Stress Response Gene Nupr1 Alleviates Cyclosporin A Nephrotoxicity In Vivo

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title:

STRESS RESPONSE GENE *NUPR1* ALLEVIATES CYCLOSPORINE NEPHROTOXICITY IN VIVO

running title:

NUPR1 IN CYCLOSPORINE TOXICITY

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ABSTRACT

Acute tubular damage is a major cause of renal failure, especially at the early phase of kidney transplantation when ischaemia-reperfusion injury and cyclosporin toxicity may coexist. The latter's mechanisms are largely unknown. Using an mRNA microarray on microdissected tubules from a rat model of cyclosporin toxicity to describe its transcriptional epithelial-specific signature *in vivo*, we found that cyclosporin induces ATF4-dependent pathways and identified *Nupr1*, a gene induced by ATF4, as the most strongly upregulated. *Nupr1* expression was induced upon injury in cultured human tubular epithelial cells and in kidney transplants. Using *Nupr1*-deficient mice, we show that *Nupr1* protects the tubular epithelium from cyclosporin toxicity, preventing structural damage, apoptosis and ATP depletion. *Nupr1* decreased cell proliferation and limited protein synthesis in proximal tubular cells treated with cyclosporin. Finally, NUPR1 was also upregulated in models of ischaemia-reperfusion injury, urinary obstruction and hypertension. Taken together, these results suggest that epithelial expression of NUPR1 plays a protective role in response to injury after renal transplantation and, presumably, in other forms of acute tubular damage.

Keywords: acute renal failure / cell survival / ATP / injury response / transcriptomics

INTRODUCTION

Tubular damage is a major cause of renal failure, and both ischaemic and toxic tubular injuries are very frequent causes of acute and chronic renal failure.[1] The course of any renal tubular injury typically starts with loss of specialised function (e.g., proximal tubular cells lose the brush border and their ability to reabsorb low-molecular-weight proteins) and ends with cell death through necrosis, apoptosis or necroptosis.[2] Repair occurs through proliferation of the surviving epithelial cells and their redifferentiation into specialised tubular cells.[3]

Most kidney-transplanted patients are treated with calcineurin inhibitors, which cause vascular and tubular damage.[4] These drugs, mainly cyclosporin A (CsA) and tacrolimus, can initiate tubular lesions,[5, 6] but the exact mechanism is currently unknown. Calcineurin is a serine phosphatase involved in the dephosphorylation of various proteins and, most importantly, a family of transcription factors – the nuclear factors of activated T cells (NFATs). There are five of these; NFATs 1 to 4 are regulated by calcineurin, and NFAT5 is regulated by osmotic stress.[7] Calcineurin, by dephosporylating NFAT, allows it to enter the nucleus and begin its transcriptional activity. NFAT target genes involved in the inflammatory response have been extensively studied in lymphocytes, where NFAT acts as a transcriptional activator, but also as a repressor for some genes.[8] *In vivo*, CsA induces renal vasoconstriction and tubular lesions.[9] The spontaneous development in mice deficient for calcineurin A alpha of a renal phenotype reminiscent of cyclosporin toxicity indicates that the decrease in calcineurin activity is sufficient to trigger renal damage.[10, 11] Genetic deficiency of either cyclophilin or NFATc1 (i.e., the two substrates known to be inhibited by cyclosporin) is not sufficient to initiate tubular damage, but may increase it by impeding the tubular repair process.[12-14]

The mechanisms by which cyclosporin alters tubular function or repair are still ill-understood. Its vasoconstrictive properties on afferent arterioles might be involved *in vivo*, by causing subintrant ischaemia downstream.[4] A direct effect within the epithelium is also plausible since, like many xenobiotics, calcineurin inhibitors are metabolised by tubular epithelial cells. Endoplasmic reticulum (ER) stress is one hallmark of *in vitro* cyclosporin toxicity.[15-17] It is a complex phenomenon with antagonistic consequences.[18] The term refers both to the accumulation of misfolded proteins in the ER and to the molecular events triggered in response to this accumulation. The accumulation of misfolded proteins recruits the chaperone protein BiP, thus in turn activating double-stranded RNA activated protein kinase-like ER kinase (PERK), a kinase that phosphorylates the transcription factor EIF2alpha. EIF2alpha phosphorylation is the common end-signal of kinases activated by amino-acid limitation (general control non repressible 2, GCN2), viral infection (double-strand RNA-activated kinase), heme limitation (heme-regulated inhibitor kinase) and protein misfolding (PERK).[19] The biological role of EIF2alpha phosphorylation is to decrease protein translation in general, except for that of adaptive proteins, including ATF4, a master transcription factor. ATF4 induces the expression of adaptive genes. If sustained, however, ATF4-induced upregulation of protein synthesis eventually causes ATP depletion and cell death.[20] It is thus essential to control the ER stress pathway. Cyclosporin toxicity is known to be associated with impaired energy status and can be alleviated by ATP.[21] Together, these data strengthen the hypothesis that ER stress plays a role in cyclosporin-induced renal injury.

Our group has extensively studied the phenotypic changes observed in tubular epithelial cells from human kidney recipients exposed to cyclosporin and has repeatedly shown, in particular, that immunohistochemical staining of two mesenchymal markers, vimentin and beta-catenin, in tubular epithelial cells detects cyclosporin tubular toxicity at an early, reversible stage.[5, 22] We have also shown that the expression of these mesenchymal markers in tubular epithelial

cells of kidney grafts in patients treated with cyclosporin is associated with initial ischaemic injury and is predictive of further development of kidney fibrosis.[23, 24] To further investigate the mechanisms of CsA-induced tubular injury, we characterised the *in vivo* tubular transcriptomic changes that occur at an early stage of cyclosporin toxicity. Our findings point to a new response gene encoding nuclear protein, transcriptional regulator, 1 *(Nupr1),* which has a central role in the ER stress pathway. We show here that *Nupr1* is induced in several animal models of acute tubular damage and confers resistance to renal tubular damage in these animals presenting cyclosporin toxicity.

RESULTS

Cyclosporin induces tubular transcriptomic changes that are related to protein synthesis and stress.

We used laser microdissection coupled to an mRNA microarray to perform an *in vivo* comparative transcriptomic analysis of rat renal tubules exposed to either vehicle or nephrotoxic doses of cyclosporin (Figure 1, Dataset 1). Using a 1.5-fold threshold (with $P<0.05$ by t-test), we found that 179 genes were downregulated and 286 genes upregulated by cyclosporin (Dataset 1). The gene expression pattern confirmed that this transcriptomic analysis was limited to tubular epithelium, since the expression of endothelial (*Cd31*) and podocyte-specific (*Nephrin*) genes was very low (respectively 3 and 2 on a logarithmic scale ranging from 2 to 14). Markers specific to the proximal tubule (*Npt2a* and *Lrp2*) were very strongly expressed (12 on the same logarithmic scale), whereas *Aqp2*, a marker of collecting ducts, was expressed only moderately (7 on the logarithmic scale). None of these cell-specific markers differed between the cyclosporin- and vehicle-treated groups. In contrast, we found that known markers of tubular damage — *Havcr1* (aka *Kim1*) and osteopontin (*Opn*) — were

induced in renal tubules exposed to cyclosporin (3 to 7 for *Kim1* and 5 to 9 for *Opn* on the logarithmic scale). Figure 1 presents these expression data.

The pathway analysis using the Pathway Analysis using Logistic Regression (LRpath) identified significant changes in the expression of genes involved in five Kyoto Encyclopedia of Genes and Genomes (KEGG) pathways: ribosome, protein processing in the endoplasmic reticulum, protein export, peroxisome, and terpenoid synthesis (Figure 1, Supplemental Table 1 and 2). Notably, searching the TRANSFAC® database for transcription factors associated with the observed transcriptomic changes did not identify NFAT or any other transcription factor. The first 3 pathways (ribosome, protein processing in the endoplasmic reticulum, and protein export), all involved in protein synthesis, showed overexpression in the CsA group, whereas the latter 2 (peroxisome and terpenoid synthesis) were underexpressed. This transcriptional signature of cyclosporin *in vivo* in the tubular epithelium is strongly reminiscent of the ATF4-dependent gene expression induced by tunicamycin (an ER stress inducer) *in vitro*.[20] Accordingly, we observed that nephrotoxic doses of cyclosporin consistently enhanced the level of ATF4 in renal tubular cells, as shown by immunohistochemical analysis of kidney sections from CsA-treated mice. Moreover, ATF4 was induced by CsA *in vitro* in cultured mouse tubular epithelial cells, as shown by western blot (Figure 2). Interestingly, *Nupr1*, an ATF4-responsive gene,[25, 26] was the gene most highly overexpressed (86 times) under cyclosporin in this microarray analysis (Supplemental Table 1). To our knowledge, the role of *Nupr1* in acute tubular damage has not previously been studied *in vivo*.

Nupr1 confers resistance to epithelial injury

To gain insight into the role of *Nupr1* in CsA nephrotoxicity, we translated our experimental model to mice. C57bl6/J wild-type (WT) mice showed evidence of epithelial toxicity with renal failure after 2 weeks of cyclosporin at doses between 50 and 100 mg/kg/day SC. A dose of 100 mg/kg/day induced acute kidney injury, weight loss, tubular damage, apoptosis and proliferation together with dose-dependent *Nupr1* induction by CsA and ER stress (Supplemental Figures 1, 2 and 3). We used *Nupr1* knockout mice to investigate the role of this gene in cyclosporin-induced renal injury. Although these *Nupr1*-deficient mice showed no spontaneous renal phenotype, the renal tubular lesions they developed when challenged with cyclosporin were substantially worse than those observed in WT mice. They had more tubular vacuolisation and dilation than their WT littermates (semi-quantitative score 2 [0.88-2.5] vs 0.5 [0.5-1], P= 0.009 for vacuolisation and 1.75 [0.5-2] vs 0 [0-0.5], P=0.003 for dilation, Figure 3 A, B, G, F). Accordingly, *Kim-1* mRNA expression was significantly higher in the cortex of *Nupr1*$^{-/-}$ compared with WT mice; a trend towards higher plasma urea levels in the *Nupr1*$^{-/-}$ mice was also observed, but did not reach statistical significance (Supplemental Figure 4).

The mechanism by which Nupr1 protects the renal epithelium involves cell survival but not decreased cyclosporin exposure, vascular reactivity or enhanced tubular repair.

Measurements of serum cyclosporin trough levels showed that the groups did not differ for cyclosporin exposure (Supplemental Figure 5A). Nor did the knockout mice differ from the WT in their expression of the *Il27* gene, a close neighbour of the *Nupr1* gene on the mouse genome and a potential regulator of cyclosporin-induced inflammation[27] (Supplemental Figure 5B). Measurements of aortic blood pressure and renal blood flow in *Nupr1*$^{-/-}$ and WT

mice after 5 days of cyclosporin (100 mg/kg/d SC) or 5 days of vehicle showed no haemodynamic effect of *Nupr1* (Supplemental Figure 5C-D).

After cyclosporin treatment, apoptosis, assessed by TUNEL, was more frequent in renal tubular cells from *Nupr1*$^{-/-}$ (18.5 [9.8-33.3] nuclei/field) than in WT mice (4 [1.75-6.5], *P*= 0.01) (Figure 3 E, F, J). This observation suggests that *Nupr1* protects tubular cells from death. Tubular proliferation assessed by Ki67 staining was again more frequent in the renal tubular cells of the *Nupr1*$^{-/-}$ (89.5 [55.5-117.3] nuclei/field) than WT animals (43.5 [33.3-56.5], *P*= 0.03) (Figure 3 C, D, I). Both tubular apoptosis and proliferative repair increased in the absence of *Nupr1*.

Nupr1 limits protein synthesis, proliferation and cell death, and preserves the energy status of epithelial proximal tubular cells during* in vitro *cyclosporin toxicity.

We used primary cultures of proximal epithelial tubular cells from *Nupr1* knockout and WT mice to investigate the effect of *Nupr1* on apoptosis under CsA treatment. In wild type cells, we measured ATF4 protein, *Nupr1*, *Atf4, Chop* and *Bip* mRNA expression before and after 1, 2, 3, 6 and 24 hours of cyclosporin exposure. All these parameters were induced already after one hour, with ATF4 protein induction being the strongest at this early time point, except *Bip* that was induced only after 3 hours (Figure 2C). *Nupr1*$^{-/-}$ cells had a higher level of ATF4 expression after CsA treatment than wild type cells (Supplemental Figure 6). Using a pulse of homopropargylglycine (a methionine analogue) to evaluate protein synthesis by immunofluorescence and flow cytometry, we showed that cyclosporin decreased protein synthesis in wild type cells but didn't do so in *Nupr1*$^{-/-}$ cells (Figure 4).

We measured cell proliferation using 3 different techniques: a simple cell count 48 hours after seeding various numbers of cells, continuous monitoring of cell density with xCELLigence technology, and BrdU incorporation (Figure 5, Figure 6A-B and Supplemental Figure 7). All

techniques showed that *Nupr1-/-* proximal tubular cells proliferated faster than wild-type cells. Treatment with CsA virtually abolished proliferation in wild-type cells, but only decreased proliferation in knock out cells (Figure 6A-B). Although proliferation was maintained, assessment by xCELLigence of CsA-treated *Nupr1-/-* cells showed a decrease in cell density, suggesting cell death.

Similar to CsA renal toxicity *in vivo*, 5 µg/mL CsA induced cell death, with more dead cells in *Nupr1-/-* cells compared to WT cells (Figure 6C).

We investigated the effect of *Nupr1* on the energy status of proximal tubular epithelial cells by measuring ATP and ADP in *Nupr1*$^{-/-}$ and WT cells incubated for 24 hours with or without 1 µg/mL CsA (Figure 6D). ATP/ADP ratio were lower in the *Nupr1-/-* mice compared to wild type mice. Moreover, the ATP/ADP ratio decreased still further after cyclosporin was added. The effect of *Nupr1* on the ATP/ADP ratio was explained mainly by a fall in ATP, although ADP increased slightly as well (Supplemental Figure 8).

Rescuing *Nupr1* deficiency by transfecting a *flag-Nupr1* transgene into *Nupr1-/-* proximal tubular cells did inhibit proliferation (less cells in S phase, and more cells in G2/M) in cells expressing the transgene, thus confirming the instrumental role of *Nupr1* in proliferation and apoptosis (Figure 7 and Supplemental Figure 9).

Nupr1 induction is relevant to other models of kidney injury in mice and in human kidney transplantation.

To determine if *Nupr1* was specifically upregulated after CsA treatment, we measured *Nupr1* mRNA in kidney cortices of mice in control conditions and after ischaemia-reperfusion injury, unilateral ureteral obstruction, and angiotensin II-induced hypertension. As shown in Supplemental Figure 10, we found that *Nupr1* was upregulated in each of these different experimental models. This finding suggests that *Nupr1* may exert its protective effects in many forms of kidney injury.

We studied the expression of *Nupr1* in cultured human renal epithelial cells. Increasing the cyclosporin concentration dose-dependently induced *Nupr1* mRNA expression in human proximal tubular cells (Figure 8A). We also performed immunohistochemical analysis for NUPR1 on normal kidney (stable renal allografts) and on injured kidney (pre-implantation biopsies from donors with acute tubular necrosis and allografts undergoing acute tubular necrosis or allograft dysfunction). Using multiple stainings for NUPR1, Megalin and nuclei, we found that, in normal kidney, NUPR1 expression was absent in nuclei from renal proximal tubules. Conversely, in injured kidneys, NUPR1 was strongly expressed in many nuclei from renal proximal tubules. (Figure 8B-F)

DISCUSSION

Kidney resistance to injury varies greatly,[28] as exemplified by cyclosporin toxicity; it is widely prescribed to patients in standardised conditions and results in variable toxicity, depending on the dose, on additional insults, and on the patient's own characteristics.[4] Several genes involved in xenobiotic detoxification have been suggested as risk factors for calcineurin inhibitor nephrotoxicity.[29] Cyclosporin nephrotoxicity nonetheless remains poorly understood, especially its *in vivo* effect on renal tubular epithelium. Our investigation provides the first description of this drug's genome-wide transcriptional effect there. Our primary hypothesis was that calcineurin inhibition would cause toxic effects by inactivating NFAT, a pleiotropic transcription factor. NFAT-induced genes (e.g., *Il2*) are expected to be downregulated by cyclosporin through calcineurin inhibition.[8] Other genes have been shown to be repressed by NFAT (e.g., *Cdk4*) and might thus be enhanced under cyclosporin treatment.[8, 30-32] Interestingly, one of the genotypes at risk of cyclosporin toxicity is a low-activity variant of *Cyp2c9*,[29] the gene most downregulated by cyclosporin in our data (Figure 1). However, the *Cyp2c9* promoter contains no NFAT-response-element,[33] and neither the NFAT nor the calcineurin pathways were modified by cyclosporin on a transcriptional level

in our data. These seemingly contradictory results can be interpreted in two ways: 1) the calcineurin and NFAT pathways in the tubular epithelium (our data) are very different from these pathways in the lymphocytes (previously published data); thus, bioinformatic tools like LRpath do not link our data to calcineurin and NFAT, and 2) the pattern of gene expression we observed is not directly caused by the inhibition of the calcineurin and NFAT pathways. Other substrates of calcineurin might be involved, or a secondary transcriptomic response to injury. This pattern is reminiscent of the genes induced by ATF4, a master transcription factor that orchestrates the expression of stress genes, including *Nupr1* and other stress related genes that were overexpressed in our analysis, like *Asparagine synthetase* and several aminoacyl-tRNA-synthetases. ATF4 induces a transcriptional program that upregulates the energy-expending mechanisms of protein synthesis potentially leading to cell death.[20] Decreased ATP levels are instrumental in cell death, whether due to diminished ATP production (decreased fatty acid oxidation) or to enhanced ATP consumption (increased protein synthesis).[20, 34] Here, after administration of toxic doses of cyclosporin *in vitro* and *in vivo*, renal tubular cells expressed ATF4-dependent pathways associated with decreased expression of peroxisome genes and increased rates of protein synthesis, energy depletion and cell death.

Nupr1, essentially unstudied in renal diseases, is a chromatin-binding protein induced by various epithelial stresses and has important properties: it is anti-apoptotic and anti-inflammatory, and it regulates cell proliferation.[35] Its expression is instrumental in endothelin-mediated mesangial hypertrophy.[36] Because *Nupr1* is an early stress response gene induced by ATF4 in the renal tubular epithelium and protects tubular cells from cell death,[25] we hypothesised that it might protect against apoptosis by preserving the cell energy status.

We found that *Nupr1* was strongly expressed during cyclosporin-induced renal epithelial lesions *in vivo* and *in vitro* and that it exerted a protective role on cell survival and energy status. *Nupr1* also contributed to inhibiting protein synthesis and slowing the proliferation of

proximal tubular cells. Ischaemia-reperfusion injury causes p53-dependent G2/M arrest of renal tubular cells and subsequent renal fibrosis.[37] *Nupr1* is a positive regulator of p53.[38] Because we found a consistent increase in *Nupr1* levels in all the kidney injury models we tested (including ischaemia-reperfusion injury), *Nupr1* induction appears to be a generic response to any epithelial injury and is not cyclosporin-specific. Whether *Nupr1* induction is also protective in these other models remains to be tested. The mechanism by which the ATF4-NUPR1 pathway might influence evolution toward cell death or survival is outlined in Figure 9. Overall, *Nupr1* inhibits energetically costly processes (proliferation and protein synthesis) and preserves ATP cellular concentrations. ADP/ATP ratio is associated to apoptosis, and may be instrumental in this model. The molecular targets of *Nupr1* that lead to cell protection are still unknown, however. Further studies should therefore 1) investigate the precise mechanisms that regulate energy consumption, protein synthesis and proliferation downstream of *Nupr1*; 2) test strategies aimed at producing a time-limited expression of *Nupr1*-related pathways in acute kidney injury, and 3) determine whether *Nupr1* variants are involved in susceptibility to kidney injury in humans.

CONCISE METHODS

Animals. We used a model of *in vivo* renal toxicity by daily injections cyclosporin for 2 weeks.[39] JL Iovanna created the *Nupr1*$^{-/-}$ mouse strain.[38] Blood and kidneys were harvested under general anaesthesia. For creatinine clearance measurements, animals were placed overnight in metabolic cages for urine collection, and blood was collected from the retro-orbital sinus under isoflurane anesthesia. *Morphologic studies and laser microdissection*. Ki67 and TUNEL quantification were performed with the particle analysis function of ImageJ 1.45o software. For each sample, 200 cortical tubules were harvested by laser capture microdissection (Supplemental Figure 11). *RT-PCR and mRNA microarray*. Microdissected tubules were studied with the GeneChip Rat Genome 230 2.0 microarrays (Affymetrix). The

pathway analysis was performed with LrPath web-based software.[40] The quantitative RT-PCR expression results relative to the housekeeping gene were obtained by the ΔCp method. *In vitro studies*. Proximal epithelial cells were isolated from fresh kidneys of *Nupr1*$^{-/-}$ and WT mice.[41, 42] *Statistics*. Statistical analysis used JMP Pro 9.0.2 software. Data are presented by their median values and interquartile ranges, and a nonparametric Wilcoxon test was used to assess statistical significance, except where otherwise indicated. A *P*-value<5% was defined as significant. *Study approval.* Animals were handled in a licensed facility (approval number B-75-20-01) in compliance with French legislation and INSERM standards. Biopsies from renal-transplanted patients receiving cyclosporin treatment were used for NUPR1 immunohistochemistry. The biopsies were indicated for state-of-the-art routine care, and all patients provided written consent for use of the leftover material for research purposes. The study performed on human biospies was approved by our institutional review board.

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AUTHOR CONTRIBUTIONS

PG designed and performed the experiments and drafted the manuscript. MW, AB and CM participated in the *in vivo* experiments. DL and SV participated in the *in vitro* experiments. SP performed the haemodynamics study. NB participated in the *in vivo* studies and RT-qPCRs. YCXD, CJ and DB participated in the histological evaluation of the kidneys (mice and humans). AH participated in the interpretation of the results and reviewed the manuscript. JI created the *Nupr1*$^{-/-}$ mice and reviewed the manuscript. ER participated in the study design and in writing the manuscript.

CONFLICT OF INTEREST

The authors have no conflict of interest to declare.

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FIGURE LEGENDS

Figure 1. *In vivo* renal tubular transcriptome analysis. **A.** Principal component analysis of the gene expression results. The 6 samples circled in red passed the quality check for further analysis. **B.** Volcano plot with -log *P*-value (t-test) along the y-axis and log fold-change along the x-axis. *Nupr1* is circled in red. **C.** mRNA expression by microarray (on a logarithmic scale ranging from 2 to 14) of representative markers for various segments of the nephron (*Megalin* and *Npt2a* for the proximal renal tubule, *Aqp2* for the collecting duct, *Nephrin* for the glomeruli, and *Cd31* for the endothelium) and known markers of renal tubular injury (*Kim1* and *Opn*). CsA-treated animals (CsA, n=3) were compared to the control group (CTL, n=3). Results were considered nonsignificant (NS) if the *P*-value (t-test) > 0.05. **D.** Summary of the logistic regression pathway analysis on KEGG pathways. The 5 pathways were enriched in the differential analysis between the CsA and the CTL group. Genes from the first 3 pathways were upregulated by cyclosporin, and genes from the last 2 pathways downregulated by it.

Figure 2. ATF4 protein expression 24h after CsA treatment assessed by immunohistochemical analysis (**A**) and by western blot (**B**) in renal tubules of mice, and at different time points (**C**). **A.** Tubules injured by CsA 100 mg/kg/d, for 14 days (CsA) overexpressed ATF4, compared with control kidneys (CTL). **B.** Photograph of the full western blots for ATF4 and GAPDH, with the protein ladder on the left (ATF4 and GAPDH corresponding to 50 and 40 kDa respectively), showing induction of ATF4 after 24 h exposure to 5 µg/mL of CsA in a primary cell culture of mouse proximal tubular cells (representative of 3 independent experiments). Extinction of ATF4 staining after transfection with an anti-ATF4 siRNA attests to the specificity of the anti-ATF4 antibody. **C.** Time course of ATF4 protein (n=2) with *Nupr1*, *Atf4, Chop* and *Bip* mRNA (n=4), after 1, 2, 3, 6 and 24 hours of CsA (1µg/mL) exposure, compared to vehicle.

Figure 3. **A, C, E**. Wild-type mice treated by cyclosporin 100 mg/kg/d for 14 days. **B, D, F**. *Nupr1*$^{-/-}$ animals treated by cyclosporin 100 mg/kg/d for 14 days. **A & B**. Masson's Trichrome. *Nupr1* deficiency exacerbated histological tubular lesions caused by cyclosporin: tubular vacuolisation and dilation. **C & D**. Ki67 immunohistochemistry. *Nupr1* deficiency was associated with increased tubular cell proliferation. **E & F**. TUNEL assay. *Nupr1* deficiency was associated with increased apoptosis. **G, H, I, J**. Quantification for tubular dilation (G), tubular vacuolisation (H) in wild type (n=12) and knock out (n=10) mice, Ki67 (I) and TUNEL (J) in wild type (n=6) and knock out (n=6) mice.

Figure 4. Assessment of protein synthesis using a pulse of L-homopropargylglycine (methionine analog) revealed by Alexa Fluor 488. **A.** Protein synthesis evaluation by immunofluorescence (in green) in wild type and *Nupr1-/-* proximal tubular cells incubated with 5 µg/mL CsA or vehicle for 24 hours. **B.** Protein synthesis evaluation by flow cytometry showing the percentage of cells in cell-cycle phase G1 undergoing protein synthesis, and the rate of protein synthesis (median fluorescence intensity) in these cells for wild type and *Nupr1-/-* cells treated for 24 hours with 5µg/mL cyclosporin or vehicle.

status.

Figure 5. Differential proliferation of WT and *Nupr1* knockout cells within 48 hours after seeding. **A**. Number of cells counted by flow cytometry in a well 48h after seeding 500 to 20000 of either KO or WT proximal tubular cells/well (96-wells plate). **B.** Photograph of the cells 48 hours after seeding 5000 of KO or WT proximal tubular cells per well. **C.** Real time monitoring of cell proliferation for 48 hours after seeding 1000 to 7000 cells/ well (96-wells plate) of either KO or WT proximal tubular cells, and monitoring of cell proliferation for 24 hours after seeding 5000 of KO or WT proximal tubular cells per well, followed by 24 hours incubation with 1µg/mL cyclosporine or vehicle.

Figure 6. **A.** Cell-cycle analysis using flow cytometry to assess DNA content by Propidium Iodide staining and DNA synthesis by BrdU incorporation, under normal conditions or under 1 µg/mL cyclosporin for 24 hours, according to *Nupr1* status (n=3). **B.** Rate of BrdU incorporation in BrdU positive cells assessed by flow cytometry, under normal conditions or under 1 µg/mL cyclosporin for 24 hours, according to *Nupr1* status (n=3). **C.** Apoptosis quantified by flow cytometry (prodidium iodide for necrosis and YO-PRO®-1 for apoptosis) *in vitro* under normal conditions or under 5 µg/mL cyclosporin for 24 hours, according to *Nupr1* status (n=5). **D.** ATP/ADP ratio *in vitro* under normal conditions (n=12) or under 1 µg/mL cyclosporin for 24 hours (n=6), according to *Nupr1*

Figure 7. Rescue of Nupr1-/- cells by transfection of a flag-Nupr1 transgene (n=3). A. Gating of single cells on DNA content using an area vs height dot-plot. B. Transfection resulted in only ~1% of flag-expressing cells. C. Transfection selective cell-cycle analysis, based on DNA content assessed by Hoechst staining.

Figure 8. A. Analysis of *Nupr1* expression (normalised on housekeeping gene *Hprt*) in human proximal tubular HK2 cells showed a dose-dependent induction of *Nupr1* mRNA by cyclosporin. **B, C, D, E.** Immunohistochemical analysis for NUPR1 in human renal allografts showing a normal biopsy 3 months after transplantation with no NUPR1 expression (C, E), and a biopsy with acute antibody-mediated rejection and chronic allograft dysfunction (D, F). C-D show NUPR1 expression, and E-F show the triple staining for nuclei (DAPI, blue), megalin (green), and NUPR1 (magenta) .

Figure 9. Schematic representation of the relations between kidney injury, the ATF4-NUPR1 pathway and epithelial fate.

SUPPORTING DOCUMENTS

Supplemental Figure 1. Dose-dependent cyclosporin nephrotoxicity at day 14 in C57bl6/J WT mice. **A.** Plasma urea in mice treated for 14 days with various doses of CsA (■ $P<0.05$; ◆ $P<0.005$ vs 0 mg/kg/d), and *Nupr1* relative quantification (normalised on the geometrical mean of the housekeeping genes *Rpl32* and *Gusb*) in the cortex of mice treated with various doses of CsA for 14 days. **B & C.** Masson's Trichrome of the kidneys of mice injected with vehicle, 60mg/kg/d or 100 mg/kg/d for 14 days (B: magnification x400, C: magnification x100). **D.** TUNEL assay of the kidneys of mice injected with vehicle, 60mg/kg/d or 100 mg/kg/d for 14 days (magnification x600). **E.** Ki67 staining of the kidneys of mice injected with vehicle, 60mg/kg/d or 100 mg/kg/d for 14 days (magnification x100).

Supplemental Figure 2. Time course of weight change (A), plasma urea (B), plasma creatinine (C), and creatinine clearance (D) in mice treated for 2 weeks by 100 mg/kg/day cyclosporine (CsA) or vehicle (CTL).

Supplemental Figure 3. Serial sections of control (A & B) and CsA-treated (C & D) mouse kidneys stained by immunohistochemistry for megalin (A & C) and CD44 (B & D).

Supplemental Figure 4. Additional markers of kidney injury in wild type (WT) or *Nupr1*-/- (KO) mice, with cyclosporine 100 mg/kg/j (CsA) or vehicle (CTL) for 14 days. A. Blood urea was significantly increased after CsA treatment, but did not differ significantly between genotypes (WTCTL: n=5, KOCTL, n=8, WTCsA: n=12, KOCsA: n=10). B. The level of mRNA from a kidney injury molecule 1 (KIM 1) after 14 days of CsA was significantly higher in *Nupr1*$^{-/-}$ than in WT mice (n=6 for each group).

Supplemental Figure 5. A. Serum cyclosporine trough levels after 2 weeks of 60 mg/kg SC cyclosporine daily were not different in wild type and *Nupr1-/-* mice (n=5). B. Expression of Il27 in the renal cortex of WT and *Nupr1* knockout mice (n=6). C and D. Mean aortic blood pressure and mean renal blood flow of knockout (KO) and wild-type (WT) mice treated by cyclosporin (CsA) or vehicle (CTL).

Supplemental Figure 6. Western blot of ATF4 normalized on GAPDH in wild-type (WT) and knock-out (KO) proximal tubular cells treated by cyclosporin (CsA) or vehicle (CTL).

Supplemental Figure 7. Gating strategy used for assessment of BrdU incorporation by flow cytometry in wild type and *Nupr1-/-* cells. BrdU-positive cells gated on the autofluorescence vs BrdU-FITC plot are shown in blue on the propidium iodide vs BrdU-FITC plot.

Supplemental Figure 8. ATP and ADP levels (arbitrary unit) in WT and *Nupr1* knockout cells after 24 hours exposure to 1 µg/mL cyclosporin (n=6) or its vehicle (n=12).

Supplemental Figure 9. Cell-cycle analysis of wild-type and *Nupr1-/-* proximal tubular cells after transfection with the *flag-Nupr1* transgene. Cells without expression of the transgene are shown in red, and cells expressing the transgene (identified with the anti-FLAG antibody) are shown in blue.

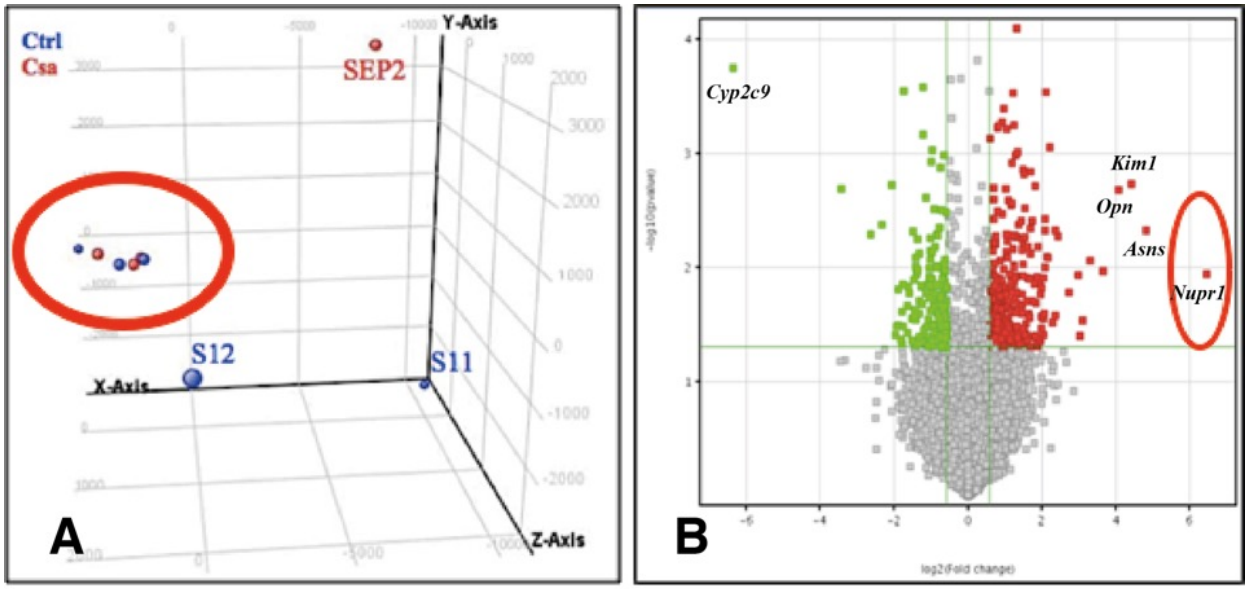
Supplemental Figure 10. Induction of *Nupr1* expression in various models of kidney injury. Moderate hypertension (HTA) was obtained through infusion of angiotensin 2 and low-dose of L-NAME, severe hypertension through infusion of angiotensin 2 plus high dose of L-NAME L-Name treatment. Ischaemia-reperfusion (IR) was performed by occluding the renal artery bilaterally for 35 minutes. Unilateral ureteral occlusion was performed by ureteral ligature for 10 days, and the contralateral kidney served as the control.

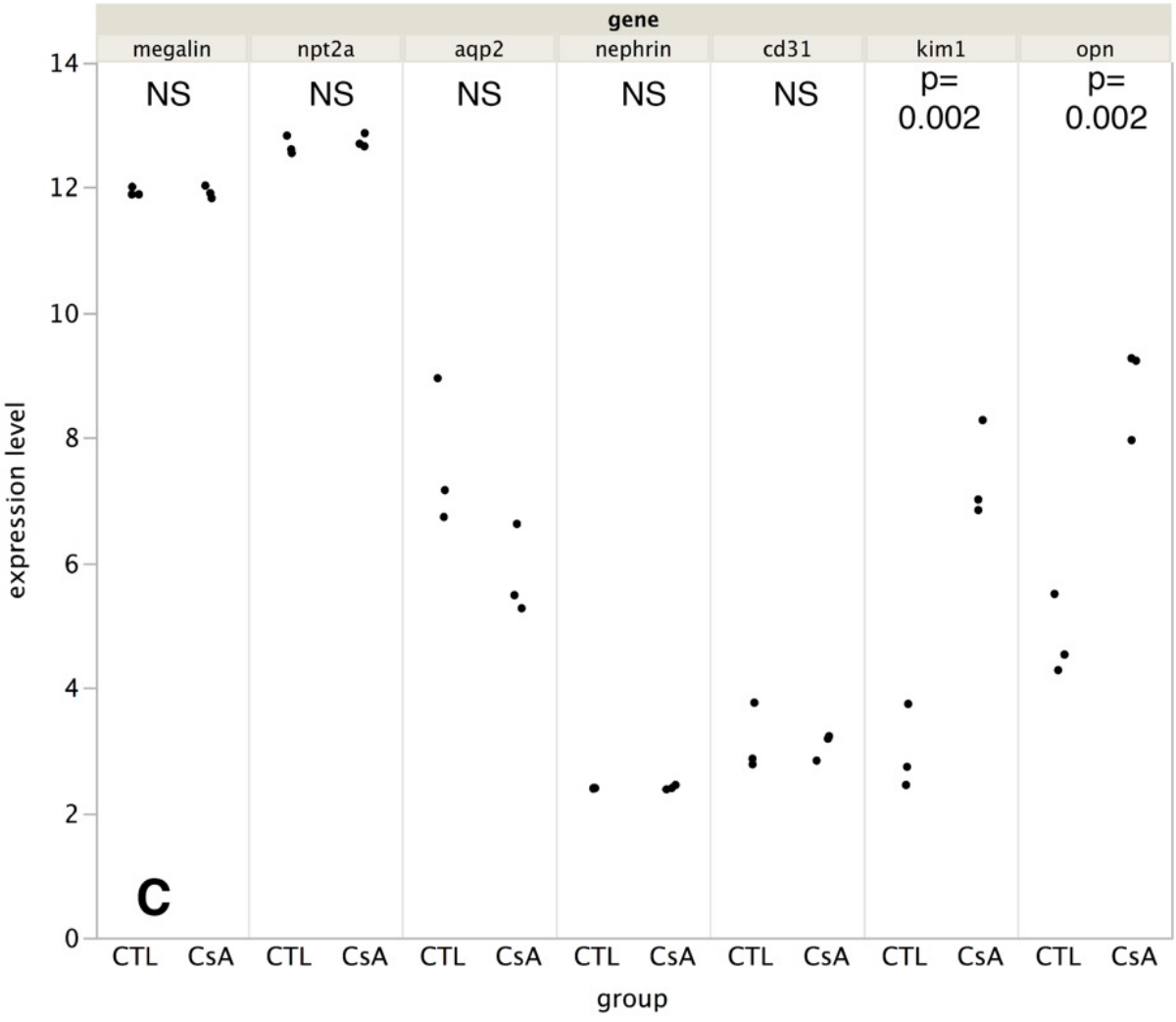
Supplemental Figure 11. A slide used for renal tubule microdissection. Note that the tubule contour was burned by the LASER, thus precluding extratubular contamination.

Dataset 1. Full results of the mRNA microarray analysis with expression data and comparison between the cyclosporin and control groups.

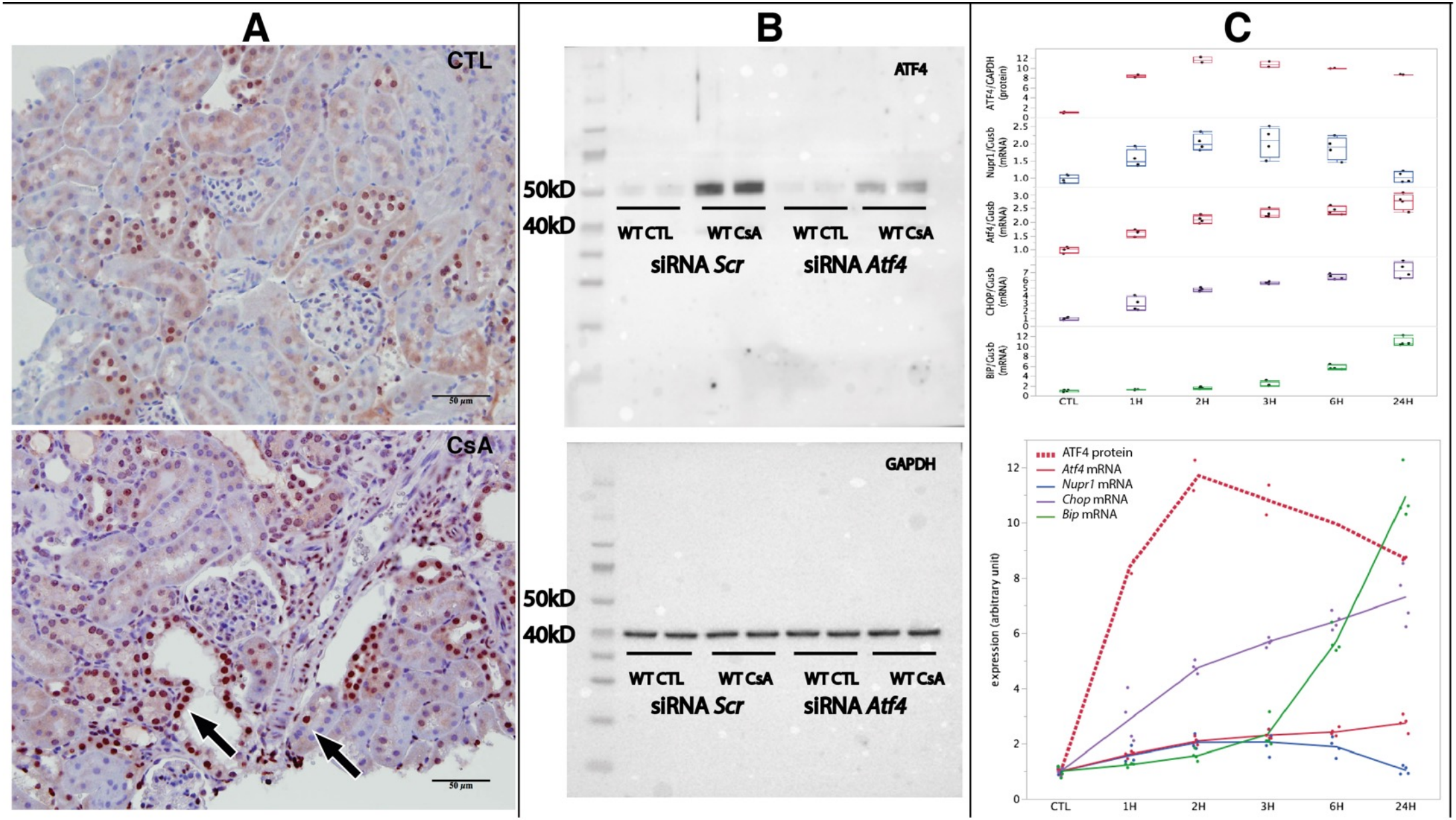
Supplemental Table 1. Results of the logistic regression pathway analysis with the details of the genes involved in enriched pathways.

Supplemental Table 2. Sequences of the primers used for RT-qPCR and details of the amplicon and spanned intron size.





D KEGG pathway red: genes overexpressed blue: genes underexpressed	Number of genes	Odds ratio	*P*-value	False discovery rate
Ribosome	66	47	6.97×10^{-18}	1.44×10^{-15}
Protein processing in endoplasmic reticulum	140	10	2.86×10^{-09}	2.96×10^{-07}
Protein export	21	46	7.29×10^{-09}	5.03×10^{-07}
Peroxisome	68	8	2.2×10^{-04}	9.13×10^{-03}
Terpenoid backbone synthesis	12	26	4.12×10^{-04}	1.22×10^{-02}


A
CTL
50 μm
CsA
50 μm
B
ATF4
50kD
40kD
WT CTL
WT CsA
WT CTL
WT CsA
siRNA Scr
siRNA Atf4
GAPDH
50kD
40kD
WT CTL
WT CsA
WT CTL
WT CsA
siRNA Scr
siRNA Atf4
C
ATF4/GAPDH (protein)
Nupr1/Gusb (mRNA)
Atf4/Gusb (mRNA)
CHOP/Gusb (mRNA)
BiP/Gusb (mRNA)
CTL
1H
2H
3H
6H
24H
ATF4 protein
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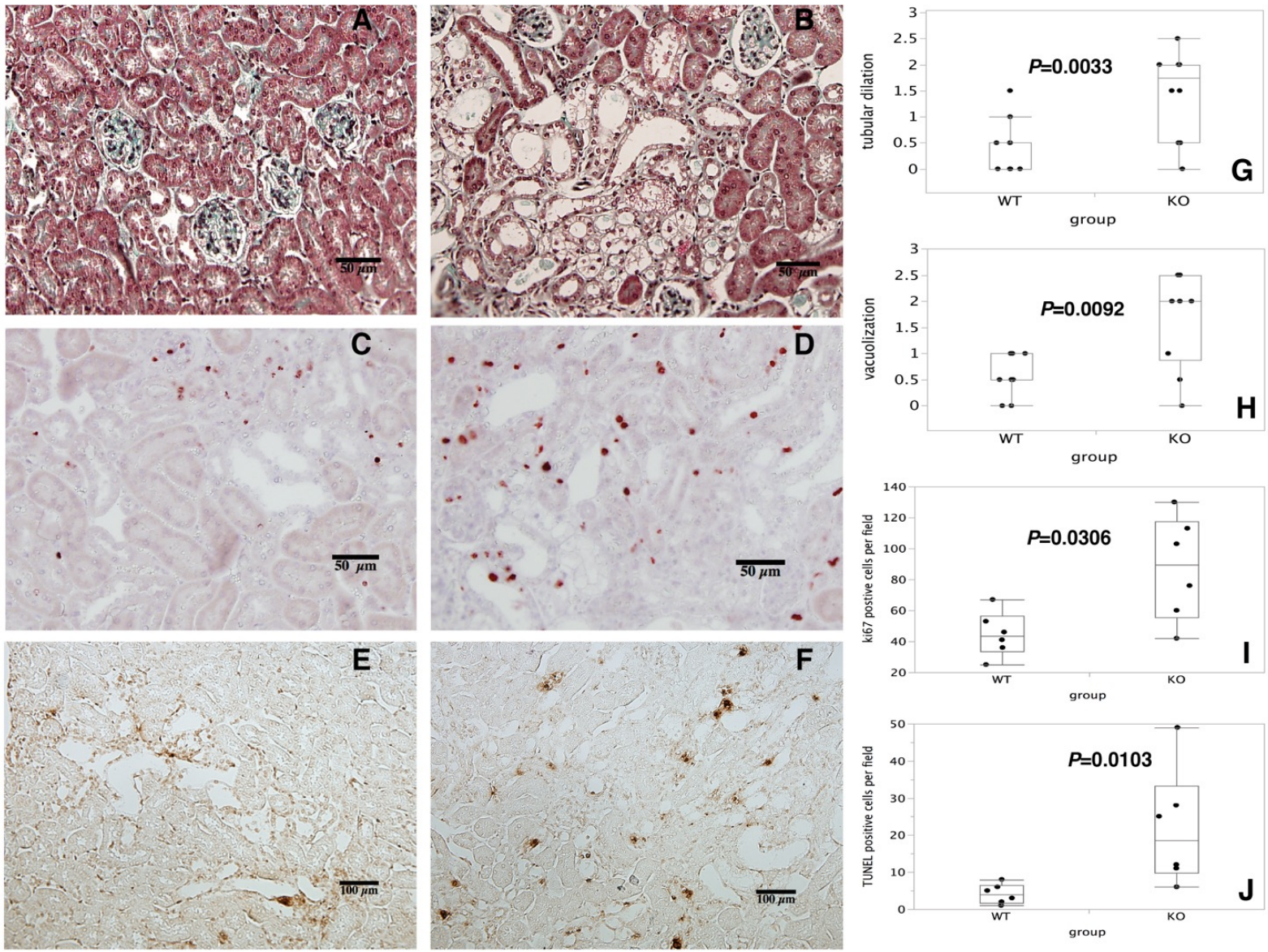
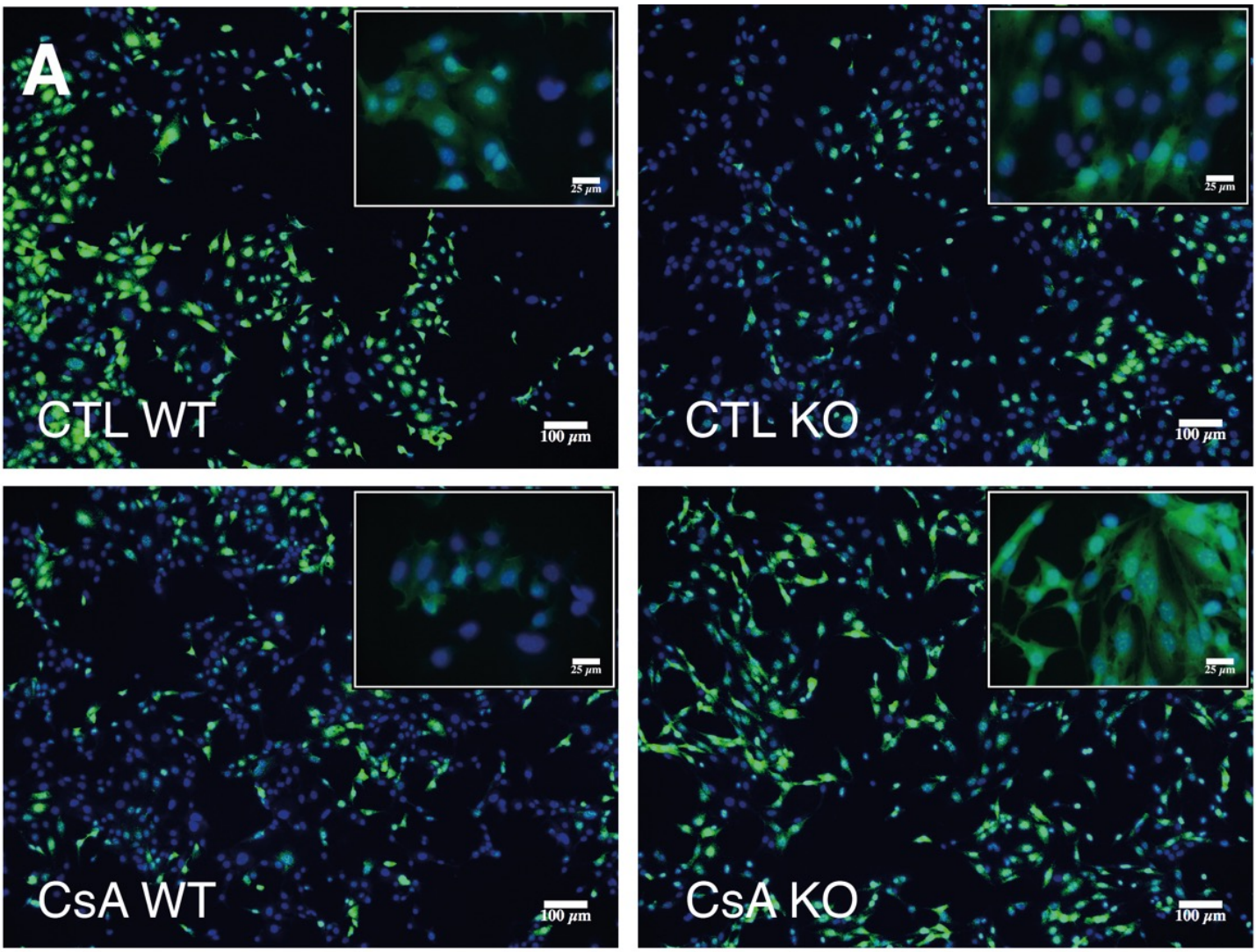
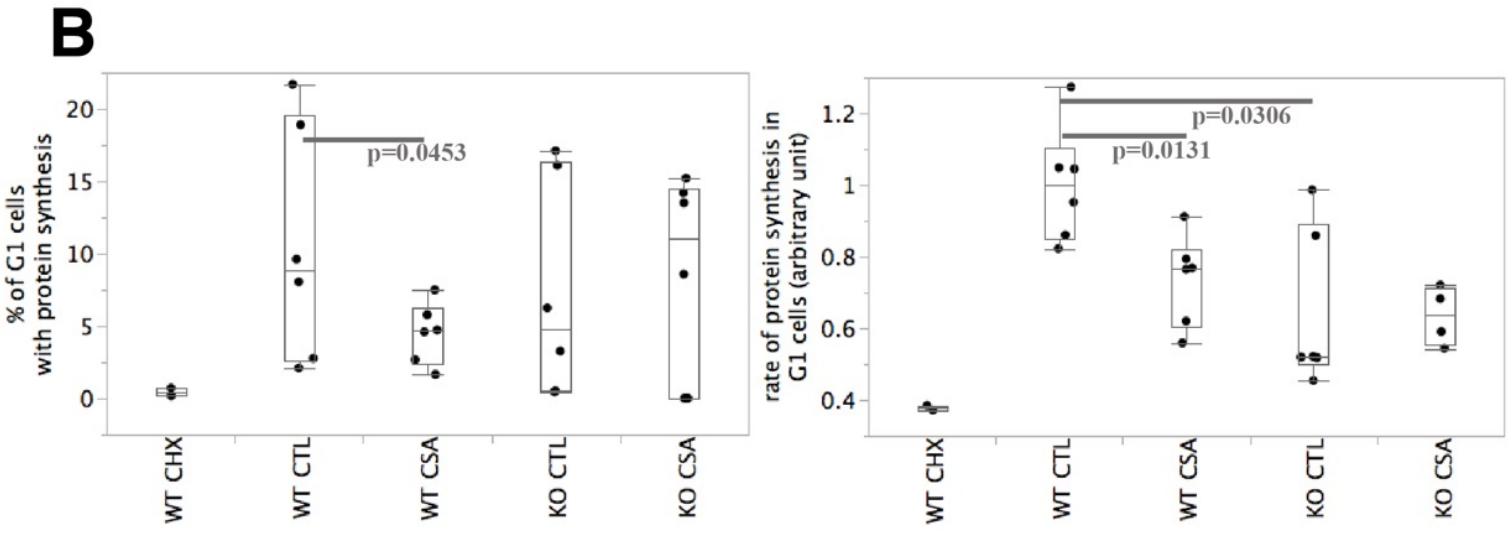
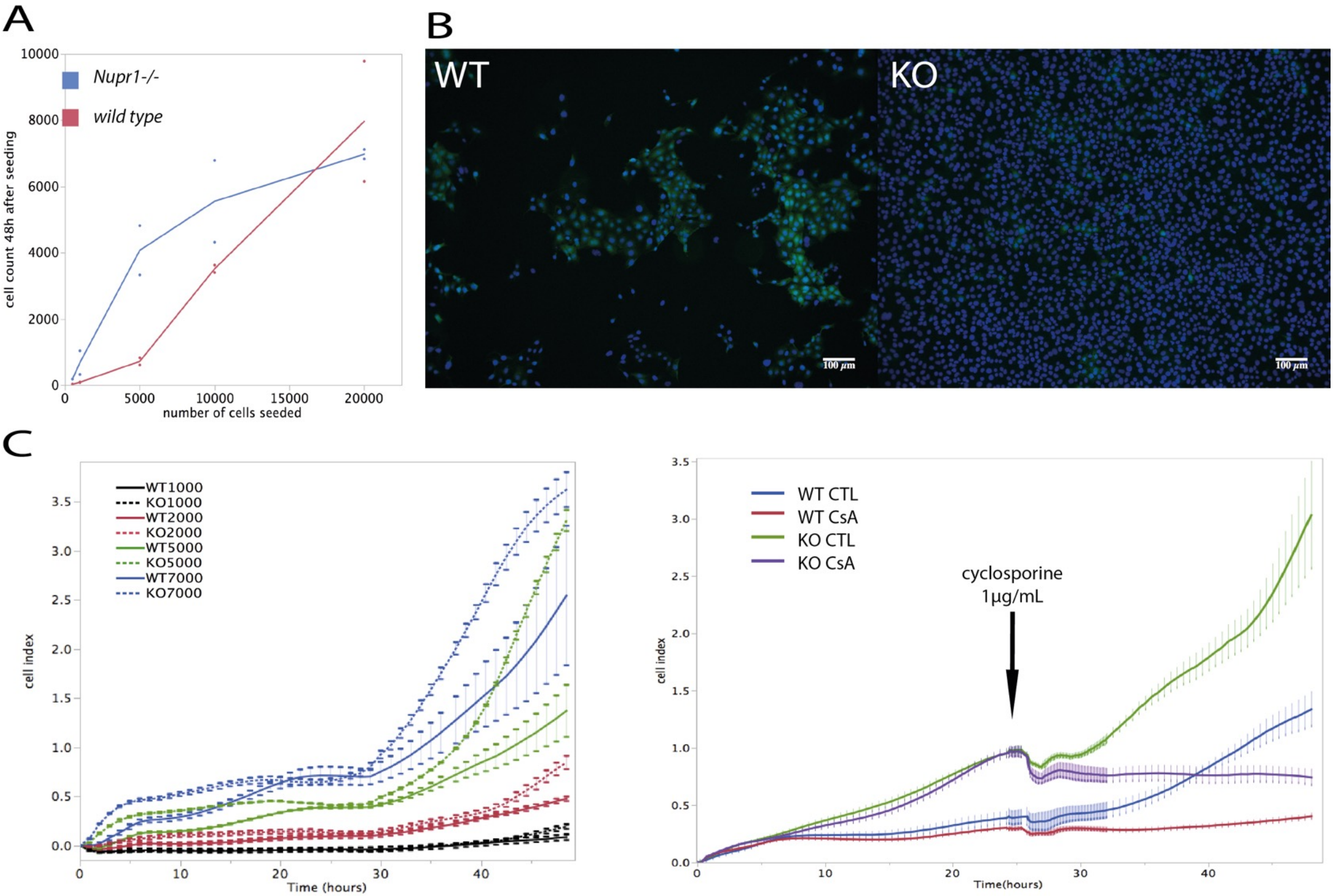
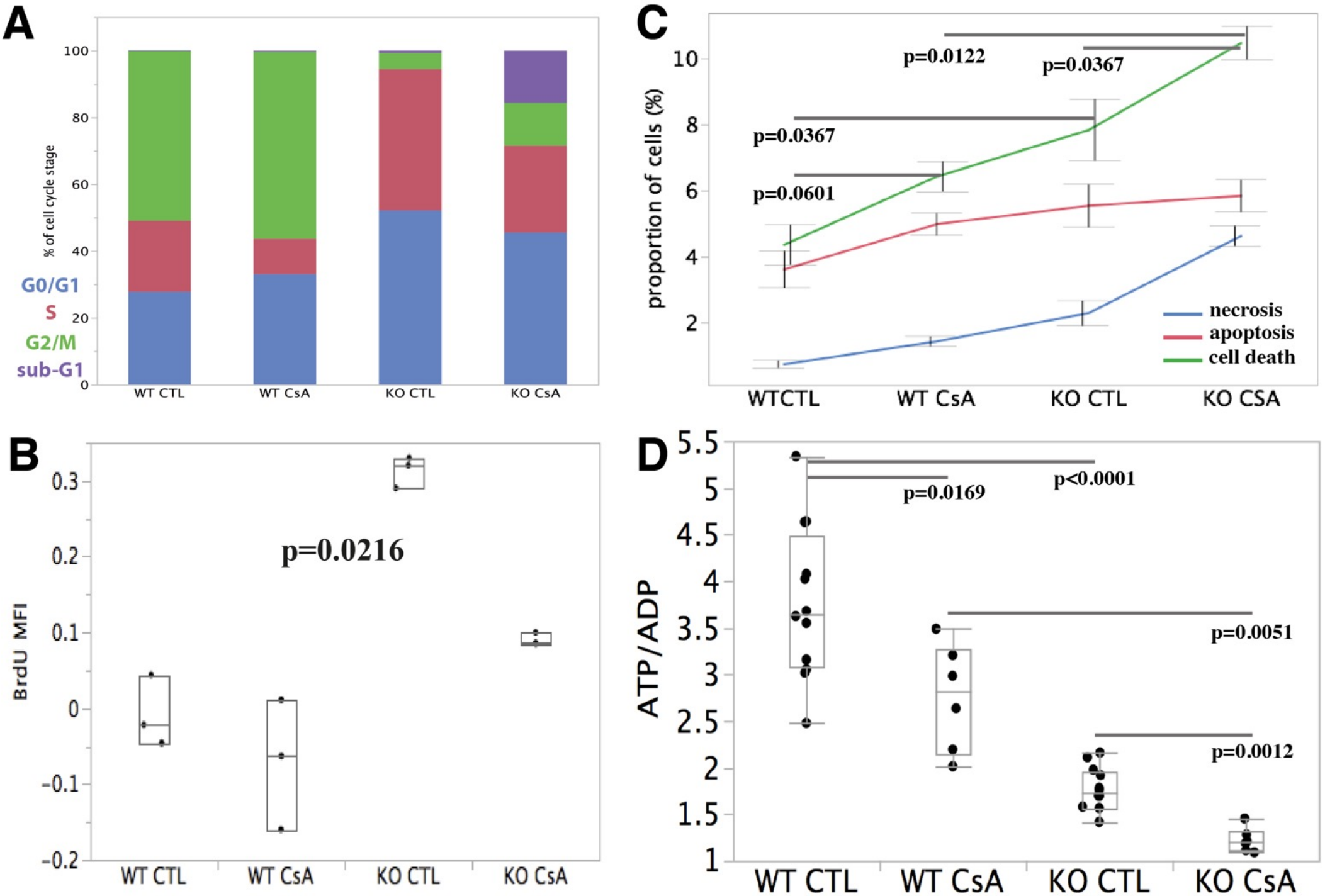
2H
3H
6H
24H

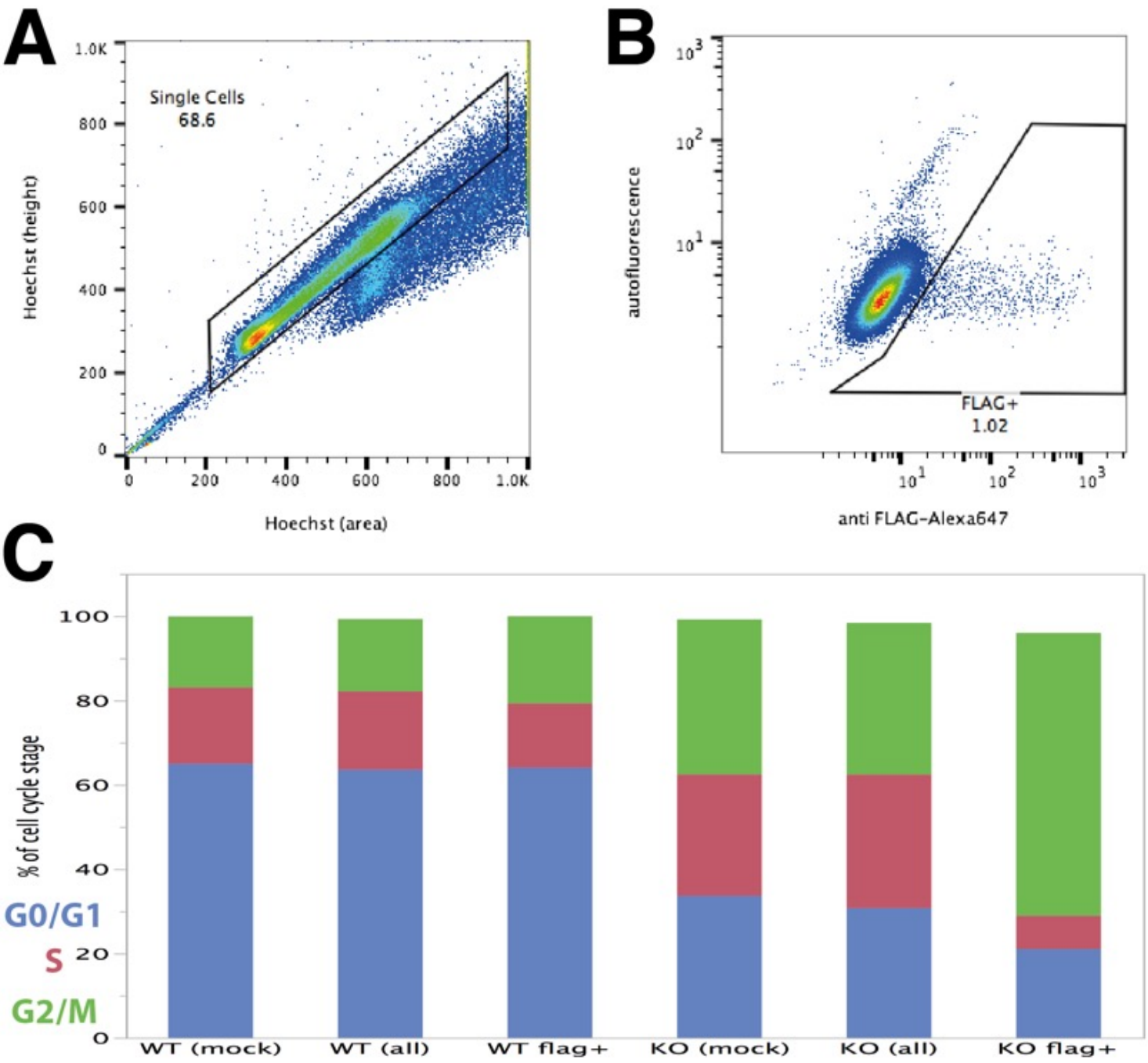

A
50 μm
B
50 μm
C
50 μm
D
50 μm
E
100 μm
F
100 μm
tubular dilation
P=0.0033
G
WT
KO
group
vacuolization
P=0.0092
H
WT
KO
group
ki67 postive cells per field
P=0.0306
I
WT
KO
group
TUNEL positive cells per field
P=0.0103
J
WT
KO
group

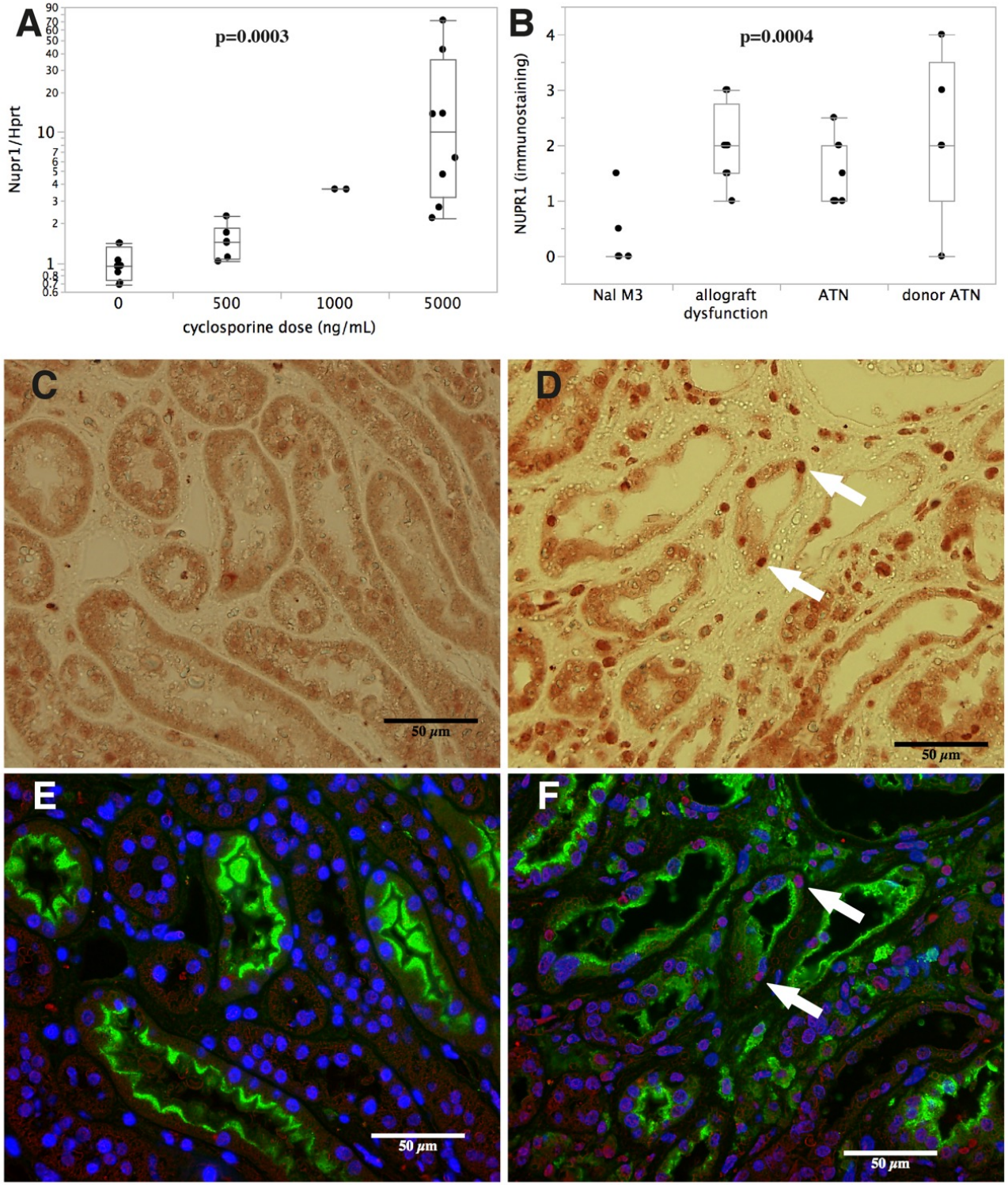

A
CTL WT
CTL KO
CsA WT
CsA KO
25 µm
100 µm

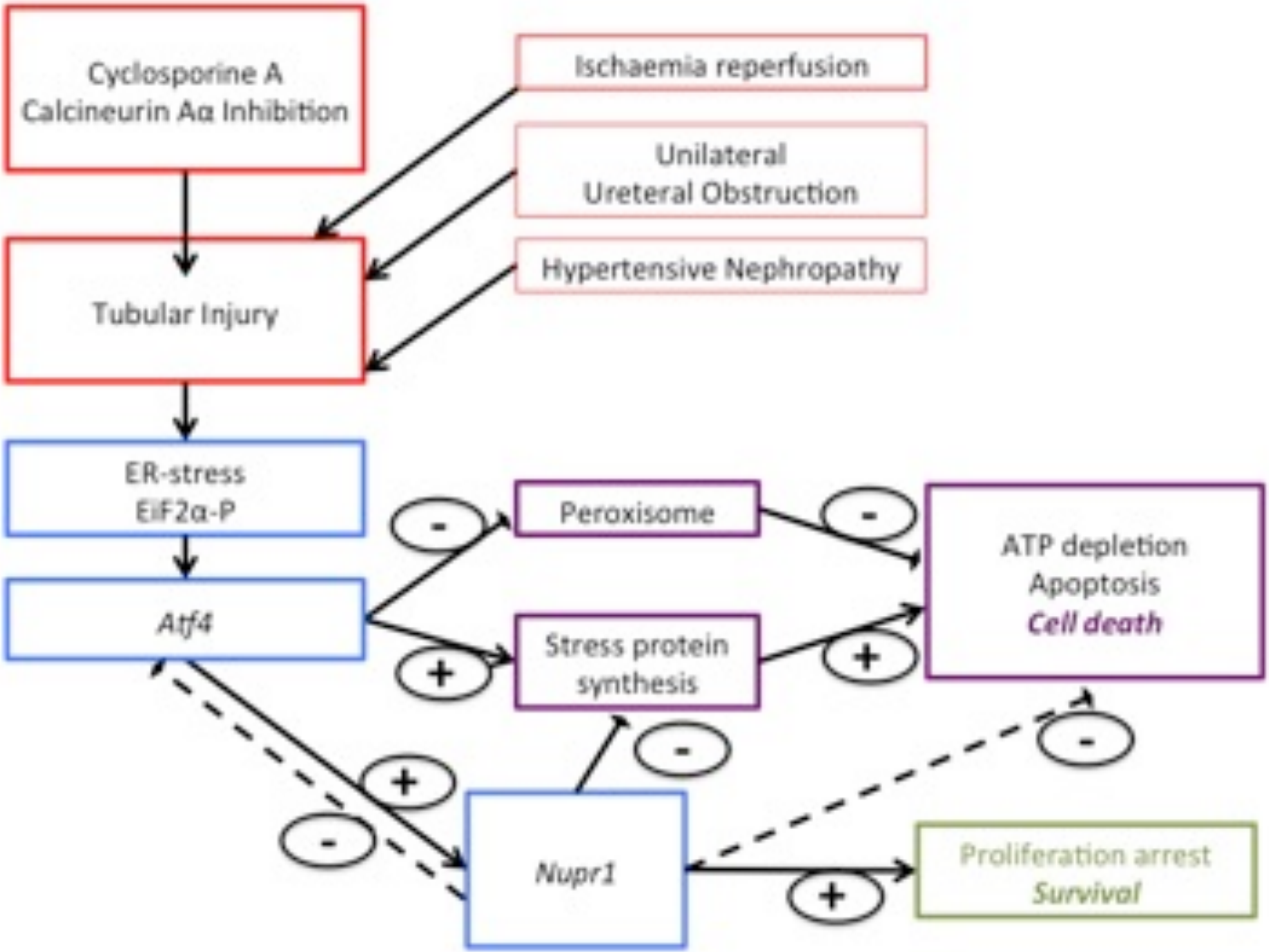

B
% of G1 cells with protein synthesis
p=0.0453
rate of protein synthesis in G1 cells (arbitrary unit)
p=0.0306
p=0.0131
WT CHX
WT CTL
WT CSA
KO CTL
KO CSA


A
Nupr1-/-
wild type
cell count 48h after seeding
number of cells seeded
B
WT
KO
100 µm
C
WT1000
KO1000
WT2000
KO2000
WT5000
KO5000
WT7000
KO7000
cell index
Time (hours)
WT CTL
WT CsA
KO CTL
KO CsA
cyclosporine
1µg/mL
cell index
Time(hours)


A
% of cell cycle stage
G0/G1
S
G2/M
sub-G1
WT CTL
WT CsA
KO CTL
KO CsA
B
BrdU MFI
p=0.0216
C
proportion of cells (%)
p=0.0122
p=0.0367
p=0.0367
p=0.0601
necrosis
apoptosis
cell death
WTCTL
WT CsA
KO CTL
KO CSA
D
ATP/ADP
p=0.0169
p<0.0001
p=0.0051
p=0.0012


A
Single Cells
68.6
Hoechst (height)
Hoechst (area)
1.0K
800
600
400
200
0
0
200
400
600
800
1.0K
B
autofluorescence
anti FLAG-Alexa647
FLAG+
1.02
C
% of cell cycle stage
G0/G1
S
G2/M
100
80
60
40
20
0
WT (mock)
WT (all)
WT flag+
KO (mock)
KO (all)
KO flag+


A
p=0.0003
Nupr1/Hprt
cyclosporine dose (ng/mL)
0
500
1000
5000
B
p=0.0004
NUPR1 (immunostaining)
Nal M3
allograft dysfunction
ATN
donor ATN
C
D
E
F
50 μm


Cyclosporine A
Calcineurin Aα Inhibition
Ischaemia reperfusion
Unilateral
Ureteral Obstruction
Hypertensive Nephropathy
Tubular Injury
ER-stress
EiF2α-P
Atf4
Peroxisome
Stress protein
synthesis
ATP depletion
Apoptosis
Cell death
Nupr1
Proliferation arrest
Survival
-
+
-
+
-
+
-
+

MATERIAL AND METHODS

Animals. Animals were housed in standard conditions in the specific pathogen-free animal facility of Inserm UMR_S 1155, in ventilated boxes with a 12/12 photoperiod, at a 20-24°C temperature with a 55+/-10% humidity. Food and water were available *ad libitum*. We used a standard murine model of *in vivo* renal toxicity with daily subcutaneous injections of cyclosporin combined with a low-salt diet started one week before the first cyclosporin injection (Safe, 0.025% Na) [1]. For rat studies (5 rats per group), cyclosporin was injected at the dose of 15 mg/kg/day for 2 weeks, and rats injected with its vehicle (ricin oil) served as control. For mice studies, WT and *Nupr1*-deficient c57bl6/J mice were given 0, 30, 50, 60, 75 or 100 mg/kg/day subcutaneous cyclosporin for 2 weeks to assess the optimal nephrotoxic dose. Olive oil, the cyclosporin vehicle for mice, served as control. JL Iovanna created the *Nupr1*$^{-/-}$ mouse strain [2].

Renal haemodynamics experiments were performed on male *Nupr1*$^{-/-}$ and WT mice. Animal surgery and renal blood flow (RBF) measurements were performed after anaesthesia by pentobarbital sodium (50–60 mg/kg body weight intraperitoneal, Nembutal, Abbott, Chicago, IL); they were placed on a servo-controlled table kept at 37°C, with trachea cannulated to facilitate respiration. The left femoral artery was catheterised to measure arterial pressure, and a femoral venous catheter was used for infusion.

Arterial pressure was measured by a pressure transducer (Statham P23 DB), and RBF by a flowmeter (0.5-v probe, Transonic Systems TS420, Ithaca, NY). RBF values were controlled for zero offset, determined at the end of an experiment after cardiac arrest. Data were recorded, stored and analysed with DataTranslation analogue-to-digital converter and IOX software (EMKA Technologies, Paris France). Experiments were planned for a total of 8 *Nupr1*$^{-/-}$ and 8 WT mice (4 CsA-treated mice and 4 control each), but 1 mouse died in each of the WT CTL, WT CsA, and KO CsA groups during the catheterisation procedure, and 1 WT

CTL, 1 KO CTL and 2 KO CsA had early renal artery bifurcation that prevented measurement of renal blood flow.

Hypertension model: Hypertension was induced in c57bl6/J male mice by two protocols. In both protocols, animals were infused subcutaneously either with vehicle (NaCl 0.9%) (control animals) or angiotensin II (1µg/kg/min) (hypertensive animals) via osmotic minipumps during 28 days. NaCl 6g/L was added to drinking water for control and hypertensive animals during the first week. Hypertensive animals also received L-Nitro-Arginine-Methyl-Esther (L-NAME) in drinking water: 50mg/kg/j for 8 days and then 10mg/kg/j for 10 days during the first protocol, and 10mg/kg/j for 20 days during the second protocol. Animals developed severe hypertension (mean systolic blood pressure 159±21 mmHg) and severe renal lesions (arteriosclerosis, glomerulosclerosis, tubulointerstitial fibrosis) in the first protocol whereas hypertension (mean systolic blood pressure 146±21 mmHg) and renal lesions were moderate in the second protocol.

Ischaemia reperfusion injury: a bilateral posterior subcostal incision was made in male c57bl6/J mice, and the renal pedicle was dissected and occluded with a small vascular clamp. After 35 min, the clamp was removed. Animals were killed and the kidneys were harvested after 2 days. The surgery and the sacrifice were performed under general anesthesia (250 mg/kg body wt, Avertine, Sigma).

Ureteral unilateral obstruction: c57bl6/J male mice underwent left ureteral ligation under general anesthesia and were sacrificed ten days later. Right unobstructed kidney was used as control. Tubular dilatation, loss of brush border, interstitial inflammation and fibrosis were observed after ureteral obstruction. [3]

Animals were sacrificed at the end of each protocol by exsanguination under general anaesthesia (pentobarbital for rats and ketamine-xylazine for mice). Blood and kidneys were harvested.

Morphologic studies and laser microdissection. Masson's trichrome staining was used for morphology, and immunostainings were performed on paraffin tissue with specific antibodies for Ki67 (rabbit polyclonal, Abcam, #ab15580), Nupr1 (rabbit, developed by JL Iovanna), ATF4 (rabbit, clone D4B8, ref 11815S, Cell Signaling), megalin (sheep, [4]), CD44 (rat, clone IM7, Exbio). After target retrieval by heating the tissue in citrate ph6 solution, the slides were incubated with primary antibodies overnight at 4°C. Next, we incubated the slides 30 minutes with a secondary antibody (Histofine Simple Stain MAX PO, Nichirei Biosciences Inc and AEC+substrate-chromogen, Dako for immunohistochemistry and anti-goat Alexa Fluor488, Invitrogen for megalin immufluorescence). 1µg/mL DAPI (forimmunofluorescence) or Hematoxylin (for immunohistochemistry) was used to stain nuclei.

Apoptosis was studied by terminal deoxynucleotidyl transferase dUTP nick end labelling (TUNEL) assays. Ki67 and TUNEL quantification were performed with the particle analysis function of ImageJ 1.45o software after setting the threshold for the detection of nuclei on a control slide. For laser capture microdissection, 8-µm thick slices of kidney were placed on nuclease-free polyethylene naphthalate (PEN)-coated glass slides, stained with toluidine blue and fixed with ethanol. For each sample, 200 cortical tubules were carefully harvested to avoid contamination by extratubular material (Supplemental Figure 6).

RT-PCR and mRNA microarray. Microdissected tubules were immediately stored in lysis buffer for mRNA extraction with the RNeasy micro kit (Qiagen), and reverse transcription was performed with a WT-Ovation kit (Nugen). Target cDNA was marked and hybridised on GeneChip Rat Genome 230 2.0 microarrays (Affymetrix). After washing, images were acquired and computed into normalised intensities. The pathway analysis was performed with LrPath web-based software [5].

For RT-PCR, a piece of renal cortex was frozen in RNA Later (Qiagen, Courtaboeuf, France). RNA extraction was performed with TRIzol (Life Technologies, BRL, Gaithersburg, MD).

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Protein synthesis was assessed using the Click-iT® HPG Alexa Fluor® 488 Protein Synthesis Assay Kit (Molecular Probes, Life Technologies). Cells were incubated with L-homopropargylglycine (a methionin analog) for 30 minutes, and stained with Alexa Fluor 488 following the manufacturer's instructions. After acquiring the photographs, cells were trypsinized in the 96-well plates, and directly analyzed by flow cytometry.

Transfection with a pcDNA3 plasmid containing the *Flag-Nupr1* construct was performed using Attractene (#301005, Qiagen) following the manufacturer protocol for traditional transfection. Cells were trypsinized and permeabilized using the Cytofix/Cytoperm kit (#554714, Becton Dickinson) and following the manufacturer instructions, with an AlexaFluor 647 conjugated anti-FLAG antibody (#3916, Cell Signaling). Cell cycle analysis was performed after Hoechst 3342 was added.

Statistics. Statistical analysis used JMP Pro 9.0.2 software. Data are presented by their median values and interquartile ranges, and a nonparametric Wilcoxon test was used to assess statistical significance, except where otherwise indicated. A *P*-value<5% was defined as significant.

Study approval. Animals were handled in a licensed facility (approval number B-75-20-01) in compliance with French legislation and INSERM standards for laboratory animal care, including when necessary approval by our institutional review board (Comité National de Réflexion Ethique sur l'Experimentation animal, numéro 5) and the French Research Ministry (authorised project n° 00797.02, authorisation for animal experimentation n°A-75-1934). Biopsies from renal-transplanted patients receiving cyclosporin treatment were used for NUPR1 immunohistochemistry. The biopsies were indicated for state-of-the-art routine care, and all patients provided written consent for use of the leftover material for research purposes. The study on human renal biopsies was approved by our local Institutional Review Board.

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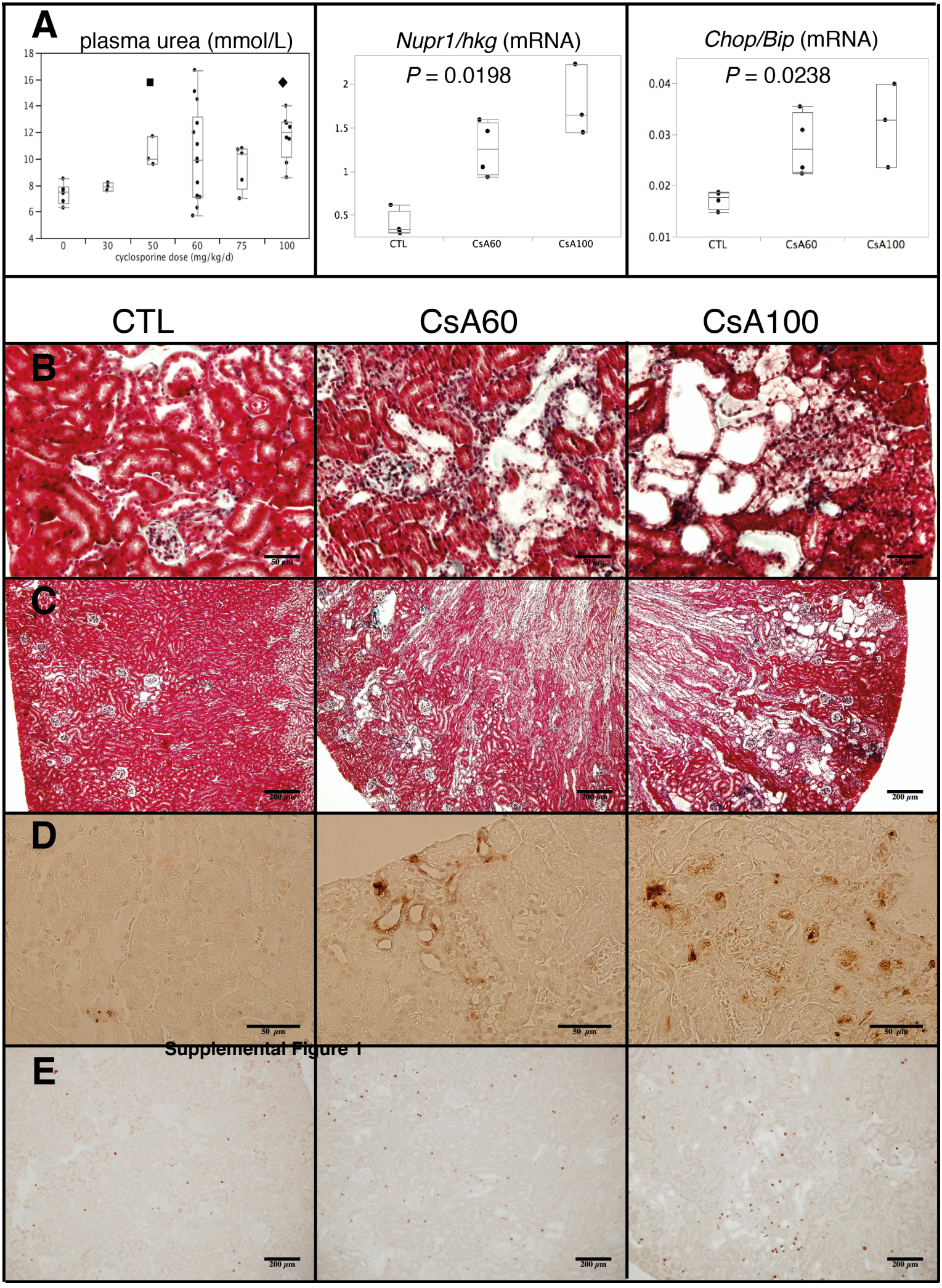
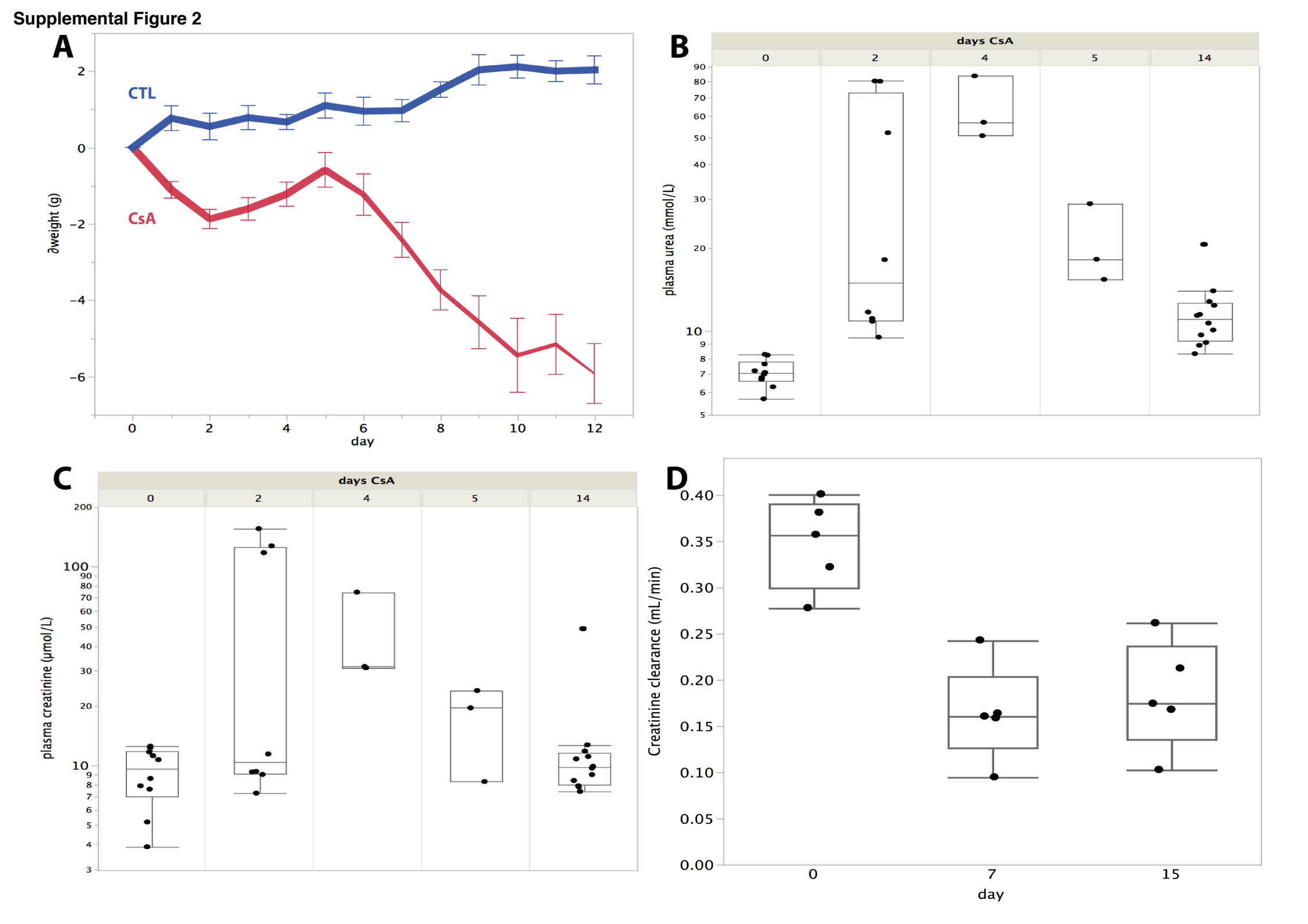
Supplemental Figure 1



Supplemental Figure 1

Supplemental Figure 2



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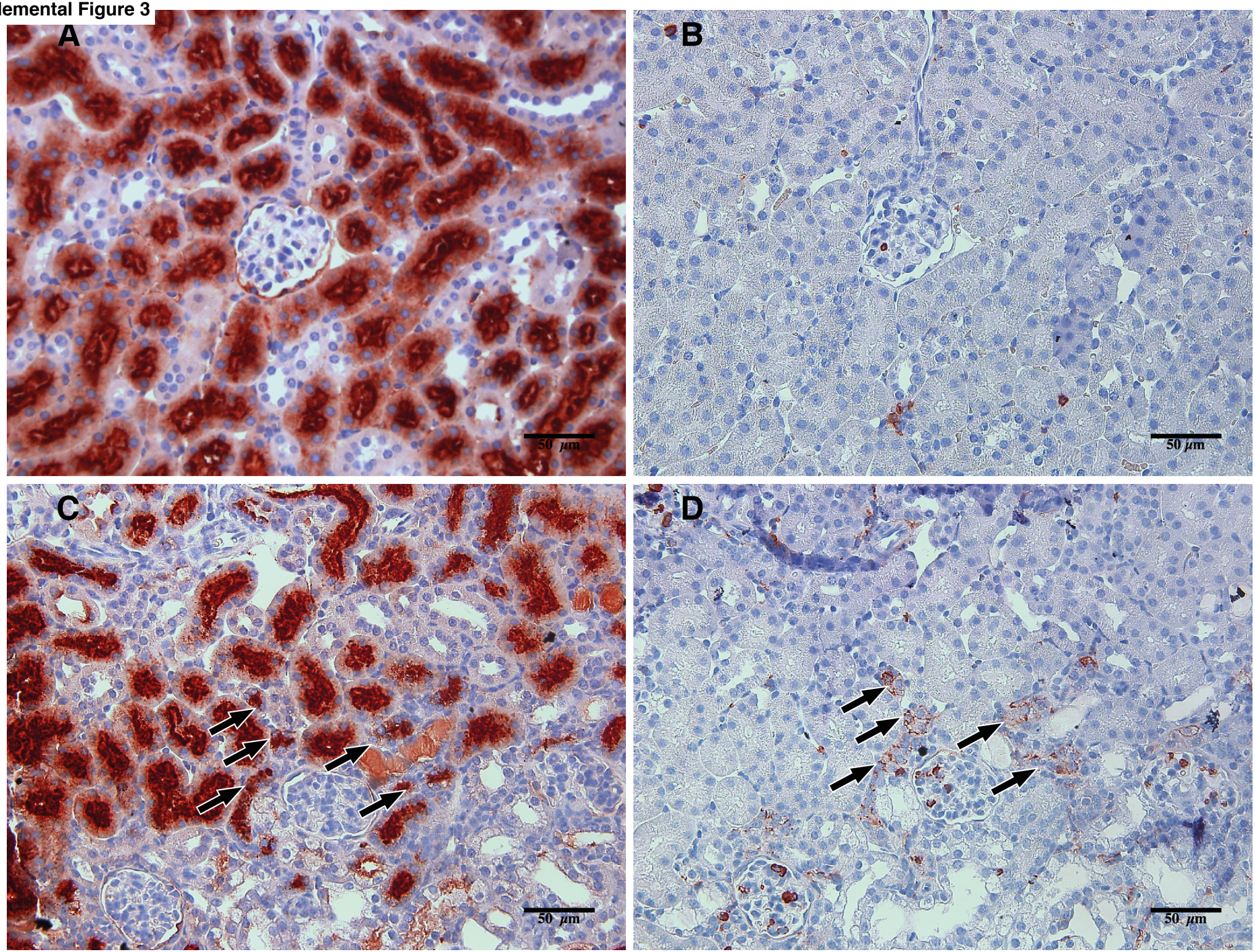

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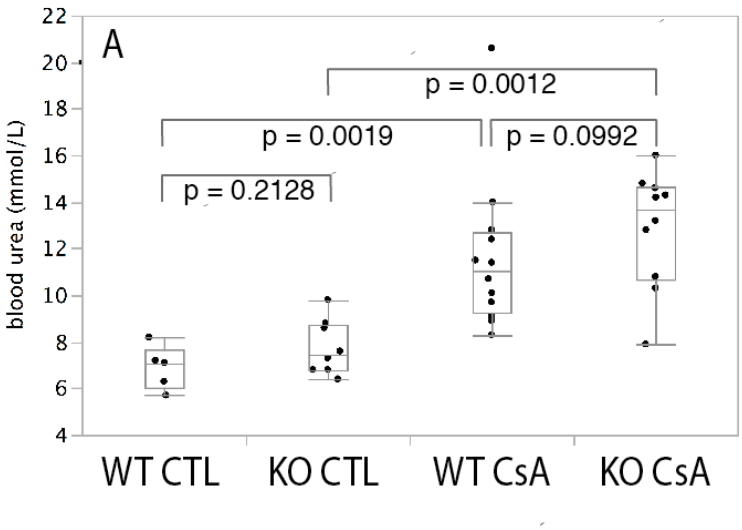

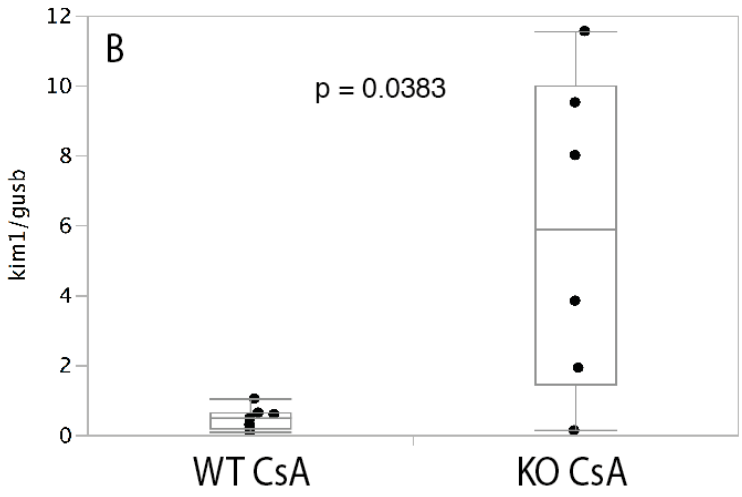

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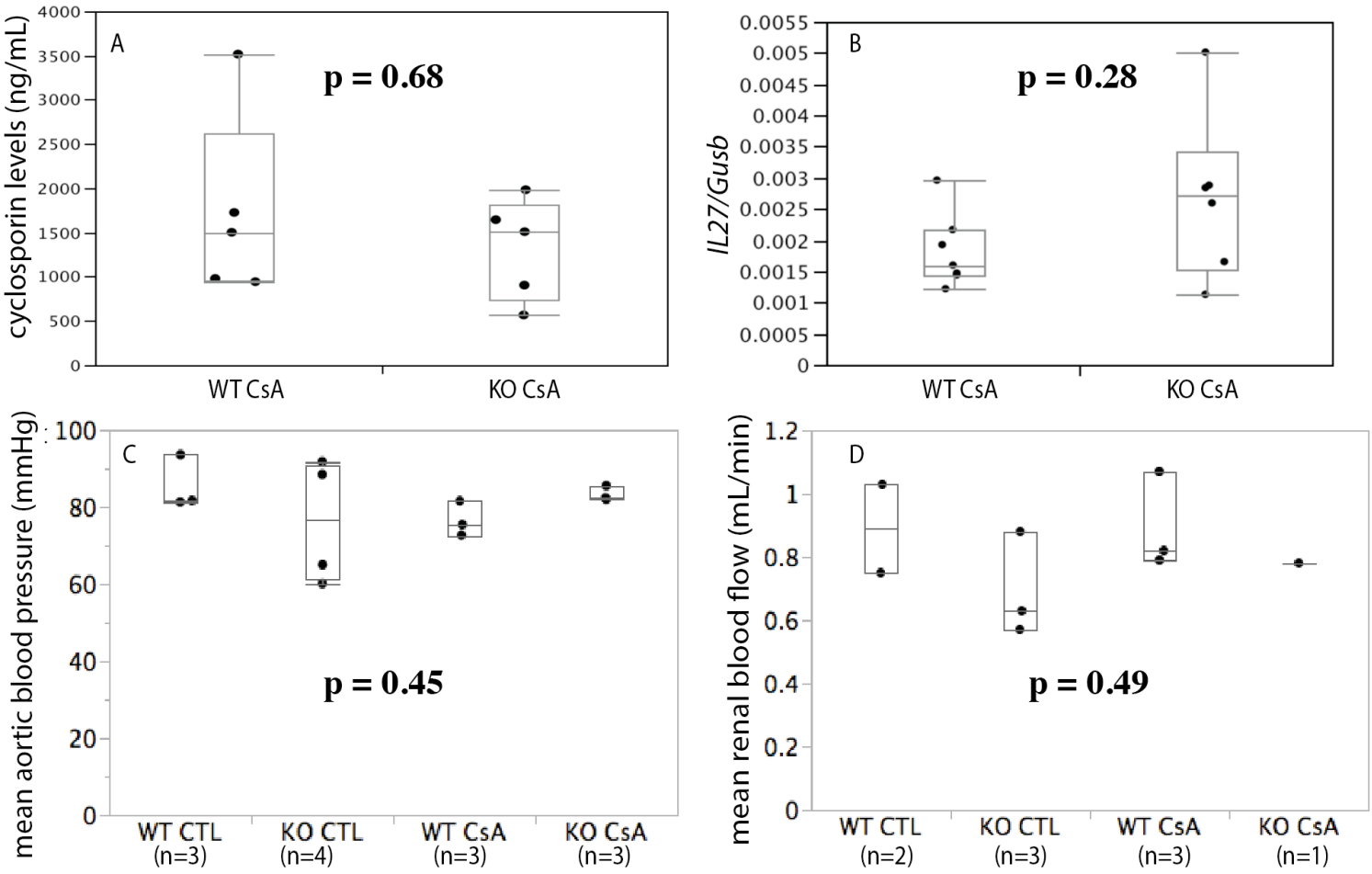

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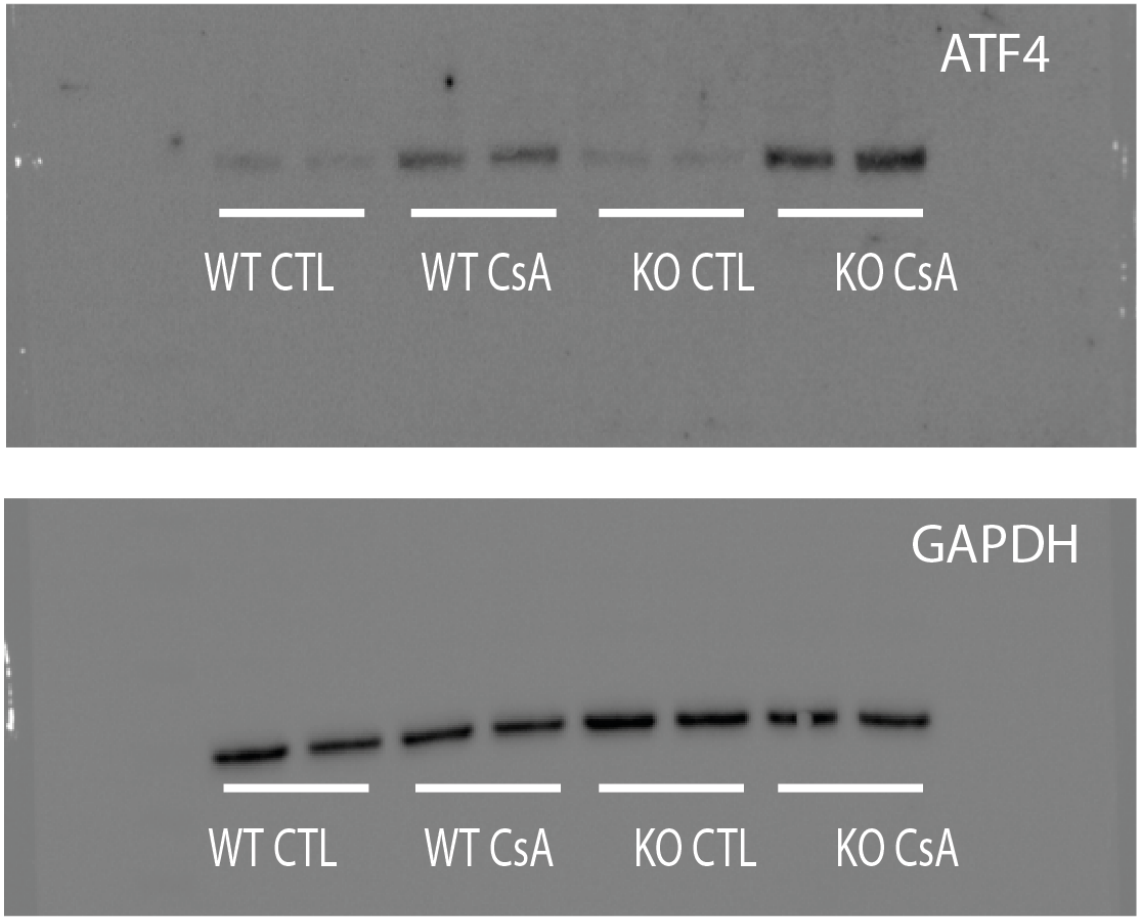

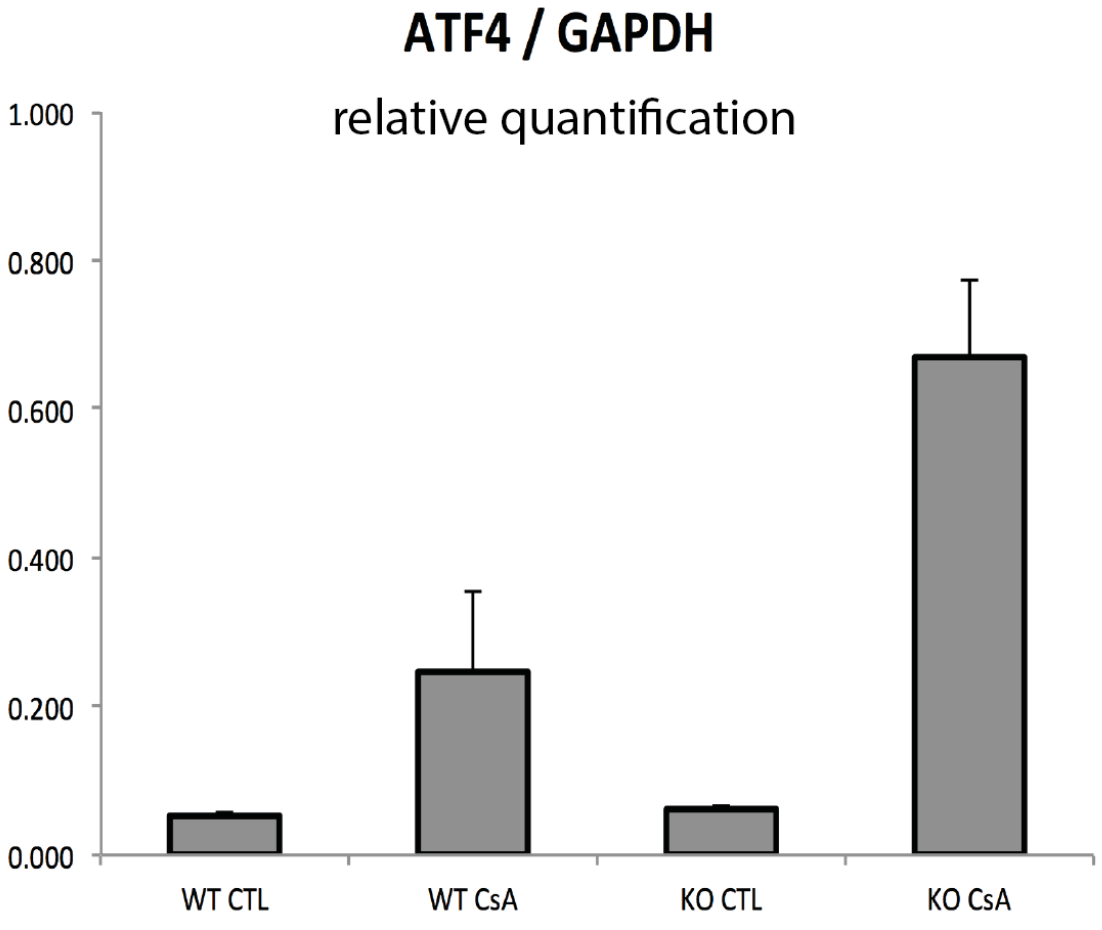

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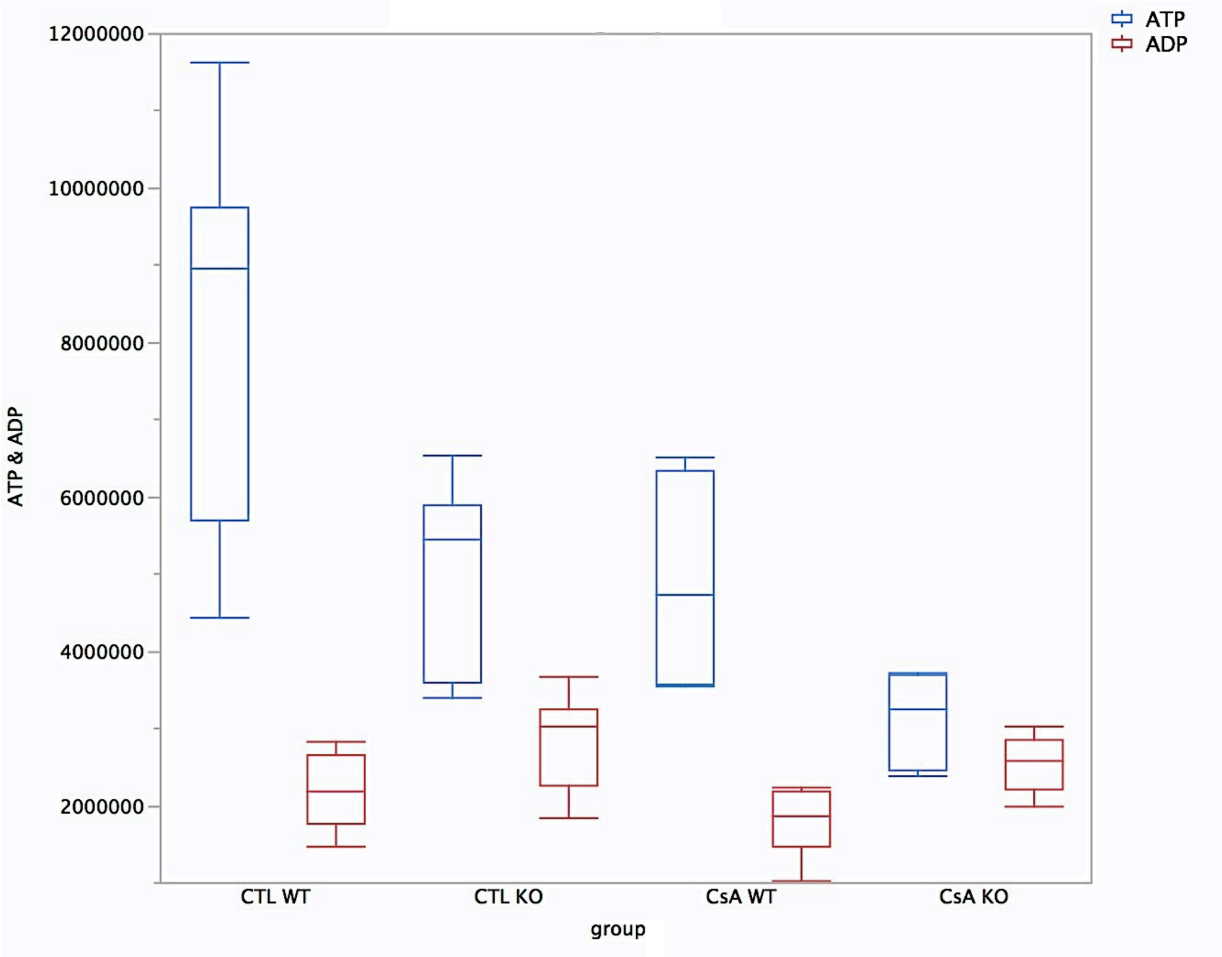

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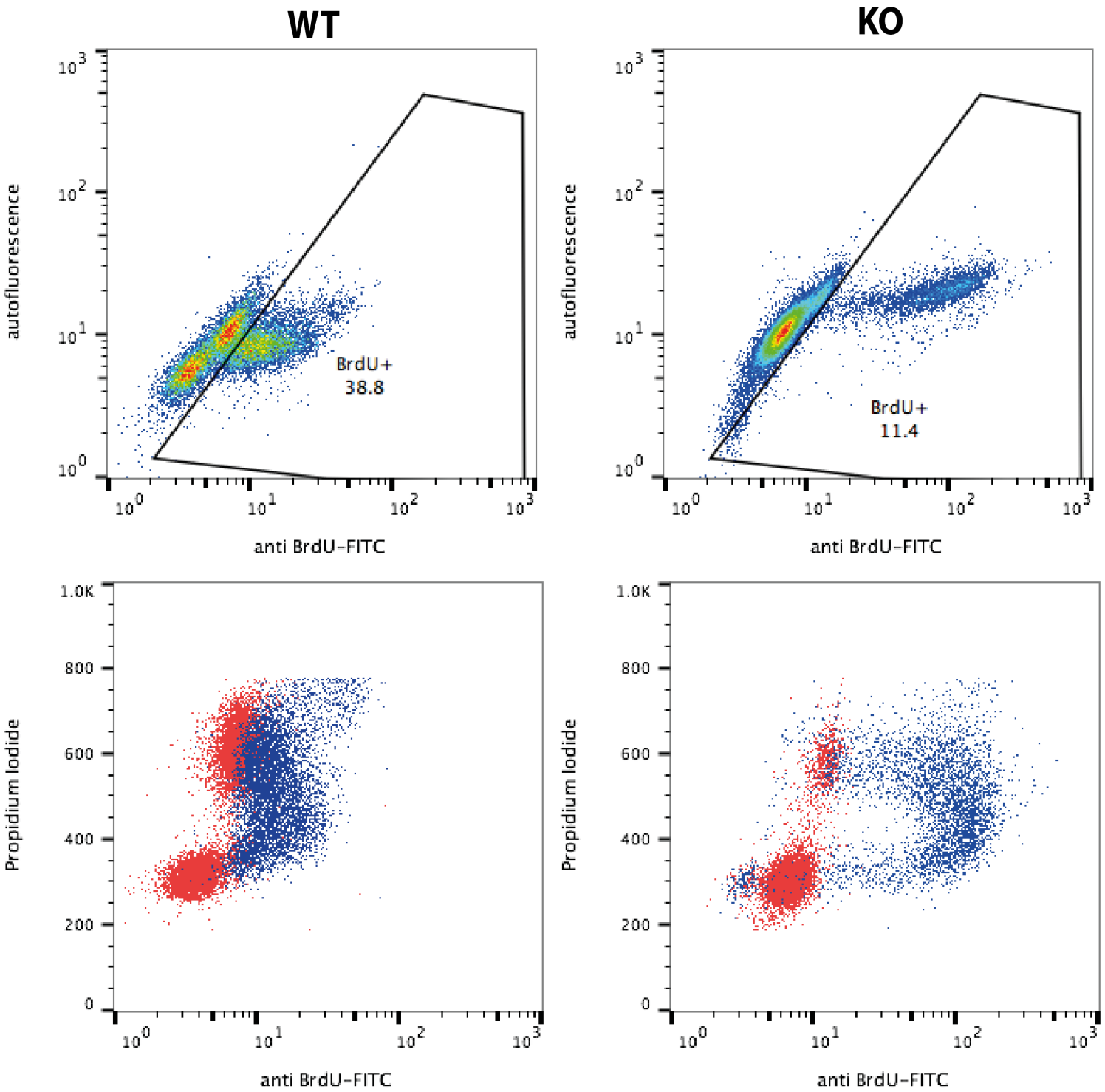

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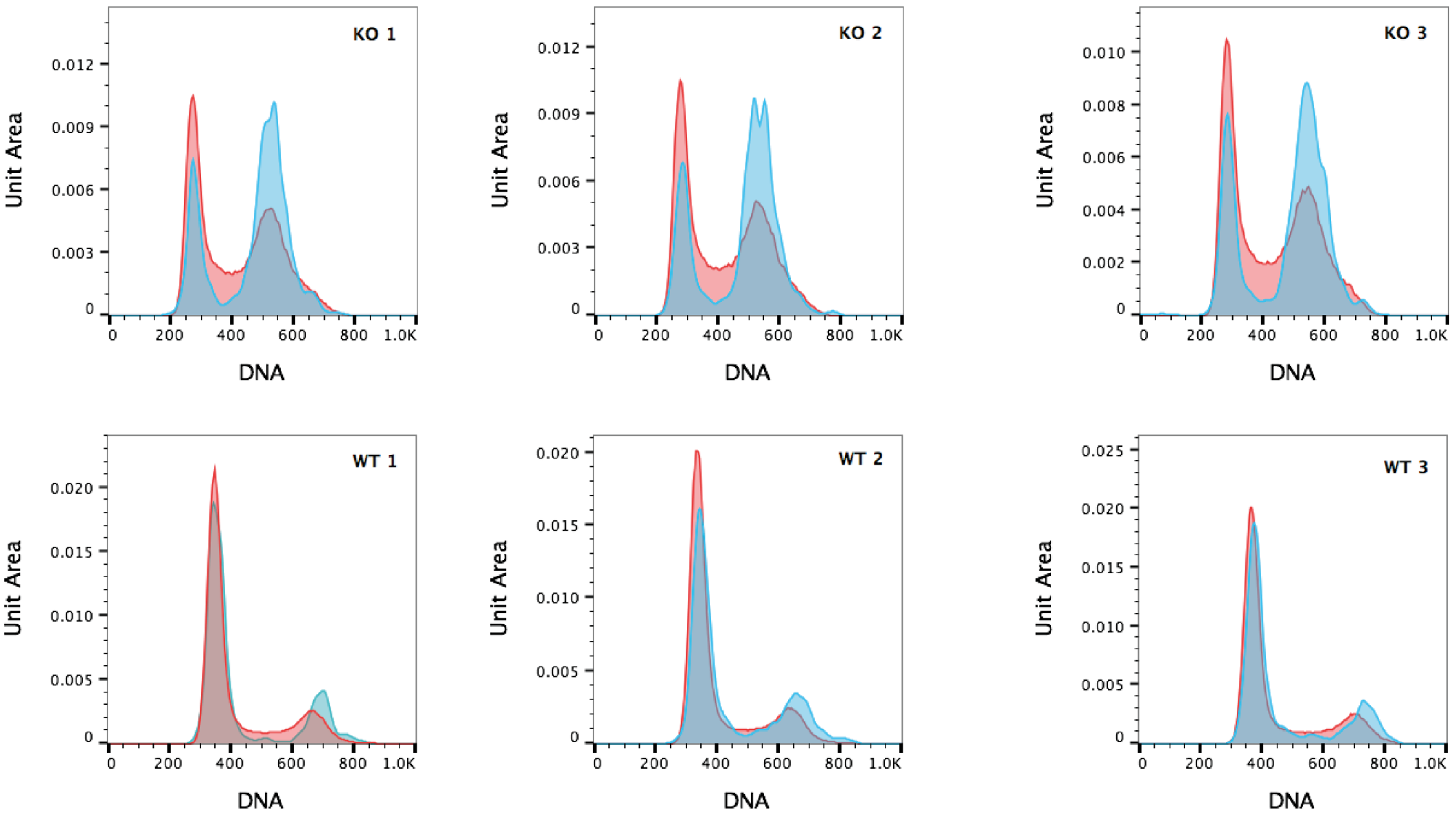

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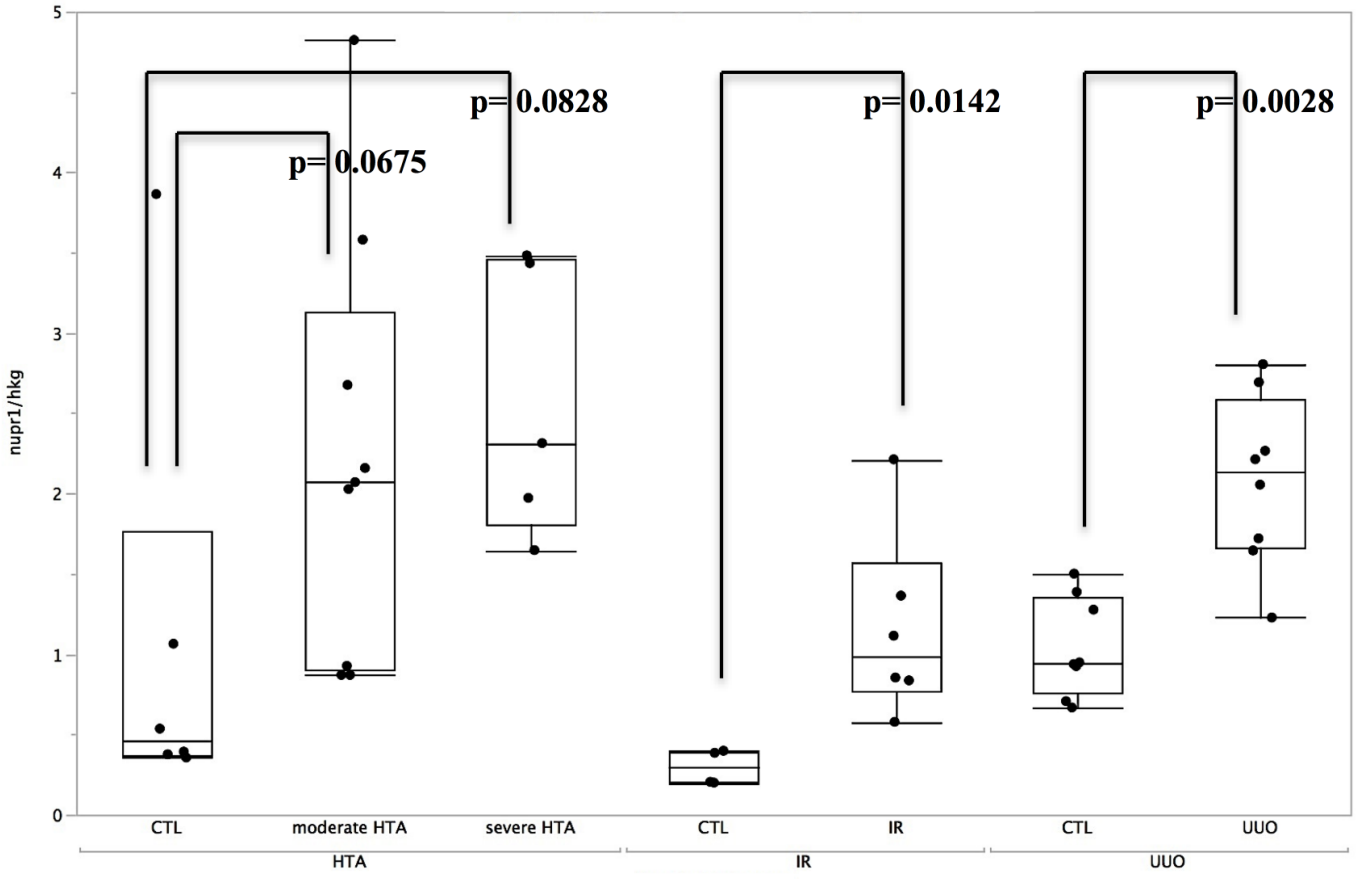
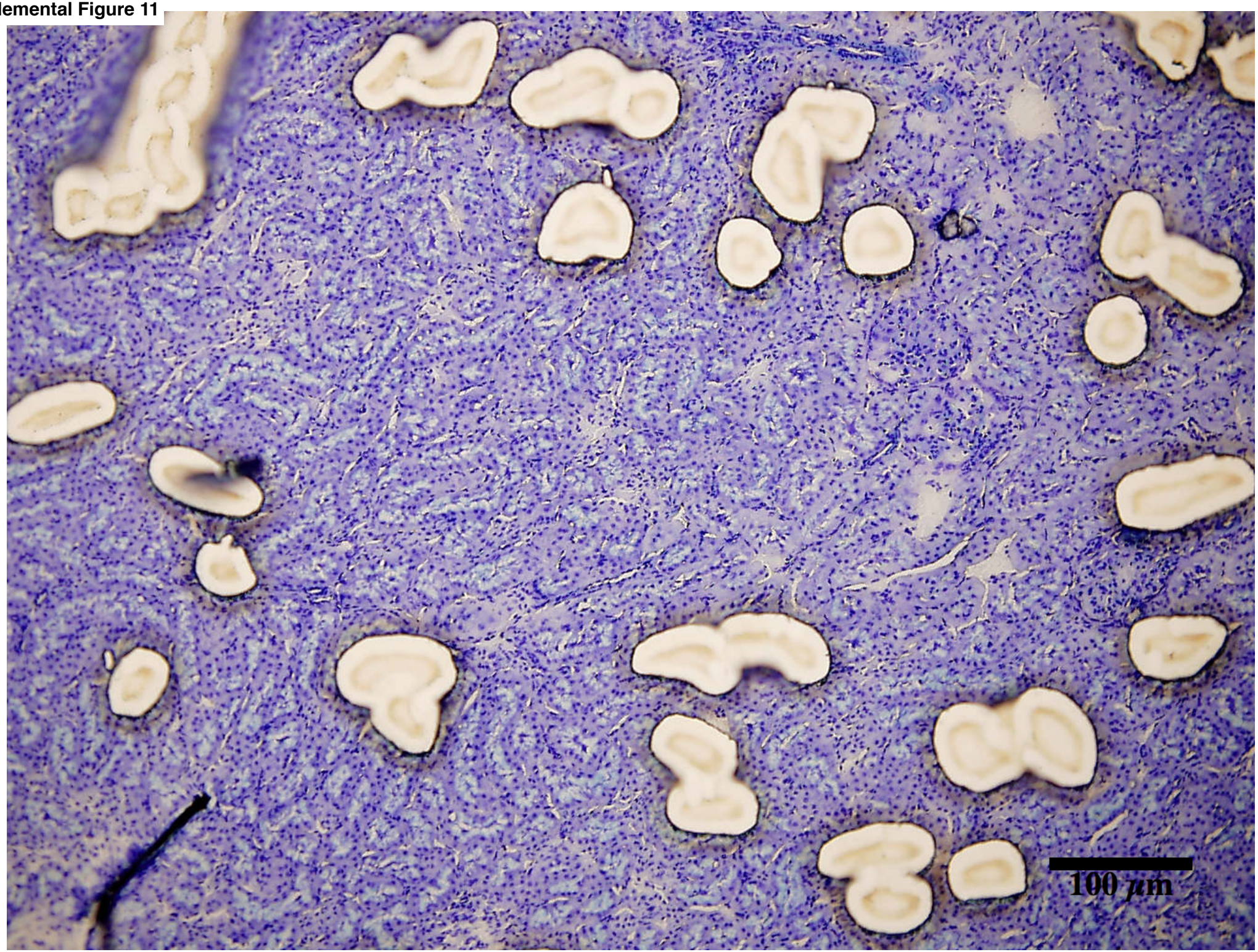


Supplemental Figure 11



MATERIAL AND METHODS

Animals. Animals were housed in standard conditions in the specific pathogen-free animal facility of Inserm UMR_S 1155, in ventilated boxes with a 12/12 photoperiod, at a 20-24°C temperature with a 55+/-10% humidity. Food and water were available *ad libitum*. We used a standard murine model of *in vivo* renal toxicity with daily subcutaneous injections of cyclosporin combined with a low-salt diet started one week before the first cyclosporin injection (Safe, 0.025% Na) [1]. For rat studies (5 rats per group), cyclosporin was injected at the dose of 15 mg/kg/day for 2 weeks, and rats injected with its vehicle (ricin oil) served as control. For mice studies, WT and *Nupr1*-deficient c57bl6/J mice were given 0, 30, 50, 60, 75 or 100 mg/kg/day subcutaneous cyclosporin for 2 weeks to assess the optimal nephrotoxic dose. Olive oil, the cyclosporin vehicle for mice, served as control. JL Iovanna created the *Nupr1*$^{-/-}$ mouse strain [2].

Renal haemodynamics experiments were performed on male *Nupr1*$^{-/-}$ and WT mice. Animal surgery and renal blood flow (RBF) measurements were performed after anaesthesia by pentobarbital sodium (50–60 mg/kg body weight intraperitoneal, Nembutal, Abbott, Chicago, IL); they were placed on a servo-controlled table kept at 37°C, with trachea cannulated to facilitate respiration. The left femoral artery was catheterised to measure arterial pressure, and a femoral venous catheter was used for infusion.

Arterial pressure was measured by a pressure transducer (Statham P23 DB), and RBF by a flowmeter (0.5-v probe, Transonic Systems TS420, Ithaca, NY). RBF values were controlled for zero offset, determined at the end of an experiment after cardiac arrest. Data were recorded, stored and analysed with DataTranslation analogue-to-digital converter and IOX software (EMKA Technologies, Paris France). Experiments were planned for a total of 8 *Nupr1*$^{-/-}$ and 8 WT mice (4 CsA-treated mice and 4 control each), but 1 mouse died in each of the WT CTL, WT CsA, and KO CsA groups during the catheterisation procedure, and 1 WT

CTL, 1 KO CTL and 2 KO CsA had early renal artery bifurcation that prevented measurement of renal blood flow.

Hypertension model: Hypertension was induced in c57bl6/J male mice by two protocols. In both protocols, animals were infused subcutaneously either with vehicle (NaCl 0.9%) (control animals) or angiotensin II (1µg/kg/min) (hypertensive animals) via osmotic minipumps during 28 days. NaCl 6g/L was added to drinking water for control and hypertensive animals during the first week. Hypertensive animals also received L-Nitro-Arginine-Methyl-Esther (L-NAME) in drinking water: 50mg/kg/j for 8 days and then 10mg/kg/j for 10 days during the first protocol, and 10mg/kg/j for 20 days during the second protocol. Animals developed severe hypertension (mean systolic blood pressure 159±21 mmHg) and severe renal lesions (arteriosclerosis, glomerulosclerosis, tubulointerstitial fibrosis) in the first protocol whereas hypertension (mean systolic blood pressure 146±21 mmHg) and renal lesions were moderate in the second protocol.

Ischaemia reperfusion injury: a bilateral posterior subcostal incision was made in male c57bl6/J mice, and the renal pedicle was dissected and occluded with a small vascular clamp. After 35 min, the clamp was removed. Animals were killed and the kidneys were harvested after 2 days. The surgery and the sacrifice were performed under general anesthesia (250 mg/kg body wt, Avertine, Sigma).

Ureteral unilateral obstruction: c57bl6/J male mice underwent left ureteral ligation under general anesthesia and were sacrificed ten days later. Right unobstructed kidney was used as control. Tubular dilatation, loss of brush border, interstitial inflammation and fibrosis were observed after ureteral obstruction. [3]

Animals were sacrificed at the end of each protocol by exsanguination under general anaesthesia (pentobarbital for rats and ketamine-xylazine for mice). Blood and kidneys were harvested.

Morphologic studies and laser microdissection. Masson's trichrome staining was used for morphology, and immunostainings were performed on paraffin tissue with specific antibodies for Ki67 (rabbit polyclonal, Abcam, #ab15580), Nupr1 (rabbit, developed by JL Iovanna), ATF4 (rabbit, clone D4B8, ref 11815S, Cell Signaling), megalin (sheep, [4]), CD44 (rat, clone IM7, Exbio). After target retrieval by heating the tissue in citrate ph6 solution, the slides were incubated with primary antibodies overnight at 4°C. Next, we incubated the slides 30 minutes with a secondary antibody (Histofine Simple Stain MAX PO, Nichirei Biosciences Inc and AEC+substrate-chromogen, Dako for immunohistochemistry and anti-goat Alexa Fluor488, Invitrogen for megalin immufluorescence). 1µg/mL DAPI (forimmunofluorescence) or Hematoxylin (for immunohistochemistry) was used to stain nuclei.

Apoptosis was studied by terminal deoxynucleotidyl transferase dUTP nick end labelling (TUNEL) assays. Ki67 and TUNEL quantification were performed with the particle analysis function of ImageJ 1.45o software after setting the threshold for the detection of nuclei on a control slide. For laser capture microdissection, 8-µm thick slices of kidney were placed on nuclease-free polyethylene naphthalate (PEN)-coated glass slides, stained with toluidine blue and fixed with ethanol. For each sample, 200 cortical tubules were carefully harvested to avoid contamination by extratubular material (Supplemental Figure 6).

RT-PCR and mRNA microarray. Microdissected tubules were immediately stored in lysis buffer for mRNA extraction with the RNeasy micro kit (Qiagen), and reverse transcription was performed with a WT-Ovation kit (Nugen). Target cDNA was marked and hybridised on GeneChip Rat Genome 230 2.0 microarrays (Affymetrix). After washing, images were acquired and computed into normalised intensities. The pathway analysis was performed with LrPath web-based software [5].

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ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1367847_at	Nupr1	nuclear protein 1	113900	Rn.11182	NM_053611	3.63	7.65	3.55	11.26	10.55	12.34	86.81	up	1.14E-02	8.95E-01	UR	-
1387328_at	Cyp2c	cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase)	29277	Rn.10870	NM_019184	10.18	8.65	9.82	3.15	3.35	3.04	82.57	down	1.76E-04	8.95E-01	DR	-
1387925_at	Aars	asparagine synthetase	25612	Rn.11172	U07202	3.54	5.18	2.40	8.37	8.18	9.00	28.03	up	4.68E-03	8.95E-01	UR	-
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1367581_a_at	Spp1	secreted phosphoprotein 1	25353	Rn.8871	AB001382	4.28	4.53	5.50	9.27	7.96	9.23	16.54	up	2.06E-03	8.95E-01	UR	-
1372601_at	Atf5	activating transcription factor 5	282840	Rn.195729	BM391471	3.38	5.47	3.70	7.76	7.04	8.69	12.54	up	1.06E-02	8.95E-01	UR	-
1370240_x_at	a-a2 /// LOC360	hemoglobin alpha, adult chain 2 /// hemoglobin alpha 2 chain	25632 /// 360504	Rn.107334	AI179404	9.72	9.55	8.85	3.47	8.11	6.19	10.94	down	6.55E-02	8.95E-01	-	-
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1370239_at	a-a2 /// LOC360	hemoglobin alpha, adult chain 2 /// hemoglobin alpha 2 chain	25632 /// 360504	Rn.107334	AI179404	9.48	9.36	8.60	3.50	7.95	5.97	10.13	down	6.40E-02	8.95E-01	-	-
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1371245_a_at	LOC689064	beta-globin	689064	---	BI287300	7.65	8.23	6.65	2.89	6.55	4.81	6.78	down	7.51E-02	8.95E-01	-	-
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1383455_at	Eprs	glutamyl-prolyl-tRNA synthetase	289352	Rn.21240	BF553211	4.49	7.49	5.21	8.21	7.83	8.88	5.95	up	5.43E-02	8.95E-01	-	-
1380426_at	Ankrd52	ankyrin repeat domain 52	362611	Rn.8972	BF404433	8.02	4.18	2.33	2.31	2.32	2.31	5.77	down	2.06E-01	8.95E-01	-	-
1386985_at	Gstm1	glutathione S-transferase mu 1	24423	Rn.202644	M28241	8.27	4.17	7.89	4.87	4.69	3.30	5.62	down	1.50E-01	8.95E-01	-	-
1370201_at	Calb1	calbindin 1	83839	Rn.3908	X04280	6.92	3.36	5.44	2.81	2.93	2.53	5.60	down	7.47E-02	8.95E-01	-	-
1393402_at	---	---	---	Rn.171114	BG670858	2.36	2.73	10.20	2.42	2.36	3.06	5.59	down	3.88E-01	8.95E-01	-	-
1371102_x_at	30134877 /// LOC8	beta globin minor gene /// beta-globin	30134877 /// 68906	Rn.216394	X05080	7.65	7.07	6.20	2.71	6.32	4.61	5.37	down	9.74E-02	8.95E-01	-	-
1377940_at	Fam101b	family with sequence similarity 101, member B	287534	Rn.13078	BF398271	4.74	6.19	2.84	6.14	8.21	6.68	5.36	up	1.04E-01	8.95E-01	-	-
1372182_at	Pfkp	phosphofructokinase, platelet	60416	Rn.2278	BM389769	3.50	3.33	3.44	5.11	5.82	6.61	5.35	up	5.23E-03	8.95E-01	UR	-
1367553_x_at	Hbb	hemoglobin, beta	24440	Rn.202646	NM_033234	8.78	8.66	7.36	4.56	7.31	5.67	5.35	down	5.88E-02	8.95E-01	-	-
1392965_a_at	Smoc2	SPARC related modular calcium binding 2	292401	Rn.6092	AI028877	2.42	6.51	5.59	7.97	6.98	6.67	5.14	up	1.43E-01	8.95E-01	-	-
1396047_at	Rere	arginine-glutamic acid dipeptide (RE) repeats	116665	Rn.10277	AW920332	3.16	4.91	2.71	6.02	5.67	6.17	5.12	up	2.63E-02	8.95E-01	UR	-
1385706_at	---	---	---	Rn.177359	BI292758	3.48	4.18	3.31	5.55	5.85	6.61	5.09	up	4.72E-03	8.95E-01	UR	-
1368878_at	Idi1	isopentenyl-diphosphate delta isomerase 1	89784	Rn.10780	NM_053539	6.82	5.15	5.54	3.13	2.58	3.78	5.06	down	4.17E-03	8.95E-01	DR	-
1370563_at	Akr1c14	aldo-keto reductase family 1, member C14	191574	Rn.10021	D17310	2.46	2.54	2.46	2.58	6.18	5.66	5.00	up	1.07E-01	8.95E-01	-	-
1383661_at	---	---	---	Rn.15645	AA926037	2.51	4.86	2.49	4.59	5.83	6.30	4.87	up	7.18E-02	8.95E-01	-	-
1387818_at	Casp4	caspase 4, apoptosis-related cysteine peptidase	114555	Rn.16195	NM_053736	3.17	2.72	2.83	4.00	5.21	6.35	4.85	up	3.01E-02	8.95E-01	UR	-
1370892_at	C4-2 /// C4b	complement component 4, gene 2 /// complement component 4B (Childo bloc	24233 /// 406161	Rn.81052	BI285347	5.23	8.16	5.29	8.66	8.50	8.32	4.82	up	8.02E-02	8.95E-01	-	-
1388608_x_at	a-a2 /// LOC360	hemoglobin alpha, adult chain 2 /// hemoglobin alpha 2 chain	25632 /// 360504	Rn.107334	AI577319	9.02	8.84	7.87	5.32	7.77	5.85	4.80	down	5.20E-02	8.95E-01	-	-
1372889_at	---	---	---	Rn.164359	AI407489	5.87	5.36	3.69	8.12	7.34	6.14	4.67	up	6.38E-02	8.95E-01	-	-
1391413_at	LOC365090	similar to 5-nucleotidase, cytosolic II	365090	---	BM387140	2.85	2.83	2.85	2.83	9.54	2.81	4.65	up	3.78E-01	8.95E-01	-	-
1389573_at	Chac1	ChaC, cation transport regulator homolog 1 (E. coli)	362196	Rn.23367	AI170665	2.75	2.78	2.76	4.67	4.78	5.46	4.61	up	8.74E-04	8.95E-01	UR	-
1370228_at	Srprb /// Tf	signal recognition particle receptor, B subunit /// transferrin	24825 /// 300965	Rn.91296	AA945178	5.53	8.86	7.33	8.73	9.54	9.93	4.47	up	1.03E-01	8.95E-01	-	-
1395586_at	---	---	---	Rn.163742	BF545930	5.79	4.86	4.56	7.19	7.62	6.82	4.40	up	8.11E-03	8.95E-01	UR	-
1389611_at	Vldlr	very low density lipoprotein receptor	25696	Rn.9975	AA849857	3.68	3.22	3.85	5.00	5.76	6.32	4.32	up	7.92E-03	8.95E-01	UR	-
1367904_at	Resp18	regulated endocrine-specific protein 18	50561	Rn.66430	NM_019278	7.12	7.74	6.08	6.59	4.49	3.54	4.31	down	1.08E-01	8.95E-01	-	-
1376293_at	Trim26	tripartite motif-containing 26	309586	Rn.163420	AI556246	2.42	2.91	2.39	4.76	4.64	4.61	4.28	up	2.83E-04	8.95E-01	UR	-
1370566_at	Rdh2	retinol dehydrogenase 2	29591	Rn.94108	U33500	8.13	6.52	8.85	6.80	6.07	4.38	4.24	down	1.04E-01	8.95E-01	-	-
1371003_at	Map1b	microtubule-associated protein 1B	29456	Rn.98152	BG378086	3.15	2.77	2.52	5.23	4.08	5.37	4.22	up	9.80E-03	8.95E-01	UR	-
1394676_at	Oxa1l	oxidase assembly 1-like	691393	Rn.105893	BF420216	4.52	4.60	3.84	6.74	5.86	6.59	4.21	up	4.72E-03	8.95E-01	UR	-
1384499_at	Bucs1	butyrobetaine (gamma), 2-oxoglutarate 3 dioxygenase 1	361638	Rn.38622	BG373566	7.96	7.36	8.88	9.30	9.38	9.73	4.20	up	3.68E-03	8.95E-01	UR	-
1392726_at	Pdpr	pyruvate dehydrogenase phosphatase regulatory subunit	307852	Rn.21088	AI059453	5.62	5.04	5.06	3.36	2.76	3.41	4.19	down	1.86E-03	8.95E-01	DR	-
1391616_at	---	---	---	Rn.203183	BF542832	6.76	7.90	9.60	7.80	4.49	5.78	4.17	down	1.80E-01	8.95E-01	-	-
1377334_at	RT1-Ba	RT1 class II, locus Ba	309821	Rn.25717	BG378249	2.79	6.90	5.00	7.50	7.94	5.39	4.12	up	2.24E-01	8.95E-01	-	-
1398618_a_at	---	---	---	Rn.137969	AW435170	6.03	7.53	6.58	8.19	9.49	8.57	4.11	up	2.52E-02	8.95E-01	UR	-
1372867_at	Rnmt	RNA (guanine-7-) methyltransferase	291534	Rn.20871	AI177333	2.99	5.88	2.48	5.50	6.02	5.94	4.09	up	1.30E-01	8.95E-01	-	-
1368160_at	Igfbp1	insulin-like growth factor binding protein 1	25685	Rn.34026	NM_013144	2.74	2.24	2.46	4.29	3.86	5.35	4.05	up	1.23E-02	8.95E-01	UR	-
1375585_at	---	---	---	Rn.164975	BE111820	3.57	4.06	3.10	6.64	5.11	5.02	4.04	up	2.79E-02	8.95E-01	UR	-
1368143_at	Anxa7	annexin A7	155423	Rn.106184	AI013902	4.06	6.34	5.08	7.25	7.22	7.04	4.04	up	3.85E-02	8.95E-01	UR	-
1384312_at	Irx1	iroquois homeobox 1	306659	Rn.46018	BF543574	3.53	7.10	5.10	6.96	7.13	7.67	4.02	up	1.30E-01	8.95E-01	-	-
1384149_at	Ccdc75	coiled-coil domain containing 75	362685	Rn.57800	H32531	6.99	7.39	4.57	8.35	9.09	7.50	4.00	up	1.15E-01	8.95E-01	-	-
1393951_at	LOC684934	similar to coiled-coil domain containing 9	684934	---	BI302706	4.14	4.92	2.82	6.80	5.33	5.71	3.97	up	5.78E-02	8.95E-01	-	-
1383978_at	---	---	---	Rn.34561	BM384029	5.25	3.96	3.48	5.56	6.36	6.68	3.92	up	3.38E-02	8.95E-01	UR	-
1379626_at	Satb1	SATB homeobox 1	316164	Rn.21462	AA946353	4.32	4.70	3.53	5.50	6.62	6.35	3.92	up	1.49E-02	8.95E-01	UR	-
1383128_at	Fam69a	family with sequence similarity 69, member A	360906	Rn.219993	AW921382	5.07	4.55	2.47	4.49	7.22	6.29	3.92	up	1.55E-01	8.95E-01	-	-
1387253_at	Guca2b	guanylate cyclase activator 2B	64055	Rn.97593	NM_022284	6.09	7.28	6.26	4.75	3.15	5.82	3.92	down	8.35E-02	8.95E-01	-	-
1376754_at	Cars	cysteinyl-tRNA synthetase	293638	Rn.14865	AI176610	3.09	4.12	3.00	5.84	4.48	5.80	3.91	up	2.66E-02	8.95E-01	UR	-
1390119_at	Sfrp2	secreted frizzled-related protein 2	310552	Rn.102416	BF396602	5.74	3.67	4.46	2.58	3.09	2.31	3.90	down	3.83E-02	8.95E-01	DR	-
1384036_s_at	LOC685277	similar to liver-specific bHLH-Zip transcription factor	685277	Rn.165356	AW536030	2.91	3.05	3.35	6.48	5.25	3.46	3.89	up	9.10E-02	8.95E-01	-	-
1396291_at	---	---	---	---	BI290733	3.64	3.82	2.96	4.13	6.66	5.48	3.86	up	6.56E-02	8.95E-01	-	-
1379452_at	Gas2	growth arrest-specific 2	29196	Rn.19800	AI411492	5.43	3.38	4.75	2.50	2.54	2.69	3.84	down	3.27E-02	8.95E-01	DR	-
1384035_at	LOC685277	similar to liver-specific bHLH-Zip transcription factor	685277	Rn.165356	AW536030	2.47	2.62	3.17	5.85	4.55	3.68	3.83	up	4.37E-02	8.95E-01	UR	-
1372004_at	Hebp1	heme binding protein 1	362454	Rn.6886	AI102065	3.98	4.08	3.75	5.15	5.67	6.79	3.83	up	1.71E-02	8.95E-01	UR	-
1369274_a_at	Cdkl3	cyclin-dependent kinase-like 3	60396	Rn.154405	NM_021772	3.38	3.59	4.08	6.41	5.04	5.38	3.81	up	1.36E-02	8.95E-01	UR	-
1387100_at	Aqp3	aquaporin 3	65133	Rn.11109	NM_031703	8.16	5.56	8.25	6.01	3.96	4.25	3.78	down	1.30E-01	8.95E-01	-	-
1370453_at	Tex101	testis expressed 101	207113	Rn.27161	AF347056	4.29	3.01	6.81	3.00	2.73	2.65	3.76	down	1.63E-01	8.95E-01	-	-
1382714_at	LOC313672	kazrin	313672	Rn.3753	AA875186	5.75	3.81	5.26	2.93	3.05	3.13	3.74	down	3.15E-02	8.95E-01	DR	-
1389365_at	LOC690000	similar to CG3740-PA	690000	Rn.2361	AI228291	8.75	7.40	8.49	6.54	6.53	5.89	3.72	down	1.53E-02	8.95E-01	DR	-
1386662_at	---	---	---	---	BF553981	2.80	2.43	2.77	4.72	5.05	3.89	3.69	up	6.55E-03	8.95E-01	UR	-
1375504_at	Polg2	polymerase (DNA directed), gamma 2, accessory subunit	303612	Rn.25075	BM390747	5.67	6.59	4.80	7.15	7.12	8.43	3.68	up	4.89E-02	8.95E-01	UR	-
1395879_at	Ttc39b	tetratricopeptide repeat domain 39B	298186	Rn.204942	BF412784	3.47	3.93	2.48	5.37	4.28	5.85	3.67	up	4.10E-02	8.95E-01	UR	-
1393822_at	Tmcc3	transmembrane and coiled-coil domain family 3	314751	Rn.19106	AA925789	4.75	4.66	8.86	5.23	3.00	4.45	3.64	down	2.90E-01	8.95E-01	-	-
1384436_at	LOC683001	similar to Transmembrane protein 16B	683001	---	BI294669	3.92	6.42	6.16	3.46	3.31	4.13	3.64	down	8.86E-02	8.95E-01	-	-
1372602_at	Sbd1	starch binding domain 1	305234	Rn.1935	BI295979	5.07	4.13	4.06	6.06	5.95	6.83	3.63	up	1.20E-02	8.95E-01	UR	-
1368508_at	Psma3 /// Psma3	proteasome (prosome, macropain) subunit, alpha type 3 /// proteasome subur	29670 /// 408248	Rn.3997	BI294912	5.31	5.62	6.03	7.57	6.67	6.58	3.58	up	6.11E-02	8.95E-01	-	-
1378600_at	Taf1d	TATA box binding protein (TBP)-associated factor, RNA polymerase I, D, 41kD	363017	Rn.137575	AI112986	4.87	5.21	3.24	6.37	6.56	5.92	3.58	up	4.44E-02	8.95E-01	UR	-
1371442_at	Hyou1	hypoxia up-regulated 1	192235	Rn.10542	BI282904	7.58	8.21	6.57	9.39	9.44	9.04	3.57	up	2.04E-02	8.95E-01	UR	-
1377717_at	LOC690008	hypothetical protein LOC690008	690008	Rn.196760	AI501409	2.56	4.25	6.00	2.58	2.24	2.50	3.56	down	1.40E-01	8.95E-01	-	-
1379287_at	Cyld	cylindromatosis (turban tumor syndrome)	312937	Rn.168938	BF391639	7.34	4.39	3.11	3.03	3.12	3.20	3.56	down	2.18E-01	8.95E-01	-	-
1368568_at	Aqp2	aquaporin 2 (collecting duct)	25386	Rn.90076	D13906	8.95	7.16	6.73	5.27	6.62	5.48	3.55	down	8.43E-02	8.95E-01	-	-
1373661_a_at	Cxcr4	chemokine (C-X-C motif) receptor 4	60628	Rn.44431	AA945737	6.34	4.33	2.81	2.64	2.79	2.57	3.55	down	1.49E-01	8.95E-01	-	-
1384219_at	---	---	---	Rn.32015	BF522747	4.84	4.43	6.42	3.13	3.55	3.53	3.54	down	4.28E-02	8.95E-01	DR	-
1389631_at	Znf609	Zinc finger protein 609	363412	Rn.161077	AA943109	5.59	5.47	2.69	2.78	2.67	2.84	3.53	down	1.28E-01	8.95E-01	-	-
1378755_at	LOC680656	hypothetical protein LOC680656	680656	---	AW523689	5.60	7.79	3.80	6.86	7.96	7.83	3.52	up	2.06E-01	8.95E-01	-	-
1387040_at	Mal	mal, T-cell differentiation protein	25263	Rn.10174	NM_012798	7.00	4.68	4.45	3.51	4.58	2.59	3.52	down	1.43E-01	8.95E-01	-	-
1369660_at	Delb1	deltamin beta 1	83687	Rn.31800	AF068860	8.02	5.77	6.53	6.11	5.54	3.23	3.52	down	1.75E-01	8.95E-01	-	-
1370310_at	Hmgcs2	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 2 (mitochondrial)	24450	Rn.29594	M33648	5.36	3.70	4.51	3.07	2.59	2.48	3.50	down	2.41E-02	8.95E-01	DR	-
1372653_at	Fkbp11	FK506 binding protein 11	300211	Rn.100569	BI276210	2.61	2.61	2.54	3.94	4.45	4.79	3.50	up	1.89E-03	8.95E-01	UR	-
1382274_at	Rarres1	retinoic acid receptor responder (tazarotene induced) 1	310486	Rn.16737	AA819288	5.26	7.50	6.41	4.61	4.43	4.72	3.49	down	5.07E-02	8.95E-01	-	-
1389244_x_at	Cxcr4	chemokine (C-X-C motif) receptor 4	60628	Rn.44431	AA945737	7.20	3.21	2.51	2.50	2.51	2.50	3.49	down	2.85E-01	8.95E-01	-	-
1370204_at	Frag1	FGF receptor activating protein 1	116675	Rn.94200	BG373817	7.66	4.51	7.35	3.99	4.70	5.44	3.47	down	1.73E-01	8.95E-01	-	-
1382467_at	Bex1 /// Bex2	brain expressed gene 1 /// brain expressed X-linked 2	363498 /// 501625	Rn.9150	C07140	3.26	3.96	3.20	3.94	6.11	5.75	3.47	up	6.59E-02	8.95E-01	-	-
1387077_at	---	---	---	Rn.208153	BE111570	3.21	4.08	2.90	5.88	5.75	3.92	3.46	up	6.88E-02	8.95E-01	-	-
1396211_at	---	---	---	Rn.169091	BE100009	2.66	2.83	2.71	4.80	5.37	3.39	3.45	up	3.91E-02	8.95E-01	UR	-
1388968_at	Mpped1	metallophosphoesterase domain containing 1	362971	Rn.19156	BF402842	5.57	5.99	7.17	4.40	5.17	3.79	3.45	down	4.61E-02	8.95E-01	DR	-
1388691_at	Fbxo36	F-box protein 36	363268	Rn.218093	BF565191	6.85	5.42	5.17	3.34	3.94	4.81	3.44	down	5.72E-02	8.95E-01	-	-
1377388_at	---	---	---	Rn.172726	BF394830	2.48	4.23	6.17	2.56	2.52	2.45	3.44	down	1.70E-01	8.95E-01	-	-
1375790_at	---	---	---	Rn.205603	BI300458	7.15	2.86	2.35	2.34	2.34	2.33	3.43	down	3.07E-01	8.95E-01	-	-
1391856_at	Sema3g	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (se	290562	Rn.32183	BE108859	7.05	2.65	3.76	2.72	3.17	2.23	3.43	down	2.58E-01	8.95E-01	-	-
1387007_at	Gfra1	GDNF family receptor alpha 1	25454	Rn.88489	NM_012959	4.07	4.52	5.48	2.72	2.95	3.07	3.43	down	1.40E-02	8.95E-01	DR	-
1371012_at	Hacl1	2-hydroxyacyl-CoA lyase 1	85255	Rn.219233	AJ245707	8.25	7.38	9.09	6.30	6.95	6.14	3.42	down	3.22E-02	8.95E-01	DR	-
1381616_at	---	---	---	Rn.199327	AI072140	4.37	6.19	7.07	4.10	3.21	5.00	3.42	down	1.35E-01	8.95E-01	-	-
1391611_at	Bhlhb9	basic helix-loop-helix domain containing, class B, 9	317407	Rn.154656	AI137509	2.74	2.86	2.82	5.42	4.20	4.12	3.41	up	1.37E-02	8.95E-01	UR	-
1391253_at	---	---	---	Rn.38294	BI294271	2.45	2.40	2.45	2.58	7.52	2.49	3.40	up	3.47E-01	8.95E-01	-	-
1395986_at	Slit2	slit homolog 2 (Drosophila)	360272	Rn.146652	BF391439	6.50	6.33	7.13	5.49	3.59	5.58	3.40	down	6.35E-02	8.95E-01	-	-
1385965_at	Ankhd1-Eif4ebp3	Ankhd1-Eif4ebp3 fusion transcript	679725	Rn.11853	BI293870	6.13	7.40	6.38	5.95	3.78	4.89	3.38	down	7.53E-02	8.95E-01	-	-
1391458_at	Ndrg1	N-myc downstream regulated gene 1	299923	Rn.153992	BE120446	8.79	8.68	9.16	7.05	7.14	7.16	3.38	down	2.82E-04	8.95E-01	DR	-
1396914_at	---	---	---	---	BF545104	2.33	3.44	3.48	5.82	5.45	3.26	3.38	up	1.18E-01	8.95E-01	-	-
1391439_at	---	---	---	---	BI278193	4.01	3.60	7.67	3.50	3.05	3.49	3.36	down	2.52E-01	8.95E-01	-	-
1372229_at	Pdk3	pyruvate dehydrogenase kinase, isozyme 3	296849	Rn.18101	AI171519	5.88	6.15	6.39	4.94	3.02	5.26	3.33	down	7.24E-02	8.95E-01	-	-
1389511_s_at	---	---	---	---	BF403383	4.80	7.35	7.82	8.25	9.00	7.90	3.32	up	1.56E-01	8.95E-01	-	-
1397294_at	---	---	---	Rn.206712	AW529486	7.60	4.01	4.03	4.02	2.65	3.79	3.31	down	2.44E-01	8.95E-01	-	-
1391307_at	Zfp259	zinc finger protein 259	500989	Rn.102011	AW251406	2.94	3.44	3.06	6.73	3.54	4.34	3.31	up	1.50E-01	8.95E-01	-	-
1370694_at	Trib3	tribbles homolog 3 (Drosophila)	246273	Rn.22325	AB020967	3.17	2.43	3.26	4.76	4.44	4.83	3.30	up	3.83E-03	8.95E-01	UR	-
1371762_at	Rbp4	retinol binding protein 4, plasma	25703	Rn.108214	AA858962	7.81	8.96	5.76	9.18	8.46	10.04	3.28	up	1.75E-01	8.95E-01	-	-
1399144_at	Srp72	signal recognition particle 72	498351	Rn.2930	BG670236	6.36	5.12	6.25	8.06	7.42	7.39	3.28	up	1.96E-02	8.95E-01	UR	-
1394805_at	Mll2	myeloid/lymphoid or mixed-lineage leukemia 2	362996	---	AI177041	5.49	2.27	5.77	3.55	2.21	2.64	3.28	down	2.24E-01	8.95E-01	-	-
1369407_at	Tnfrsf11b	tumor necrosis factor receptor superfamily, member 11b	25341	Rn.202973	NM_012870	5.76	8.22	7.48	5.06	5.34	5.93	3.27	down	9.11E-02	8.95E-01	-	-
1371560_at	Ifi3	interferon regulatory factor 3	292892	Rn.1499	AA893384	6.71	8.08	5.98	9.41	8.67	7.78	3.25	up	9.43E-02	8.95E-01	-	-
1385556_at	RGD1308616	similar to KIAA0467 protein	362573	Rn.143183	AW521143	6.41	5.33	3.69	3.68	2.91	3.76	3.23	down	1.13E-01	8.95E-01	-	-
1369590_a_at	Ddit3	DNA-damage inducible transcript 3	29467	Rn.11183	NM_024134	8.26	6.42	3.91	8.10	7.14	8.41	3.23	up	2.68E-01	8.95E-01	-	-
1394117_at	---	---	---	Rn.154614	AA799317	4.61	4.17	3.31	6.36	5.85	4.94	3.22	up	4.02E-02	8.95E-01	UR	-
1378757_at	RGD1310257	similar to RIKEN cDNA 6330408A02 gene	308381	Rn.207230	BG375931	3.54	5.55	4.19	5.77	7.12	5.45	3.21	up	9.85E-02	8.95E-01	-	-
1370000_at	Nucb2	nucleobindin 2	59295	Rn.41602	NM_021663	5.76	7.35	6.96	7.88	8.01	9.21	3.21	up	5.82E-02	8.95E-01	-	-
1385865_at	Wdr51a	WD repeat domain 51A	501048	Rn.24652	BM390351	2.72	2.76	2.94	5.89	4.18	3.39	3.20	up	8.62E-02	8.95E-01	-	-
1379284_at	Ubash3b	ubiquitin associated and SH3 domain containing, B	315579	Rn.11924	AI411760	5.63	7.57	6.19	7.96	7.99	8.46	3.20	up	4.88E-02	8.95E-01	UR	-
1373368_at	PCOLCE2	procollagen C-endopeptidase enhancer 2	684050	Rn.216411	BI276680	3.43	2.95	3.48	4.50	5.11	5.27	3.19	up	4.53E-03	8.95E-01	UR	-
1389676_at	Ccdc101	coiled-coil domain containing 101	293488	Rn.34983	BI294925	3.42	5.41	3.57	5.93	5.39	6.10	3.18	up	6.85E-02	8.95E-01	-	-
1396803_at	Thoc2	THO complex 2	313308	Rn.35526	BE117119	5.58	5.86	5.89	4.38	2.77	5.18	3.18	down	7.99E-02	8.95E-01	-	-
1368834_at	Camk2d	calcium/calmodulin-dependent protein kinase II delta	24246	Rn.87208	AA894330	3.48	3.60	2

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1374049_at	Myl6b	myosin, light chain 6B, alkali, smooth muscle and non-muscle	685883	---	AI230220	4.32	5.11	4.33	5.14	7.34	5.94	2.93	up	8.95E-02	8.95E-01	-	-
1377029_at	Rora	RAR-related orphan receptor alpha	300807	An.43530	AI235414	5.43	6.62	5.22	7.35	6.98	7.59	2.93	up	3.04E-02	8.95E-01	UR	-
1379443_at	Hpx3	Hemansky-Pudlak syndrome 3 homolog (human)	310288	Rn.159782	BE120719	4.41	6.12	5.07	6.75	6.61	6.89	2.93	up	3.76E-02	8.95E-01	UR	-
1379411_at	RGD1563825	similar to ENSANGP00000020885	306366	Rn.132418	AI180253	7.51	8.63	10.57	7.12	6.93	8.02	2.92	down	1.81E-01	8.95E-01	-	-
1374292_at	RGD1305007	similar to RIKEN cDNA 1110031I02	303749	Rn.101104	BF414124	4.72	4.23	3.29	5.54	4.68	6.65	2.92	up	9.49E-02	8.95E-01	-	-
1377526_at	Snx27	sorting nexin family member 27	260323	Rn.7581	BE113239	4.58	6.48	4.85	7.20	6.83	6.51	2.91	up	6.89E-02	8.95E-01	-	-
1397950_at	Smg7	Smg-7 homolog, nonsense mediated mRNA decay factor (C. elegans)	360855	Rn.60213	H34608	2.32	2.35	2.49	2.32	7.13	2.34	2.91	up	3.91E-01	8.95E-01	-	-
1391570_at	Ablim3	actin binding LIM protein family, member 3	307395	An.39037	AI105070	5.24	4.80	3.32	6.02	5.83	6.12	2.90	up	5.90E-02	8.95E-01	-	-
1380850_at	---	---	---	An.26628	AI111767	3.95	3.67	5.36	2.80	2.83	2.75	2.89	down	4.33E-02	8.95E-01	DR	-
1391921_at	Rngtt	RNA guanylyltransferase and 5'-phosphatase	313131	Rn.8497	AW530941	3.46	3.48	7.17	3.47	3.46	2.59	2.89	down	2.94E-01	8.95E-01	-	-
1395620_at	Fam133b	family with sequence similarity 133, member B	362320	Rn.162728	AI710510	3.36	3.55	2.91	4.40	5.02	4.99	2.88	up	5.31E-03	8.95E-01	UR	-
1378993_at	---	---	---	---	BF386397	4.50	2.53	5.19	2.56	2.56	2.53	2.88	down	1.28E-01	8.95E-01	-	-
1387028_a_at	Id1	inhibitor of DNA binding 1	25261	Rn.2113	M86708	3.54	5.57	5.29	2.48	4.27	3.08	2.88	down	1.39E-01	8.95E-01	-	-
1395357_at	Map1b	microtubule-associated protein 1B	29456	Rn.98152	BG672052	2.51	2.40	2.47	4.67	3.01	4.27	2.88	up	3.83E-02	8.95E-01	UR	-
1369244_at	Arnt	aryl hydrocarbon receptor nuclear translocator	25242	Rn.10520	NM_012780	3.73	3.89	3.14	5.23	5.04	5.06	2.87	up	2.98E-03	8.95E-01	UR	-
1378328_at	---	---	---	An.28012	AI169255	3.91	5.18	2.26	2.26	2.26	2.25	2.87	down	1.46E-01	8.95E-01	-	-
1372012_at	Dhcr24	24-dehydrocholesterol reductase	298298	Rn.9470	BF417479	4.99	5.71	6.28	4.60	4.09	3.73	2.87	down	2.79E-02	8.95E-01	DR	-
1375643_at	Ckap4	cytoskeleton-associated protein 4	362859	Rn.99508	BM384259	7.37	5.74	7.42	8.63	8.28	8.17	2.86	up	5.64E-02	8.95E-01	-	-
1369431_at	Galnt7	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltran	29750	Rn.207200	NM_022926	6.70	6.62	3.50	6.16	7.67	7.54	2.86	up	2.61E-01	8.95E-01	-	-
1395582_at	---	---	---	An.166318	BF398623	7.70	5.98	5.56	6.22	3.47	5.00	2.86	down	2.15E-01	8.95E-01	-	-
1382783_at	Blm	Bloom syndrome homolog (human)	308755	Rn.211198	BF406187	4.56	2.75	5.63	3.17	2.49	2.72	2.86	down	1.54E-01	8.95E-01	-	-
1385512_at	Atg4d	ATG4 autophagy related 4 homolog D (S. cerevisiae)	686505	Rn.202643	AW526908	6.80	5.48	4.76	4.29	3.53	4.69	2.85	down	9.30E-02	8.95E-01	-	-
1386031_at	Prkd3	Protein kinase D3	313834	Rn.3990	BF288135	5.91	5.06	4.62	7.22	7.70	5.20	2.85	up	1.52E-01	8.95E-01	-	-
1388742_at	---	---	---	Rn.7933	AA945877	3.12	2.51	2.57	4.21	4.27	4.23	2.85	up	1.50E-03	8.95E-01	UR	-
1376292_at	---	---	---	Rn.18142	BM383423	2.34	4.19	2.54	4.01	4.03	5.56	2.84	up	1.25E-01	8.95E-01	-	-
1368288_at	Gc	group specific component	24384	Rn.1437	AA944965	7.11	7.45	7.13	5.30	6.14	5.74	2.84	down	4.80E-03	8.95E-01	DR	-
1388946_at	RGD1311910	similar to hypothetical p38 protein	307235	Rn.105128	AI233763	7.88	7.01	8.27	6.71	4.95	6.97	2.84	down	1.10E-01	8.95E-01	-	-
1382122_at	Etv5	Ets variant 5	303828	Rn.18397	BE113124	6.88	6.36	6.50	3.66	5.55	6.01	2.84	down	1.11E-01	8.95E-01	-	-
1389571_at	Stat2	signal transducer and activator of transcription 2	288774	Rn.24237	BG666368	4.10	4.88	6.22	3.33	4.06	3.29	2.84	down	8.77E-02	8.95E-01	-	-
1370349_a_at	OC680367 /// Rup	similar to Urinary protein 3 precursor (RUP-3) /// urinary protein 2	619560 /// 680367	Rn.162992	AF368860	2.45	2.45	2.96	2.45	2.47	2.44	2.83	down	3.74E-01	8.95E-01	-	-
1384750_at	Numb	numb homolog (Drosophila)	29419	Rn.102078	BF403834	3.57	5.01	5.66	3.06	3.06	3.61	2.83	down	8.06E-02	8.95E-01	-	-
1381080_at	---	---	---	Rn.169378	AI169081	7.17	5.03	6.18	5.13	5.19	3.56	2.83	down	1.40E-01	8.95E-01	-	-
1398395_at	Itgb1bp1	integrin beta 1 binding protein 1	298914	Rn.29469	AW434272	4.78	5.10	4.23	6.71	5.41	6.49	2.83	up	3.37E-02	8.95E-01	UR	-
1382349_at	Tbccd1	TBCC domain containing 1	303830	Rn.23183	AI408238	2.80	2.82	2.80	2.82	5.24	4.84	2.82	up	1.16E-01	8.95E-01	-	-
1398206_at	---	---	---	Rn.208041	BE109223	3.65	3.48	6.61	2.75	3.36	3.15	2.82	down	2.21E-01	8.95E-01	-	-
1376275_at	---	---	---	Rn.32291	BE101108	7.03	3.21	2.96	2.52	3.02	3.18	2.82	down	3.25E-01	8.95E-01	-	-
1389177_at	Perp	PERP, TP53 apoptosis effector	292949	Rn.101762	AI568971	5.40	6.76	5.70	7.07	7.88	7.38	2.81	up	3.51E-02	8.95E-01	UR	-
1385231_at	---	---	---	---	AI044528	6.58	2.95	2.58	2.56	2.55	2.53	2.81	down	3.07E-01	8.95E-01	-	-
1379402_at	Abcc4	ATP-binding cassette, sub-family C (CFTR/MRP), member 4	170924	An.13195	BE100533	3.85	4.79	4.55	5.54	5.93	6.19	2.80	up	1.17E-02	8.95E-01	UR	-
1383423_at	---	---	---	Rn.6470	BI295136	3.20	4.06	2.46	3.69	5.61	4.88	2.80	up	1.10E-01	8.95E-01	-	-
1374969_at	Pgm5	phosphoglucomutase 5	679990	Rn.108629	AA799832	5.99	7.46	4.01	7.07	7.00	7.84	2.80	up	2.25E-01	8.95E-01	-	-
1393559_at	---	---	---	Rn.205013	AI235210	4.27	3.83	4.97	2.71	3.05	2.86	2.80	down	1.26E-02	8.95E-01	DR	-
1386479_at	---	---	---	Rn.204289	AI071163	2.42	4.32	2.57	3.48	6.33	3.95	2.80	up	2.39E-01	8.95E-01	-	-
1369445_at	Mre11a	MRE11 meiotic recombination 11 homolog A (S. cerevisiae)	64046	Rn.209040	NM_022279	2.81	4.08	5.58	2.41	2.83	2.80	2.79	down	1.42E-01	8.95E-01	-	-
1375170_at	S100a11	S100 calcium binding protein A11 (calizzarin)	445415	Rn.104930	BG378926	5.63	5.82	6.24	7.39	7.27	7.46	2.79	up	1.37E-03	8.95E-01	UR	-
1367960_at	Arl4a	ADP-ribosylation factor-like 4A	29308	Rn.9258	NM_019186	6.58	6.05	3.82	6.81	7.14	6.93	2.78	up	1.57E-01	8.95E-01	-	-
1390110_at	Uckl1	uridine-cytidine kinase 1-like 1	499956	Rn.35240	BG372998	3.96	4.60	2.27	4.98	6.03	4.26	2.78	up	1.63E-01	8.95E-01	-	-
1389061_at	Nsun5	NOL1/NOP2/Sun domain family, member 5	288595	Rn.220169	AI171164	4.57	3.11	4.58	4.69	5.61	4.78	2.78	up	8.33E-02	8.95E-01	-	-
1388715_at	Gars	glycyl-tRNA synthetase	297113	Rn.3338	AA818089	5.52	6.96	6.71	7.58	7.66	8.38	2.78	up	4.53E-02	8.95E-01	UR	-
1374190_at	Clybl	citrate lyase beta like	306198	Rn.137340	BG380750	5.48	6.20	5.91	7.80	7.09	7.12	2.78	up	9.28E-03	8.95E-01	UR	-
1377431_at	RGD1307648	similar to CG13901-PA	294004	Rn.50057	BE106000	4.54	6.60	4.65	2.96	4.21	4.21	2.77	down	1.35E-01	8.95E-01	-	-
1390767_at	Sar1	signal sequence receptor, alpha	361233	Rn.123918	BF391148	5.63	6.28	5.85	7.72	6.55	7.90	2.77	up	3.36E-02	8.95E-01	UR	-
1372950_at	Bet1l	blocked early in transport 1 homolog (S. cerevisiae) like	54400	An.90025	AI600006	4.56	4.75	4.59	6.17	6.53	5.60	2.77	up	6.15E-03	8.95E-01	UR	-
1398456_a_at	---	---	---	Rn.29073	BF389045	2.77	2.89	2.84	4.66	5.61	2.62	2.76	up	1.72E-01	8.95E-01	-	-
1380623_at	Taz	tafazzin	363521	Rn.7267	BM389775	4.60	3.55	5.07	3.35	2.39	3.09	2.76	down	5.06E-02	8.95E-01	-	-
1380961_at	---	---	---	Rn.169523	AW526232	4.73	4.15	3.99	6.32	5.75	5.19	2.76	up	2.12E-02	8.95E-01	UR	-
1386669_at	LOC679127	similar to Protein KIAA0690	679127	---	BF565188	4.50	3.50	3.79	5.23	5.96	4.98	2.75	up	2.53E-02	8.95E-01	UR	-
1386934_at	Slc6a8	solute carrier family 6 (neurotransmitter transporter, creatine), member 8	50690	Rn.10336	NM_017348	6.52	7.23	7.30	8.40	8.28	8.75	2.75	up	6.87E-03	8.95E-01	UR	-
1377188_at	---	---	---	Rn.147846	BI296291	3.80	4.39	4.35	6.01	5.91	5.01	2.75	up	1.70E-02	8.95E-01	UR	-
1373220_at	---	---	---	Rn.219230	BI296489	2.94	4.42	3.56	4.49	5.60	5.19	2.74	up	5.33E-02	8.95E-01	-	-
1375530_at	Gnpnat1	glucosamine-phosphate N-acetyltransferase 1	498486	Rn.14702	BG374612	6.67	6.86	6.02	8.07	8.03	7.81	2.74	up	5.47E-03	8.95E-01	UR	-
1388547_at	Cldn4	claudin 4	304407	Rn.6830	BE328951	5.04	3.69	3.36	6.78	4.64	5.02	2.73	up	1.58E-01	8.95E-01	-	-
1378224_at	---	---	---	Rn.147029	BE105981	2.37	2.72	2.57	5.58	2.38	4.05	2.73	up	1.94E-01	8.95E-01	-	-
1379724_at	Phldb2	pleckstrin homology-like domain, family B, member 2	685611	Rn.201706	BE103244	5.59	6.19	6.32	4.38	4.13	5.25	2.73	down	2.34E-02	8.95E-01	DR	-
1371424_at	Jmjd5	jumonji domain containing 5	308976	Rn.22093	BG378621	6.51	5.63	6.34	3.54	3.57	5.04	2.72	down	9.10E-02	8.95E-01	-	-
1379239_at	Uimc1	Ubiquitin interaction motif containing 1	290997	Rn.103261	AI705987	4.22	3.73	3.06	6.18	5.03	4.12	2.72	up	1.03E-01	8.95E-01	-	-
1381264_at	---	---	---	Rn.160196	BE099664	4.07	3.65	4.99	2.84	3.00	2.55	2.71	down	2.63E-02	8.95E-01	DR	-
1378133_at	Slc7a11	solute carrier family 7 (cationic amino acid transporter, y+ system), member 1	310392	Rn.28160	AW532618	2.61	2.60	2.66	2.64	4.32	5.22	2.71	up	1.30E-01	8.95E-01	-	-
1383401_at	Tes	testis derived transcript	500040	Rn.44841	BI288769	2.38	2.47	2.31	3.11	3.87	4.49	2.71	up	2.31E-02	8.95E-01	UR	-
1367866_at	Fbln5	fibulin 5	29158	Rn.1699	NM_019153	6.82	5.82	6.86	4.91	5.78	4.50	2.71	down	4.77E-02	8.95E-01	DR	-
1378690_at	Ly6al	lymphocyte antigen 6 complex, locus A-like	362935	Rn.203167	BI291986	4.36	6.26	6.55	5.97	2.20	4.69	2.70	down	3.32E-01	8.95E-01	-	-
1397546_at	Spata2	spermatogenesis associated, serine-rich 2	300221	Rn.52841	BF567095	7.45	5.57	6.92	5.56	4.88	5.20	2.70	down	7.35E-02	8.95E-01	-	-
1393639_at	Myo10	myosin X	310178	Rn.20775	AI044576	5.90	5.67	7.24	3.26	5.57	5.68	2.70	down	1.97E-01	8.95E-01	-	-
1373495_at	Ube2j1	ubiquitin-conjugating enzyme E2, J1	297961	Rn.18843	AW915822	3.71	4.95	2.41	4.58	5.92	4.87	2.70	up	1.62E-01	8.95E-01	-	-
1367881_at	Sirpa	signal-regulatory protein alpha	25528	Rn.53971	NM_013016	2.53	3.51	4.65	5.04	3.76	6.19	2.70	up	1.99E-01	8.95E-01	-	-
1398983_at	Mrpl30	mitochondrial ribosomal protein L30	301352	Rn.7068	AW435012	7.03	7.75	5.59	8.07	8.54	8.06	2.70	up	9.37E-02	8.95E-01	-	-
1376185_at	Klfc1	kinesin family member C1	294286	Rn.38181	AW253880	6.84	6.73	6.60	4.78	5.35	5.76	2.70	down	8.02E-03	8.95E-01	DR	-
1382615_at	Sec61a1	Sec61 alpha 1 subunit (S. cerevisiae)	80843	An.47029	BI284366	3.45	4.07	4.74	5.88	4.75	5.92	2.70	up	5.56E-02	8.95E-01	-	-
1388665_at	D130today /// Rna	similar to RIKEN cDNA 1110020A23 /// ribonuclease, RNase K	287452 /// 287453	Rn.1025	BM390489	5.44	4.20	4.94	3.00	3.76	3.52	2.70	down	2.81E-02	8.95E-01	DR	-
1382593_at	Etv1	ets variant 1	362733	Rn.76536	AA963276	5.15	4.00	5.68	3.73	3.13	3.67	2.70	down	5.42E-02	8.95E-01	-	-
1382556_a_at	RGD1309388	similar to DIP13 alpha	290537	An.34413	AI412140	5.84	7.55	4.89	7.42	7.87	7.28	2.69	up	1.48E-01	8.95E-01	-	-
1368016_at	Pecr	peroxisomal trans-2-enoyl-CoA reductase	113956	Rn.163081	NM_133299	10.12	9.54	10.59	8.66	8.68	8.64	2.69	down	9.57E-03	8.95E-01	DR	-
1395632_at	---	---	---	---	AI715532	5.20	5.10	3.35	5.60	6.03	6.30	2.69	up	8.86E-02	8.95E-01	-	-
1389995_at	Srrm1	serine/arginine repetitive matrix 1	313620	Rn.39266	BF546042	5.68	4.77	3.80	3.25	3.30	3.43	2.68	down	6.05E-02	8.95E-01	-	-
1383385_at	---	---	---	Rn.22852	AI136674	5.63	5.71	3.99	5.35	7.24	7.01	2.68	up	1.57E-01	8.95E-01	-	-
1379341_at	Usp6nl	USP6 N-terminal like	291309	Rn.56101	BG376132	2.91	3.99	4.74	5.47	5.20	5.23	2.68	up	5.73E-02	8.95E-01	-	-
1382217_at	---	---	---	Rn.91997	AI009517	4.49	4.35	3.46	5.77	4.38	6.41	2.67	up	1.06E-01	8.95E-01	-	-
1391533_at	Slc5a12	solute carrier family 5 (sodium/glucose cotransporter), member 12	362188	Rn.14711	AI058978	2.68	2.47	2.66	4.43	3.97	3.66	2.67	up	3.84E-03	8.95E-01	UR	-
1378359_at	Nkrf	NFKB repressing factor	298316	Rn.198468	AI072632	5.93	4.47	5.44	2.49	4.75	4.34	2.67	down	1.58E-01	8.95E-01	-	-
1379997_at	---	---	---	Rn.172995	BF398462	6.55	2.50	2.50	2.43	2.44	2.45	2.66	down	3.55E-01	8.95E-01	-	-
1367682_at	Mdk	midkine	81517	Rn.17447	NM_030859	4.31	2.94	3.49	4.84	6.37	3.75	2.66	up	1.75E-01	8.95E-01	-	-
1375587_at	Adss	Adenylosuccinate synthase	298276	Rn.9047	AI412674	8.30	6.27	5.11	4.77	4.59	6.10	2.65	down	2.50E-01	8.95E-01	-	-
1391356_at	Iws1	IWS1 homolog (S. cerevisiae)	291705	Rn.206133	BI282688	2.59	5.14	3.40	6.66	4.56	4.12	2.65	up	2.65E-01	8.95E-01	-	-
1390781_at	Abcb10	ATP-binding cassette, sub-family B (MDR/TAP), member 10	361439	Rn.22937	AA900411	5.80	6.80	7.94	4.97	5.11	6.25	2.65	down	1.30E-01	8.95E-01	-	-
1392601_at	---	---	---	Rn.165898	AI030043	7.68	5.31	8.24	5.47	7.07	4.48	2.64	down	2.98E-01	8.95E-01	-	-
1389636_at	362665 /// LOC50	similar to KIAA0833 protein /// similar to calmodulin-binding transcription activ	362665 /// 500591	Rn.22493	AI231088	7.16	5.25	5.32	4.43	4.54	4.55	2.64	down	8.93E-02	8.95E-01	-	-
1384131_at	Arl6ip2	ADP-ribosylation factor-like 6 interacting protein 2	298757	Rn.203081	AW914046	5.73	7.04	5.71	7.02	8.33	7.33	2.64	up	7.75E-02	8.95E-01	-	-
1383251_at	Parp2	poly (ADP-ribose) polymerase 2	290027	An.22730	AW524533	5.83	4.08	5.97	4.29	2.72	4.67	2.64	down	1.76E-01	8.95E-01	-	-
1372510_at	Snx1	sulfredoxin 1 homolog (S. cerevisiae)	299271	Rn.2835	AI172302	2.75	3.83	3.42	4.89	3.85	5.46	2.64	up	6.91E-02	8.95E-01	-	-
1373749_at	Srlta1	syntrophin, acidic 1	362242	Rn.139656	BF395599	5.41	5.87	8.01	4.67	5.07	5.37	2.63	down	1.68E-01	8.95E-01	-	-
1370144_at	LOC689842 /// RG	GTP binding protein 4 /// similar to Nucleolar GTP-binding protein 1 (Chronic	00 /// 291269 /// 68	Rn.199031	NM_053689	8.01	9.68	8.46	7.13	7.72	7.12	2.63	down	6.00E-02	8.95E-01	-	-
1379281_at	Sostdc1	sclerostin domain containing 1	266803	Rn.2415	AA892798	8.24	6.06	4.96	6.59	5.21	3.28	2.63	down	3.63E-01	8.95E-01	-	-
1377981_at	Ccdc109a	Coiled-coil domain containing 109A	294560	Rn.44172	AI408685	3.24	5.29	3.37	5.68	5.12	5.29	2.63	up	1.10E-01	8.95E-01	-	-
1368164_at	Blvra	biliverdin reductase A	116599	Rn.9865	NM_053850	10.20	10.33	9.81	8.67	8.28	9.22	2.63	down	1.14E-02	8.95E-01	DR	-
1378999_a_at	Usp49	ubiquitin specific peptidase 49	316211	Rn.147913	AW252553	6.67	2.59	2.69	2.60	2.66	2.52	2.62	down	3.60E-01	8.95E-01	-	-
1394251_x_at	Irx3	iroquois homeobox 3	307721	Rn.22133	AI719965	3.98	4.63	3.92	3.94	3.73	2.71	2.62	down	1.12E-01	8.95E-01	-	-
1382489_at	RGD1564964	similar to WD repeat domain 11 protein	315843	Rn.23174	BE116698	6.64	7.14	7.64	5.65	4.98	6.63	2.62	down	6.79E-02	8.95E-01	-	-
1383806_at	Smarce1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin,	303518	Rn.8513	BF556825	7.26	6.75	6.87	6.33	3.58	6.79	2.62	down	2.43E-01	8.95E-01	-	-
1382484_at	---	---	---	Rn.94369	AI408899	4.31	2.87	5.72	2.81	3.04	2.89	2.61	down	1.69E-01	8.95E-01	-	-
1374833_at	---	---	---	Rn.15513	AA944485	6.51	6.41	7.02	5.41	5.58	4.79	2.61	down	1.05E-02	8.95E-01	DR	-
1376698_at	---	---	---	Rn.25396	BF418869	5.87	6.23	7.81	5.21	5.07	5.49	2.61	down	8.55E-02	8.95E-01	-	-
1370898_at	Snn	stannin	29140	Rn.6147	BF288101	7.08	7.27	6.21	4.58	6.26	5.59	2.60	down	7.84E-02	8.95E-01	-	-
1368597_at	Snf1lk	SNF1-like kinase	99329	Rn.42905	AB020480	2.81	3.82	2.95	4.66	5.04	4.02	2.60	up	3.34E-02	8.95E-01	UR	-
1389522_at	Plekha6	pleckstrin homology domain containing, family A member 6	360842	Rn.21422	BE109446	4.98	6.14	3.08	6.40	6.47	5.45	2.60	up	2.21E-01	8.95E-01	-	-
1380430_at	---	---	---	Rn.204854	BI386177	2.57	2.60	2.51	4.82	2.55	4.45	2.59	up	1.22E-01	8.95E-01	-	-
1392758_at	Tra2a	transformer-2 alpha	500116	Rn.220184	AA943056	4.32	4.62	4.21	3.18	2.57	3.28	2.59	down	5.62E-03	8.95E-01	DR	-
1395948_at	---	---	---	Rn.43688	AI410644	3.06	3.05	3.03	3.05	4.25	5.95	2.59	up	1.79E-01	8.95E-01	-	-
1382004_at	---	---	---	Rn.21256	AI175827	2.79	3.59	2.61	4.87	4.60	3.63	2.59	up	4.67E-02	8.95E-01	UR	-
1395638_at	Cpsf7	cleavage and polyadenylation specific factor 7, 59kDa	365407	Rn.98627	BF558937	8.18	6.26	6.28	5.84	5.51	5.26	2.58	down	1.06E-01	8.95E-01	-	-
1370752_a_at	Tp53	tumor protein p53	24842	Rn.54443	AY009504	8.09	6.28	7.46	5.75	5.34	6.63	2.58	down	1.04E-01	8.95E-01	-	-
1384677_at	RGD1561963	similar to Dedicator of cytokinesis protein 10 (Protein zizimin 3)	301556	---	AI236595	7.13	3.28	2.70	2.94	3.18	2.90	2.58	down	3.82E-01	8.95E-01	-	-
1371905_at	MGC94190	similar to 0610007L01Rik protein	288616	Rn.99691	BM384949	7.59	8.17	8.41	10.35	8.68	9.24	2.58	up	6.76E-02	8.95E-01	-	-
1396202_at	---	---	---	Rn.32525	BF401339	4.66	4.09	6.83	3.45	3.27	4.77	2.58	down	2.28E-01	8.95E-01	-	-
1385101_a_at	Ccdc127	coiled-coil domain containing 127	308060	Rn.21696	AI712625	7.29	6.48	6.99	6.38	4.81	5.49	2.57	down	5.66E-02	8.95E-01	-	-
1374169_at	RGD1310686	similar to chromosome 16 open reading frame 5	360480	Rn.101805	AI236128	3.03	4.49	5.96	2.81	2.51	4.07	2.57	down	2.35E-01	8.95E-01	-	-
1389345_at	---	---	---	Rn.203739	AI231218	3.82	4.13	6.98	3.80	2.96	4.10	2.57	down	2.70E-01	8.95E-01	-	-
1371902_at	---	---	---	---	AI227832	7.23	3.59	3.06	3.44	3.10	3.27	2.56	down	3.60E-01	8.95E-01	-	-
1371969_at	---	---	---	Rn.87384	BI291848	4.79	5.15	5.72	5.73	6.69	7.31	2.55	up	6.39E-02	8.95E-01	-	-
1387358_at	Arl1	ADP-ribosylation factor-like 1	64187	Rn.3065	NM_022385	6.65	7.29	5.65	7.92	7.30	8.42	2.55	up	7.92E-02	8.95E-01	-	-
1376423_at	Fbxl19	F-box and leucine-rich repeat protein 19	308999	Rn.50190	BG381739	3.34	3.99	2.33	4.76	4.89	4.07	2.55	up	6.89E-02	8.95E-01	-	-
1376272_s_at	---	---	---	---	AI178914	4.06	4.88	3.55	5.80	4.51	6.23	2.55	up	1.04E-01	8.95E-01	-	-
1375441_at	Sars	seryl-tRNA synthetase	266975	Rn.73067	BI278468	7.60	7.63	7.43	8.91	8.52	9.28	2.55	up	4.13E-03	8.95E-01	UR	-
1393243_at	rCG_20380	hypothetical protein LOC100125367	100125367	Rn.159977	BG372316	4.67	4.78	3.42	5.49	5.79	5.62	2.54	up	3.88E-02	8.95E-01	UR	-
1384511_at	Dnajb5	Dnaj (Hsp40) homolog, subfamily B, member 5	313811	Rn.92865	BF556851	5.30	4.03	3.89	3.29	2.80	3.10	2.54	down	4.62E-02	8.95E-01	DR	-
1377891_at	LOC685079	similar to Protein SYS1 homolog	685079	An.31818	AI407265	7.20	7.25	3.92	7.23	7.95	7.22	2.54	up	2.99E-01	8.95E-01	-	-
1377986_at	Scoc	short coiled-coil protein	364981	Rn.18315	AI029749	8.41	8.53	8.71	7.55	6.34	7.74	2.53	down	4.00E-02	8.95E-01	DR	-
1368476_at	Nr3c2	nuclear receptor subfamily 3, group C, member 2	25672	Rn.9674	NM_013131	6.97	4.46	5.71	4.11	4.35	4.66	2.53	down	1.45E-01	8.95E-01	-	-
1389089_at	Slc39a7	solute carrier family 39 (zinc transporter), member 7	294281	Rn.103977	BM389027	8.23	8.73	9.18	9.81	9.83	10.52	2.53	up	2.06E-02	8.95E-01	UR	-
1386968_at	Ppp1r1a	protein phosphatase 1, regulatory (inhibitor) subunit 1A	58977	Rn.9756	NM_022676	6.82	6.06

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1377992_at	---	---	---	Rn.204418	AI111775	9.57	8.21	6.57	9.32	9.65	9.26	2.45	up	2.13E-01	8.95E-01	-	-
1397336_at	Papolg	poly(A) polymerase gamma	305586	Rn.27992	AI168993	2.37	4.04	5.52	2.97	2.55	2.52	2.45	down	2.32E-01	8.95E-01	-	-
1373079_at	---	---	---	Rn.8272	BI286427	5.59	5.92	4.98	6.32	6.70	7.36	2.45	up	3.35E-02	8.95E-01	UR	-
1377474_at	Abhd13	abhydrolase domain containing 13	306630	Rn.6621	AI007668	2.91	2.54	5.32	4.20	6.03	4.43	2.45	up	2.83E-01	8.95E-01	-	-
1398599_at	Stt3a	STT3, subunit of the oligosaccharyltransferase complex, homolog A (S. cerev	500972	Rn.98525	BG664929	4.83	4.63	4.62	6.07	5.94	5.96	2.45	up	7.94E-05	8.95E-01	UR	-
1386541_at	Spata9	spermatogenesis associated 9	294594	Rn.211979	BF567705	3.81	3.79	2.56	5.23	3.63	5.20	2.45	up	1.26E-01	8.95E-01	-	-
1385079_at	LOC685209	similar to Zinc finger BED domain containing protein 4	685209	---	BE120749	7.70	4.98	5.24	4.07	5.08	4.90	2.45	down	2.34E-01	8.95E-01	-	-
1386628_at	---	---	---	---	BF550445	2.50	2.49	2.51	3.60	5.32	2.45	2.44	up	1.96E-01	8.95E-01	-	-
1371173_a_at	Cast	calpastatin	25403	Rn.17481	Y13591	7.05	6.49	7.20	4.86	5.98	6.04	2.44	down	4.35E-02	8.95E-01	DR	-
1376770_at	Efhd1	EF-hand domain family, member D1	501181	Rn.12816	BM389214	7.95	5.46	5.24	5.22	4.71	4.85	2.44	down	2.18E-01	8.95E-01	-	-
1385587_at	Mcoln2	mucolipin 2	292168	Rn.35113	AI555000	4.46	7.21	6.59	6.45	8.05	7.62	2.43	up	2.52E-01	8.95E-01	-	-
1369113_at	Grem1	gremlin 1, cysteine knot superfamily, homolog (Xenopus laevis)	50566	Rn.42929	NM_019282	5.95	2.59	2.62	2.36	2.62	2.34	2.43	down	3.15E-01	8.95E-01	-	-
1389387_at	rCG_37297	similar to Proteasome inhibitor PI31 subunit	689852	Rn.103325	BF561377	6.38	5.81	5.90	7.66	7.46	6.87	2.43	up	1.17E-02	8.95E-01	-	-
1371540_at	Krtcap2	keratinocyte associated protein 2	295243	Rn.103147	AI102711	5.77	6.38	6.07	7.48	7.05	7.53	2.43	up	5.33E-03	8.95E-01	UR	-
1376837_at	H6pd	hexose-6-phosphate dehydrogenase (glucose 1-dehydrogenase)	298655	Rn.17292	BE109381	5.46	5.87	5.72	7.15	6.88	6.86	2.43	up	1.02E-03	8.95E-01	UR	-
1373676_at	---	---	---	Rn.20033	AI712626	3.87	4.11	5.61	5.64	6.08	5.70	2.43	up	8.56E-02	8.95E-01	-	-
1393569_at	Rbm18	RNA binding motif protein 18	311902	Rn.2745	AI058532	5.76	6.50	7.44	5.44	5.35	5.08	2.42	down	6.20E-02	8.95E-01	-	-
1377994_at	---	---	---	Rn.161395	AI501237	2.60	3.94	2.65	3.56	4.26	5.20	2.42	up	1.19E-01	8.95E-01	-	-
1380888_at	LOC684841	similar to CG31613-PA	684841	---	AI176481	2.50	2.44	6.46	2.44	2.46	2.68	2.42	down	3.93E-01	8.95E-01	-	-
1380632_at	Prkd3	protein kinase D3	313834	Rn.3990	BF288135	4.91	4.62	4.68	6.39	6.93	4.70	2.42	up	1.33E-01	8.95E-01	-	-
1368208_at	Nat8b	N-acetyltransferase 8B	171084	Rn.3643	NM_153558	10.99	11.23	11.69	10.08	9.62	10.41	2.41	down	1.45E-02	8.95E-01	DR	-
1383425_at	C5	complement component 5	362119	Rn.21259	BI290729	4.70	3.99	3.52	5.54	5.15	5.33	2.41	up	2.46E-02	8.95E-01	UR	-
1368837_at	Arid4b	AT rich interactive domain 4B (Rbp1 like)	84481	Rn.47249	NM_053421	6.13	5.55	7.12	5.20	4.23	5.55	2.41	down	1.04E-01	8.95E-01	-	-
1379580_at	Chd6	chromodomain helicase DNA binding protein 6	311607	Rn.43055	BF398050	5.84	6.53	6.26	4.01	5.76	5.06	2.41	down	8.06E-02	8.95E-01	-	-
1367655_at	Tmsb10	thymosin, beta 10	50665	Rn.5983	NM_021261	4.49	5.59	6.14	6.67	6.91	6.44	2.41	up	6.46E-02	8.95E-01	-	-
1379939_a_at	RGD1306063	Similar to HT021	289928	Rn.16932	AW526107	5.02	6.53	3.82	7.06	6.37	5.74	2.41	up	2.19E-01	8.95E-01	-	-
1388781_at	---	---	---	Rn.95130	AW434329	6.05	6.52	7.26	5.26	4.65	6.12	2.41	down	8.39E-02	8.95E-01	-	-
1370008_at	Psmc3ip	proteasome (prosome, macropain) 26S subunit, ATPase 3, interacting protein	140938	Rn.144650	NM_134458	2.55	4.41	3.96	4.69	4.76	5.27	2.41	up	9.81E-02	8.95E-01	-	-
1376975_at	---	---	---	Rn.6502	AA849719	7.77	7.12	8.13	6.26	6.51	6.45	2.41	down	1.41E-02	8.95E-01	DR	-
1393128_at	Gpatch4	G patch domain containing 4	295228	Rn.20166	BI288424	2.51	2.94	2.44	3.90	2.84	4.94	2.40	up	1.13E-01	8.95E-01	-	-
1370245_at	Clst1	calthepain L1	25697	Rn.1294	AI232474	9.81	11.11	10.80	11.56	12.13	11.83	2.40	up	4.10E-02	8.95E-01	UR	-
1393376_at	Sox6	SRY (sex determining region Y)-box 6	293165	Rn.76073	BI289559	4.44	4.79	8.33	4.71	4.38	4.68	2.40	down	3.68E-01	8.95E-01	-	-
1378092_at	Mdp-1	magnesium-dependent phosphatase 1	290230	Rn.19870	AI408718	7.20	4.94	4.74	3.95	3.76	5.38	2.40	down	2.49E-01	8.95E-01	-	-
1380044_x_at	---	---	---	---	BM388738	2.65	2.66	2.68	6.47	2.67	2.64	2.40	up	3.77E-01	8.95E-01	-	-
1384904_at	Neto2	neuropilin (NRP) and tolloid (TLL)-like 2	307757	Rn.147067	AW527233	5.32	5.43	4.82	3.62	4.50	3.66	2.40	down	2.08E-02	8.95E-01	DR	-
1388394_at	Aars	alanyl-tRNA synthetase	292023	Rn.8645	BI282672	6.94	7.12	6.52	8.39	7.91	8.07	2.40	up	5.14E-03	8.95E-01	UR	-
1387448_at	Bet1l	blocked early in transport 1 homolog (S. cerevisiae) like	54400	Rn.90025	NM_019368	2.30	3.41	3.18	4.72	4.66	3.29	2.40	up	9.41E-02	8.95E-01	-	-
1374827_at	Ndst2	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 2	114002	Rn.7781	BI276137	5.83	4.82	5.21	5.92	5.89	5.82	2.39	up	1.74E-01	8.95E-01	-	-
1370600_at	Fgd4	FYVE, RhoGEF and PH domain containing 4	246174	Rn.29988	AF038388	2.64	3.90	3.06	3.98	4.96	4.44	2.39	up	5.43E-02	8.95E-01	-	-
1393762_at	Pcaf	p300/CBP-associated factor	301164	Rn.4126	AA901054	3.67	4.81	3.47	4.87	4.92	5.93	2.39	up	8.04E-02	8.95E-01	-	-
1385164_at	---	---	---	Rn.17147	BE108640	4.28	4.08	5.63	3.70	2.80	3.72	2.39	down	9.25E-02	8.95E-01	-	-
1377790_at	---	---	---	Rn.49288	BE115859	4.25	3.92	3.66	4.74	5.42	5.44	2.39	up	1.22E-02	8.95E-01	UR	-
1389745_at	---	---	---	---	BI290604	6.58	9.19	7.82	8.83	8.71	9.82	2.39	up	2.04E-01	8.95E-01	-	-
1383563_at	---	---	---	Rn.199354	BI282373	7.00	7.25	6.46	5.88	4.93	6.12	2.39	down	4.42E-02	8.95E-01	DR	-
1369583_at	Jdp2	Jun dimerization protein 2	116674	Rn.10721	NM_053894	2.68	2.76	2.71	2.77	4.12	5.03	2.39	up	1.26E-01	8.95E-01	-	-
1374685_at	---	---	---	Rn.169246	BE117446	4.32	4.72	4.09	6.43	5.68	4.78	2.39	up	7.06E-02	8.95E-01	-	-
1396801_at	---	---	---	Rn.199344	AI764598	2.51	2.46	2.85	5.21	2.56	3.81	2.39	up	1.81E-01	8.95E-01	-	-
1370719_a_at	Clcc1	chloride channel CLIC-like 1	170927	Rn.26586	AB052921	5.64	6.15	3.74	6.68	6.33	6.28	2.39	up	1.67E-01	8.95E-01	-	-
1394627_at	Snx19	sorting nexin 19	315478	Rn.8862	AW527508	6.23	4.75	5.38	3.66	4.20	4.75	2.38	down	7.72E-02	8.95E-01	-	-
1371014_at	Plcb1	phospholipase C, beta 1 (phosphoinositide-specific)	24654	Rn.45523	BE097028	6.73	5.90	6.52	4.59	4.53	6.27	2.38	down	1.14E-01	8.95E-01	-	-
1372726_at	Hist1h4b	histone cluster 1, H4b	64627	Rn.1659	AI176792	6.86	6.09	6.06	5.44	5.61	4.21	2.38	down	7.09E-02	8.95E-01	-	-
1395362_at	---	---	---	Rn.49234	BG670699	5.90	3.70	7.14	4.82	4.00	4.17	2.38	down	2.93E-01	8.95E-01	-	-
1381145_at	---	---	---	Rn.154146	BE112469	6.45	4.94	5.35	4.85	3.82	4.32	2.38	down	8.20E-02	8.95E-01	-	-
1388521_at	Pycs	pyrroline-5-carboxylate synthetase (glutamate gamma-semialdehyde synthet	361755	Rn.3148	BG380693	2.48	2.76	2.75	3.32	4.03	4.39	2.38	up	1.88E-02	8.95E-01	UR	-
1392961_at	Mob4r1b	MOB1, Mps One Binder kinase activator-like 1B (yeast)	297387	Rn.74475	AW534383	4.26	5.07	5.73	3.70	3.52	4.09	2.38	down	5.19E-02	8.95E-01	-	-
1390954_at	Ppm1h	protein phosphatase 1H (PP2C domain containing)	314897	Rn.198204	AI548159	5.71	5.14	4.24	6.40	6.87	5.58	2.38	up	9.36E-02	8.95E-01	-	-
1381118_at	RGD1311463	similar to RIKEN cDNA 2700007P21	311279	Rn.40865	AW526652	5.71	3.94	4.69	3.34	3.22	4.04	2.38	down	9.50E-02	8.95E-01	-	-
1383813_at	Arl2bp	ADP-ribosylation factor-like 2 binding protein	498910	Rn.985	BF567478	8.56	8.14	9.45	7.26	7.08	8.06	2.38	down	6.26E-02	8.95E-01	-	-
1392839_at	Bri3bp	Bri3 binding protein	498176	Rn.136726	BE114818	8.59	9.20	9.73	7.83	7.88	8.07	2.37	down	2.07E-02	8.95E-01	DR	-
1395525_at	Wwc2	WW and C2 domain containing 2	498630	Rn.114731	AW921946	4.88	5.51	6.26	4.06	4.11	4.75	2.37	down	5.23E-02	8.95E-01	-	-
1370007_at	Pdia4	protein disulfide isomerase family A, member 4	116598	Rn.39305	NM_053849	6.63	7.41	6.84	8.02	6.88	9.70	2.36	up	2.19E-01	8.95E-01	-	-
1387611_at	Bcl2	B-cell CLL/lymphoma 2	24224	Rn.9996	NM_016993	2.39	2.38	2.39	3.66	3.15	4.07	2.36	up	9.50E-03	8.95E-01	UR	-
1379511_at	---	---	---	Rn.35732	AA875275	2.56	3.16	2.71	2.81	4.78	4.56	2.36	up	1.28E-01	8.95E-01	-	-
1383987_at	---	---	---	Rn.170876	AI112807	3.52	6.30	6.64	6.63	6.70	6.85	2.36	up	2.79E-01	8.95E-01	-	-
1374721_at	---	---	---	Rn.167320	AI178647	6.15	6.65	5.22	7.07	7.38	7.29	2.36	up	4.48E-02	8.95E-01	UR	-
1375362_at	Sppl2a	signal peptide peptidase-like 2A	311401	Rn.8666	BI304125	4.96	6.83	3.90	5.42	6.52	7.47	2.36	up	3.01E-01	8.95E-01	-	-
1382040_at	Eprs	glutamyl-prolyl-tRNA synthetase	289352	Rn.21240	AI234919	6.59	6.04	6.24	7.50	7.17	7.91	2.36	up	9.90E-03	8.95E-01	UR	-
1389979_at	684513 /// LOC68	similar to SWI/SNF-related matrix-associated actin-dependent regulator of chi	684513 /// 685179	Rn.20004	BF396079	5.56	6.95	5.15	7.76	6.88	6.73	2.36	up	1.22E-01	8.95E-01	-	-
1398311_a_at	Kdins220	kinase D-interacting substrate 220	116457	Rn.21470	AF313464	4.65	6.83	5.15	6.31	7.48	6.54	2.36	up	1.75E-01	8.95E-01	-	-
1390868_at	RGD1308695	similar to RIKEN cDNA 1200016B10	289088	Rn.101917	BF403073	5.66	4.65	4.25	3.13	3.69	4.04	2.35	down	6.74E-02	8.95E-01	-	-
1397622_at	---	---	---	Rn.170961	AI578003	7.25	7.31	5.59	8.18	7.86	7.83	2.35	up	9.82E-02	8.95E-01	-	-
1367536_at	Apip	APAF1 interacting protein	295961	Rn.15482	AI172106	6.02	5.29	5.00	8.90	5.83	5.29	2.35	up	3.48E-01	8.95E-01	-	-
1379616_at	---	---	---	Rn.206265	BM383436	3.42	3.13	6.66	3.18	3.18	3.16	2.35	down	3.37E-01	8.95E-01	-	-
1368627_at	Rgn	regucalcin (senescence marker protein-30)	25106	Rn.10006	NM_031546	12.01	11.67	11.79	10.60	10.57	10.60	2.35	down	2.59E-04	8.95E-01	DR	-
1379905_at	Gtpbp1	GTP binding protein 1	300077	Rn.97210	BM386324	4.31	6.05	2.62	5.07	6.06	5.54	2.35	up	2.99E-01	8.95E-01	-	-
1393321_at	Klhdc1	kelch domain containing 1	314190	Rn.96357	AW525577	3.65	2.81	6.01	2.88	2.97	2.94	2.35	down	2.68E-01	8.95E-01	-	-
1371368_at	Sec61a1	Sec61 alpha 1 subunit (S. cerevisiae)	80843	Rn.47029	BI279499	7.85	8.13	7.80	8.89	8.88	9.71	2.35	up	1.35E-02	8.95E-01	UR	-
1383436_at	---	---	---	Rn.216674	BG376768	3.14	6.58	3.91	4.72	7.07	5.52	2.35	up	3.81E-01	8.95E-01	-	-
1373754_at	---	---	---	Rn.1545	AI599232	5.68	5.61	4.56	6.60	6.09	6.85	2.34	up	4.52E-02	8.95E-01	UR	-
1378958_at	Ccdc86	coiled-coil domain containing 86	293738	Rn.40466	AA998314	2.42	3.75	2.33	3.47	4.98	3.74	2.34	up	1.34E-01	8.95E-01	-	-
1393365_at	Chd1	chromodomain helicase DNA binding protein 1	208215	Rn.218360	AW433625	7.64	5.99	7.48	6.29	5.58	5.56	2.34	down	1.01E-01	8.95E-01	-	-
1384442_at	Cldn6	claudin 6	287098	Rn.18647	AI030970	4.43	4.68	4.55	3.43	3.12	3.44	2.34	down	6.74E-04	8.95E-01	DR	-
1370665_at	Hyou1	hypoxia up-regulated 1	192235	Rn.10542	U41853	4.68	4.92	5.39	6.22	5.21	7.23	2.34	up	1.19E-01	8.95E-01	-	-
1395553_at	Zfp68	zinc finger protein 68	304337	Rn.144939	BG672614	3.48	4.86	3.49	4.52	6.07	4.91	2.34	up	1.34E-01	8.95E-01	-	-
1387693_a_at	Slc6a9	solute carrier family 6 (neurotransmitter transporter, glycine), member 9	116509	Rn.32110	M95413	2.35	2.35	2.36	3.60	3.76	3.36	2.34	up	5.51E-04	8.95E-01	UR	-
1386076_at	---	---	---	Rn.169580	BF563176	6.01	3.24	2.71	2.80	2.69	2.80	2.34	down	2.97E-01	8.95E-01	-	-
1367631_at	Ctgf	connective tissue growth factor	64032	Rn.17145	NM_022266	7.02	7.64	4.41	6.34	4.57	4.49	2.33	down	3.51E-01	8.95E-01	-	-
1374663_at	---	---	---	Rn.163668	AW526756	5.28	2.66	5.64	3.22	3.43	3.27	2.33	down	2.64E-01	8.95E-01	-	-
1379755_at	---	---	---	---	BE116194	6.08	4.10	4.56	3.53	2.75	4.80	2.33	down	2.22E-01	8.95E-01	-	-
1382233_a_at	---	---	---	Rn.216446	AI030449	6.44	7.34	6.58	7.30	7.97	8.75	2.33	up	7.18E-02	8.95E-01	-	-
1385980_at	Dcun1d1	DCN1, defective in cullin neddylation 1, domain containing 1 (S. cerevisiae)	310324	Rn.116073	BE108839	4.62	6.27	6.76	6.17	7.58	7.56	2.33	up	2.01E-01	8.95E-01	-	-
1377890_at	---	---	---	Rn.41920	AI411360	4.45	3.94	3.83	4.85	5.66	5.37	2.33	up	1.60E-02	8.95E-01	UR	-
1374567_at	Psrc2	proline/serine-rich coiled-coil 2	314836	Rn.19449	AI408443	5.15	5.56	4.28	6.70	6.72	5.23	2.33	up	1.21E-01	8.95E-01	-	-
1374475_at	Abhd1	abhydrolase domain containing 1	313917	Rn.162847	AI105131	5.95	6.33	6.28	5.85	3.82	5.23	2.32	down	1.18E-01	8.95E-01	-	-
1376057_at	Pde8a	Phosphodiesterase 8A	308776	Rn.24771	BG377309	3.03	3.58	3.58	4.90	4.41	4.53	2.32	up	6.77E-03	8.95E-01	UR	-
1392454_at	Znhit6	zinc finger, HIT type 6	292160	Rn.162633	BI286999	6.87	7.50	4.27	6.98	7.46	7.85	2.32	up	3.00E-01	8.95E-01	-	-
1381795_at	---	---	---	Rn.147524	AA963295	6.09	2.50	2.59	2.50	2.56	2.48	2.32	down	3.63E-01	8.95E-01	-	-
1388764_at	Iqgap1	IQ motif containing GTPase activating protein 1	361598	Rn.106939	BM387072	4.99	5.24	2.98	6.08	5.66	5.11	2.32	up	1.90E-01	8.95E-01	-	-
1383931_at	---	---	---	---	AA901043	3.73	3.11	5.70	2.42	3.10	3.38	2.32	down	2.18E-01	8.95E-01	-	-
1386890_at	S100a10	S100 calcium binding protein A10	81778	Rn.4083	NM_031114	6.54	8.19	8.12	8.85	8.43	9.20	2.31	up	1.06E-01	8.95E-01	-	-
1368888_a_at	Rtn4	reticulon 4	83765	Rn.1348	AF051335	4.62	6.47	5.38	6.45	6.49	7.16	2.31	up	1.07E-01	8.95E-01	-	-
1381277_at	Hoxb3	homeo box B3	303488	Rn.208556	BI295467	3.64	4.81	3.89	6.43	4.03	5.50	2.31	up	1.98E-01	8.95E-01	-	-
1389527_at	LOC378467	promethin	378467	Rn.185772	BM384073	5.96	5.69	4.08	6.13	6.68	6.54	2.31	up	1.19E-01	8.95E-01	-	-
1389531_at	Zfp330	zinc finger protein 330	361387	Rn.137414	AW523471	5.97	5.12	4.47	6.40	5.97	6.82	2.31	up	7.26E-02	8.95E-01	-	-
1388171_at	Cdk7	cyclin-dependent kinase 7	171150	Rn.98896	AW916118	7.46	6.67	7.71	5.99	5.72	6.49	2.31	down	3.53E-02	8.95E-01	DR	-
1383921_at	---	---	---	Rn.113924	AW916957	3.67	4.37	3.78	5.40	6.18	3.86	2.31	up	1.67E-01	8.95E-01	-	-
1373254_at	Krt10	keratin 10	450225	Rn.125065	BI282479	3.62	4.35	3.47	4.83	4.81	5.43	2.31	up	2.34E-02	8.95E-01	UR	-
1379210_at	---	---	---	Rn.34519	AI500867	5.06	4.93	6.04	2.66	5.47	4.28	2.31	down	2.46E-01	8.95E-01	-	-
1379950_at	---	---	---	Rn.160578	AI071581	4.74	5.49	5.66	4.96	3.36	3.95	2.31	down	9.13E-02	8.95E-01	-	-
1398472_at	Peo1	progressive external ophthalmoplegia 1 (human)	309441	Rn.105678	AA925995	3.60	3.52	2.55	3.75	5.43	4.11	2.31	up	1.20E-01	8.95E-01	-	-
1385705_at	Pcbp3	poly(rC) binding protein 3	294336	Rn.107537	AI072571	3.54	4.14	4.56	2.57	2.52	3.53	2.30	down	5.22E-02	8.95E-01	-	-
1393127_at	Zfp358	zinc finger protein 358	360754	Rn.22648	AI707002	5.62	5.33	3.39	6.22	5.56	6.15	2.30	up	1.75E-01	8.95E-01	-	-
1385619_at	Kif11	kinesin family member 11	171304	Rn.58850	BF562797	7.21	6.32	5.25	4.65	4.82	5.71	2.30	down	1.41E-01	8.95E-01	-	-
1379662_a_at	---	---	---	Rn.165314	AI011832	3.76	6.94	4.49	5.39	7.91	5.49	2.30	up	3.97E-01	8.95E-01	-	-
1375964_at	Psph	phosphoserine phosphatase	304429	Rn.8734	BF282282	7.18	7.07	9.01	6.74	6.34	6.58	2.30	down	1.34E-01	8.95E-01	-	-
1378172_at	---	---	---	Rn.203733	AI008119	4.13	3.12	4.84	2.95	2.55	3.00	2.30	down	8.23E-02	8.95E-01	-	-
1379981_at	Thoc1	THO complex 1	291797	Rn.202648	AI170356	5.51	4.07	3.30	3.81	2.29	3.18	2.29	down	2.01E-01	8.95E-01	-	-
1373147_at	Fbxl3	F-box and leucine-rich repeat protein 3	306129	Rn.36356	AI145387	8.46	8.12	9.55	7.44	7.08	8.02	2.29	down	7.95E-02	8.95E-01	-	-
1392825_at	RGD1559600	RGD1559600	499256	Rn.15230	AA923852	2.81	2.88	2.95	3.90	4.10	4.23	2.29	up	2.94E-04	8.95E-01	UR	-
1388486_at	Dpp8	dipeptidylpeptidase 8	315758	Rn.17532	BG671315	6.81	7.35	5.73	7.81	8.36	7.31	2.29	up	1.01E-01	8.95E-01	-	-
1386687_at	LOC686234	similar to Peptide chain release factor 1, mitochondrial precursor (MRF-1)	686234	---	BF563196	5.47	3.69	4.29	2.99	2.95	3.93	2.29	down	1.23E-01	8.95E-01	-	-
1389169_at	Pgrmc2	progesterone receptor membrane component 2	361940	Rn.7685	AA944158	4.14	6.16	4.64	6.05	5.86	6.61	2.29	up	1.39E-01	8.95E-01	-	-
1377869_at	Ccrn4l	CCR4 carbon catabolite repression 4-like (S. cerevisiae)	310395	Rn.15040	BI284261	4.10	5.30	5.26	5.58	5.57	7.09	2.29	up	1.37E-01	8.95E-01	-	-
1369089_at	Erbb3	v-erb-b2 erythroblastic leukemia viral oncogene homolog 3 (avian)	29496	Rn.10228	NM_017218	6.85	5.98	7.28	5.59	5.35	5.60	2.28	down	3.87E-02	8.95E-01	DR	-
1384140_at	---	---	---	Rn.204876	BF288836	6.11	2.62	2.70	2.61	2.65	2.59	2.28	down	3.59E-01	8.95E-01	-	-
1390525_a_at	Stra6	stimulated by retinoic acid gene 6	363071	Rn.12735	BI284420	4.72	4.78	3.08	2.74	3.48	2.79	2.28	down	1.20E-01	8.95E-01	-	-
1388409_at	Zc3h7b	zinc finger CCCH-type containing 7B	315158	Rn.91605	AW142595	7.69	5.85	5.39	5.35	4.80	5.21	2.28	down	1.74E-01	8.95E-01	-	-
1370091_at	Gnaq	guanine nucleotide binding protein, alpha q polypeptide	81666	Rn.22817	NM_031036	3.56	5.46	4.66	6.11	6.47	4.68	2.28	up	1.99E-01	8.95E-01	-	-
1392655_at	---	---	---	Rn.199231	AA997266	2.65	2.50	2.92	6.18	2.82	2.63	2.28	up	3.63E-01	8.95E-01	-	-
1378544_at	Rbbp6	retinoblastoma binding protein 6	308968	Rn.95305	BE117471	6.35	7.19	5.83	7.67	7.87	7.41	2.28	up	4.64E-02	8.95E-01	UR	-
1391469_at	---	---	---	Rn.216418	AI548930	6.05	3.93	4.36	3.93	4.03	2.81	2.28	down	1.91E-01	8.95E-01	-	-
1384091_at	---	---	---	Rn.203333	AA899909	6.20	3.20	2.59	2.52	2.95	2.95	2.28	down	3.49E-01	8.95E-01	-	-
1383023_at	---	---	---	---	AI235658	4.28	4.05	5.78	3.94	3.35	3.23	2.28	down	1.12E-01	8.95E-01	-	-
1374716_at	Rrp15	ribosomal RNA processing 15 homolog (S. cerevisiae)	360895	Rn.137835	AI411620	4.68	4.58	3.59	5.34	5.71	5.36	2.28	up	3.21E-02	8.95E-01	UR	-
1385458_a_at	RGD1306959	similar to C11orf17 protein	361624	Rn.106344	AA799992	4.06	5.90	3.84	4.79	6.18	6.39	2.28	up	2.23E-01	8.95E-01	-	-
1397648_at	Frs2	fibroblast growth factor receptor substrate 2	314850	Rn.22182	BE112403	4.77	3.78	4.89	2.41	3.10	4.37	2.28	down	1.52E-01	8.95E-01	-	-
1369286_at	Proc	protein C	25268	Rn.91064	NM_012803	4.49	5.22	4.61	2.56	3.95	4.25	2.28	down	1.04E-01	8.95E-01	-	-
1385582_at	Osbpl2	oxysterol binding protein-like 2	296461	Rn.12390	AI548374	2.77	3.83	4.70	4.69	5.13	5.04	2.28	up	1.07E-01	8.95E-01	-	-
1376382_at	B3galt2	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 2	305571	Rn.1970	BE100018	4.39	6.35	5.47	6.13	7.28	6.35	2.27	up	1.50E-01	8.95E-01	-	-
1381507_at	---	---	---	Rn.169470	BE097981	2.61	3.28	3.10	4.22	5.08	3.25	2.27	up	1.05E-01	8.95E-01	-	-
1391628_at	Ss18	synovial sarcoma transloc

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicats)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1373787_at	Slc6a9	solute carrier family 6 (neurotransmitter transporter, glycine), member 9	116509	Rn.32110	AA943735	2.57	2.65	2.65	5.15	2.89	3.31	2.24	up	1.69E-01	8.95E-01	-	-
1383247_a_at	rCG_35099	spinster homolog 2	100270678	Rn.159761	BI291029	5.75	5.34	5.61	6.91	6.39	6.89	2.24	up	5.20E-03	8.95E-01	UR	-
1370019_at	Sult1a1	sulfotransferase family, cytosolic, 1A, phenol-preferring, member 1	83783	Rn.1507	AF394783	6.35	6.56	5.51	6.34	6.49	9.07	2.24	up	2.85E-01	8.95E-01	-	-
1385823_s_at	Podxl	podocalyxin-like	192181	Rn.162741	AI172520	8.15	2.72	2.87	3.04	4.26	2.96	2.24	down	5.61E-01	8.95E-01	-	-
1390825_at	Slc35b3	solute carrier family 35, member B3	306866	Rn.6323	AI010087	5.32	6.46	6.03	4.81	4.20	5.32	2.24	down	6.67E-02	8.95E-01	-	-
1395839_at	Znf142	zinc finger protein 142 (clone pHZ-49)	316524	Rn.164982	BF561078	4.75	4.46	4.77	3.97	3.01	3.51	2.24	down	1.66E-02	8.95E-01	DR	-
1395799_at	Itsn2	intersectin 2	313934	Rn.37673	AI177767	4.81	4.80	5.70	2.51	4.81	4.51	2.23	down	2.12E-01	8.95E-01	-	-
1371185_at	Itga6	integrin, alpha 6	114517	Rn.161799	AA955091	5.20	5.85	4.87	3.75	4.19	4.51	2.23	down	3.29E-02	8.95E-01	DR	-
1384804_at	Dnmt3a	DNA (cytosine-5-)-methyltransferase 3 alpha	444984	Rn.92659	AI029751	5.79	4.83	5.98	4.63	3.59	4.92	2.23	down	9.82E-02	8.95E-01	-	-
1373245_at	Col4a1	collagen, type IV, alpha 1	290905	Rn.53801	BE111752	6.44	6.07	4.04	6.99	6.96	6.06	2.23	up	2.24E-01	8.95E-01	-	-
1387434_at	Slc22a4	solute carrier family 22 (organic cation transporter), member 4	64037	Rn.163093	NM_022270	5.72	6.54	6.79	7.60	7.48	7.45	2.23	up	2.41E-02	8.95E-01	UR	-
1376481_at	Adamts9	a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin t	312566	Rn.162758	BF416285	3.19	3.66	2.64	5.00	3.71	4.24	2.23	up	7.19E-02	8.95E-01	-	-
1375105_at	Aven	Apoptosis, caspase activation inhibitor	311299	Rn.145049	BF419036	2.73	2.45	6.58	2.58	2.73	2.99	2.23	down	4.37E-01	8.95E-01	-	-
1378370_at	---	---	---	Rn.20112	BF401705	5.03	4.87	7.48	4.28	4.44	5.19	2.23	down	2.65E-01	8.95E-01	-	-
1384544_at	Pon3	paraoxonase 3	312086	Rn.16469	BM385409	6.73	4.92	4.39	7.33	5.89	6.29	2.23	up	2.36E-01	8.95E-01	-	-
1389636_a_at	Timp3	TIMP metallopeptidase inhibitor 3	25358	Rn.119634	AI599265	10.66	8.67	8.47	8.57	7.93	7.83	2.23	down	1.93E-01	8.95E-01	-	-
1375491_at	---	---	---	---	BI299116	4.57	2.52	3.97	2.26	2.30	3.03	2.23	down	1.54E-01	8.95E-01	-	-
1395520_at	Rbm28	RNA binding motif protein 28	312182	Rn.50022	AW530017	9.13	7.24	7.07	6.79	6.74	6.44	2.22	down	1.59E-01	8.95E-01	-	-
1376972_at	Slc40a1	Solute carrier family 39 (iron-regulated transporter), member 1	170840	Rn.15324	AI407028	4.73	5.18	5.26	6.34	6.13	6.16	2.22	up	2.83E-03	8.95E-01	UR	-
1390775_at	Galnt2	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltrar	292090	Rn.144772	AW254382	2.27	3.15	4.90	2.27	2.33	2.26	2.22	down	2.12E-01	8.95E-01	-	-
1376202_at	B3galt1	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 1	293667	Rn.219653	BF416236	5.67	6.33	5.79	6.73	7.32	7.19	2.22	up	1.33E-02	8.95E-01	UR	-
1372448_at	Zdhhc5	zinc finger, DHHC-type containing 5	362156	Rn.4240	D86711	3.70	5.28	5.08	5.39	6.04	6.08	2.22	up	1.03E-01	8.95E-01	-	-
1368313_a_at	Trpv1	transient receptor potential cation channel, subfamily V, member 1	83810	Rn.3073	AB041029	4.79	4.06	4.63	3.39	2.47	4.17	2.22	down	9.99E-02	8.95E-01	-	-
1389013_at	Rpl7l1	ribosomal protein L7-like 1	317275	Rn.102202	BF420644	7.58	7.41	10.66	7.53	7.28	7.39	2.22	down	3.38E-01	8.95E-01	-	-
1373169_at	Agpat5	1-acylglycerol-3-phosphate O-acyltransferase 5 (lysophosphatidic acid acyltra	306582	Rn.199010	AI175416	4.05	4.12	2.85	5.31	4.98	4.19	2.22	up	9.50E-02	8.95E-01	-	-
1379636_at	Fam82a	family with sequence similarity 82, member A	313840	Rn.25365	AW528443	4.77	5.37	6.12	4.03	3.87	4.91	2.22	down	8.65E-02	8.95E-01	-	-
1382534_at	---	---	---	Rn.48679	BF284898	5.20	3.61	5.81	3.80	4.94	2.42	2.22	down	3.06E-01	8.95E-01	-	-
1390395_at	---	---	---	Rn.3812	BF284768	4.23	3.20	3.74	4.48	5.29	4.85	2.22	up	3.84E-02	8.95E-01	UR	-
1388898_at	Hsph1	heat shock 105kDa/110kDa protein 1	288444	Rn.37805	AI236601	9.14	8.80	9.15	7.94	7.65	8.06	2.22	down	2.42E-03	8.95E-01	DR	-
1371131_a_at	Txnip	thioredoxin interacting protein	117514	Rn.2758	U30789	8.13	7.90	6.81	9.17	9.18	7.93	2.22	up	1.19E-01	8.95E-01	-	-
1376766_at	Fmnl1	formin-like 1	287746	Rn.45477	BF416786	5.90	5.74	5.43	7.66	6.58	6.29	2.22	up	5.88E-02	8.95E-01	-	-
1374920_at	---	---	---	Rn.19095	AI228955	7.11	6.24	6.12	5.91	4.86	5.26	2.22	down	5.84E-02	8.95E-01	-	-
1392618_at	---	---	---	Rn.153757	BG379597	3.71	5.09	5.15	6.17	4.70	6.53	2.22	up	1.91E-01	8.95E-01	-	-
1389673_a_at	Surf4	surfeit 4	619346	Rn.107863	BE112262	5.91	6.83	7.44	6.24	7.29	8.09	2.22	up	9.86E-02	8.95E-01	-	-
1371023_at	Megf8	multiple EGF-like-domains 8	114029	Rn.21378	AW524873	3.78	4.56	2.36	2.41	2.35	2.49	2.22	down	1.50E-01	8.95E-01	-	-
1377787_at	Rbm6	RNA binding motif protein 6	315997	Rn.94277	BF407266	2.81	3.29	2.76	4.22	3.67	4.42	2.22	up	1.52E-02	8.95E-01	UR	-
1383472_at	Aldh1b1	aldehyde dehydrogenase 1 family, member B1	298079	Rn.12547	AA997683	5.98	6.66	6.71	6.04	4.46	5.40	2.21	down	9.09E-02	8.95E-01	-	-
1384990_at	---	---	---	Rn.210164	BF393943	2.43	2.41	5.79	2.36	2.42	2.41	2.21	down	3.65E-01	8.95E-01	-	-
1384863_at	Cpne7	copine VII	361433	Rn.145177	AW534032	6.56	5.32	5.61	3.84	5.34	4.87	2.21	down	1.21E-01	8.95E-01	-	-
1397847_at	---	---	---	Rn.23514	AW921990	4.89	5.50	7.77	4.90	4.80	5.02	2.21	down	2.63E-01	8.95E-01	-	-
1389246_at	B4galt1	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 1	24390	Rn.17157	BF282414	3.65	3.36	3.41	5.46	4.76	3.63	2.21	up	1.01E-01	8.95E-01	-	-
1384797_at	Atl3	atlastin GTPase 3	309187	Rn.202359	BF404325	2.95	4.22	4.69	2.53	2.96	2.94	2.21	down	1.00E-01	8.95E-01	-	-
1372747_at	Slc20a2	solute carrier family 20 (phosphate transporter), member 2	29502	Rn.13642	AI409899	2.95	5.66	3.35	4.20	5.84	5.34	2.21	up	3.06E-01	8.95E-01	-	-
1393238_at	Ints7	integrator complex subunit 7	289380	Rn.156180	AA900649	6.16	7.19	6.32	5.55	4.61	6.10	2.20	down	1.03E-01	8.95E-01	-	-
1371808_at	Blmh	bleomycin hydrolase	288752	Rn.100672	AI012747	8.76	8.40	7.55	7.47	6.18	7.64	2.20	down	1.22E-01	8.95E-01	-	-
1395984_at	RGD1307682	similar to hypothetical protein FLJ21827	300675	Rn.13688	AI043648	5.74	7.37	9.08	6.32	6.39	6.05	2.20	down	3.05E-01	8.95E-01	-	-
1392783_at	---	---	---	Rn.203237	AI136436	6.17	6.15	4.14	6.52	6.73	6.62	2.20	up	1.69E-01	8.95E-01	-	-
1377346_at	---	---	---	Rn.129546	AI112298	3.87	4.57	3.31	5.41	4.58	5.17	2.20	up	6.10E-02	8.95E-01	-	-
1391572_at	Cars	cysteinyl-tRNA synthetase	293638	Rn.14865	BE109168	2.66	2.85	2.61	4.80	2.92	3.81	2.20	up	1.07E-01	8.95E-01	-	-
1377523_at	LOC686314	similar to dachshund b	686314	---	BE113698	3.09	5.59	2.92	4.83	4.42	5.76	2.20	up	2.97E-01	8.95E-01	-	-
1369991_at	Sec13a	SEC13 homolog A (S. cerevisiae)	65166	Rn.13070	NM_031723	7.23	8.84	7.40	8.57	8.73	9.58	2.20	up	1.31E-01	8.95E-01	-	-
1377012_at	Smarcad1	SWI/SNF-related, matrix-associated actin-dependent regulator of chromatin, s	312398	Rn.7758	AI012630	5.79	5.05	6.15	5.15	3.15	5.29	2.19	down	2.12E-01	8.95E-01	-	-
1374303_at	Alkbh2	alkB, alkylation repair homolog 2 (E. coli)	304578	Rn.107582	BI288146	5.70	3.48	3.60	4.78	6.04	5.35	2.19	up	2.34E-01	8.95E-01	-	-
1393333_at	---	---	---	---	BF561617	4.77	5.16	6.52	4.75	4.68	3.62	2.19	down	1.55E-01	8.95E-01	-	-
1382942_at	---	---	---	Rn.210384	BF397627	3.10	3.12	3.15	3.37	6.48	2.90	2.19	up	3.72E-01	8.95E-01	-	-
1383273_a_at	Pcbp3	poly(rC) binding protein 3	294336	Rn.107537	AA956005	8.34	6.85	7.28	5.27	5.47	8.35	2.19	down	3.59E-01	8.95E-01	-	-
1374788_at	Tp53bp1	tumor protein p53 binding protein 1	296099	Rn.160605	AI235252	5.85	4.43	3.86	4.22	2.92	3.62	2.19	down	1.83E-01	8.95E-01	-	-
1371631_at	Eif1ad	eukaryotic translation initiation factor 1A domain containing	293673	Rn.4163	BF420639	4.80	4.56	3.70	5.25	5.11	6.08	2.19	up	6.62E-02	8.95E-01	-	-
1391163_at	Eftud1	elongation factor Tu GTP binding domain containing 1	308789	Rn.204399	BM385306	5.74	6.26	7.22	5.05	5.16	5.63	2.18	down	7.43E-02	8.95E-01	-	-
1389234_at	Vwf	Von Willebrand factor homolog	116669	Rn.35561	BI298314	6.41	7.59	7.00	4.80	6.22	6.60	2.18	down	1.56E-01	8.95E-01	-	-
1396434_at	---	---	---	Rn.217015	BF414402	3.84	4.44	6.69	4.50	3.75	3.35	2.18	down	2.93E-01	8.95E-01	-	-
1374034_at	Cars	cysteinyl-tRNA synthetase	293638	Rn.14865	BG379410	4.30	3.43	4.21	5.01	5.15	5.15	2.18	up	1.63E-02	8.95E-01	UR	-
1398447_at	---	---	---	Rn.28439	AA801323	4.97	6.13	4.19	5.82	6.55	6.29	2.18	up	1.37E-01	8.95E-01	-	-
1387348_at	Igfbp5	insulin-like growth factor binding protein 5	25285	Rn.1593	BE113270	9.69	8.39	9.32	8.36	8.47	7.20	2.18	down	1.16E-01	8.95E-01	-	-
1390169_at	LOC688749	similar to Tubby-related protein 3 (Tubby-like protein 3)	688749	Rn.8754	AW144331	3.50	4.82	5.56	3.01	3.94	3.56	2.18	down	1.65E-01	8.95E-01	-	-
1396849_at	---	---	---	Rn.48310	AW534332	2.33	2.78	5.24	2.33	2.34	2.32	2.18	down	2.82E-01	8.95E-01	-	-
1398471_at	Cog6	component of oligomeric golgi complex 6	310411	Rn.105874	BF288063	4.01	5.00	4.80	6.17	5.64	5.37	2.18	up	4.28E-02	8.95E-01	UR	-
1370199_at	Nucb1	nucleobindin 1	84595	Rn.1492	Z36277	4.58	4.79	3.12	4.97	5.01	5.88	2.18	up	1.37E-01	8.95E-01	-	-
1375961_at	Frzb	secreted-related protein	295891	Rn.12034	AI072892	5.85	4.97	6.27	3.74	5.42	4.57	2.17	down	1.44E-01	8.95E-01	-	-
1391812_at	---	---	---	Rn.103569	AI145876	3.30	4.92	4.52	4.98	4.64	6.48	2.17	up	2.07E-01	8.95E-01	-	-
1375922_at	Cox15	COX15 homolog, cytochrome c oxidase assembly protein (yeast)	309391	Rn.1309	BI296988	6.70	7.30	7.14	7.11	9.91	7.49	2.17	up	2.80E-01	8.95E-01	-	-
1387620_at	Klk11	kallikrein 11-like peptidase	24523	Rn.207160	NM_012593	6.79	2.69	2.91	6.41	6.66	2.68	2.17	up	5.79E-01	8.95E-01	-	-
1387841_at	Exoc5	exocyst complex component 5	60627	Rn.44430	NM_022204	6.65	7.95	9.34	6.37	6.73	7.49	2.17	down	2.56E-01	8.95E-01	-	-
1373580_at	---	---	---	Rn.222043	BI289991	4.81	4.99	5.65	5.89	6.10	6.80	2.17	up	4.06E-02	8.95E-01	UR	-
1371037_at	Pros1	protein S (alpha)	81750	Rn.2888	U06230	4.81	5.15	5.32	5.74	6.24	6.65	2.17	up	2.11E-02	8.95E-01	UR	-
1374276_at	---	---	---	Rn.204421	BE104102	2.63	3.21	3.52	3.40	5.49	3.81	2.17	up	1.82E-01	8.95E-01	-	-
1389140_at	Spcs2	signal peptidase complex subunit 2 homolog (S. cerevisiae)	293142	Rn.7939	AI172437	6.96	7.23	7.00	8.00	7.85	8.69	2.16	up	1.51E-02	8.95E-01	UR	-
1376098_a_at	Myo1g	myosin IG	289785	Rn.198974	BF282304	4.04	5.29	6.66	7.15	5.04	7.14	2.16	up	3.41E-01	8.95E-01	-	-
1383818_at	Thnsl1	threonine synthase-like 1 (S. cerevisiae)	498805	Rn.198366	BF565324	6.41	2.36	2.64	2.31	3.18	2.57	2.16	down	4.49E-01	8.95E-01	-	-
1384400_at	Pde4c	phosphodiesterase 4C, cAMP-specific (phosphodiesterase E1 dunce homolo	290646	Rn.92465	BM389421	4.64	4.93	4.77	5.63	6.36	5.70	2.16	up	1.12E-02	8.95E-01	UR	-
1399133_at	Fbxo7	F-box protein 7	366854	Rn.20218	AW520767	3.98	4.91	4.21	4.83	6.20	5.40	2.16	up	8.40E-02	8.95E-01	-	-
1372332_at	---	---	---	Rn.13655	AI170687	2.97	3.34	4.54	4.54	5.71	3.95	2.16	up	1.88E-01	8.95E-01	-	-
1388583_at	Cxcl12	chemokine (C-X-C motif) ligand 12 (stromal cell-derived factor 1)	24772	Rn.54439	BF283398	6.10	5.82	4.25	6.66	7.25	5.60	2.16	up	2.12E-01	8.95E-01	-	-
1367856_at	G6pd	glucose-6-phosphate dehydrogenase	24377	Rn.11040	NM_017006	6.24	7.79	7.99	8.59	8.34	8.43	2.16	up	1.16E-01	8.95E-01	-	-
1395351_at	---	---	---	Rn.205010	BF543381	3.87	4.46	2.65	2.65	2.36	2.64	2.16	down	1.09E-01	8.95E-01	-	-
1384092_at	C1ql3	Complement component 1, q subcomponent-like 3	680404	Rn.13498	AW921638	2.18	3.10	2.19	3.44	4.52	2.85	2.16	up	1.26E-01	8.95E-01	-	-
1391631_at	---	---	---	Rn.23065	AA924498	2.38	2.37	2.44	2.42	4.52	3.58	2.16	up	1.42E-01	8.95E-01	-	-
1368994_a_at	Garnl1	GTPase activating Rap/RanGAP domain-like 1	56785	Rn.86984	AF041107	4.03	6.16	5.48	5.86	7.38	5.76	2.16	up	2.46E-01	8.95E-01	-	-
1372091_at	Mid1ip1	MID1 interacting protein 1 (gastrulation specific G12 homolog (zebrafish))	404280	Rn.8267	BI276959	3.81	3.46	2.55	4.63	4.46	4.06	2.16	up	5.54E-02	8.95E-01	-	-
1392924_at	---	---	---	Rn.154194	BG371591	3.51	3.85	3.54	4.23	4.29	5.72	2.16	up	9.04E-02	8.95E-01	-	-
1371785_at	Tnfrsf12a	tumor necrosis factor receptor superfamily, member 12a	302965	Rn.105040	BI303379	4.57	5.02	3.94	5.31	4.84	6.71	2.16	up	1.61E-01	8.95E-01	-	-
1371901_at	---	---	---	Rn.3633	AI176646	4.82	4.34	4.93	4.99	7.32	5.11	2.16	up	2.28E-01	8.95E-01	-	-
1391711_at	---	---	---	Rn.171889	BM386534	5.47	5.36	4.32	4.49	3.20	4.14	2.16	down	1.06E-01	8.95E-01	-	-
1388887_at	Ggta1	glycoprotein, alpha-galactosyltransferase 1	246766	Rn.916	AI178222	4.26	4.04	3.84	5.47	3.76	6.23	2.15	up	2.09E-01	8.95E-01	-	-
1377463_at	Man2a2	Mannosidase 2, alpha 2	308757	Rn.41796	BE099244	5.76	6.12	4.88	6.39	6.92	6.76	2.15	up	5.02E-02	8.95E-01	-	-
1371005_at	Abcc1	ATP-binding cassette, sub-family C (CFTR/MRP), member 1	24565	Rn.10495	AI059506	5.82	5.64	4.01	4.65	5.58	5.15	2.15	down	8.11E-02	8.95E-01	-	-
1385374_at	---	---	---	Rn.203752	AA997236	6.51	5.96	8.01	6.02	5.60	5.54	2.15	down	1.54E-01	8.95E-01	-	-
1377932_at	---	---	---	Rn.105786	AI556083	3.87	4.51	3.33	4.81	4.20	6.01	2.15	up	1.57E-01	8.95E-01	-	-
1382028_at	Pex19	peroxisomal biogenesis factor 19	289233	Rn.203104	BE115406	5.50	5.28	5.57	4.42	3.44	5.17	2.15	down	9.56E-02	8.95E-01	-	-
1370817_at	Sec11c	SEC11 homolog C (S. cerevisiae)	266758	Rn.16883	AB022714	7.25	8.42	7.74	8.58	8.68	9.48	2.15	up	6.77E-02	8.95E-01	-	-
1392603_at	---	---	---	Rn.167218	AI174525	7.15	6.76	8.78	5.31	7.11	6.96	2.15	down	2.62E-01	8.95E-01	-	-
1374437_at	Nars	asparaginyl-tRNA synthetase	291556	Rn.48209	BF419336	7.47	7.50	6.95	8.01	8.26	8.96	2.15	up	3.10E-02	8.95E-01	UR	-
1386382_at	Osbpl1a	Oxysterol binding protein-like 1A	259221	Rn.178864	AW534220	8.01	10.61	8.51	8.24	7.97	7.62	2.14	down	2.49E-01	8.95E-01	-	-
1369754_a_at	Cast	calpastatin	25403	Rn.17481	NM_053295	5.13	5.45	5.10	7.14	5.82	6.02	2.14	up	6.19E-02	8.95E-01	-	-
1370946_at	Nflx	nuclear factor I/X (CCAAT-binding transcription factor)	81524	Rn.56776	BF420722	6.95	5.21	6.88	5.10	5.27	5.37	2.14	down	1.28E-01	8.95E-01	-	-
1397469_at	Dst	dystonin	316313	Rn.79807	BI296305	7.60	6.89	6.50	5.58	5.69	6.41	2.14	down	5.66E-02	8.95E-01	-	-
1378333_at	---	---	---	Rn.50362	BI284174	4.31	3.06	4.22	2.75	2.72	2.83	2.14	down	5.30E-02	8.95E-01	-	-
1387716_at	Utrn	utrophin	25600	Rn.9901	NM_013070	3.73	2.81	2.83	3.89	5.05	3.73	2.14	up	1.01E-01	8.95E-01	-	-
1381036_at	---	---	---	Rn.166670	AW434394	5.74	3.34	4.43	3.63	3.32	3.28	2.14	down	1.94E-01	8.95E-01	-	-
1383834_at	Agap3	GTPase activating protein	362300	Rn.98623	BI285391	6.52	6.75	5.97	6.92	7.52	7.19	2.14	up	4.38E-02	8.95E-01	UR	-
1394320_at	Cdk2	cyclin dependent kinase 2	362817	Rn.104460	BF542448	2.59	5.42	2.37	2.36	2.38	2.34	2.14	down	3.27E-01	8.95E-01	-	-
1372869_at	/// RGD156	similar to Nucleolar GTP-binding protein 1 (Chronic renal failure gene protein	291269 /// 689842	Rn.199031	BE109202	8.08	10.58	9.23	7.44	9.41	7.75	2.14	down	3.11E-01	8.95E-01	-	-
1397853_s_at	Arhgef9	Cdc42 guanine nucleotide exchange factor (GEF) 9	296013	Rn.163449	BG672534	3.62	5.07	4.76	6.63	5.32	4.78	2.14	up	1.95E-01	8.95E-01	-	-
1369644_at	Lphn2	latrophilin 2	171447	Rn.12089	NM_134408	3.49	5.64	3.32	5.10	4.80	5.83	2.14	up	2.47E-01	8.95E-01	-	-
1397729_x_at	LOC363060	similar to RIKEN cDNA 1600029D21	363060	Rn.39346	BF283642	2.81	2.61	2.85	4.83	4.13	2.60	2.14	up	1.74E-01	8.95E-01	-	-
1387915_at	Sels	selenoprotein S	286900	Rn.4197	AF367467	6.77	7.09	6.40	7.40	7.79	8.36	2.13	up	3.34E-02	8.95E-01	UR	-
1382269_at	Cnnm2	cyclin M2	294014	Rn.205139	BM388183	4.42	4.94	3.17	5.39	5.17	5.26	2.13	up	1.07E-01	8.95E-01	-	-
1398636_at	RGD1305420	similar to Nef associated protein 1	298072	Rn.51866	BE110303	3.37	3.21	4.85	4.44	5.82	4.44	2.13	up	1.92E-01	8.95E-01	-	-
1387629_at	Bspry	B-box and SPRY domain containing	64027	Rn.53996	NM_022261	5.91	4.52	5.74	4.86	5.06	2.98	2.13	down	2.41E-01	8.95E-01	-	-
1382118_at	Apeg3	Antisense paternally expressed gene 3	619476	Rn.49740	BE104676	3.59	4.45	2.93	4.95	5.48	3.81	2.13	up	1.75E-01	8.95E-01	-	-
1381837_at	---	---	---	Rn.35623	AI502137	2.63	3.23	3.60	4.72	4.40	3.60	2.13	up	6.66E-02	8.95E-01	-	-
1384873_at	---	---	---	Rn.205325	AI555547	2.39	2.36	2.40	5.65	2.40	2.37	2.13	up	3.74E-01	8.95E-01	-	-
1381434_s_at	LOC302022	similar to nidogen 2 protein	302022	Rn.13869	AW253721	6.67	2.62	2.60	2.68	2.68	3.25	2.13	down	4.70E-01	8.95E-01	-	-
1385994_at	Spo11	SPO11 meiotic protein covalently bound to DSB homolog (S. cerevisiae)	366261	Rn.31584	AI232279	6.73	5.76	7.29	5.55	5.23	5.73	2.13	down	8.21E-02	8.95E-01	-	-
1381567_at	Zufsp	zinc finger with UFM1-specific peptidase domain	294390	Rn.3372	BG381715	2.49	2.47	2.51	2.47	5.66	2.60	2.13	up	3.55E-01	8.95E-01	-	-
1369098_at	Vldlr	very low density lipoprotein receptor	25696	Rn.9975	NM_013155	4.49	3.78	3.87	4.91	4.51	5.97	2.13	up	9.02E-02	8.95E-01	-	-
1398341_at	lsd3 /// LOC688169	CDGSH iron sulfur domain 3 /// similar to CG3420-PA	287661 /// 688169	Rn.107812	BI295767	7.06	7.49	8.44	6.85	6.07	6.81	2.13	down	8.50E-02	8.95E-01	-	-
1378582_at	Trabd	TraB domain containing	300142	Rn.3565	BM383666	5.21	5.73	6.37	6.56	7.20	6.81	2.12	up	4.77E-02	8.95E-01	UR	-
1393145_at	Kdsr	3-ketodihydrosphingosine reductase	360833	Rn.22924	AA899892	3.79	4.57	3.91	5.65	4.86	5.02	2.12	up	3.39E-02	8.95E-01	UR	-
1372858_at	---	---	---	---	AA900367	5.97	5.11	5.29	4.39	3.87	4.85	2.12	down	4.84E-02	8.95E-01	DR	-
1374704_at	Kdelc2	KDEL (Lys-Asp-Glu-Leu) containing 2	315664	Rn.98686	BM384752	4.22	4.83	6.36	4.90	3.07	4.20	2.12	down	2.61E-01	8.95E-01	-	-
1369592_at	Wbp2	WW domain binding protein 2	192645	Rn.198920	NM_138975	8.71	7.71	7.50	7.49	6.73	6.45	2.12	down	8.88E-02	8.95E-01	-	-
1384315_at	Pdk3	pyruvate dehydrogenase kinase, isozyme 3	296849	Rn.18101	BM389330	6.25	6.22	5.64	5.11	5.14	4.62	2.12	down	1.40E-02	8.95E-01	DR	-
1375936_at	Dsc2	desmocollin 2	291760	Rn.3954	BI279683	2.56	2.61	2.62	3.86	2.65	4.53	2.12	up	1.20E-01	8.95E-01	-	-
1386693_at	Csnk1e	casein kinase 1, epsilon	58822	Rn.203721	BF565397	3.50	2.84	3.53	5.87	3.57	3.68	2.12	up	2.39E-01	8.95E-01	-	-
1383774_at	Ncrna00117	non-protein coding RNA 117	289864	Rn.108544	BG376677	5.24	6.34	4.79	6.28	6.52	6.82	2.12	up	8.91E-02	8.95E-01	-	-
1392922_at	---	---	---	Rn.23625	BE116619	2.79	5.19	3.43	5.25	5.35	4.06	2.12	up	2.62E-01	8.95E-01	-	-
1373162_at	LOC681708	similar to transmembrane protein 41a	681708	Rn.199221	AI600085	6.78	7.16	7.09

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1392933_a_at	---	---	---	Rn.9084	BF288704	4.12	3.22	4.17	4.92	4.61	5.15	2.08	up	3.72E-02	8.95E-01	UR	-
1368692_a_at	Chka	choline kinase alpha	29194	Rn.10985	AW140851	3.97	4.78	6.02	3.91	3.95	3.73	2.08	down	1.53E-01	8.95E-01	-	-
1388397_at	Ebna1bp2	EBNA1 binding protein 2	114021	Rn.9598	BI281160	4.80	6.81	7.12	6.57	7.65	7.88	2.08	up	2.64E-01	8.95E-01	-	-
1373425_at	Cik2	CDC-like kinase 2	365842	Rn.17201	BF284224	6.74	7.56	6.54	4.71	6.49	6.47	2.08	down	1.87E-01	8.95E-01	-	-
1370859_at	Pdia6	protein disulfide isomerase family A, member 6	286906	Rn.2685	BI284965	6.79	7.26	6.81	7.90	7.42	8.71	2.08	up	5.91E-02	8.95E-01	-	-
1395518_at	---	---	---	---	---	6.34	5.01	5.24	3.65	4.30	5.47	2.08	down	1.90E-01	8.95E-01	-	-
1396189_at	---	---	---	---	---	6.47	7.72	8.33	7.42	6.93	7.00	2.08	down	1.84E-02	8.95E-01	DR	-
1382042_at	---	---	---	Rn.220205	AI137817	8.22	6.80	8.14	6.19	6.77	7.02	2.08	down	1.13E-01	8.95E-01	-	-
1369680_at	Slc2a13	solute carrier family 2 (facilitated glucose transporter), member 13	171147	Rn.21287	NM_133611	3.46	3.75	3.62	3.78	5.34	4.88	2.08	up	8.88E-02	8.95E-01	-	-
1368442_at	F2	coagulation factor II (thrombin)	29251	Rn.54498	NM_022924	7.19	5.57	6.23	4.91	5.56	5.35	2.08	down	1.07E-01	8.95E-01	-	-
1383809_at	---	---	---	Rn.25407	BF562237	4.00	5.04	4.29	4.90	5.91	5.68	2.08	up	7.23E-02	8.95E-01	-	-
1372940_at	RGD1562339	RGD1562339	498107	Rn.95097	BM389329	4.27	6.10	6.51	6.45	6.80	6.78	2.08	up	2.05E-01	8.95E-01	-	-
1380163_at	Sec23ip	SEC23 interacting protein	309010	Rn.138256	BI302685	5.35	5.70	5.29	6.79	6.29	6.42	2.08	up	5.83E-03	8.95E-01	UR	-
1384357_at	---	---	---	Rn.165895	BI665592	5.39	5.07	4.11	3.29	4.08	4.03	2.07	down	8.40E-02	8.95E-01	-	-
1375645_at	RGD1560286	similar to DNA segment, Chr 4, ERATO Doi 22, expressed	500575	Rn.22136	AI408842	7.55	7.12	6.73	6.32	5.53	6.39	2.07	down	4.43E-02	8.95E-01	DR	-
1399155_at	LOC296637	similar to HLA-B associated transcript-2 isoform a	296637	Rn.98457	AA944347	4.88	3.19	4.45	2.66	3.45	3.25	2.07	down	1.33E-01	8.95E-01	-	-
1379833_at	Lingo4 /// Rorc	leucine rich repeat and Ig domain containing 4 /// RAR-related orphan recepto	368158 /// 499668	Rn.21421	BE110171	4.43	5.27	4.64	5.48	5.82	6.19	2.07	up	3.14E-02	8.95E-01	UR	-
1376409_at	Rab23	RAB23, member RAS oncogene family	367242	Rn.24441	AI176677	7.52	7.38	7.97	6.25	6.73	6.74	2.07	down	1.19E-02	8.95E-01	DR	-
1394461_at	---	---	---	Rn.216877	BF409715	5.34	5.65	6.34	5.22	4.57	4.38	2.07	down	5.41E-02	8.95E-01	-	-
1368325_at	Egf	epidermal growth factor	25313	Rn.6075	NM_012842	9.54	8.09	7.91	7.33	9.73	5.33	2.07	down	4.86E-01	8.95E-01	-	-
1391194_at	Sall1	Sal-like 1 (Drosophila)	307740	Rn.32153	BG377337	4.77	4.07	3.58	5.28	5.08	5.21	2.07	up	3.92E-02	8.95E-01	UR	-
1379515_at	Pigt	phosphatidylinositol glycan anchor biosynthesis, class T	296360	Rn.40489	AW144664	5.84	4.32	4.29	3.65	3.60	4.05	2.07	down	1.19E-01	8.95E-01	-	-
1381449_s_at	Tgfa	transforming growth factor alpha	24827	Rn.9952	BG670310	2.58	2.68	2.81	2.57	5.72	2.92	2.07	up	3.53E-01	8.95E-01	-	-
1374929_at	Ccdc126	coiled-coil domain containing 126	500117	Rn.22388	AI010233	5.31	5.77	6.14	5.05	3.56	5.46	2.07	down	1.68E-01	8.95E-01	-	-
1378396_at	---	---	---	Rn.23485	AI007647	4.32	4.16	3.15	5.13	4.79	4.86	2.07	up	5.19E-02	8.95E-01	-	-
1374906_at	Rnf113a1	ring finger protein 113A1	313450	Rn.34457	BF407585	4.19	2.90	5.37	2.91	2.93	3.48	2.07	down	2.28E-01	8.95E-01	-	-
1373385_at	---	---	---	Rn.154543	BF550271	8.23	7.60	8.37	7.54	7.10	6.42	2.07	down	5.96E-02	8.95E-01	-	-
1370456_at	Fat3	FAT tumor suppressor homolog 3 (Drosophila)	191571	Rn.210528	AB076401	6.31	4.72	5.02	3.39	5.23	4.28	2.07	down	2.19E-01	8.95E-01	-	-
1369895_s_at	Podxl	podocalyxin-like	192181	Rn.162741	AB020726	6.68	6.04	7.44	5.58	5.66	5.78	2.07	down	6.29E-02	8.95E-01	-	-
1389474_at	Mylip	myosin regulatory light chain interacting protein	306825	Rn.1844	AA818380	5.40	3.42	4.70	3.58	3.31	3.49	2.07	down	1.48E-01	8.95E-01	-	-
1382526_at	RGD1309308	similar to RIKEN cDNA 1810074P20	313115	Rn.12784	BF281921	4.67	4.69	5.37	4.74	7.54	5.61	2.07	up	2.90E-01	8.95E-01	-	-
1383182_at	Srpk1	SFRS protein kinase 1	361811	Rn.2688	AW144184	6.79	6.32	7.14	4.94	6.01	6.16	2.07	down	8.05E-02	8.95E-01	-	-
1373323_at	Eps15l1	epidermal growth factor receptor pathway substrate 15-like 1	361120	Rn.20801	BF397730	5.28	2.44	2.42	2.26	2.41	2.32	2.07	down	3.32E-01	8.95E-01	-	-
1397274_at	---	---	---	Rn.23194	AI555780	2.66	3.84	3.03	3.09	4.31	5.27	2.07	up	1.21E-01	8.95E-01	-	-
1375395_at	Zfp324	zinc finger protein 324	365192	Rn.39324	BE116886	2.81	2.80	2.40	3.20	5.13	2.81	2.07	up	2.25E-01	8.95E-01	-	-
1375174_at	Dpy19l1	dpy-19-like 1 (C. elegans)	315496	Rn.22725	BI296653	3.87	4.57	4.50	3.23	3.23	3.34	2.07	down	1.00E-02	8.95E-01	DR	-
1395570_at	---	---	---	Rn.22097	BF548061	2.57	2.53	5.66	2.50	2.55	2.57	2.06	down	3.70E-01	8.95E-01	-	-
1368444_at	Sgta	small glutamine-rich tetratricopeptide repeat (TPR)-containing, alpha	64667	Rn.9655	NM_022703	6.07	6.70	7.21	5.85	5.85	5.15	2.06	down	6.11E-02	8.95E-01	-	-
1392966_at	Zfp410	zinc finger protein 410	314310	Rn.106064	BF396256	4.05	4.88	4.22	5.25	6.08	4.96	2.06	up	6.74E-02	8.95E-01	-	-
1369756_a_at	Slc4a4	solute carrier family 4 (anion exchanger), member 4	84484	Rn.11114	AF210250	6.85	4.70	7.51	7.02	4.15	4.76	2.06	down	4.39E-01	8.95E-01	-	-
1371310_s_at	Serpinh1	serine (or cysteine) peptidase inhibitor, clade H, member 1	29345	Rn.98159	BI285495	8.35	7.17	7.46	6.70	6.35	6.79	2.06	down	5.13E-02	8.95E-01	-	-
1372945_at	Ing3	inhibitor of growth family, member 3	312154	Rn.52988	BI296751	3.85	4.49	4.32	3.81	2.52	3.18	2.06	down	6.75E-02	8.95E-01	-	-
1390628_at	Cpeb2	cytoplasmic polyadenylation element binding protein 2	360949	Rn.162283	AI010275	5.19	4.63	5.04	3.84	3.38	4.50	2.06	down	4.68E-02	8.95E-01	DR	-
1374118_at	Lars	leucyl-tRNA synthetase	291624	Rn.7687	AA944176	5.51	6.34	6.55	7.33	6.88	7.32	2.06	up	4.05E-02	8.95E-01	UR	-
1398350_at	Basp1	brain abundant, membrane attached signal protein 1	64180	Rn.37779	BG380454	8.95	9.39	9.75	8.54	8.10	8.32	2.06	down	1.65E-02	8.95E-01	DR	-
1389197_at	Ktelc1	KTEL (Lys-Tyr-Glu-Leu) containing 1	288091	Rn.7051	BI290535	7.23	6.47	5.50	6.97	8.33	7.03	2.06	up	1.93E-01	8.95E-01	-	-
1383116_at	Alg13	asparagine-linked glycosylation 13 homolog (S. cerevisiae)	300284	Rn.29819	BI298383	3.17	3.98	3.07	4.20	5.17	3.99	2.06	up	8.78E-02	8.95E-01	-	-
1378373_at	---	---	---	Rn.112702	BF522207	5.64	6.13	3.93	5.85	7.52	5.46	2.06	up	3.20E-01	8.95E-01	-	-
1380710_at	---	---	---	Rn.211418	BF418003	5.52	2.45	2.65	2.49	2.52	2.48	2.06	down	3.52E-01	8.95E-01	-	-
1392337_at	Ccdc75	coiled-coil domain containing 75	362685	Rn.57800	BF399475	2.61	2.62	2.59	2.63	4.05	4.26	2.06	up	1.12E-01	8.95E-01	-	-
1378445_at	RGD1561537	similar to putative repair and recombination helicase RAD26L	361197	Rn.12539	BM388759	6.00	5.23	7.00	4.53	4.85	5.72	2.06	down	1.70E-01	8.95E-01	-	-
1374217_at	RGD1310686	similar to chromosome 16 open reading frame 5	360480	Rn.101805	BG375463	6.14	6.17	5.65	4.70	4.50	5.64	2.06	down	5.59E-02	8.95E-01	-	-
1380251_at	---	---	---	---	BM386280	3.26	3.22	3.25	3.93	5.02	3.90	2.06	up	4.70E-02	8.95E-01	UR	-
1397689_at	---	---	---	---	BF288445	3.07	3.43	3.03	5.00	3.19	4.46	2.06	up	1.33E-01	8.95E-01	-	-
1388750_at	Tfrc	transferrin receptor	64678	Rn.98672	BF417032	7.06	6.98	7.39	5.86	6.35	6.10	2.06	down	5.43E-03	8.95E-01	DR	-
1387026_at	Smc1a	structural maintenance of chromosomes 1A	63996	Rn.11763	NM_031683	5.50	5.76	6.21	5.12	3.53	5.69	2.06	down	2.01E-01	8.95E-01	-	-
1375032_at	Kndc1	kinase non-catalytic C-lobe domain (KIND) containing 1	361672	Rn.99397	AI412533	5.46	2.35	2.37	2.35	2.36	2.34	2.06	down	3.71E-01	8.95E-01	-	-
1369064_a_at	Scn8a	sodium channel, voltage gated, type VIII, alpha subunit	29710	Rn.91216	NM_019266	3.58	6.76	3.58	3.69	3.52	3.59	2.05	down	3.83E-01	8.95E-01	-	-
1399093_at	LOC293589	putative GTP-binding protein	293589	Rn.219621	BM392394	4.18	4.86	3.62	5.08	5.19	5.52	2.05	up	5.31E-02	8.95E-01	-	-
1383718_at	Ctbp2	C-terminal binding protein 2	81717	Rn.138124	AI011604	3.25	2.81	2.72	3.91	3.85	4.14	2.05	up	5.03E-03	8.95E-01	UR	-
1384194_at	Fzd7	Frizzled homolog 7 (Drosophila)	301440	Rn.1806	BF411054	2.39	2.38	5.49	2.39	2.39	2.37	2.05	down	3.73E-01	8.95E-01	-	-
1380980_at	RGD1309414	similar to KIAA0913 protein	361004	Rn.24931	AW523336	3.08	2.73	2.70	4.08	4.01	3.53	2.05	up	7.97E-03	8.95E-01	UR	-
1388569_at	Serpinf1	serine (or cysteine) peptidase inhibitor, clade F, member 1	287526	Rn.16993	AI179984	8.84	10.15	9.86	10.55	10.54	10.87	2.05	up	6.50E-02	8.95E-01	-	-
1376593_at	---	---	---	Rn.12150	BF283990	5.47	6.93	5.36	6.33	7.42	7.14	2.05	up	1.60E-01	8.95E-01	-	-
1371428_at	Sec61g	Sec61, gamma subunit	689134	Rn.1965	AI170002	9.62	9.96	9.35	10.52	10.64	10.88	2.05	up	7.20E-03	8.95E-01	UR	-
1377913_at	---	---	---	Rn.216727	AI598485	2.66	3.73	5.19	3.17	2.64	2.66	2.05	down	2.41E-01	8.95E-01	-	-
1373613_at	Slc48a1	solute carrier family 48 (heme transporter), member 1	300191	Rn.32236	AI408827	4.89	5.78	6.54	6.27	7.38	6.67	2.05	up	1.47E-01	8.95E-01	-	-
1376673_at	---	---	---	Rn.16704	BM391853	5.91	5.94	7.43	5.28	5.89	5.01	2.05	down	1.42E-01	8.95E-01	-	-
1391040_at	Rbbp8	retinoblastoma binding protein 8	291787	Rn.128724	AA997052	5.48	5.55	4.37	4.51	2.85	4.94	2.05	down	2.35E-01	8.95E-01	-	-
1384811_at	Hlf /// LOC690286	hepatic leukemia factor /// similar to hepatic leukemia factor	363667 /// 690286	Rn.137741	AI136334	5.94	4.11	6.32	4.63	3.49	5.14	2.05	down	2.84E-01	8.95E-01	-	-
1388104_at	Lgr4	leucine-rich repeat-containing G protein-coupled receptor 4	286994	Rn.162671	BI300274	3.68	5.03	5.05	5.37	5.59	5.90	2.05	up	9.76E-02	8.95E-01	-	-
1383250_at	Utp14a	U14 ribonucleolar ribonucleoprotein, homolog A (yeast)	317579	Rn.16331	BE105819	5.54	5.17	4.52	5.58	6.57	6.17	2.05	up	6.73E-02	8.95E-01	-	-
1385471_at	Ddx27	DEAD (Asp-Glu-Ala-Asp) box polypeptide 27	362274	Rn.206923	BF396345	4.26	6.19	6.05	5.62	8.35	5.65	2.05	up	4.00E-01	8.95E-01	-	-
1384006_at	---	---	---	---	AI045457	5.39	3.26	2.85	2.75	2.74	2.91	2.05	down	2.61E-01	8.95E-01	-	-
1367919_at	Nup210	nucleoporin 210	58958	Rn.3189	NM_053322	3.06	3.83	2.80	4.15	3.65	4.99	2.05	up	1.07E-01	8.95E-01	-	-
1392678_a_at	Dnmt3a	DNA (cytosine-5-)-methyltransferase 3 alpha	444984	Rn.92659	AA956455	7.95	7.99	5.68	8.55	8.41	7.76	2.05	up	2.68E-01	8.95E-01	-	-
1395693_at	Txndc4	thioredoxin domain containing 4 (endoplasmic reticulum)	298066	Rn.2459	BF553613	7.29	8.12	7.12	8.93	7.76	8.94	2.05	up	1.07E-01	8.95E-01	-	-
1390088_at	Slc25a46	solute carrier family 25, member 46	291709	Rn.12583	AW141957	8.05	8.49	8.48	7.21	7.02	7.69	2.05	down	1.42E-02	8.95E-01	DR	-
1373418_at	Eprs	glutamyl-prolyl-tRNA synthetase	289352	Rn.21240	BM388143	7.41	7.62	8.69	8.47	8.94	9.42	2.04	up	9.89E-02	8.95E-01	-	-
1395455_at	Hnrnph3	heterogeneous nuclear ribonucleoprotein H3 (2H9)	361838	Rn.60652	AI713082	4.56	5.78	4.69	5.74	6.53	5.85	2.04	up	8.74E-02	8.95E-01	-	-
1398796_at	Tmed10	transmembrane emp24-like trafficking protein 10 (yeast)	84599	Rn.8509	NM_053467	6.29	7.51	6.91	7.73	7.94	8.13	2.04	up	4.92E-02	8.95E-01	UR	-
1373742_at	Spsb2	spIA/ryanodine receptor domain and SOCS box containing 2	297592	Rn.162769	AW526082	5.18	3.86	3.93	3.41	3.46	3.00	2.04	down	8.57E-02	8.95E-01	-	-
1389685_at	Znf655	zinc finger protein 655	360764	Rn.6640	AI009613	5.43	5.19	5.44	6.42	6.25	6.47	2.04	up	5.99E-04	8.95E-01	UR	-
1374909_at	Ankhd1-Eif4ebp3	Ankhd1-Eif4ebp3 fusion transcript	679725	Rn.11853	BI296626	4.18	4.68	4.22	5.01	5.92	5.24	2.04	up	3.16E-02	8.95E-01	UR	-
1389133_at	Slc30a6	solute carrier family 30 (zinc transporter), member 6	298786	Rn.7189	AI104670	4.72	6.17	4.64	6.43	5.79	6.41	2.04	up	1.29E-01	8.95E-01	-	-
1391724_at	---	---	---	Rn.204785	AI102641	3.71	3.94	4.22	2.43	3.22	3.14	2.04	down	2.37E-02	8.95E-01	DR	-
1388215_at	Pvrl1	poliovirus receptor-related 1	192183	Rn.207176	BF404656	2.67	2.55	5.36	2.43	2.56	2.51	2.04	down	3.26E-01	8.95E-01	-	-
1394511_at	Mysm1	myb-like, SWIRM and MPN domains 1	298247	Rn.63856	BF419160	2.63	3.35	3.67	3.92	5.20	3.63	2.04	up	1.47E-01	8.95E-01	-	-
1382047_at	D2hgdh	D-2-hydroxyglutarate dehydrogenase	301624	Rn.49283	AA899888	5.10	2.96	2.72	2.31	2.70	2.68	2.04	down	2.52E-01	8.95E-01	-	-
1394041_at	Ankhd1-Eif4ebp3	Ankhd1-Eif4ebp3 fusion transcript	679725	Rn.11853	BI293870	6.27	7.13	6.83	6.46	5.36	5.33	2.04	down	8.35E-02	8.95E-01	-	-
1372107_at	Fhl1	four and a half LIM domains 1	25177	Rn.54261	BG673187	7.69	7.46	7.44	6.12	6.79	6.59	2.04	down	8.48E-03	8.95E-01	DR	-
1396449_at	---	---	---	---	BF560693	4.58	6.33	5.49	3.87	5.00	4.42	2.04	down	1.65E-01	8.95E-01	-	-
1372398_at	Kctd15	potassium channel tetramerisation domain containing 15	499129	Rn.23171	BG373314	4.78	3.51	2.90	5.23	4.32	4.72	2.04	up	1.69E-01	8.95E-01	-	-
1378784_at	---	---	---	Rn.12649	BE111117	6.12	7.27	6.41	7.60	7.78	7.51	2.04	up	4.44E-02	8.95E-01	UR	-
1376847_at	LOC690745	MOCO sulphurase C-terminal domain containing-like	690745	Rn.26676	BI302283	2.85	2.72	2.37	4.17	4.12	2.73	2.04	up	1.05E-01	8.95E-01	-	-
1392406_at	Ipp	intracisternal A particle-promoted polypeptide	299439	Rn.47908	BE120827	8.95	7.88	7.72	7.29	6.81	7.38	2.04	down	7.32E-02	8.95E-01	-	-
1375325_at	Adamts13	ADAM metallopeptidase with thrombospondin type 1 motif, 13	362091	Rn.105899	BF415016	3.70	4.08	4.11	5.40	5.63	3.95	2.04	up	1.32E-01	8.95E-01	-	-
1383533_at	---	---	---	---	AI715743	3.24	3.25	3.23	3.17	6.46	3.17	2.04	up	4.03E-01	8.95E-01	-	-
1374070_at	Gpx2	glutathione peroxidase 2	29326	Rn.3503	AA800587	4.22	2.38	3.70	3.77	4.65	4.95	2.04	up	1.91E-01	8.95E-01	-	-
1373620_at	Nus1	nuclear undecaprenyl pyrophosphate synthase 1 homolog (S. cerevisiae)	294400	Rn.23082	AI102038	6.21	7.65	6.43	7.26	7.81	8.29	2.04	up	1.30E-01	8.95E-01	-	-
1393565_at	RGD1563441	similar to RIKEN cDNA A030009H04	497935	Rn.148168	BF406306	5.77	2.65	2.66	2.67	2.71	2.62	2.04	down	3.79E-01	8.95E-01	-	-
1388192_at	Rwdd3	RWD domain containing 3	65026	Rn.54470	AI711028	6.61	6.52	8.03	5.97	5.43	6.69	2.03	down	1.70E-01	8.95E-01	-	-
1372098_at	Tmem141	transmembrane protein 141	499755	Rn.220638	AI172089	6.78	5.52	5.95	5.14	4.61	5.44	2.03	down	8.17E-02	8.95E-01	-	-
1371583_at	Rbm3	RNA binding motif (RNP1, RRM) protein 3	114488	Rn.18057	AI598399	7.21	7.40	8.24	8.37	8.56	8.99	2.03	up	4.82E-02	8.95E-01	UR	-
1377751_at	---	---	---	Rn.24708	AI233227	5.80	5.61	5.63	4.63	4.36	4.98	2.03	down	5.49E-03	8.95E-01	DR	-
1373652_at	RGD1564833	similar to 9630058J23Rik protein	498297	Rn.140756	BG374986	5.25	4.45	5.13	5.95	4.05	5.89	2.03	up	3.08E-01	8.95E-01	-	-
1388565_at	Spg21	spastic paraplegia 21 homolog (human)	300791	Rn.19459	BI289536	4.49	6.23	6.31	6.51	6.75	6.84	2.03	up	1.65E-01	8.95E-01	-	-
1397487_at	Xpnpep3	X-prolyl aminopeptidase (aminopeptidase P) 3, putative	685823	Rn.19478	AW535011	5.57	6.64	7.85	5.06	5.82	6.12	2.03	down	2.35E-01	8.95E-01	-	-
1383377_at	Gabpa	GA binding protein transcription factor, alpha subunit	363735	Rn.145253	BG372192	5.61	6.43	6.36	4.94	4.12	6.27	2.03	down	2.07E-01	8.95E-01	-	-
1383961_a_at	Dnajc11	DnaJ (Hsp40) homolog, subfamily C, member 11	362666	Rn.66161	AI556478	6.35	6.09	6.73	5.63	5.35	5.13	2.03	down	1.23E-02	8.95E-01	DR	-
1386344_at	Ankh	Ankylosis, progressive homolog (mouse)	114506	Rn.211841	BG662519	2.92	4.17	5.29	5.08	5.75	4.63	2.03	up	2.49E-01	8.95E-01	-	-
1367511_at	Ncstn	nicastrin	289231	Rn.51975	BI285459	7.40	7.64	7.66	7.42	4.97	7.25	2.03	down	2.68E-01	8.95E-01	-	-
1375912_at	Galnt2	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltrar	292090	Rn.144772	BI285430	5.66	6.02	7.40	5.31	4.87	5.85	2.03	down	1.66E-01	8.95E-01	-	-
1397886_at	Zc3h8	zinc finger CCCH type containing 8	311414	Rn.137486	BF564624	3.56	4.84	4.30	5.32	6.27	4.16	2.03	up	2.27E-01	8.95E-01	-	-
1368189_at	Dhcr7	7-dehydrocholesterol reductase	64191	Rn.228	NM_022389	7.88	8.28	8.07	6.73	7.19	7.25	2.03	down	7.02E-03	8.95E-01	DR	-
1383242_a_at	---	---	---	Rn.165375	BF561222	7.08	6.29	3.92	6.04	7.39	6.92	2.03	up	3.78E-01	8.95E-01	-	-
1392207_at	Luc7l	LUC7-like (S. cerevisiae)	360503	Rn.99992	BG373449	3.58	4.72	2.68	4.66	4.76	4.62	2.03	up	1.81E-01	8.95E-01	-	-
1373494_at	Bcr	breakpoint cluster region	309696	Rn.12782	BE120831	4.31	5.46	3.54	3.46	3.16	3.64	2.03	down	1.51E-01	8.95E-01	-	-
1380410_at	---	---	---	Rn.96000	AI043958	3.20	3.59	3.28	3.20	6.07	3.86	2.03	up	3.10E-01	8.95E-01	-	-
1387495_at	Tle4	transducin-like enhancer of split 4 (E(spl) homolog, Drosophila)	25565	Rn.162515	NM_019141	4.07	5.28	4.47	4.07	3.04	3.65	2.03	down	9.32E-02	8.95E-01	-	-
1386394_at	Prps1	phosphoribosyl pyrophosphate synthetase 1	29562	Rn.9761	AA956971	6.07	5.68	7.60	5.57	5.51	5.21	2.03	down	1.62E-01	8.95E-01	-	-
1379317_a_at	Pdcd11	programmed cell death 11	309458	Rn.136636	BI280308	5.05	5.18	5.97	3.67	4.88	4.60	2.03	down	9.51E-02	8.95E-01	-	-
1374682_at	Sox13	SRY (sex determining region Y)-box 13	289026	Rn.30532	BM383170	9.47	6.94	6.37	6.16	6.47	7.09	2.02	down	3.63E-01	8.95E-01	-	-
1396076_at	---	---	---	---	AW914907	5.75	2.65	2.44	2.66	2.48	2.65	2.02	down	3.97E-01	8.95E-01	-	-
1380550_at	Arid1a	AT rich interactive domain 1A (SWI-like)	297867	Rn.61077	AW251646	6.16	4.79	6.37	6.51	7.96	5.89	2.02	up	2.66E-01	8.95E-01	-	-
1391660_at	---	---	---	---	AI412900	2.87	3.80	4.96	3.15	2.58	2.85	2.02	down	1.81E-01	8.95E-01	-	-
1399142_at	---	---	---	Rn.144353	BF398045	5.23	4.26	5.56	4.68	3.27	4.06	2.02	down	1.46E-01	8.95E-01	-	-
1369958_at	Rhob	ras homolog gene family, member B	64373	Rn.2042	NM_022542	5.35	6.40	7.02	7.30	7.03	7.49	2.02	up	1.16E-01	8.95E-01	-	-
1383628_at	---	---	---	Rn.13182	BG376623	3.10	3.61	3.76	4.77	4.21	4.53	2.02	up	1.69E-02	8.95E-01	UR	-
1374432_at	---	---	---	---	BE118251	5.97	4.43	4.43	4.36	3.40	3.14	2.02	down	1.92E-01	8.95E-01	-	-
1388885_at	Aph1a	anterior pharynx defective 1 homolog A (C. elegans)	365872	Rn.22786	BI275921	4.46	6.01	5.73	5.75	7.09	6.40	2.02	up	1.73E-01	8.95E-01	-	-
1387115_at	Ikbkap	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase complex-	140934	Rn.162816	NM_080899	5.70	5.09	5.55	4.70	3.44	5.16	2.02	down	1.37E-01	8.95E-01	-	-
1393282_at	rCG_35099	spinster homolog 2	100270678	Rn.159761	AA942816	2.90	3.60	4.04	5.66	3.94	3.98	2.02	up	1.98E-01	8.95E-01	-	-
1386988_at	Deaf1	deformed epidermal autoregulatory factor 1 (Drosophila)	83632	Rn.11134	NM_031801	3.64	3.03	5.32	2.73	3.33	2.89	2.02	down	2.25E-01	8.95E-01	-	-
1399138_at	Wdr42a	WD repeat domain 42A	364050	Rn.203073	BG672805	5.10	7.45	8.16	6.84	9.98	6.93	2.02	up	5.05E-01	8.95E-01	-	-
1375640_at	Fkbp9	FK506 binding protein 9, 63 kDa	297123	Rn.105976	AI236786	7.96	8.83	8.37	8.68	10.31	9.21	2.02	up	1.36E-01	8.95E-01	-	-
1368333_at	Umod	uromodulin	25128	Rn.31982	NM_017082	9.43	9.

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)				
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG MTC
1398444_at	RGD1311742	similar to RIKEN cDNA 5133400G04	291676	Rn.136857	BF405417	4.48	6.12	4.47	5.72	6.38	5.95	1.99	up	1.63E-01	8.95E-01	- -
1395019_at	Usp38	ubiquitin specific peptidase 38	307764	Rn.17881	AI101440	5.64	5.04	6.68	5.34	5.14	3.90	1.99	down	2.06E-01	8.95E-01	- -
1368517_at	Ssbp3	single stranded DNA binding protein 3	84354	Rn.162074	NM_053358	5.93	6.62	4.67	6.65	6.84	6.71	1.99	up	1.60E-01	8.95E-01	- -
1389281_at	---	---	---	Rn.8592	BE116601	5.05	4.32	4.74	3.59	3.88	3.68	1.99	down	1.24E-02	8.95E-01	DR -
1394416_at	---	---	---	Rn.199890	AI176741	4.06	2.75	2.79	3.87	4.96	3.75	1.99	up	1.60E-01	8.95E-01	- -
1393831_at	RGD1308677	Similar to RIKEN cDNA C630028N24 gene	300723	Rn.149113	BM383212	10.42	9.11	9.88	8.91	9.31	8.22	1.99	down	1.17E-01	8.95E-01	- -
1392687_at	Pigq	phosphatidylinositol glycan anchor biosynthesis, class Q	287159	Rn.12777	BF288309	2.60	2.67	5.37	2.53	2.55	2.59	1.99	down	3.39E-01	8.95E-01	- -
1378152_at	---	---	---	Rn.148001	AI170349	4.45	5.87	5.20	4.23	4.10	4.22	1.99	down	7.47E-02	8.95E-01	- -
1370428_x_at	2 /// RT1-A3 /// RT	RT1 class Ia, locus A2 /// RT1 class I, A3 /// RT1 class Ib, locus Aw2	37 /// 24974 /// 309	Rn.40130	AJ249701	2.73	4.80	2.75	4.28	3.75	5.20	1.99	up	2.87E-01	8.95E-01	- -
1382396_at	Ubfd1	ubiquitin family domain containing 1	294554	Rn.198517	BE101337	5.50	5.65	6.63	4.63	5.00	5.18	1.99	down	6.36E-02	8.95E-01	- -
1398594_at	---	---	---	Rn.22289	AI029767	5.70	4.89	4.85	5.80	6.70	5.92	1.99	up	6.58E-02	8.95E-01	- -
1369777_a_at	Shank2	SH3 and multiple ankyrin repeat domains 2	171093	Rn.14545	NM_133440	5.39	4.01	4.19	5.46	5.72	5.39	1.99	up	9.01E-02	8.95E-01	- -
1376031_at	---	---	---	Rn.7441	BE099769	5.48	6.80	8.13	7.38	8.32	7.68	1.99	up	2.91E-01	8.95E-01	- -
1386653_at	Prickle2	prickle homolog 2 (Drosophila)	312563	Rn.85011	AW917558	5.30	3.05	3.65	5.71	4.22	5.03	1.98	up	2.84E-01	8.95E-01	- -
1383874_at	RGD1560812	RGD1560812	500640	Rn.16708	BG670036	3.19	3.25	3.35	3.25	4.22	5.29	1.98	up	1.70E-01	8.95E-01	- -
1372677_at	Dohh	deoxyhypusine hydroxylase/monooxygenase	314644	Rn.38296	BM392053	4.45	4.48	3.84	4.90	6.07	4.75	1.98	up	1.01E-01	8.95E-01	- -
1384913_at	---	---	---	Rn.149241	AI030882	6.14	6.79	6.80	5.25	5.54	5.98	1.98	down	3.12E-02	8.95E-01	DR -
1395278_at	---	---	---	Rn.206043	BI299865	5.81	3.24	3.37	3.43	3.36	2.66	1.98	down	3.20E-01	8.95E-01	- -
1381640_at	---	---	---	---	BM389537	3.07	4.32	4.74	5.16	5.81	4.12	1.98	up	2.31E-01	8.95E-01	- -
1383438_at	Sucla2	Succinate-CoA ligase, ADP-forming, beta subunit	361071	Rn.62159	H31112	5.54	6.49	5.70	3.91	5.51	5.34	1.98	down	1.67E-01	8.95E-01	- -
1395326_at	Rbm9	RNA binding motif protein 9	362950	Rn.137551	AI548193	3.61	4.11	3.12	4.50	6.18	3.12	1.98	up	3.48E-01	8.95E-01	- -
1390762_at	Cbfa2t2	core-binding factor, runt domain, alpha subunit 2, translocated to, 2 (human)	296293	Rn.92167	BE103006	5.58	4.54	4.66	4.23	3.67	3.92	1.98	down	5.35E-02	8.95E-01	- -
1374171_at	---	---	---	Rn.164431	AI170507	5.10	4.52	4.85	3.95	3.91	3.64	1.98	down	7.19E-03	8.95E-01	DR -
1386853_s_at	Stx5	syntaxin 5	65134	Rn.5782	BI286446	2.68	3.18	3.15	5.28	3.18	3.51	1.98	up	2.16E-01	8.95E-01	- -
1371327_a_at	Actg1	actin, gamma 1	287876	Rn.101464	BG666668	8.94	9.09	8.99	8.21	7.87	7.98	1.98	down	9.15E-04	8.95E-01	DR -
1383855_at	Degs2	degenerative spermatocyte homolog 2, lipid desaturase (Drosophila)	314438	Rn.166717	AI136525	8.03	5.46	7.08	6.99	7.05	3.58	1.98	down	5.12E-01	8.95E-01	- -
1396087_at	Rgnef	Rho-guanine nucleotide exchange factor	361882	Rn.33912	BG669452	2.49	3.05	2.38	4.69	3.64	2.54	1.98	up	2.06E-01	8.95E-01	- -
1395760_at	---	---	---	Rn.64137	BF552848	4.80	3.49	3.01	2.54	3.09	2.70	1.98	down	1.53E-01	8.95E-01	- -
1379194_at	Klhdc5	kelch domain containing 5	500367	Rn.203842	BF407258	5.29	2.36	2.39	2.36	2.37	2.36	1.98	down	3.69E-01	8.95E-01	- -
1379650_a_at	Gtf2ird1	GTF2I repeat domain containing 1	246770	Rn.84872	BF290483	2.87	2.91	3.02	3.25	3.91	4.59	1.98	up	6.44E-02	8.95E-01	- -
1372885_at	Cebpg	CCAAT/enhancer binding protein (C/EBP), gamma	25301	Rn.10332	AI230467	6.45	7.18	6.87	7.30	7.50	8.66	1.98	up	1.06E-01	8.95E-01	- -
1386711_a_at	Dnajc11	DnaJ (Hsp40) homolog, subfamily C, member 11	362666	Rn.66161	BF566761	5.78	5.86	6.90	5.21	5.17	5.21	1.98	down	5.26E-02	8.95E-01	- -
1395993_at	Stk16	serine/threonine kinase 16	286927	Rn.13308	AI764408	2.60	2.49	2.60	5.58	2.56	2.52	1.98	up	3.87E-01	8.95E-01	- -
1389665_at	Habp4	hyaluronan binding protein 4	361196	Rn.13726	BG375819	3.61	3.42	3.37	5.47	3.69	4.19	1.98	up	1.40E-01	8.95E-01	- -
1393606_at	RGD735140	hypothetical protein LK44	362219	Rn.11612	AI137411	3.43	4.71	4.89	5.51	6.09	4.38	1.98	up	2.21E-01	8.95E-01	- -
1394342_at	---	---	---	Rn.154103	BF557463	4.80	4.94	3.32	5.20	6.01	4.80	1.97	up	1.93E-01	8.95E-01	- -
1373403_at	LOC684871	similar to Protein C8orf4 (Thyroid cancer protein 1) (TC-1)	684871	Rn.216648	AI230625	4.57	5.11	3.94	6.33	3.92	6.31	1.97	up	3.22E-01	8.95E-01	- -
1376682_at	Lpin3	lipin 3	362261	Rn.145057	AI709541	5.89	6.64	6.41	7.88	6.62	7.38	1.97	up	8.34E-02	8.95E-01	- -
1376472_at	---	---	---	Rn.220454	AI714119	5.14	3.88	5.27	5.26	6.53	5.44	1.97	up	1.74E-01	8.95E-01	- -
1373917_at	Eif1	Eukaryotic translation termination factor 1	307503	Rn.98549	BE100459	4.96	5.90	4.58	5.89	6.04	6.46	1.97	up	8.39E-02	8.95E-01	- -
1367910_at	Smad4	SMAD family member 4	50554	Rn.9774	NM_019275	4.88	5.21	5.38	4.01	3.52	4.99	1.97	down	9.91E-02	8.95E-01	- -
1374499_at	LOC682999	hypothetical protein LOC682999	682999	Rn.217221	BM383402	5.50	5.12	6.34	4.44	3.76	5.83	1.97	down	2.40E-01	8.95E-01	- -
1388692_at	Alkbh7	alkB, alkylation repair homolog 7 (E. coli)	679944	Rn.101790	AI411102	2.94	3.77	3.37	4.73	3.75	4.54	1.97	up	6.36E-02	8.95E-01	- -
1368562_at	Sulf4a1	sulfotransferase family 4A, member 1	58953	Rn.162965	NM_031641	2.31	5.17	4.96	4.16	6.27	4.95	1.97	up	4.27E-01	8.95E-01	- -
1383500_at	Rtkp1	ribosome binding protein 1	311483	Rn.14242	BI279795	6.10	7.11	6.83	7.82	6.68	8.48	1.97	up	1.82E-01	8.95E-01	- -
1379232_at	---	---	---	---	AA955771	6.97	6.04	3.78	6.69	6.86	6.18	1.97	up	3.69E-01	8.95E-01	- -
1385230_at	Aer61	glycosyltransferase Aer61	494219	Rn.162760	BF387549	2.50	2.35	2.40	4.76	2.37	3.05	1.97	up	2.43E-01	8.95E-01	- -
1387187_a_at	Nat1	N-acetyltransferase 1 (arylamine N-acetyltransferase)	116631	Rn.37420	U17260	4.05	5.22	4.39	5.60	5.68	5.71	1.97	up	2.21E-02	8.95E-01	UR -
1376065_at	Rrs1	RRS1 ribosome biogenesis regulator homolog (S. cerevisiae)	297784	Rn.15120	AI058889	6.50	6.84	5.56	6.84	7.41	7.59	1.97	up	9.36E-02	8.95E-01	- -
1369708_a_at	Creb1	cAMP responsive element binding protein 1	81646	Rn.90061	NM_031017	2.53	2.51	5.51	2.45	2.56	2.59	1.97	down	3.83E-01	8.95E-01	- -
1382683_at	---	---	---	Rn.3564	AA891943	10.05	10.34	8.65	10.93	9.96	11.09	1.97	up	1.96E-01	8.95E-01	- -
1395073_at	Evi1	ecotropic viral integration site 1	294924	Rn.20198	BI288681	4.13	3.92	2.61	4.47	5.91	3.21	1.97	up	3.45E-01	8.95E-01	- -
1385691_at	---	---	---	---	BI293900	4.29	6.86	6.96	7.21	6.54	7.29	1.97	up	3.42E-01	8.95E-01	- -
1378644_at	---	---	---	Rn.205218	BI301465	3.49	2.36	4.13	2.36	2.36	2.34	1.97	down	1.34E-01	8.95E-01	- -
1390782_at	Clec14a	C-type lectin domain family 14, member a	314148	Rn.3862	BI295930	4.47	3.64	3.08	4.95	4.12	5.04	1.97	up	1.22E-01	8.95E-01	- -
1384801_at	NIPBL	Nipped-B homolog (Drosophila)	294787	Rn.11589	AA963592	5.15	4.92	5.28	4.17	3.58	4.68	1.97	down	4.38E-02	8.95E-01	DR -
1372547_at	RGD1306583	similar to RIKEN cDNA 2410002O22 gene	294709	Rn.15285	AI175034	4.33	6.51	5.11	5.81	6.77	6.29	1.96	up	2.35E-01	8.95E-01	- -
1395260_at	---	---	---	Rn.165750	BM383147	4.63	4.64	3.92	5.45	4.98	5.69	1.96	up	3.75E-02	8.95E-01	UR -
1376851_at	---	---	---	---	AW520324	5.38	4.01	3.85	3.15	4.18	2.98	1.96	down	1.86E-01	8.95E-01	- -
1383000_at	---	---	---	Rn.167470	AI578317	2.47	2.44	2.45	5.42	2.45	2.42	1.96	up	3.83E-01	8.95E-01	- -
1395741_at	Mgea5	Meningioma expressed antigen 5 (hyaluronidase)	154968	Rn.162539	BF548107	5.60	6.38	6.44	5.16	4.59	5.75	1.96	down	8.73E-02	8.95E-01	- -
1383263_at	Ogn	osteoglycin	291015	Rn.103114	BG664221	4.32	3.40	4.82	3.03	3.07	3.53	1.96	down	9.43E-02	8.95E-01	- -
1392244_at	---	---	---	Rn.16466	AA818153	3.31	3.86	2.50	3.46	4.84	4.29	1.96	up	1.59E-01	8.95E-01	- -
1381937_at	---	---	---	---	AI045406	3.12	4.63	4.67	5.13	5.43	4.76	1.96	up	1.49E-01	8.95E-01	- -
1372343_at	Exosc8	exosome component 8	295050	Rn.220644	BM384065	3.20	5.20	5.08	5.81	5.31	5.27	1.96	up	2.21E-01	8.95E-01	- -
1398454_at	---	---	---	Rn.167679	BM389272	3.58	4.50	5.14	5.14	5.55	5.45	1.96	up	1.08E-01	8.95E-01	- -
1395742_at	---	---	---	Rn.55610	AW920352	2.43	3.44	3.02	3.11	4.38	4.32	1.96	up	1.28E-01	8.95E-01	- -
1373457_at	Ing1	inhibitor of growth family, member 1	306626	Rn.145491	AI170649	3.60	4.03	3.65	4.23	4.96	5.00	1.96	up	2.74E-02	8.95E-01	UR -
1379961_at	---	---	---	Rn.207039	AW534043	2.30	2.29	2.30	3.51	4.00	2.29	1.96	up	1.29E-01	8.95E-01	- -
1397490_at	Spata13	spermatogenesis associated 13	305938	Rn.100403	AI237039	2.85	4.06	2.79	3.34	5.50	3.77	1.96	up	2.81E-01	8.95E-01	- -
1385342_at	Twistnb	TWIST neighbor	362728	Rn.13221	AA998932	4.76	5.73	4.11	5.56	4.88	7.06	1.96	up	2.92E-01	8.95E-01	- -
1373821_at	Slc30a5	solute carrier family 30 (zinc transporter), member 5	294698	Rn.16711	BF418332	5.36	5.97	6.50	6.12	7.22	7.40	1.96	up	1.34E-01	8.95E-01	- -
1385250_at	Chd6	chromodomain helicase DNA binding protein 6	311607	Rn.43055	BF415132	3.89	5.03	3.22	3.13	3.15	2.95	1.96	down	1.43E-01	8.95E-01	- -
1380611_at	Fkbp5	FK506 binding protein 5	361810	Rn.144288	BI284255	6.72	3.87	4.43	6.25	5.84	5.83	1.96	up	3.34E-01	8.95E-01	- -
1383042_at	---	---	---	Rn.203393	AA944383	5.25	2.34	2.35	2.35	2.34	2.34	1.96	down	3.74E-01	8.95E-01	- -
1371394_x_at	---	---	---	---	BG664827	7.24	6.93	7.72	6.72	5.88	6.39	1.96	down	4.45E-02	8.95E-01	DR -
1372352_at	Armet	arginine-rich, mutated in early stage tumors	315989	Rn.161941	AI170666	7.82	7.31	6.93	8.84	7.45	8.67	1.95	up	1.31E-01	8.95E-01	- -
1376835_at	Nfkbie	Nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, ep	316241	Rn.129334	BI293600	5.16	4.15	4.46	3.14	2.90	4.81	1.95	down	2.23E-01	8.95E-01	- -
1382732_at	Lyve1	lymphatic vessel endothelial hyaluronan receptor 1	293186	Rn.22111	BE116084	2.59	2.60	2.58	4.49	3.59	2.59	1.95	up	1.53E-01	8.95E-01	- -
1379754_at	Stau2	Staufen, RNA binding protein, homolog 2 (Drosophila)	171500	Rn.73714	AI070598	4.60	4.13	3.39	3.18	2.81	3.24	1.95	down	6.20E-02	8.95E-01	- -
1370893_at	Acaca	acetyl-coenzyme A carboxylase alpha	60581	Rn.163753	BI296153	4.83	6.34	6.56	7.36	6.81	6.45	1.95	up	1.86E-01	8.95E-01	- -
1396913_at	---	---	---	Rn.145985	AW534103	3.33	2.63	3.53	4.35	4.33	3.70	1.95	up	4.92E-02	8.95E-01	UR -
1393027_at	RGD1305235	similar to RIKEN cDNA 1700052N19	292267	Rn.50425	AI058848	4.41	4.39	5.95	4.45	3.17	4.23	1.95	down	2.13E-01	8.95E-01	- -
1375458_at	Asrgl1	Asparaginase like 1	246307	Rn.22774	AI232205	7.17	7.20	8.64	6.15	7.22	6.74	1.95	down	1.69E-01	8.95E-01	- -
1374543_at	---	---	---	Rn.16899	AA858791	5.81	4.89	4.81	4.12	4.14	4.36	1.95	down	4.33E-02	8.95E-01	DR -
1397753_at	Pigq	phosphatidylinositol glycan anchor biosynthesis, class Q	287159	Rn.12777	BG371999	4.65	5.15	5.25	4.77	4.00	4.38	1.95	up	1.39E-01	8.95E-01	- -
1374288_at	Fbxl3	FtsJ homolog 3 (E. coli)	303608	Rn.47509	BG374267	4.61	5.09	3.66	5.36	5.73	5.17	1.95	up	9.97E-02	8.95E-01	- -
1392877_at	---	---	---	---	AA859524	2.58	2.48	5.47	2.56	2.63	2.45	1.95	down	3.83E-01	8.95E-01	- -
1383783_at	Pcdh9	Protocadherin 9	306091	Rn.35614	AW551192	4.18	3.63	3.02	2.77	2.57	2.61	1.95	down	4.76E-02	8.95E-01	DR -
1379018_at	---	---	---	Rn.206038	BG375236	2.44	2.43	2.45	5.33	2.45	2.42	1.95	up	3.76E-01	8.95E-01	- -
1371633_at	Ctnnbl1	catenin, beta like 1	296320	Rn.98091	BI285669	8.01	7.78	7.17	8.52	8.70	8.62	1.95	up	2.05E-02	8.95E-01	UR -
1389448_at	04-Sep	septin 4	287606	Rn.6269	AA800004	5.10	5.86	5.23	6.79	6.17	6.11	1.95	up	3.98E-02	8.95E-01	UR -
1373281_at	Lmf1	lipase maturation factor 1	360495	Rn.59746	BM384421	3.29	3.65	3.05	3.93	3.78	5.17	1.95	up	1.12E-01	8.95E-01	- -
1398343_at	LOC498996	similar to DnaJ (Hsp40) homolog, subfamily A, member 4	498996	Rn.196543	AI104324	7.76	7.20	7.16	6.13	6.36	6.75	1.95	down	2.19E-02	8.95E-01	DR -
1377612_at	Narg1	NMDA receptor regulated 1	310399	Rn.12587	BI289992	2.40	2.39	5.60	2.39	2.40	2.72	1.95	down	4.21E-01	8.95E-01	- -
1372289_at	Slc25a12	solute carrier family 25 (mitochondrial carrier, Aralar), member 12	362145	Rn.220164	AI170792	6.27	5.18	6.07	5.18	4.09	5.36	1.95	down	1.38E-01	8.95E-01	- -
1373704_at	Aqr	aquarius homolog (mouse)	366163	Rn.37299	BI294892	4.78	4.66	4.55	5.69	5.68	5.51	1.95	up	4.01E-04	8.95E-01	UR -
1373125_at	Klc2	kinesin light chain 2	309159	Rn.13031	AW915749	6.61	3.46	3.22	3.41	3.61	3.39	1.95	down	4.30E-01	8.95E-01	- -
1370527_a_at	Csnk1d	casein kinase 1, delta	64462	Rn.8048	L07578	3.03	6.05	3.09	5.23	4.28	5.55	1.95	up	4.19E-01	8.95E-01	- -
1393093_at	RGD1560601	similar to Jumonji/ARID domain-containing protein 1C (SmcX protein)	317432	Rn.147997	BF522164	2.99	3.78	3.79	4.27	5.38	3.78	1.94	up	1.50E-01	8.95E-01	- -
1382880_at	---	---	---	Rn.136535	AI235339	2.57	3.63	4.48	2.56	2.68	2.56	1.94	down	1.59E-01	8.95E-01	- -
1391816_at	---	---	---	---	AI409106	2.73	3.12	5.12	2.69	2.80	2.61	1.94	down	2.67E-01	8.95E-01	- -
1390555_at	Socs5	suppressor of cytokine signaling 5	500616	Rn.47568	AW530876	2.52	2.95	2.32	3.05	4.22	3.39	1.94	up	7.20E-02	8.95E-01	- -
1385859_at	---	---	---	Rn.204157	AI059371	3.68	3.02	4.40	2.96	2.44	2.82	1.94	down	8.86E-02	8.95E-01	- -
1367958_a_at	Scn1b	sodium channel, voltage-gated, type I, beta	29686	Rn.4958	AF182949	5.72	5.46	5.55	4.48	5.43	3.95	1.94	down	9.56E-02	8.95E-01	- -
1397300_at	---	---	---	Rn.42112	BG371544	6.82	5.79	4.86	6.26	6.92	7.16	1.94	up	2.01E-01	8.95E-01	- -
1383555_at	RGD1560258	similar to RIKEN cDNA 4930579G22	360799	Rn.145152	AW525704	2.96	5.36	2.73	2.80	2.81	2.56	1.94	down	3.21E-01	8.95E-01	- -
1372536_at	Cabc1	chaperone, ABC1 activity of bc1 complex homolog (S. pombe)	360887	Rn.160865	AI105042	7.49	7.84	8.92	7.02	7.16	7.20	1.94	down	9.13E-02	8.95E-01	- -
1395411_at	Napri1	nicotinate phosphoribosyltransferase domain containing 1	315085	Rn.22665	AW916787	3.06	4.86	3.87	2.99	3.14	2.79	1.94	down	1.46E-01	8.95E-01	- -
1373461_at	Dam-1	Defective modulator-1	501103	Rn.145714	AI176790	6.07	5.32	5.49	4.97	3.85	5.18	1.94	up	1.12E-01	8.95E-01	- -
1368194_at	Agpat4	1-acylglycerol-3-phosphate O-acyltransferase 4 (lysophosphatidic acid acyltra	170919	Rn.41595	NM_133406	4.35	5.13	3.60	5.01	5.15	5.80	1.94	up	1.30E-01	8.95E-01	- -
1392421_at	Baz2b	bromodomain adjacent to zinc finger domain, 2B	317627	Rn.139712	AW526570	3.10	3.55	3.24	6.10	3.33	3.33	1.94	up	3.62E-01	8.95E-01	- -
1392521_at	---	---	---	Rn.165872	AI030119	5.80	5.21	5.10	4.46	5.12	3.65	1.94	down	1.16E-01	8.95E-01	- -
1388426_at	Srebf1	sterol regulatory element binding transcription factor 1	78968	Rn.221929	BF398848	2.90	3.30	4.13	4.19	4.62	4.38	1.94	up	6.68E-02	8.95E-01	- -
1368434_at	Nat1	N-acetyltransferase 1 (arylamine N-acetyltransferase)	116631	Rn.37420	NM_053853	5.00	5.44	4.67	3.58	3.74	4.91	1.94	down	1.15E-01	8.95E-01	- -
1376553_at	Nthl1	nth (endonuclease III)-like 1 (E.coli)	29541	Rn.14632	BI284353	3.02	2.97	3.04	3.00	4.41	4.48	1.94	up	1.18E-01	8.95E-01	- -
1397492_at	Lmo7	LIM domain 7	361484	Rn.98417	BF410962	2.66	2.96	4.64	2.36	2.40	2.63	1.94	down	1.98E-01	8.95E-01	- -
1385006_at	Atrx	alpha thalassemia/mental retardation syndrome X-linked (RAD54 homolog, S	246284	Rn.107838	BF393029	5.48	6.36	4.46	5.01	5.14	9.02	1.94	up	5.40E-01	8.95E-01	- -
1385852_at	Crebbp	CREB binding protein	54244	Rn.108128	BF566908	3.42	6.30	5.59	3.79	3.22	5.43	1.94	down	4.30E-01	8.95E-01	- -
1397186_at	---	---	---	Rn.176997	AW529325	2.80	3.28	2.81	5.19	3.77	2.79	1.94	up	2.53E-01	8.95E-01	- -
1392705_at	Slc9a6	solute carrier family 9 (sodium/hydrogen exchanger), member 6	302863	Rn.25009	AI412070	4.22	4.37	3.17	4.40	5.75	4.47	1.94	up	1.75E-01	8.95E-01	- -
1371362_at	Kdelr3	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 3	315131	Rn.144441	BI285402	6.93	7.58	7.47	6.70	6.10	6.32	1.94	down	2.35E-02	8.95E-01	DR -
1374921_at	Rtel1	regulator of telomere elongation helicase 1	362288	Rn.98315	BI274548	2.80	3.81	3.65	4.09	4.66	4.36	1.94	up	5.40E-02	8.95E-01	- -
1377532_at	RGD1305020	similar to Hepatocellular carcinoma-associated antigen 58 homolog	311575	Rn.38255	AW434782	6.91	6.76	6.78	6.69	4.07	6.83	1.94	down	3.49E-01	8.95E-01	- -
1382496_at	Hnf4a	hepatocyte nuclear factor 4, alpha	25735	Rn.44442	BI288517	8.79	8.54	8.34	9.31	10.65	8.56	1.93	up	2.02E-01	8.95E-01	- -
1374462_at	Kifap3	kinesin-associated protein 3	289168	Rn.163223	BI286000	7.54	7.61	8.04	6.45	7.04	6.84	1.93	down	1.48E-02	8.95E-01	DR -
1379027_at	Wwc1	WW and C2 domain containing 1	303039	Rn.101912	BM390702	6.38	7.89	7.70	8.33	8.33	8.17	1.93	up	1.17E-01	8.95E-01	- -
1398561_at	Irf2	interferon regulatory factor 2	290749	Rn.107887	BI302791	7.34	5.51	5.62	5.63	4.67	5.33	1.93	down	2.21E-01	8.95E-01	- -
1396944_at	---	---	---	Rn.162924	BM391352	4.65	5.59	3.92	5.53	6.10	5.38	1.93	up	1.48E-01	8.95E-01	- -
1367909_at	Enpp3	ectonucleotide pyrophosphatase/phosphodiesterase 3	54410	Rn.44	NM_019370	7.15	7.55	6.97	6.40	5.57	6.85	1.93	down	8.21E-02	8.95E-01	- -
1372430_at	RGD1311739	similar to RIKEN cDNA 1700037H04	311428	Rn.144317	H31887	3.54	4.26	2.97	3.47	6.40	3.75	1.93	up	3.98E-01	8.95E-01	- -
1369292_at	Hsd17b1	hydroxysteroid (17-beta) dehydrogenase 1	25322	Rn.10594	NM_012851	5.33	4.49	4.84	3.75	4.55	3.51	1.93	down	7.58E-02	8.95E-01	- -
1393047_at	Rnf217	ring finger protein 217	292188	Rn.9080	BF416560	6.52	6.37	6.77	5.10	5.69	6.02	1.93	down	3.17E-02	8.95E-01	DR -
1390259_at	Ube2d1	ubiquitin-conjugating enzyme E2D 1, UBC4/5 homolog (yeast)	361831	Rn.24837	AI231279	4.92	5.58	4.90	5.34	7.35	5.55	1.93	up	2.33E-01	8.95E-01	- -
1376755_at	Rarb	retinoic acid receptor, beta	24706	Rn.220045	BF419646	2.29	3.53	2.42	3.72	3.07	4.31	1.93	up	1.49E-01	8.95E-01	- -
1393938_at	---	---	---	Rn.167905	AI501880	4.78	7.18	6.28	6.75	7.06	7.27	1.93	up	2.55E-01	8.95E-01	- -
1392898_at	---	---	---	Rn.25071	AF011367	3.96	5.14	4.99	6.60	4.83	5.51	1.93	up	2.10E-01	8.95E-01	- -
1386426_at	Atp2b1	ATPase, Ca++ transporting, plasma membrane 1	29598	Rn.7208	AI137869	5.38	5.69	3.37	5.06	5.52	6.71	1.93	up	3.40E-01	8.95E-01	- -
1373869_at	Soat1	sterol O-acyltransferase 1	81782	Rn.59	AI012418	4.06	4.08	3.28	4.05	4.35	5.85	1.93	up	1.98E-01	8.95E-01	- -
1395346_at	Aamp	angio-associated, migratory cell

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicats)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1378160_at	Frrs1	ferric-chelate reductase 1	310810	Rn.162616	AI179412	7.58	6.03	7.75	6.88	4.83	6.85	1.91	down	3.45E-01	8.95E-01	-	-
1368052_at	Tspan8	tetraspanin 8	171048	Rn.6087	NM_133526	2.95	3.32	2.81	3.69	4.95	3.23	1.91	up	1.58E-01	8.95E-01	-	-
1395654_at	Ccdc25	coiled-coil domain containing 25	361059	Rn.136803	BI278299	5.68	7.26	7.04	7.69	7.13	7.95	1.90	up	1.67E-01	8.95E-01	-	-
1374667_at	---	---	---	Rn.23465	AW433942	2.75	2.63	2.55	2.85	4.89	2.97	1.90	up	2.34E-01	8.95E-01	-	-
1386129_at	Ing2	inhibitor of growth family, member 2	290744	Rn.20482	BF523624	6.45	5.66	6.72	5.67	4.62	5.75	1.90	down	1.28E-01	8.95E-01	-	-
1374295_at	Polrmt	polymerase (RNA) mitochondrial (DNA directed)	299604	Rn.24623	AI233096	4.67	3.92	6.86	4.81	4.05	3.80	1.90	down	3.77E-01	8.95E-01	-	-
1378825_a_at	Dennd4b	DENN/MADD domain containing 4B	361987	Rn.22411	AI011101	3.61	3.65	4.33	4.79	5.22	4.38	1.90	up	5.11E-02	8.95E-01	-	-
1394431_at	Cdadc1	cytidine and dCMP deaminase domain containing 1	361052	Rn.76647	AI704014	4.61	4.48	4.85	3.75	3.88	3.54	1.90	down	3.05E-03	8.95E-01	DR	-
1374732_at	Hexim2	hexamthylene bis-acetamide inducible 2	303580	Rn.8406	BI275803	3.25	3.30	5.24	3.30	2.61	3.09	1.90	down	2.48E-01	8.95E-01	-	-
1395027_at	---	---	---	Rn.45112	BI290841	7.39	8.20	6.54	6.98	5.83	6.55	1.90	down	1.89E-01	8.95E-01	-	-
1369439_at	Agtr1b	angiotensin II receptor, type 1b	81638	Rn.9815	NM_031009	2.55	2.63	5.16	2.52	2.57	2.48	1.90	down	3.43E-01	8.95E-01	-	-
1383572_at	Zdhhc6	zinc finger, DHHC domain containing 6	361771	Rn.19409	BF414797	4.94	6.32	5.90	7.03	6.11	6.80	1.90	up	1.34E-01	8.95E-01	-	-
1388941_at	Arnt2	archaelysin family metallopeptidase 2	360650	Rn.15408	AI172403	2.69	5.50	4.16	5.18	4.38	5.56	1.90	up	3.54E-01	8.95E-01	-	-
1390863_at	Slc19a2	solute carrier family 19 (thiamine transporter), member 2	289175	Rn.19386	BF283298	4.48	4.65	5.94	6.79	4.49	6.57	1.90	up	3.46E-01	8.95E-01	-	-
1376709_at	Slc39a8	solute carrier family 39 (metal ion transporter), member 8	295455	Rn.28321	BM388442	9.64	9.66	10.38	8.75	8.84	9.32	1.90	down	3.72E-02	8.95E-01	DR	-
1383451_at	Wsb2	WD repeat and SOCS box-containing 2	288692	Rn.4063	AA848210	5.52	5.07	5.03	3.51	4.01	5.33	1.90	down	1.77E-01	8.95E-01	-	-
1374321_at	RGD1560108	similar to RIKEN cDNA 2700081O15	499309	Rn.162490	AI227598	3.63	3.09	2.76	4.08	4.87	3.30	1.90	up	1.51E-01	8.95E-01	-	-
1387051_at	Stau1	staufen RNA binding protein homolog 1 (Drosophila)	84496	Rn.9028	NM_053436	5.25	6.61	5.10	6.33	6.33	7.07	1.90	up	1.62E-01	8.95E-01	-	-
1386967_at	Rhoq	ras homolog gene family, member Q	85428	Rn.4169	NM_053522	5.74	5.21	4.27	5.55	6.12	6.31	1.90	up	1.30E-01	8.95E-01	-	-
1374232_at	Pik3ca	phosphatidylinositol 3-kinase, catalytic, alpha polypeptide	170911	Rn.44193	BI290699	6.28	6.65	5.39	6.74	7.34	7.00	1.90	up	8.95E-02	8.95E-01	-	-
1383587_at	RGD1565496	similar to Butyrate-induced transcript 1	302783	Rn.767	BF283779	6.58	6.31	6.60	4.85	5.82	6.05	1.90	down	7.27E-02	8.95E-01	-	-
1379637_at	RGD1562639	similar to c-myc promoter binding protein	315756	Rn.21843	BG670537	4.63	4.12	3.59	4.80	4.94	5.37	1.90	up	5.55E-02	8.95E-01	-	-
1375096_at	Sfn	stratifin	313017	Rn.145079	BF418337	4.07	3.05	5.03	3.12	3.13	3.13	1.90	down	1.83E-01	8.95E-01	-	-
1374868_at	---	---	---	Rn.13827	AW535434	6.02	5.69	5.63	6.69	6.28	7.14	1.90	up	2.89E-02	8.95E-01	UR	-
1373706_at	Smarcal1	Swi/SNF related matrix associated, actin dependent regulator of chromatin, s	316477	Rn.34679	BI281981	2.45	4.24	2.57	4.48	3.58	3.97	1.90	up	2.18E-01	8.95E-01	-	-
1379246_at	Prcp	prolylcarboxypeptidase (angiotensinase C)	293118	Rn.8457	AA926318	2.33	2.33	5.11	2.33	2.35	2.32	1.90	down	3.75E-01	8.95E-01	-	-
1383409_at	---	---	---	Rn.11736	BM383214	4.26	4.73	6.66	4.58	3.25	5.06	1.90	down	3.70E-01	8.95E-01	-	-
1376191_at	Hpgd	hydroxyprostaglandin dehydrogenase 15 (NAD)	79242	Rn.6386	AA848820	7.96	6.18	7.08	5.89	6.69	5.87	1.89	down	1.87E-01	8.95E-01	-	-
1368824_at	Cald1	caldesmon 1	25687	Rn.204926	BM392106	5.44	5.71	6.56	6.62	6.46	7.40	1.89	up	1.08E-01	8.95E-01	-	-
1396030_at	---	---	---	Rn.153616	BF402684	3.22	3.29	2.46	4.43	3.59	3.72	1.89	up	6.83E-02	8.95E-01	-	-
1375042_at	Alg8	asparagine-linked glycosylation 8, alpha-1,3-glucosyltransferase homolog (S.	293129	Rn.12688	BI287504	3.94	4.23	3.43	5.10	5.10	4.16	1.89	up	7.82E-02	8.95E-01	-	-
1373252_at	LOC300225	similar to formin-like 3 protein	300225	Rn.161053	AI411930	5.15	3.93	4.59	3.12	4.64	3.14	1.89	down	2.07E-01	8.95E-01	-	-
1390562_s_at	---	---	---	Rn.203304	BE102350	2.60	2.58	2.64	2.62	5.21	2.75	1.89	up	3.36E-01	8.95E-01	-	-
1376436_at	Lysmd3	LysM, putative peptidoglycan-binding, domain containing 3	315923	Rn.146128	AI072181	4.23	5.53	3.60	4.96	5.57	5.60	1.89	up	2.03E-01	8.95E-01	-	-
1389432_at	Pbx2	pre-B-cell leukemia homeobox 2	406164	Rn.901	BE101096	5.45	6.37	6.44	7.51	6.44	7.06	1.89	up	1.08E-01	8.95E-01	-	-
1374341_at	Thap7	THAP domain containing 7	287944	Rn.25455	AI237866	5.94	6.01	4.75	5.94	7.59	5.94	1.89	up	2.50E-01	8.95E-01	-	-
1377809_at	LOC681884	similar to CG14483-PA	681884	---	BE111879	7.19	6.51	6.49	7.20	10.77	4.99	1.89	up	6.17E-01	8.95E-01	-	-
1371484_at	LOC690349	hypothetical protein LOC690349	690349	Rn.198540	BM390227	7.02	7.18	6.75	6.53	5.36	6.30	1.89	down	7.28E-02	8.95E-01	-	-
1388468_at	Cdc42se1	CDC42 small effector 1	499672	Rn.111901	BI284508	6.16	5.33	4.67	3.39	4.36	5.65	1.89	down	3.06E-01	8.95E-01	-	-
1391199_at	Fadd	Fas (TNFRSF6)-associated via death domain	266610	Rn.16183	BE100715	3.77	4.43	6.24	4.36	2.98	4.34	1.89	down	3.50E-01	8.95E-01	-	-
1371369_at	Col6a2	collagen, type VI, alpha 2	361821	Rn.128903	BI287851	3.55	2.30	4.16	2.64	2.32	2.30	1.89	down	1.75E-01	8.95E-01	-	-
1392162_at	Pspc1	Paraspeckle component 1	305910	Rn.204537	BF391447	3.09	4.28	4.16	3.49	2.55	2.73	1.89	down	1.26E-01	8.95E-01	-	-
1369493_at	Prlr	prolactin receptor	24684	Rn.9757	NM_012630	7.84	8.77	8.35	7.54	6.86	7.80	1.89	down	7.55E-02	8.95E-01	-	-
1369126_at	Ptgfr	prostaglandin F receptor	25652	Rn.97602	U47287	4.91	2.50	2.98	2.58	2.59	2.47	1.89	down	2.80E-01	8.95E-01	-	-
1373260_at	---	---	---	Rn.216654	AI412606	3.83	3.71	2.49	4.56	4.47	3.75	1.89	up	1.40E-01	8.95E-01	-	-
1391817_at	RGD1304595	similar to RIKEN cDNA 6330416G13 gene	298104	Rn.15144	AA901178	6.30	6.47	7.14	6.85	7.96	7.85	1.89	up	1.04E-01	8.95E-01	-	-
1372723_at	Ipo9	Importin 9	304817	Rn.198415	BF396318	4.69	5.03	4.79	5.90	5.55	5.81	1.89	up	3.37E-03	8.95E-01	UR	-
1370047_at	Enpp1	ectonucleotide pyrophosphatase/phosphodiesterase 1	85496	Rn.1199	NM_053535	3.56	5.10	5.26	6.26	5.27	5.14	1.89	up	2.30E-01	8.95E-01	-	-
1395648_at	---	---	---	Rn.209585	BF389377	2.90	4.29	3.99	2.91	2.61	2.91	1.89	down	1.02E-01	8.95E-01	-	-
1393108_at	---	---	---	Rn.203868	BM387813	3.08	3.05	4.82	2.66	2.39	3.15	1.89	down	2.16E-01	8.95E-01	-	-
1374670_at	RGD1307722	similar to hypothetical protein MGC20700	362824	Rn.93047	BM384543	4.18	4.45	4.48	4.91	5.77	5.18	1.89	up	2.79E-02	8.95E-01	UR	-
1376449_at	Tomm40h	translocase of outer mitochondrial membrane 40 homolog B (yeast)	304971	Rn.113744	BF407964	3.90	3.27	4.46	3.06	2.45	3.38	1.89	down	1.06E-01	8.95E-01	-	-
1372145_at	Tars	threonyl-tRNA synthetase	294810	Rn.22757	BI289683	6.79	7.24	6.55	7.70	7.27	8.36	1.89	up	7.11E-02	8.95E-01	-	-
1376652_at	C1qa	complement component 1, q subcomponent, alpha polypeptide	298566	Rn.105647	BF418967	2.55	2.45	2.42	3.48	4.15	2.54	1.89	up	1.22E-01	8.95E-01	-	-
1384478_at	Mll3	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila);	114510	Rn.22828	BF549837	2.29	2.58	5.50	2.58	2.40	2.65	1.89	down	4.24E-01	8.95E-01	-	-
1372706_at	Hexb	hexosaminidase B	294673	Rn.203067	AA892845	7.40	6.40	7.03	8.35	7.56	7.67	1.88	up	7.53E-02	8.95E-01	-	-
1378281_at	---	---	---	Rn.147627	AI709975	2.52	2.65	5.11	2.50	2.54	2.51	1.88	down	3.39E-01	8.95E-01	-	-
1386803_at	Grn	granulin	29143	Rn.5820	NM_017113	7.75	7.35	7.24	8.47	8.71	7.89	1.88	up	3.36E-02	8.95E-01	UR	-
1371737_at	Trim27	tripartite motif-containing 27	291171	Rn.8393	BI281720	5.06	5.16	5.16	5.88	6.14	6.11	1.88	up	5.20E-04	8.95E-01	UR	-
1397904_at	---	---	---	Rn.200330	BI292042	2.51	2.48	5.49	2.69	2.50	2.56	1.88	down	4.13E-01	8.95E-01	-	-
1372124_at	Eif4b	eukaryotic translation initiation factor 4B	300253	Rn.95954	BI278814	8.87	9.00	8.30	9.60	9.59	9.71	1.88	up	1.37E-02	8.95E-01	UR	-
1372946_at	RGD1562747	similar to RIKEN cDNA 1110012L19	299328	Rn.98979	AI411957	3.09	4.36	4.24	4.13	5.29	5.00	1.88	up	1.64E-01	8.95E-01	-	-
1379803_at	Lmo4	LIM domain only 4	362051	Rn.2517	AI406386	3.16	3.32	5.04	3.24	2.66	2.90	1.88	down	2.18E-01	8.95E-01	-	-
1371712_at	LOC684148	similar to snRNP core protein SMX5	684148	---	AI176503	2.74	3.77	2.75	3.53	4.09	4.37	1.88	up	9.63E-02	8.95E-01	-	-
1386474_at	---	---	---	---	H31753	4.09	2.79	4.84	3.06	3.17	2.75	1.88	down	2.11E-01	8.95E-01	-	-
1384603_at	Abca4	ATP-binding cassette, sub-family A (ABC1), member 4	310836	Rn.40415	AI602131	5.90	7.53	7.38	5.75	5.93	6.40	1.88	down	1.76E-01	8.95E-01	-	-
1373233_at	Lhfpl2	lipoma HMGIC fusion partner-like 2	294643	Rn.203042	AI013502	3.89	3.03	4.15	2.72	2.77	2.84	1.88	down	5.58E-02	8.95E-01	-	-
1397830_at	Igfbp5	insulin-like growth factor binding protein 5	25285	Rn.1593	BF399783	8.75	8.44	8.25	7.69	8.31	6.72	1.88	down	1.33E-01	8.95E-01	-	-
1373358_at	---	---	---	Rn.168809	AA998150	4.01	3.81	6.75	3.83	4.20	3.80	1.88	down	3.96E-01	8.95E-01	-	-
1369184_at	Cldn16	claudin 16	155268	Rn.43852	NM_131905	6.39	5.44	5.28	5.78	4.62	3.99	1.88	down	2.21E-01	8.95E-01	-	-
1390422_at	Pxk	PX domain containing serine/threonine kinase	306203	Rn.86175	AW920759	3.30	4.56	4.67	3.25	3.22	3.33	1.88	down	1.08E-01	8.95E-01	-	-
1382431_at	---	---	---	Rn.3724	AI103530	2.80	2.77	2.79	3.12	4.98	2.99	1.88	up	2.29E-01	8.95E-01	-	-
1372930_at	Sp110	SP110 nuclear body protein	301570	Rn.6459	AI411381	6.33	5.59	7.42	4.32	6.68	5.61	1.88	down	3.53E-01	8.95E-01	-	-
1371877_at	Dexi	dexamethasone-induced transcript	497857	Rn.15447	BM391502	5.08	6.67	7.03	7.07	7.42	7.02	1.88	up	2.10E-01	8.95E-01	-	-
1373271_at	Trappc5	trafficking protein particle complex 5	363858	Rn.162083	AI104034	8.94	8.56	7.11	6.64	6.60	6.84	1.88	down	2.74E-01	8.95E-01	-	-
1388364_at	Ndufs3	NADH dehydrogenase (ubiquinone) Fe-S protein 3	295923	Rn.1261	BG381650	9.31	9.08	9.47	9.30	12.01	9.28	1.88	up	3.77E-01	8.95E-01	-	-
1396462_at	Vps4a	vacuolar protein sorting 4 homolog A (S. cerevisiae)	246772	Rn.12477	BF388609	4.07	4.14	3.31	5.53	4.20	4.52	1.88	up	1.31E-01	8.95E-01	-	-
1377446_at	Plekha8	pleckstrin homology domain containing, family A (phosphoinositide binding sp	500132	Rn.23848	BF409122	5.14	6.36	6.38	7.02	6.65	6.94	1.88	up	1.00E-01	8.95E-01	-	-
1394182_at	Mtmr4	myotubularin related protein 4	287607	Rn.2567	AI178892	2.89	4.41	4.42	4.41	4.54	5.49	1.88	up	2.12E-01	8.95E-01	-	-
1389476_at	RGD1307100	similar to RIKEN cDNA D630029K19	294978	Rn.162572	AI010238	5.38	4.38	2.96	4.49	5.86	5.08	1.88	up	3.25E-01	8.95E-01	-	-
1395297_at	RGD1309621	similar to hypothetical protein FLJ10652	316982	Rn.101585	AI556097	4.01	4.02	5.19	5.60	6.37	3.96	1.88	up	3.25E-01	8.95E-01	-	-
1389074_at	Fchsd2	FCH and double SH3 domains 2	308864	Rn.2386	AI232737	6.52	7.51	6.81	6.13	5.66	6.34	1.87	down	6.42E-02	8.95E-01	-	-
1387151_at	Nup107	nucleoporin 107	116555	Rn.11398	NM_053830	4.69	4.25	4.99	3.91	3.69	3.61	1.87	down	1.71E-02	8.95E-01	DR	-
1382605_at	---	---	---	Rn.11455	AI234026	7.06	5.11	3.36	6.37	5.52	6.36	1.87	up	4.58E-01	8.95E-01	-	-
1379359_at	---	---	---	Rn.53959	BF407675	3.14	3.17	3.03	3.33	5.57	3.16	1.87	up	3.10E-01	8.95E-01	-	-
1383352_at	---	---	---	Rn.18262	AI029580	6.33	3.35	3.36	3.15	4.06	3.10	1.87	down	4.33E-01	8.95E-01	-	-
1386689_at	Hook2	hook homolog 2 (Drosophila)	304669	Rn.46346	BF563120	5.44	6.40	7.17	5.79	5.24	5.26	1.87	down	1.64E-01	8.95E-01	-	-
1382443_at	Pabpc4	poly A binding protein, cytoplasmic 4	298510	Rn.201330	BG376950	4.61	6.05	6.52	6.28	6.68	6.94	1.87	up	2.09E-01	8.95E-01	-	-
1373797_at	Hyal3	hyaluronoglucosaminidase 3	361987	Rn.72927	BF417430	5.48	5.92	5.68	4.65	5.03	4.70	1.87	down	6.46E-03	8.95E-01	DR	-
1387581_at	Rassf9	Ras association (RalGDS/AF-6) domain family (N-terminal) member 9	65053	Rn.30013	NM_022959	3.91	5.18	4.52	5.40	6.03	4.89	1.87	up	1.39E-01	8.95E-01	-	-
1395686_at	---	---	---	Rn.205720	BE096030	3.83	5.60	5.70	5.92	5.68	6.25	1.87	up	2.24E-01	8.95E-01	-	-
1372978_at	---	---	---	Rn.33902	BI291218	4.28	3.61	2.50	4.76	3.87	4.47	1.87	up	1.94E-01	8.95E-01	-	-
1372396_at	RGD1308026	similar to 2310047B19Rik protein	363029	Rn.21057	BE113316	8.07	7.56	9.06	8.43	8.86	8.87	1.87	up	2.14E-02	8.95E-01	UR	-
1394066_at	---	---	---	---	AA875609	6.54	7.61	6.32	6.44	4.91	6.41	1.87	down	2.33E-01	8.95E-01	-	-
1382051_at	Hscb	HscB iron-sulfur cluster co-chaperone homolog (E. coli)	360826	Rn.65800	AA955489	2.83	4.55	4.70	4.73	5.94	4.11	1.87	up	3.25E-01	8.95E-01	-	-
1371627_at	---	---	---	Rn.220061	BI277433	5.51	5.38	7.21	5.17	5.37	4.85	1.87	down	2.12E-01	8.95E-01	-	-
1384878_at	Nmt2	N-myristoyltransferase 2	291318	Rn.162255	AI501085	5.53	2.84	2.64	2.60	2.84	2.86	1.87	down	3.89E-01	8.95E-01	-	-
1389620_at	Suv420h2	suppressor of variegation 4-20 homolog 2 (Drosophila)	308345	Rn.105145	AW525235	3.46	2.88	3.44	4.46	4.16	3.87	1.87	up	2.44E-02	8.95E-01	UR	-
1377562_at	Elmod3	ELMO/CED-12 domain containing 3	297342	Rn.203170	AI711257	3.54	3.57	2.68	4.37	3.71	4.42	1.87	up	7.32E-02	8.95E-01	-	-
1398572_at	Rnmt	RNA (guanine-7-) methyltransferase	291534	Rn.20871	BI294251	5.14	6.79	5.75	7.34	6.09	6.96	1.87	up	2.12E-01	8.95E-01	-	-
1374791_at	---	---	---	Rn.203296	BF282933	2.28	2.82	4.87	2.40	2.47	2.40	1.87	down	3.18E-01	8.95E-01	-	-
1376465_at	---	---	---	Rn.24047	BI295240	5.40	4.81	4.14	5.55	5.41	6.09	1.87	up	9.69E-02	8.95E-01	-	-
1385772_at	---	---	---	Rn.211569	BF416058	2.61	2.63	2.70	2.62	5.42	2.60	1.87	up	3.92E-01	8.95E-01	-	-
1381823_at	---	---	---	Rn.52538	BE115637	3.19	2.87	2.85	2.86	5.92	2.83	1.87	up	4.33E-01	8.95E-01	-	-
1375819_at	RGD1307254	similar to RIKEN cDNA 1200011I18	298712	Rn.22071	BI299678	6.27	6.86	5.11	7.22	7.00	6.72	1.86	up	1.68E-01	8.95E-01	-	-
1375669_at	Fkbp2	FK506 binding protein 2	293702	Rn.65886	BI285619	8.83	10.16	9.47	9.86	10.40	10.89	1.86	up	1.38E-01	8.95E-01	-	-
1373334_at	Tmem129	transmembrane protein 129	305458	Rn.137870	AI406609	4.59	5.23	4.41	5.41	6.06	5.46	1.86	up	5.08E-02	8.95E-01	-	-
1371467_at	LOC293103	similar to RIKEN cDNA 0610007P06	293103	Rn.96145	AA891221	6.98	6.72	8.25	6.24	6.26	6.75	1.86	down	1.48E-01	8.95E-01	-	-
1379826_at	Ccdc107	coiled-coil domain containing 107	313496	Rn.41038	AA859429	7.35	7.66	5.85	8.11	7.50	7.95	1.86	up	2.02E-01	8.95E-01	-	-
1395797_at	---	---	---	---	AW926989	5.20	2.52	2.59	2.54	2.57	2.50	1.86	down	3.67E-01	8.95E-01	-	-
1396320_at	Crkrs	Cdc2-related kinase, arginine/serine-rich	192350	Rn.48817	BF396773	8.58	7.52	7.18	7.03	6.63	6.93	1.86	down	1.10E-01	8.95E-01	-	-
1384614_at	---	---	---	---	AI169347	9.31	9.58	8.77	10.45	9.35	10.54	1.86	up	1.17E-01	8.95E-01	-	-
1381828_at	---	---	---	Rn.159957	AA955889	2.44	3.22	4.39	2.45	2.46	2.45	1.86	down	1.89E-01	8.95E-01	-	-
1383391_a_at	C2	complement component 2	24231	Rn.98333	AI716125	5.00	2.27	2.32	2.30	2.31	2.29	1.86	down	3.77E-01	8.95E-01	-	-
1385904_at	Cirbp	cold inducible RNA binding protein	81825	Rn.28931	BG153342	8.15	7.41	7.23	8.31	8.99	8.17	1.86	up	7.74E-02	8.95E-01	-	-
1398695_at	---	---	---	Rn.209550	BF389056	3.40	2.77	3.04	3.77	4.78	3.35	1.86	up	1.24E-01	8.95E-01	-	-
1388298_at	Myl9	myosin, light chain 9, regulatory	296313	Rn.6873	BI279044	4.65	5.82	7.18	6.63	4.42	3.92	1.86	down	4.65E-01	8.95E-01	-	-
1385927_at	Hoxc4	homeo box C4	24459	Rn.12051	AA965251	3.12	3.00	3.12	4.06	3.13	4.73	1.86	up	1.26E-01	8.95E-01	-	-
1375018_at	RGD1563354	similar to hypothetical protein D630003M21	311592	Rn.52207	BF409977	5.45	3.62	4.61	4.26	3.47	3.28	1.86	down	2.15E-01	8.95E-01	-	-
1389802_at	---	---	---	Rn.25416	BF396759	4.92	4.82	2.76	4.29	5.92	4.97	1.86	up	3.51E-01	8.95E-01	-	-
1370822_at	RT1-Ba	RT1 class II, locus Ba	309621	Rn.25717	AF307302	4.00	2.65	4.57	3.21	2.63	2.70	1.86	down	2.10E-01	8.95E-01	-	-
1392304_at	---	---	---	Rn.147255	BI295865	6.00	2.88	3.86	4.18	5.79	5.46	1.86	up	4.40E-01	8.95E-01	-	-
1392441_at	Zeb2	zinc finger E-box binding homeobox 2	311071	Rn.59710	BF415891	5.07	2.42	2.44	2.42	2.42	2.41	1.86	down	3.68E-01	8.95E-01	-	-
1377979_at	---	---	---	Rn.20423	AW434228	4.42	4.11	3.51	4.92	5.70	4.11	1.86	up	1.68E-01	8.95E-01	-	-
1385891_at	---	---	---	Rn.167008	AA900322	4.79	4.67	3.69	6.34	4.71	4.78	1.86	up	2.34E-01	8.95E-01	-	-
1373850_at	Smpd3b	sphingomyelin phosphodiesterase, acid-like 3B	362619	Rn.220246	AW251315	2.75	5.35	5.32	5.39	5.36	5.35	1.86	up	3.58E-01	8.95E-01	-	-
1393150_at	Klf3	Kruppel-like factor 3 (basic)	114845	Rn.218431	BF562149	5.77	6.62	4.81	6.67	6.38	6.81	1.86	up	1.72E-01	8.95E-01	-	-
1388366_at	Mrpl4	mitochondrial ribosomal protein L4	363023	Rn.13113	BI275903	4.52	5.39	4.30	5.67	5.41	5.80	1.86	up	6.41E-02	8.95E-01	-	-
1382276_at	Ssh1	slingshot homolog 1 (Drosophila)	304580	Rn.131309	BE120171	4.66	4.66	5.29	4.09	4.65	3.19	1.86	down	1.32E-01	8.95E-01	-	-
1368390_at	Araf	ras-like murine sarcoma 3611 viral oncogene homolog	64363	Rn.1714	NM_022532	5.60	5.98	7.09	4.93	5.18	5.88	1.86	down	1.66E-01	8.95E-01	-	-
1374152_at	Wdr46	WD repeat domain 46	309628	Rn.104783	BF290018	8.36	5.86	7.10	6.12	5.31	7.21	1.86	down	3.82E-01	8.95E-01	-	-
1396152_s_at	Igfbp5	insulin-like growth factor binding protein 5	25285	Rn.1593	BF399783	8.95	8.75	8.53	7.74	8.82	6.98	1.86	down	1.79E-01	8.95E-01	-	-
1390682_at	Fnbp1	formin binding protein 1	192348	Rn.20445	BE105446	4.26	3.48	4.82	2.93	3.46	3.48	1.86	down	1.05E-01	8.95E-01	-	-
1380319_at	Invs	inversin	313228	Rn.166430	BI296604	4.14	4.16	3.31	4.07	4.45	5.77	1.86	up	2.03E-01	8.95E-01	-	-
1388917_at	Myo1d	myosin ID	25485	Rn.10376	BI279786	3.47	6.86	5.56	6.74	5.61	6.21	1.86	up	4.40E-01	8.95E-01	-	-
1394797_at	---	---	---	Rn.169991	BI276075	3.69	3.74	3.18	3.98	5.49	3.81	1.86	up	1.89E-01	8.95E-01	-	-
1373737_at	Wash2	WAS protein family homolog 2	367328	Rn.15475	BG376997	4.74	4.22	4.85	3.53	3.63	3.98	1.86	down	1.93E-02	8.95E-01	DR	-
1374848_at	Gtf3c6	general transcription factor IIIC, polypeptide 6, alpha	361858	Rn.9497	AI599867	5.19	5.46	3.39	4.94	6.14	5.65	1.86	down	2.93E-01	8.95E-01	-	-
1385191_at	---	---	---	Rn.147561	AA997253	3.50	3.61	4.48	2.75	2.53	3.64	1.86	down	1.23E-01	8.95E-01	-	-
1385350_at	---	---	---	Rn.116091	BF398122	5.75	5.07

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)				
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG MTC
1397375_at	Acsl5	Acyl-CoA synthetase long-chain family member 5	94340	Rn.105862	BM384537	4.73	5.46	4.76	5.82	5.96	5.82	1.84	up	2.29E-02	8.95E-01	UR -
1390156_a_at	Prickle2	prickle homolog 2 (Drosophila)	312563	Rn.85011	BF283671	5.12	2.70	5.41	3.35	3.18	4.05	1.84	down	3.84E-01	8.95E-01	- -
1394486_at	Rab43	RAB43, member RAS oncogene family	500249	Rn.141443	BE116701	5.51	3.23	5.41	3.66	3.95	3.89	1.84	down	3.05E-01	8.95E-01	- -
1388213_a_at	H2-T23 /// H2-T24	histocompatibility 2, T region locus 23 /// histocompatibility 2, T region locus 2	294228 /// 414784	---	AJ243973	8.78	8.85	6.36	6.54	5.06	7.75	1.84	down	4.59E-01	8.95E-01	- -
1387020_at	Cyp51	cytochrome P450, subfamily 51	25427	Rn.107152	BG664123	4.19	4.68	4.66	3.04	3.66	4.19	1.84	down	7.55E-02	8.95E-01	- -
1390246_at	---	---	---	Rn.22416	AI100769	7.68	6.13	6.45	6.03	4.99	6.60	1.84	down	2.58E-01	8.95E-01	- -
1367694_at	Hadhb	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/en	171155	Rn.11253	NM_133618	9.80	9.81	9.85	8.85	8.28	9.69	1.84	down	9.88E-02	8.95E-01	- -
1375253_at	Nfe2l1	nuclear factor, erythroid derived 2,-like 1	360610	Rn.167338	BF403837	5.55	2.48	2.46	2.60	2.57	2.69	1.84	down	4.40E-01	8.95E-01	- -
1375191_at	---	---	---	Rn.4131	AI230379	3.92	4.28	4.63	4.63	5.50	5.34	1.84	up	5.87E-02	8.95E-01	- -
1371038_at	Cebpg	CCAAT/enhancer binding protein (C/EBP), gamma	25301	Rn.10332	X64403	2.64	2.72	3.01	3.62	3.26	4.12	1.84	up	3.27E-02	8.95E-01	UR -
1393798_at	Atrx	alpha thalassemia/mental retardation syndrome X-linked (RAD54 homolog, S	246284	Rn.107838	BF398451	8.36	7.86	6.68	8.33	8.64	8.56	1.84	up	1.59E-01	8.95E-01	- -
1373072_at	---	---	---	Rn.1897	AI170552	3.85	3.89	4.05	4.57	5.50	4.37	1.84	up	6.69E-02	8.95E-01	- -
1378346_at	---	---	---	Rn.41006	AI385237	7.64	6.67	7.82	6.74	5.67	7.10	1.84	down	1.91E-01	8.95E-01	- -
1385873_at	Usp42	ubiquitin specific peptidase 42	288482	Rn.25011	AA856418	3.69	3.61	5.75	2.81	3.48	4.12	1.84	down	3.32E-01	8.95E-01	- -
1378058_at	---	---	---	Rn.199165	AI137429	6.46	6.10	5.58	6.05	3.71	5.75	1.84	down	3.22E-01	8.95E-01	- -
1392954_at	---	---	---	Rn.203240	AI029637	3.16	2.97	2.49	6.17	2.59	2.49	1.84	up	5.14E-01	8.95E-01	- -
1378941_at	---	---	---	Rn.199208	AA957447	3.46	3.45	2.85	5.16	2.89	4.34	1.84	up	2.73E-01	8.95E-01	- -
1374886_at	Bcs1l	BCS1-like (yeast)	301514	Rn.15293	BF402630	3.36	2.55	3.33	5.23	3.60	3.05	1.84	up	2.81E-01	8.95E-01	- -
1370073_at	Dnajc3	DnaJ (Hsp40) homolog, subfamily C, member 3	63880	Rn.162234	NM_022232	7.97	9.10	9.25	9.60	9.13	10.23	1.84	up	1.64E-01	8.95E-01	- -
1395211_s_at	---	---	---	---	BE118557	3.75	2.99	2.32	2.58	4.95	4.17	1.84	up	3.41E-01	8.95E-01	- -
1390662_at	Pdp2	Pyruvate dehydrogenase phosphatase isoenzyme 2	246311	Rn.220381	BF290729	6.96	6.82	6.96	6.48	5.32	6.31	1.84	down	7.39E-02	8.95E-01	- -
1372451_at	OC501098 /// Med	similar to ubiquitin specific protease 49 /// mediator complex subunit 20	316209 /// 501098	Rn.17148	AI598346	6.84	6.05	5.29	6.95	6.98	6.87	1.84	up	1.22E-01	8.95E-01	- -
1384605_at	---	---	---	Rn.170876	BF419162	4.33	6.23	6.77	6.71	6.65	6.59	1.84	up	3.03E-01	8.95E-01	- -
1370642_s_at	Pdgfb	platelet derived growth factor receptor, beta polypeptide	24629	Rn.98311	BM389426	5.27	5.16	4.22	4.01	4.07	3.93	1.84	down	5.80E-02	8.95E-01	- -
1389121_at	---	---	---	Rn.116396	AA998771	3.75	4.07	3.70	3.95	5.38	4.81	1.83	up	1.13E-01	8.95E-01	- -
1374990_at	---	---	---	Rn.144604	AI233786	4.98	4.37	3.78	4.97	5.36	5.41	1.83	up	7.93E-02	8.95E-01	- -
1374972_at	Tbc1d2	TBC1 domain family, member 2	313234	Rn.168194	BI288775	4.96	2.36	2.40	2.36	2.38	2.36	1.83	down	3.67E-01	8.95E-01	- -
1389366_at	Znf553	zinc finger protein 553	308991	Rn.12466	BI293689	6.42	6.75	5.01	4.65	6.19	4.72	1.83	down	2.98E-01	8.95E-01	- -
1387408_at	Siah2	seven in absentia 2	140593	Rn.29192	NM_134457	3.63	3.38	3.76	4.26	5.12	4.01	1.83	up	6.85E-02	8.95E-01	- -
1372462_at	Acat2	acetyl-Coenzyme A acetyltransferase 2	308100	Rn.203063	AI412322	3.83	4.81	4.90	5.40	5.94	4.82	1.83	up	1.37E-01	8.95E-01	- -
1371084_at	LOC292872	kallikrein	292872	---	BI279353	6.03	2.47	2.62	2.50	2.55	2.45	1.83	down	3.52E-01	8.95E-01	- -
1383862_at	---	---	---	Rn.199139	BF404050	5.12	2.93	3.09	3.07	2.39	3.07	1.83	down	3.03E-01	8.95E-01	- -
1369319_at	Arl6ip5	ADP-ribosylation-like factor 6 interacting protein 5	66028	Rn.64512	NM_023972	2.89	3.34	2.25	4.46	3.13	3.51	1.83	up	1.61E-01	8.95E-01	- -
1394741_at	Hnrnpa3	heterogeneous nuclear ribonucleoprotein A3	362152	Rn.107690	AI409455	5.73	6.04	5.44	6.82	6.27	6.73	1.83	up	2.25E-02	8.95E-01	UR -
1395248_at	Edem1	ER degradation enhancer, mannosidase alpha-like 1	297504	Rn.8162	BF418342	7.05	8.02	7.36	8.36	8.23	8.46	1.83	up	4.15E-02	8.95E-01	UR -
1392542_at	2se2 /// LOC10019	CDC42 small effector 2 /// hypothetical LOC100191012	00191012 /// 69102	Rn.7470	AA944330	6.59	6.76	6.71	6.74	4.81	5.89	1.83	down	1.94E-01	8.95E-01	- -
1385129_at	RGD1304904	similar to mitochondrial glycerol 3-phosphate acyltransferase	296130	Rn.52060	BE112217	2.47	2.50	5.24	2.58	2.51	2.50	1.83	down	3.97E-01	8.95E-01	- -
1371803_at	---	---	---	Rn.164151	BM384012	3.46	4.33	7.02	4.26	3.52	4.42	1.83	down	4.76E-01	8.95E-01	- -
1379696_at	---	---	---	Rn.40249	BI291833	2.71	2.67	2.73	3.05	5.01	2.67	1.83	up	2.95E-01	8.95E-01	- -
1393745_at	Orc3l	origin recognition complex, subunit 3-like (yeast)	313138	Rn.162803	BE118179	4.61	3.64	5.94	3.42	3.83	4.33	1.83	down	2.92E-01	8.95E-01	- -
1372269_at	Med6	mediator complex subunit 6	299180	Rn.97814	AI229634	4.46	3.95	3.95	3.28	2.93	3.54	1.83	down	2.41E-02	8.95E-01	DR -
1392772_at	Zfp318	zinc finger protein 318	685082	Rn.28520	BF285633	5.63	6.22	5.42	5.44	4.22	5.01	1.83	down	1.13E-01	8.95E-01	- -
1370015_at	Git1	G protein-coupled receptor kinase interacting ArfGAP 1	83709	Rn.34521	NM_031814	6.83	5.84	6.42	5.84	5.27	5.37	1.83	down	6.20E-02	8.95E-01	- -
1399152_at	Eps15	epidermal growth factor receptor pathway substrate 15	313474	Rn.162085	BF559107	7.19	7.29	8.79	7.15	6.67	6.84	1.83	down	1.80E-01	8.95E-01	- -
1385822_at	---	---	---	Rn.165914	AI030314	6.47	4.89	5.41	6.79	7.26	5.34	1.83	up	3.06E-01	8.95E-01	- -
1387822_at	Gna11	guanine nucleotide binding protein, alpha 11	81662	Rn.21925	NM_031033	4.64	3.70	5.19	5.70	5.96	4.47	1.83	up	2.41E-01	8.95E-01	- -
1370979_at	Ddx20	DEAD (Asp-Glu-Ala-Asp) box polypeptide 20	84473	Rn.137424	BF282783	4.16	5.86	5.32	6.69	5.36	5.90	1.83	up	2.42E-01	8.95E-01	- -
1373266_at	Fam107a	family with sequence similarity 107, member A	361018	Rn.1569	BG380826	4.96	2.70	2.71	2.41	2.71	2.64	1.83	down	3.15E-01	8.95E-01	- -
1393458_s_at	Phf14	PHD finger protein 14	500030	Rn.117647	BE107536	6.67	7.33	7.57	6.01	5.99	6.96	1.83	down	1.06E-01	8.95E-01	- -
1367857_at	Fads1	fatty acid desaturase 1	84575	Rn.28161	NM_053445	5.29	4.30	3.60	5.37	5.15	5.28	1.83	up	1.54E-01	8.95E-01	- -
1382921_at	Sdad1	SDA1 domain containing 1	289504	Rn.12755	AA997613	3.62	5.06	4.66	5.10	5.53	5.32	1.83	up	1.25E-01	8.95E-01	- -
1389225_at	---	---	---	Rn.15421	BI296570	4.56	3.97	4.03	4.70	5.68	4.77	1.83	up	7.67E-02	8.95E-01	- -
1389660_at	Amigo3	adhesion molecule with Ig like domain 3	316003	Rn.203829	BE096098	5.40	3.89	3.42	5.04	5.20	5.08	1.83	up	2.22E-01	8.95E-01	- -
1396137_at	Zer1	zer-1 homolog (C. elegans)	311842	Rn.23384	BF567873	2.82	3.72	4.36	5.54	4.07	3.89	1.83	up	2.75E-01	8.95E-01	- -
1382163_at	Gata3	GATA binding protein 3	85471	Rn.92350	BE118901	5.19	2.45	2.51	2.61	2.49	2.44	1.82	down	3.92E-01	8.95E-01	- -
1381977_at	---	---	---	---	BI299008	4.75	4.24	5.11	2.85	4.33	4.31	1.82	down	1.91E-01	8.95E-01	- -
1398318_at	Muc1	mucin 1, cell surface associated	24571	Rn.10779	BI274326	4.64	2.80	3.24	2.80	2.65	2.63	1.82	down	1.96E-01	8.95E-01	- -
1385043_at	Inadl	InaD-like (Drosophila)	313382	Rn.129128	AA924649	6.65	7.22	6.54	7.91	7.04	8.06	1.82	up	8.60E-02	8.95E-01	- -
1368973_at	Adar	adenosine deaminase, RNA-specific	81635	Rn.10056	NM_031006	2.50	2.49	5.39	2.50	2.50	2.78	1.82	down	4.22E-01	8.95E-01	- -
1367505_at	Znf644	zinc finger protein 644	305127	Rn.8773	AW916491	5.30	5.70	4.94	5.62	6.81	6.11	1.82	up	1.02E-01	8.95E-01	- -
1385589_at	LOC679958	similar to CG10806-PB, isoform B	679958	Rn.198171	BI288737	2.57	2.82	2.43	2.56	4.90	2.96	1.82	up	3.02E-01	8.95E-01	- -
1387604_at	Dftb	DNA fragmentation factor, beta polypeptide (caspase-activated DNase)	84359	Rn.67077	NM_053362	3.72	2.70	3.34	2.39	2.40	2.37	1.82	down	4.36E-02	8.95E-01	DR -
1374551_at	Ifi35	interferon-induced protein 35	287719	Rn.44680	BM388891	4.94	6.80	5.85	7.45	5.34	7.40	1.82	up	3.80E-01	8.95E-01	- -
1397409_s_at	Wee1	wee 1 homolog (S. pombe)	308937	Rn.208255	BE113999	5.45	5.35	5.32	6.85	5.44	6.43	1.82	up	1.10E-01	8.95E-01	- -
1368968_at	Arrb1	arrestin, beta 1	25387	Rn.34876	NM_012910	2.45	3.63	2.53	3.20	4.23	3.77	1.82	up	1.49E-01	8.95E-01	- -
1386456_at	---	---	---	Rn.133418	AA892111	6.69	4.00	3.97	2.70	6.65	2.71	1.82	down	6.16E-01	8.95E-01	- -
1387010_s_at	Scn1b	sodium channel, voltage-gated, type I, beta	29686	Rn.4958	NM_017288	7.05	7.74	7.54	7.03	6.88	5.83	1.82	down	1.13E-01	8.95E-01	- -
1383176_at	RGD1306959	similar to C11orf17 protein	361624	Rn.106344	BF561368	2.75	4.55	2.88	2.86	5.35	4.57	1.82	up	4.08E-01	8.95E-01	- -
1369285_at	Pggt1b	protein geranylgeranyltransferase type I, beta subunit	81746	Rn.10031	NM_031082	4.30	4.33	5.33	2.83	4.59	3.94	1.82	down	2.33E-01	8.95E-01	- -
1377192_a_at	Clpx	ClpX caseinolytic peptidase X homolog (E. coli)	300786	Rn.203913	BM384629	7.07	7.96	6.98	7.84	8.69	8.08	1.82	up	9.75E-02	8.95E-01	- -
1374694_at	Ankrd28	ankyrin repeat domain 28	306264	Rn.11536	BF284602	6.04	6.05	7.63	5.66	5.05	6.42	1.82	down	2.62E-01	8.95E-01	- -
1390457_at	---	---	---	Rn.45780	BM385762	5.75	4.43	5.08	4.43	3.82	4.42	1.82	down	1.17E-01	8.95E-01	- -
1385929_at	---	---	---	Rn.40398	AI229697	3.93	5.74	6.64	4.51	4.70	4.50	1.82	down	3.41E-01	8.95E-01	- -
1372286_at	Tspan6	tetraspanin 6	302313	Rn.22880	BI295929	4.82	5.87	6.45	6.64	6.65	6.44	1.82	up	1.46E-01	8.95E-01	- -
1393413_at	RGD1310984	similar to RIKEN cDNA 9430031J16	304376	Rn.150211	BI290400	3.54	2.30	3.78	2.32	2.39	2.32	1.82	down	1.33E-01	8.95E-01	- -
1372688_at	Exosc7	exosome component 7	316098	Rn.45886	BI296190	6.07	6.65	5.66	7.22	6.65	7.10	1.82	up	6.18E-02	8.95E-01	- -
1391486_at	---	---	---	Rn.19658	BM388409	3.30	5.48	7.93	5.08	3.72	5.33	1.82	down	5.78E-01	8.95E-01	- -
1374235_at	Rcan2	regulator of calcineurin 2	140666	Rn.24428	AI138048	7.20	7.00	7.38	6.92	5.30	6.77	1.82	down	1.79E-01	8.95E-01	- -
1397526_at	Gcdh	glutaryl-Coenzyme A dehydrogenase	364975	Rn.99039	AI412088	10.61	10.62	10.90	10.16	9.73	9.65	1.82	down	9.88E-03	8.95E-01	DR -
1382339_a_at	---	---	---	Rn.2853	AA875265	2.62	2.98	5.81	2.89	2.92	3.01	1.82	down	4.41E-01	8.95E-01	- -
1388071_x_at	RT1-Aw2	RT1 class Ib, locus Aw2	24737	Rn.116787	M24024	7.51	7.32	9.10	7.16	6.87	7.31	1.82	down	2.11E-01	8.95E-01	- -
1396541_at	Jmjd1c	jumonji domain containing 1C	171120	Rn.99017	BI304487	3.82	4.16	3.51	2.88	3.15	2.89	1.82	down	1.41E-02	8.95E-01	DR -
1371240_at	Tpm1	Tropomyosin 1, alpha	24851	Rn.87540	AF370889	2.42	2.43	4.95	2.40	2.43	2.39	1.82	down	3.64E-01	8.95E-01	- -
1393261_at	---	---	---	Rn.203238	AI058850	4.70	4.72	3.76	3.10	3.76	3.74	1.82	down	8.94E-02	8.95E-01	- -
1390483_at	Slc25a29	solute carrier family 25, member 29	314441	Rn.15047	BF555120	4.81	4.68	3.92	4.78	6.73	4.49	1.82	up	3.19E-01	8.95E-01	- -
1370147_at	Acmsd	aminocarboxymuconate semialdehyde decarboxylase	171385	Rn.162389	NM_134372	8.58	8.39	8.71	8.30	7.32	7.48	1.82	down	5.32E-02	8.95E-01	- -
1394020_at	---	---	---	Rn.187080	AI412164	3.63	2.25	3.02	3.39	5.44	2.65	1.82	up	4.04E-01	8.95E-01	- -
1378214_at	Galnac4s-6st	B cell RAG associated protein	286974	Rn.217784	AI101388	4.11	2.74	3.51	2.72	2.71	2.35	1.82	down	1.05E-01	8.95E-01	- -
1393738_s_at	Mfhas1	malignant fibrous histiocytoma amplified sequence 1	306508	Rn.106316	AI136864	2.62	2.62	2.66	3.01	4.86	2.61	1.82	up	2.83E-01	8.95E-01	- -
1390801_at	RGD1359349	similar to hypothetical protein MGC34760	361744	Rn.23870	AI412174	7.45	8.13	6.59	7.98	8.08	8.70	1.82	up	1.59E-01	8.95E-01	- -
1367894_at	Insig1	insulin induced gene 1	64194	Rn.772	NM_022392	5.73	6.14	5.91	4.94	5.01	5.25	1.82	down	5.03E-03	8.95E-01	DR -
1370919_at	Hnrpm	heterogeneous nuclear ribonucleoprotein M	116655	Rn.10156	AI103467	7.63	8.05	8.12	7.73	10.87	7.78	1.82	up	4.58E-01	8.95E-01	- -
1369518_at	Pik3r3	phosphoinositide-3-kinase, regulatory subunit 3 (gamma)	60664	Rn.44448	NM_022213	5.11	2.39	2.39	2.39	2.54	2.38	1.82	down	3.97E-01	8.95E-01	- -
1373640_at	Pycr2	pyrroline-5-carboxylate reductase family, member 2	364064	Rn.137266	AW525211	4.08	3.75	3.77	4.81	4.45	4.92	1.82	up	8.52E-03	8.95E-01	UR -
1380805_at	Pvrl3	Poliovirus receptor-related 3	288124	Rn.56373	BF397707	4.44	4.53	2.53	4.62	5.62	3.83	1.81	up	3.60E-01	8.95E-01	- -
1389509_at	Sap130	Sin3A associated protein	307527	Rn.46066	BE097016	5.41	4.50	3.19	4.38	5.76	5.54	1.81	up	3.28E-01	8.95E-01	- -
1379536_at	Plekha6	pleckstrin homology domain containing, family A member 6	360842	Rn.21422	BF547014	6.45	6.74	7.29	6.81	5.01	6.08	1.81	down	2.11E-01	8.95E-01	- -
1389717_at	Fam175b	family with sequence similarity 175, member B	293570	Rn.105667	AI171467	7.07	5.95	6.73	6.27	4.40	6.51	1.81	down	3.13E-01	8.95E-01	- -
1378943_at	---	---	---	Rn.203050	AI501626	5.04	2.47	2.49	2.47	2.48	2.46	1.81	down	3.71E-01	8.95E-01	- -
1397582_at	---	---	---	Rn.147739	AW529518	4.94	4.16	4.10	5.44	4.73	5.61	1.81	up	8.77E-02	8.95E-01	- -
1386879_at	Lgals3	lectin, galactoside-binding, soluble, 3	83781	Rn.764	NM_031832	2.92	2.70	2.79	4.31	3.34	3.34	1.81	up	5.92E-02	8.95E-01	- -
1372146_at	---	---	---	Rn.164176	AA851264	4.62	6.08	5.85	5.84	7.06	6.22	1.81	up	2.13E-01	8.95E-01	- -
1367835_at	Pcsk1n	proprotein convertase subtilisin/kexin type 1 inhibitor	246333	Rn.25745	NM_019279	4.94	4.68	3.35	4.89	5.81	4.85	1.81	up	2.16E-01	8.95E-01	- -
1387776_at	Tgm2	transglutaminase 2, C polypeptide	56083	Rn.10	BI275994	4.14	4.72	5.62	6.28	5.65	5.13	1.81	up	1.90E-01	8.95E-01	- -
1395166_at	Ehd2	EH-domain containing 2	361512	Rn.16016	AW252627	6.99	4.71	3.95	4.66	3.60	4.82	1.81	down	4.35E-01	8.95E-01	- -
1391451_at	Pck2	Phosphoenolpyruvate carboxykinase 2 (mitochondrial)	361042	Rn.35508	AI229633	2.86	2.85	3.21	5.01	3.19	3.29	1.81	up	2.28E-01	8.95E-01	- -
1396133_at	Itgb5	Integrin, beta 5	257645	Rn.16988	AA944325	2.38	2.37	2.39	2.38	4.96	2.38	1.81	up	3.75E-01	8.95E-01	- -
1378592_at	Trim59	tripartite motif-containing 59	365813	Rn.205621	BF396210	6.72	5.62	5.82	5.31	4.91	5.38	1.81	down	8.06E-02	8.95E-01	- -
1376035_at	Ttc7b	tetratricopeptide repeat domain 7B	362768	Rn.64438	BI274308	5.61	6.42	5.70	6.79	6.69	6.82	1.81	up	3.03E-02	8.95E-01	UR -
1381077_at	---	---	---	Rn.12430	AA998643	3.80	3.63	6.33	4.49	3.04	3.67	1.81	down	4.26E-01	8.95E-01	- -
1385543_at	---	---	---	Rn.173632	BF413374	3.89	3.97	5.98	3.55	3.52	4.21	1.81	down	2.99E-01	8.95E-01	- -
1381106_at	---	---	---	Rn.207917	BE108055	2.39	2.37	2.40	2.39	4.95	2.38	1.81	up	3.73E-01	8.95E-01	- -
1371146_at	Tfec	transcription factor EC	26296	Rn.9659	L08812	5.19	5.48	6.33	5.03	4.24	5.16	1.81	down	1.29E-01	8.95E-01	- -
1389298_at	---	---	---	Rn.199100	AI412864	4.36	4.96	4.44	5.80	4.73	5.80	1.81	up	1.01E-01	8.95E-01	- -
1385709_x_at	---	---	---	Rn.81030	AW529028	5.47	4.14	3.38	3.95	3.27	3.22	1.81	down	2.61E-01	8.95E-01	- -
1375282_at	Ccm2	cerebral cavernous malformation 2	305505	Rn.106599	BM391433	4.93	4.06	3.31	4.62	4.66	5.58	1.81	up	2.05E-01	8.95E-01	- -
1392724_at	Tom1l2	target of myb1-like 2 (chicken)	360537	Rn.807	AI705674	2.71	2.41	4.67	2.41	2.41	2.40	1.81	down	2.94E-01	8.95E-01	- -
1379250_at	Galm	galactose mutarotase (aldose 1-epimerase)	313843	Rn.83639	AI012955	6.13	7.15	7.85	6.42	5.88	6.26	1.81	down	1.79E-01	8.95E-01	- -
1388154_at	E2f5	E2F transcription factor 5	116651	Rn.52317	U31668	4.34	4.66	5.41	5.82	5.44	5.71	1.81	up	6.51E-02	8.95E-01	- -
1388872_at	---	---	---	Rn.165929	BI290053	5.01	5.03	4.39	3.30	3.81	4.75	1.81	down	1.46E-01	8.95E-01	- -
1394387_at	Ccdc34	coiled-coil domain containing 34	362187	Rn.18453	BM383527	5.31	4.37	2.53	2.52	2.61	4.52	1.81	down	4.60E-01	8.95E-01	- -
1388267_a_at	Mt1a	metallothionein 1a	24567	Rn.54397	M24327	11.64	10.96	11.38	10.97	10.10	10.35	1.81	down	5.95E-02	8.95E-01	- -
1377222_at	---	---	---	Rn.147414	BF400700	3.36	4.39	3.52	4.72	4.95	4.16	1.81	up	9.86E-02	8.95E-01	- -
1374322_at	LOC678741	similar to Zinc finger CCCH-type domain containing protein 6	678741	Rn.98823	AA893980	6.72	5.46	5.36	5.83	4.41	4.74	1.81	down	2.37E-01	8.95E-01	- -
1388798_at	Ube2e2	ubiquitin-conjugating enzyme E2E 2 (UBC4/5 homolog, yeast)	361013	Rn.15203	AW921519	5.15	6.34	5.06	5.66	6.16	7.29	1.81	up	2.49E-01	8.95E-01	- -
1396383_at	Aldh3b1	aldehyde dehydrogenase 3 family, member B1	309147	Rn.162510	BF412690	6.25	3.73	3.74	3.36	3.96	3.85	1.80	down	3.77E-01	8.95E-01	- -
1375945_at	Pkdcc	pikachurin domain containing 2	361282	Rn.36200	BG375285	8.28	8.73	8.89	7.80	7.20	8.35	1.80	down	8.86E-02	8.95E-01	- -
1392725_at	A2ld1	AIG2-like domain 1	290500	Rn.17263	AA924588	2.41	3.69	4.28	2.52	2.35	2.95	1.80	down	2.17E-01	8.95E-01	- -
1370597_at	Stx17	syntaxin 17	252853	Rn.204688	AF115435	3.36	3.58	2.77	3.59	5.10	3.58	1.80	up	2.03E-01	8.95E-01	- -
1393953_at	Epsti1	EPSB-like 3	295361	Rn.138008	BI284392	2.68	2.87	4.40	2.85	4.89	4.75	1.80	up	3.75E-01	8.95E-01	- -
1367599_at	Atp5g1	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit C1 (subun	29754	Rn.3357	NM_017311	7.09	7.64	7.00	8.01	8.01	8.25	1.80	up	1.65E-02	8.95E-01	UR -
1381043_at	---	---	---	Rn.169208	AI639256	2.43	2.47	2.47	4.98	2.45	2.48	1.80	up	3.69E-01	8.95E-01	- -
1396581_at	---	---	---	Rn.172471	BF389197	3.12	3.19	3.36	3.20	4.89	4.13	1.80	up	1.61E-01	8.95E-01	- -
1397881_at	Ccdc88a	coiled coil domain containing 88A	305605	Rn.163266	AI572768	5.08	5.08	5.68	3.27	4.99	5.03	1.80	down	2.37E-01	8.95E-01	- -
1379524_at	Wdr34	WD repeat domain 34	296618	Rn.116904	AI136576	4.63	6.44	6.27	6.87	6.64	6.39	1.80	up	2.25E-01	8.95E-01	- -
1392595_at	Znf618	zinc finger protein 618	313253	Rn.25240	AI228656	2.45	3.89	5.00	2.95	2.95	2.89	1.80	down	3.14E-01	8.95E-01	- -
1384465_at	Papc1	paraspeckle component 1	305910	Rn.204537	AI136893	8.25	7.27	7.89	7.36	6.22	7.28	1.80	down	1.43E-01	8.95E-01	- -
1376468_at	Hars	histidyl-tRNA synthetase	307492	Rn.35537	AI411501	7.63	8.16	8.02	9.10	8.47	8.80	1.80	down	2.50E-02	8.95E-01	UR -
1379336_at	---	---	---	Rn.45452	BF289150	8.39	7.38	7.35	6.37	6.75	7.45	1.80	down	1.44E-01	8.95E-01	- -
1393987_s_at	Grk6	G protein-coupled receptor kinase 6	59076	Rn.10633	BI274742	8.55	9.22	9.19	9.82	9.79	9.

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1391179_at	---	---	---	Rn.209805	BF390958	4.79	2.55	2.42	2.42	2.42	2.41	1.79	down	3.37E-01	8.95E-01	-	-
1372120_at	Uba5	ubiquitin-like modifier activating enzyme 5	300968	Rn.18210	AI408025	5.16	4.65	4.04	5.15	5.45	5.75	1.79	up	8.54E-02	8.95E-01	-	-
1395412_at	Caprin1	cell cycle associated protein 1	362173	Rn.22572	BF546337	8.12	7.76	9.22	7.27	7.32	8.00	1.79	down	1.68E-01	8.95E-01	-	-
1379747_at	Prss35	Protease, serine, 35	315866	Rn.161916	AA866443	2.52	3.86	3.67	2.53	2.55	2.46	1.79	down	1.17E-01	8.95E-01	-	-
1374496_at	RGD1310827	similar to RIKEN cDNA 1200009O22; EST AI316813	362364	Rn.25045	BG380570	2.87	4.55	5.14	4.30	2.97	2.79	1.78	down	3.71E-01	8.95E-01	-	-
1398566_at	---	---	---	Rn.161133	AW526014	2.34	2.33	4.84	2.33	2.34	2.33	1.78	down	3.74E-01	8.95E-01	-	-
1373577_at	Nrp1	Neuropilin 1	246331	Rn.10815	BE116566	7.36	7.09	6.29	7.73	7.89	7.63	1.78	up	6.54E-02	8.95E-01	-	-
1368004_at	Mrpl23	mitochondrial ribosomal protein L23	64360	Rn.1608	NM_022529	7.64	7.50	7.56	7.04	5.82	7.34	1.78	down	1.48E-01	8.95E-01	-	-
1368358_a_at	Ptprr	protein tyrosine phosphatase, receptor type, R	94202	Rn.6277	NM_053594	2.49	2.39	2.41	2.44	4.94	2.42	1.78	up	3.76E-01	8.95E-01	-	-
1393269_at	---	---	---	Rn.24292	BF3860949	2.50	2.93	4.36	2.40	2.40	2.48	1.78	down	2.13E-01	8.95E-01	-	-
1372313_at	Gpr89	G protein-coupled receptor 89	362003	Rn.160685	BI275972	4.94	6.07	4.42	4.92	6.64	6.37	1.78	up	3.14E-01	8.95E-01	-	-
1368031_at	Nolc1	nucleolar and coiled-body phosphoprotein 1	64896	Rn.9517	BI290791	6.37	6.32	4.98	7.27	6.34	6.56	1.78	up	1.94E-01	8.95E-01	-	-
1371988_at	Man1a1	mannosidase, alpha, class 1A, member 1	294410	Rn.3576	AA892549	4.20	5.55	5.53	5.35	6.64	5.80	1.78	up	2.28E-01	8.95E-01	-	-
1377976_at	---	---	---	---	AI137539	5.62	3.20	2.85	3.28	2.96	2.93	1.78	down	3.96E-01	8.95E-01	-	-
1384230_at	LOC683980	similar to keratinocytes associated protein 3	683980	Rn.202673	AI576177	3.28	5.00	5.11	5.11	5.47	5.31	1.78	up	2.38E-01	8.95E-01	-	-
1374221_at	Slc29a3	Solute carrier family 29 (nucleoside transporters), member 3	353307	Rn.15870	BM385468	6.46	7.19	7.92	5.99	6.10	6.99	1.78	down	1.91E-01	8.95E-01	-	-
1371891_at	RGD1308430	similar to 1700123O20Rik protein	361038	Rn.2583	BG371476	4.99	4.29	5.11	5.48	6.25	5.15	1.78	up	1.14E-01	8.95E-01	-	-
1379397_at	Rora	RAR-related orphan receptor alpha	300807	Rn.43530	BE106199	7.41	8.01	6.65	7.61	8.44	8.52	1.78	up	1.64E-01	8.95E-01	-	-
1390566_a_at	Ckmt1	creatine kinase, mitochondrial 1, ubiquitous	29593	Rn.155589	BI301453	7.73	4.99	6.01	6.13	6.34	3.77	1.78	down	5.09E-01	8.95E-01	-	-
1370932_at	Lrp4	low density lipoprotein receptor-related protein 4	83469	Rn.21381	AI070976	6.86	6.36	7.35	5.53	5.46	7.09	1.78	down	2.40E-01	8.95E-01	-	-
1384117_at	RGD1564887	similar to 9130011E15Rik protein	499363	Rn.23632	BF556676	3.05	4.30	4.26	5.16	3.95	4.99	1.78	up	2.11E-01	8.95E-01	-	-
1392528_at	Csf2ra	Granulocyte-macrophage colony stimulating receptor alpha	652957	Rn.216620	AI555854	6.12	5.95	4.50	5.20	2.78	6.10	1.78	down	4.97E-01	8.95E-01	-	-
1396451_at	---	---	---	Rn.148773	BF393275	2.84	2.52	2.58	3.66	2.84	3.95	1.78	up	7.49E-02	8.95E-01	-	-
1368192_at	Cxcr3	chemokine (C-X-C motif) receptor 3	84475	Rn.24787	NM_053415	2.39	2.38	4.87	2.38	2.39	2.37	1.78	down	3.73E-01	8.95E-01	-	-
1379026_at	Rhbdl3	rhomboid, veinlet-like 3 (Drosophila)	287556	Rn.20693	AI072008	3.88	4.99	3.76	4.11	5.54	5.47	1.78	up	2.42E-01	8.95E-01	-	-
1377232_at	---	---	---	Rn.199467	BF406608	8.29	8.14	6.38	8.68	8.19	8.44	1.78	up	2.56E-01	8.95E-01	-	-
1380780_at	Smc3	structural maintenance of chromosomes 3	29486	Rn.11074	NM_053483	5.79	5.92	6.79	5.54	4.25	6.23	1.78	down	2.76E-01	8.95E-01	-	-
1387952_a_at	Cd44	Cd44 molecule	25406	Rn.1120	AF065147	2.85	3.00	2.93	3.38	3.84	4.05	1.78	up	1.45E-02	8.95E-01	UR	-
1375869_at	Ulk1	Unc-51 like kinase 1 (C. elegans)	360827	Rn.24509	AI603439	6.04	6.55	5.50	6.92	7.03	6.63	1.78	up	6.24E-02	8.95E-01	-	-
1387064_at	Pxmp3	peroxisomal membrane protein 3	29534	Rn.4065	NM_017234	3.79	4.53	4.30	3.96	5.98	5.17	1.78	up	2.56E-01	8.95E-01	-	-
1383722_at	Prosc	proline synthetase co-transcribed homolog (bacterial)	306544	Rn.1880	H53436	4.31	5.06	4.40	4.64	6.38	5.25	1.78	up	2.14E-01	8.95E-01	-	-
1375392_at	---	---	---	Rn.207343	BF405277	2.43	2.44	4.94	2.44	2.45	2.43	1.78	down	3.77E-01	8.95E-01	-	-
1375382_at	Mdc1	mediator of DNA damage checkpoint 1	309595	Rn.106312	BE120346	2.41	2.43	2.43	3.24	4.06	2.45	1.78	up	1.47E-01	8.95E-01	-	-
1381336_at	---	---	---	Rn.14788	BF408248	5.03	4.68	5.62	5.02	6.45	6.36	1.78	up	1.97E-01	8.95E-01	-	-
1381515_at	---	---	---	Rn.47887	AW532132	2.69	2.56	5.01	2.58	2.60	2.60	1.78	down	3.55E-01	8.95E-01	-	-
1385252_at	Trim6	tripartite motif-containing 6	293294	Rn.212480	BI280655	4.48	3.56	2.69	2.78	2.75	2.72	1.78	down	1.82E-01	8.95E-01	-	-
1390520_at	Dnajb3	DnaJ (Hsp40) homolog, subfamily B, member 3	680216	Rn.198850	AI180165	2.33	2.62	5.00	3.69	5.05	3.69	1.78	up	4.36E-01	8.95E-01	-	-
1398137_at	---	---	---	Rn.205136	AI500919	4.15	3.30	2.56	2.64	2.56	2.32	1.78	down	1.51E-01	8.95E-01	-	-
1389135_at	Ctps2	CTP synthase II	619580	Rn.13683	AW140637	5.50	6.80	6.14	7.16	7.13	6.64	1.78	up	1.13E-01	8.95E-01	-	-
1398771_at	Slc3a2	solute carrier family 3 (activators of dibasic and neutral amino acid transport),	50567	Rn.5801	NM_019283	6.08	5.29	5.52	5.68	6.92	6.79	1.78	up	1.45E-01	8.95E-01	-	-
1392324_at	Epb82	EPSB-like 2	361673	Rn.23793	AI137983	5.02	5.73	6.74	4.88	4.81	5.30	1.78	down	1.88E-01	8.95E-01	-	-
1389217_at	Rfng	RFNG O-fucosylpeptide 3-beta-N-acetylglucosaminyltransferase	60433	Rn.168817	AI599568	5.53	5.28	4.66	5.91	6.43	5.61	1.78	up	7.84E-02	8.95E-01	-	-
1375789_at	Pthr1	Parathyroid hormone receptor 1	56813	Rn.48025	BE100627	5.40	5.53	7.83	6.05	4.96	5.26	1.78	down	3.87E-01	8.95E-01	-	-
1378985_at	Pust1	Pseudouridylate synthase-like 1	362681	Rn.139877	AW533698	5.62	2.88	2.53	3.06	2.75	2.74	1.78	down	4.46E-01	8.95E-01	-	-
1388674_at	Cdkn1a	cyclin-dependent kinase inhibitor 1A (p21, Cip1)	114851	Rn.10089	AI010427	2.43	3.83	2.45	2.47	5.08	3.65	1.78	up	4.02E-01	8.95E-01	-	-
1376896_at	RGD1309308	Similar to RIKEN cDNA 1810074P20	313115	Rn.12784	AI227699	4.25	4.31	4.99	5.70	4.99	5.34	1.78	up	5.84E-02	8.95E-01	-	-
1373025_at	C1qc	complement component 1, q subcomponent, C chain	362634	Rn.2393	AI411618	3.32	2.68	4.20	4.56	4.92	3.22	1.78	up	2.90E-01	8.95E-01	-	-
1397820_at	---	---	---	Rn.199355	BF553729	2.42	3.69	3.27	3.18	5.51	3.18	1.78	up	3.92E-01	8.95E-01	-	-
1374634_at	Plh1d2	PIH1 domain containing 2	315645	Rn.105880	AA818131	3.18	4.38	3.05	4.16	4.40	4.53	1.78	up	1.30E-01	8.95E-01	-	-
1373057_at	---	---	---	Rn.7646	AI229142	6.13	5.97	5.45	4.67	5.15	5.23	1.78	down	3.76E-02	8.95E-01	DR	-
1379560_at	Nsd1	nuclear receptor binding SET domain protein 1	36764	Rn.19435	BE099674	3.53	4.44	6.34	4.45	3.16	4.21	1.78	down	4.19E-01	8.95E-01	-	-
1397672_at	---	---	---	Rn.51837	AT006319	5.55	5.56	5.83	4.63	4.79	5.04	1.77	down	5.16E-03	8.95E-01	DR	-
1384557_at	---	---	---	Rn.203305	AI136444	4.03	4.19	3.98	4.52	5.45	4.71	1.77	up	4.59E-02	8.95E-01	UR	-
1377519_a_at	691036 /// RGD155	similar to SET binding factor 2 /// similar to SET binding factor 2	308934 /// 691036	Rn.37595	AI059932	2.67	3.35	4.75	2.61	2.54	3.14	1.77	down	2.66E-01	8.95E-01	-	-
1396313_at	---	---	---	Rn.26625	AI111750	2.76	2.91	3.03	3.75	4.40	3.04	1.77	up	1.09E-01	8.95E-01	-	-
1373542_at	Sphk2	sphingosine kinase 2	308589	Rn.41053	BM386306	6.73	7.39	7.45	6.28	6.44	6.37	1.77	down	2.50E-02	8.95E-01	DR	-
1389760_at	Pcgf6	polycomb group ring finger 6	309457	Rn.16897	AA858786	4.71	2.81	2.82	2.38	2.62	2.86	1.77	down	2.69E-01	8.95E-01	-	-
1395766_at	---	---	---	---	BM391518	3.59	4.56	2.89	2.73	2.81	3.02	1.77	down	1.68E-01	8.95E-01	-	-
1368087_a_at	Ptpn21	protein tyrosine phosphatase, non-receptor type 21	171070	Rn.11310	NM_133545	7.33	7.21	5.68	8.19	7.38	7.12	1.77	up	2.55E-01	8.95E-01	-	-
1382634_at	Med14	mediator complex subunit 14	317343	Rn.17025	AI044343	5.19	6.52	5.42	6.21	6.56	6.85	1.77	up	1.41E-01	8.95E-01	-	-
1377379_at	Irf6	interferon regulatory factor 6	364081	Rn.12385	BF410603	6.36	6.60	6.56	7.45	6.79	7.76	1.77	up	4.99E-02	8.95E-01	UR	-
1368420_at	Cp	ceruloplasmin	24268	Rn.32777	NM_012532	2.81	3.99	2.83	4.04	4.20	3.87	1.77	up	1.10E-01	8.95E-01	-	-
1367497_at	Ptdss1	phosphatidylserine synthase 1	314553	Rn.103732	AA851302	6.11	6.35	8.03	6.00	5.73	6.29	1.77	down	2.58E-01	8.95E-01	-	-
1394435_at	Vangl1	vang-like 1 (van gogh, Drosophila)	690366	Rn.35269	AI703874	5.64	5.95	6.33	5.02	4.68	5.76	1.77	down	9.40E-02	8.95E-01	-	-
1391827_at	Flnb	filamin, beta	306204	Rn.1761	AI013675	4.20	4.58	3.67	4.31	5.49	5.11	1.77	up	1.33E-01	8.95E-01	-	-
1381705_at	---	---	---	Rn.220617	BE110067	4.89	2.64	2.85	2.65	2.63	2.63	1.77	down	3.13E-01	8.95E-01	-	-
1389497_at	Smyd5	SET and MYND domain containing 5	312503	Rn.3127	BF414808	5.05	3.46	3.31	2.72	2.70	3.93	1.77	down	2.99E-01	8.95E-01	-	-
1378717_at	---	---	---	Rn.57341	BF390952	5.00	2.57	2.56	2.51	2.56	2.59	1.77	down	3.68E-01	8.95E-01	-	-
1377925_at	---	---	---	Rn.35414	BE105762	5.69	5.84	5.96	3.46	6.17	5.39	1.77	down	3.66E-01	8.95E-01	-	-
1377143_at	Slc35b1	solute carrier family 35, member B1	287642	Rn.124916	BM388792	5.97	6.28	5.51	6.57	6.83	6.82	1.77	up	2.62E-02	8.95E-01	UR	-
1382099_at	Vps26a	vacuolar protein sorting 26 homolog A (S. pombe)	361846	Rn.3673	BI289595	6.08	5.94	4.51	6.47	6.22	6.30	1.77	up	1.80E-01	8.95E-01	-	-
1397870_at	---	---	---	Rn.146439	BF390925	6.41	3.37	2.83	3.33	3.33	3.49	1.77	down	5.01E-01	8.95E-01	-	-
1373339_at	Letmd1	LETM1 domain containing 1	681352	Rn.102946	AI599410	6.20	5.34	5.61	5.57	8.62	5.43	1.77	up	4.85E-01	8.95E-01	-	-
1378210_at	Mll1	myeloid/lymphoid or mixed-lineage leukemia 1	315606	Rn.62341	BE114473	5.24	5.91	7.64	5.94	4.94	5.44	1.77	down	3.47E-01	8.95E-01	-	-
1372729_at	Procr	protein C receptor, endothelial	362248	Rn.144312	AI137406	3.82	2.55	2.67	5.41	2.82	3.48	1.77	up	4.22E-01	8.95E-01	-	-
1377926_at	Centg2	centaurin, gamma 2	316611	Rn.25493	AA924061	2.50	2.43	5.29	7.00	2.44	3.25	1.77	up	6.52E-01	8.97E-01	-	-
1375461_at	Atp5sl	ATP5S-like	361520	Rn.31959	BI285588	4.86	3.83	5.51	3.56	4.03	4.15	1.77	down	1.89E-01	8.95E-01	-	-
1378824_at	---	---	---	Rn.15216	BF389173	4.34	4.86	5.36	3.90	3.04	5.16	1.77	down	2.96E-01	8.95E-01	-	-
1379918_at	---	---	---	Rn.203894	BE115821	3.79	4.33	5.72	3.82	3.86	3.69	1.77	down	2.27E-01	8.95E-01	-	-
1386293_at	---	---	---	---	AA892593	4.42	7.19	4.30	4.43	6.92	7.03	1.77	up	5.52E-01	8.95E-01	-	-
1398886_at	RGD1563348	similar to Selenoprotein H	502642	Rn.63	BI285703	6.44	7.80	7.72	7.94	8.14	8.34	1.77	up	1.46E-01	8.95E-01	-	-
1389838_at	Fam160a2	family with sequence similarity 160, member A2	293343	Rn.22692	BG380701	2.44	2.45	2.46	3.36	4.02	2.44	1.77	up	1.48E-01	8.95E-01	-	-
1387785_at	Mtpn	myotrophin	79215	Rn.3239	AI711244	7.02	7.60	7.85	6.31	6.39	7.29	1.77	down	1.08E-01	8.95E-01	-	-
1381943_at	Chic2	Cysteine-rich hydrophobic domain 2	83835	Rn.106037	BE112096	2.39	2.63	2.36	5.05	2.40	2.39	1.77	up	4.08E-01	8.95E-01	-	-
1383670_at	Hoxb6	homeo box B6	497986	Rn.203800	BI303863	4.90	5.92	4.57	6.77	5.73	5.35	1.77	up	2.35E-01	8.95E-01	-	-
1390645_at	---	---	---	Rn.34130	AI406837	2.46	3.16	4.20	2.45	2.48	2.43	1.77	down	1.79E-01	8.95E-01	-	-
1398371_at	Ccdc132	coiled-coil domain containing 132	312083	Rn.1875	AI409075	5.87	4.80	5.58	3.99	5.00	4.79	1.77	down	1.38E-01	8.95E-01	-	-
1368651_at	Pklr	pyruvate kinase, liver and RBC	24651	Rn.48821	NM_012624	8.07	8.36	7.94	7.02	7.32	7.55	1.77	down	1.43E-02	8.95E-01	DR	-
1369952_at	Pabpc1	polyA binding protein, cytoplasmic 1	171350	Rn.127813	NM_134353	7.99	8.47	7.93	8.66	9.05	9.14	1.77	up	2.21E-02	8.95E-01	UR	-
1393203_at	Fam136a	family with sequence similarity 136, member A	297415	Rn.198157	BG665886	5.38	4.98	5.15	3.56	4.22	5.26	1.77	down	1.80E-01	8.95E-01	-	-
1368102_at	Hsd11b2	hydroxysteroid 11-beta dehydrogenase 2	25117	Rn.10186	NM_017081	8.26	6.00	5.83	7.32	6.17	4.15	1.77	down	5.35E-01	8.95E-01	-	-
1373263_at	Wdr74	WD repeat domain 74	690229	Rn.14606	AW523737	7.07	6.84	5.96	7.54	6.97	7.82	1.77	up	1.23E-01	8.95E-01	-	-
1389645_at	Rilpl1	Rab interacting lysosomal protein-like 1	304469	Rn.62627	AW916694	2.77	2.69	2.68	2.72	4.45	3.42	1.77	up	1.77E-01	8.95E-01	-	-
1382466_at	Snrnp48	small nuclear ribonucleoprotein 48k (U11/U12)	291060	Rn.39699	BF407231	5.70	6.54	6.44	7.95	6.76	6.42	1.76	up	1.99E-01	8.95E-01	-	-
1391637_at	Arhgap15	Rho GTPase activating protein 15	295635	Rn.15607	AI178168	5.01	2.44	2.50	2.50	2.50	2.49	1.76	down	3.88E-01	8.95E-01	-	-
1388900_at	RGD1566118	RGD1566118	361797	Rn.128917	BG381414	4.93	5.61	4.86	5.47	6.30	6.09	1.76	up	7.78E-02	8.95E-01	-	-
1372884_at	Large	like-glycosyltransferase	361368	Rn.24338	BG381486	5.45	6.31	5.14	6.26	6.45	6.64	1.76	up	8.84E-02	8.95E-01	-	-
1367871_at	Cyp2e1	cytochrome P450, family 2, subfamily e, polypeptide 1	25086	Rn.1372	NM_031543	9.46	8.52	7.90	9.50	9.45	9.40	1.76	up	1.45E-01	8.95E-01	-	-
1397918_at	---	---	---	---	BF414420	6.57	6.71	6.45	7.11	7.01	8.06	1.76	up	7.52E-02	8.95E-01	-	-
1373119_at	Kctd3	potassium channel tetramerisation domain containing 3	305055	Rn.19263	BF407757	4.02	4.92	5.32	3.90	3.96	4.35	1.76	down	1.41E-01	8.95E-01	-	-
1379565_at	Creb3l2	cAMP responsive element binding protein 3-like 2	362339	Rn.23031	AA956791	5.05	5.28	3.86	4.81	6.66	5.18	1.76	up	3.16E-01	8.95E-01	-	-
1389414_at	---	---	---	Rn.13770	BI285335	3.04	2.58	3.04	3.46	3.10	4.56	1.76	up	1.53E-01	8.95E-01	-	-
1382944_at	---	---	---	Rn.7257	AA891161	5.23	6.39	6.07	6.03	6.67	7.45	1.76	up	2.02E-01	8.95E-01	-	-
1368511_at	Bhlhe41	basic helix-loop-helix family, member e41	117095	Rn.10784	NM_133303	3.72	6.73	3.73	4.69	5.98	5.96	1.76	up	4.94E-01	8.95E-01	-	-
1374876_at	Leprotl1	leptin receptor overlapping transcript-like 1	361160	Rn.94288	BE098368	5.73	6.98	6.01	7.66	7.07	6.44	1.76	up	1.87E-01	8.95E-01	-	-
1387703_a_at	Usp2	ubiquitin specific peptidase 2	115771	Rn.203590	AF106659	8.24	7.21	7.91	8.98	7.78	9.06	1.76	up	1.86E-01	8.95E-01	-	-
1379368_at	Bcl6	B-cell CLL/lymphoma 6	303836	Rn.20571	AI237606	5.03	8.48	6.60	4.86	6.67	6.13	1.76	down	5.11E-01	8.95E-01	-	-
1390519_at	---	---	---	Rn.167279	BM387032	2.70	2.69	2.71	2.69	5.18	2.67	1.76	up	3.82E-01	8.95E-01	-	-
1393251_at	---	---	---	Rn.86568	BM391286	6.55	6.41	4.03	5.99	6.53	6.92	1.76	up	3.96E-01	8.95E-01	-	-
1383643_at	RGD1560328	similar to UPF0197 protein C11orf10 homolog	499317	Rn.162493	BI282584	9.54	8.96	9.31	10.11	9.72	10.42	1.76	up	3.60E-02	8.95E-01	UR	-
1372619_at	Mrpl49	mitochondrial ribosomal protein L49	309176	Rn.101724	AI172185	4.23	6.13	5.97	5.96	6.50	6.32	1.76	up	2.63E-01	8.95E-01	-	-
1382940_at	Glb1l2	galactosidase, beta 1-like 2	503194	Rn.162985	BI281084	4.71	4.01	7.15	3.91	3.96	5.56	1.76	down	4.97E-01	8.95E-01	-	-
1372658_at	Synm	synemin, intermediate filament protein	308709	Rn.46362	BG373779	2.90	4.12	4.48	2.78	2.80	3.46	1.76	down	1.97E-01	8.95E-01	-	-
1389304_at	---	---	---	Rn.164465	AI176323	6.09	6.15	6.30	6.64	7.63	6.72	1.76	up	6.68E-02	8.95E-01	-	-
1374328_at	C2cd3	C2 calcium-dependent domain containing 3	293148	Rn.48	BF403886	2.54	2.59	5.08	2.60	2.45	2.72	1.76	down	3.89E-01	8.95E-01	-	-
1383592_at	Armc8	Armadillo repeat containing 8	315949	Rn.8146	AA925988	6.83	3.64	3.72	4.44	7.74	4.47	1.76	up	6.20E-01	8.95E-01	-	-
1392914_at	---	---	---	---	BI275467	6.99	7.83	6.26	7.89	7.70	7.95	1.76	up	1.50E-01	8.95E-01	-	-
1390306_at	---	---	---	Rn.47844	AW531909	4.27	5.12	4.84	5.29	6.09	5.29	1.76	up	9.04E-02	8.95E-01	-	-
1387860_at	Capn2	calpain 2	29154	Rn.6822	BF281377	7.93	7.47	6.96	7.94	8.34	8.52	1.76	up	6.88E-02	8.95E-01	-	-
1376393_at	---	---	---	Rn.212090	BI296409	2.34	2.34	4.78	2.34	2.35	2.33	1.76	down	3.73E-01	8.95E-01	-	-
1395445_at	Rfxap	regulatory factor X-associated protein	499617	Rn.198587	AI548975	2.68	3.03	2.53	4.17	3.42	3.10	1.76	up	8.00E-02	8.95E-01	-	-
1367941_at	Tfam	transcription factor A, mitochondrial	83474	Rn.18266	NM_031326	6.10	5.92	5.39	6.77	6.58	6.51	1.76	up	2.35E-02	8.95E-01	UR	-
1397496_at	RGD1560620	similar to hypothetical protein	291940	Rn.29121	BE108753	7.48	3.96	4.33	4.09	5.10	4.13	1.76	down	5.23E-01	8.95E-01	-	-
1394077_at	Rnd3	Rho family GTPase 3	295588	Rn.25153	BF548080	3.16	4.96	5.36	3.17	4.55	3.32	1.76	down	3.69E-01	8.95E-01	-	-
1397889_at	---	---	---	Rn.26698	BF402043	3.04	3.67	2.88	4.09	3.07	4.88	1.76	up	2.31E-01	8.95E-01	-	-
1396401_at	Rbm17	RNA binding motif protein 17	291295	Rn.20694	AW433899	2.91	2.86	3.08	3.06	4.57	3.66	1.76	up	1.41E-01	8.95E-01	-	-
1389389_at	Ddx56	DEAD (Asp-Glu-Ala-Asp) box polypeptide 56	289780	Rn.39458	BF420168	4.10	3.90	4.77	4.68	4.68	5.85	1.76	up	1.59E-01	8.95E-01	-	-
1396853_at	---	---	---	Rn.213839	AI549156	6.07	7.21	6.77	5.60	4.88	7.13	1.76	down	3.34E-01	8.95E-01	-	-
1368596_at	Snf1lk	SNF1-like kinase	59329	Rn.42905	AB020480	8.66	8.12	8.59	9.56	8.74	9.50	1.76	up	6.19E-02	8.95E-01	-	-
1390147_at	RGD1559904	similar to mKIAA1429 protein	313061	Rn.102580	AI549079	4.11	3.81	4.44	3.26	2.97	3.69	1.76	down	4.34E-02	8.95E-01	DR	-
1384648_at	Fam164a	Family with sequence similarity 164, member A	310244	Rn.8041	AA963844	7.08	5.87	4.28	6.51	6.26	6.90	1.76	up	3.84E-01	8.95E-01	-	-
1387079_at	Gucy1a3	guanylate cyclase 1, soluble, alpha 3	497757	Rn.1974	M57405	2.95	2.91	2.73	5.00	3.13	2.90	1.76	up	2.91E-01	8.95E-01	-	-
1378237_at	---	---	---	Rn.166147	BG376172	5.96	4.92	4.81	6.50	5.55	6.08	1.76	up	1.52E-01	8.95E-01	-	-
1390728_at	Limd1	LIM domains containing 1	316101	Rn.3986	AI501517	4.15	3.81	3.49	5.23	4.84	3.82	1.76	up	1.52E-01	8.95E-01	-	-
1382266_at	Gpr146	G protein-coupled receptor 146	498153	Rn.41446	AI500893	5.39	2.73	2.72	2.80	2.87	2.73	1.75	down	4.13E-01	8.95E-01	-	-
1397987_at	---	---	---	Rn.147447	BF390656	3.09	3.91	4.88	2.90	3.41	3.14	1.75	down	2.06E-01	8.95E-01	-	-
1372959_at	Nme4	non-metastatic cells 4, protein expressed in	685879	Rn.145948	BI289467	6.93	4.39	5.34	5.46	4.10	4.66	1.75	down	3.89E-01	8.95E-01	-	-
1397568_at	Trp53inp2	tumor protein p53 inducible nuclear protein 2	362246	Rn.86075	AW521373	2.95	2.69	2.63	2.74	5.29	2.68	1.75	up	4.02E-01	8.95E-01	-	-
1397529_at	Ddx17	DEAD (Asp-Glu-Ala-Asp) box polypeptide 17	315133	Rn.105298	BI296754	8.24	8.94	7.63	8.36	6.56	7.46	1.75	down	2.77E-01	8.95E-01	-	-
1373118_at	LOC689074	similar to Protein KIAA1543	689074	Rn.24684	BM387460	7.27	5.30	5.41	5.24	5.22

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1392701_at	Gmppb	GDP-mannose pyrophosphorylase B	363145	Rn.102187	BI285572	5.28	6.59	5.73	6.71	5.87	7.43	1.74	up	2.48E-01	8.95E-01	-	-
1375862_at	Pxdn	peroxidasin homolog (Drosophila)	554172	Rn.40541	BM384701	2.49	2.76	4.67	2.49	2.55	2.48	1.74	down	3.08E-01	8.95E-01	-	-
1368137_at	Mapt	microtubule-associated protein tau	29477	Rn.2455	BE107978	7.65	7.59	8.18	6.86	7.24	6.92	1.74	down	2.20E-02	8.95E-01	DR	-
1374281_at	Ino80	INO80 homolog (S. cerevisiae)	296084	Rn.100690	BE109901	2.71	3.28	2.67	3.11	4.59	3.36	1.74	up	1.83E-01	8.95E-01	-	-
1394574_at	---	---	---	Rn.210473	BF398290	4.87	2.50	2.63	2.78	2.59	2.22	1.74	down	3.67E-01	8.95E-01	-	-
1372216_at	Cyb561d1	cytochrome b-561 domain containing 1	362017	Rn.17547	AI010259	2.38	2.81	2.36	2.80	2.90	4.25	1.74	up	1.77E-01	8.95E-01	-	-
1382032_at	---	---	---	Rn.164681	AI407730	5.90	5.92	5.36	5.08	4.63	5.07	1.74	down	2.73E-02	8.95E-01	DR	-
1378345_at	Ogfod1	2-oxoglutarate and iron-dependent oxygenase domain containing 1	307657	Rn.19163	BF389196	3.35	3.45	5.91	3.21	3.70	3.39	1.74	down	3.99E-01	8.95E-01	-	-
1379285_at	Rtp4	receptor (chemosensory) transporter protein 4	360733	Rn.4244	AA819788	2.82	3.39	4.82	2.94	2.94	2.75	1.74	down	2.52E-01	8.95E-01	-	-
1389355_at	Ier5	immediate early response 5	498256	Rn.8590	BF285187	3.33	3.15	2.74	3.79	4.64	3.19	1.74	up	1.52E-01	8.95E-01	-	-
1370954_at	P4ha1	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alp	64475	Rn.8531	BI274401	4.27	5.09	5.01	4.38	3.22	4.37	1.74	down	1.61E-01	8.95E-01	-	-
1375298_at	Ppp2r5c	protein phosphatase 2, regulatory subunit B' gamma isoform	691318	Rn.2153	BF408443	5.42	6.02	4.62	6.24	5.41	6.81	1.74	up	2.35E-01	8.95E-01	-	-
1383988_at	LOC690274	hypothetical protein LOC690274	690274	Rn.9543	AI028887	5.68	6.05	3.47	5.78	6.17	5.65	1.74	up	3.85E-01	8.95E-01	-	-
1376240_at	RGD1566399	similar to MYST histone acetyltransferase monocytic leukemia 4	305681	Rn.221977	BG378240	2.86	2.72	2.58	3.29	3.36	3.92	1.74	up	2.11E-02	8.95E-01	UR	-
1379205_at	---	---	---	Rn.148149	BG374111	5.47	3.13	3.19	3.15	3.16	3.09	1.74	down	3.57E-01	8.95E-01	-	-
1373011_at	Fam134b	family with sequence similarity 134, member B	619558	Rn.162560	BE109520	5.42	5.45	5.28	6.08	6.66	5.80	1.74	up	3.63E-02	8.95E-01	UR	-
1395139_at	Kif16b	kinesin family member 16B	311478	Rn.7029	BM388214	3.90	4.35	4.30	2.42	3.99	3.75	1.74	down	1.91E-01	8.95E-01	-	-
1374174_at	---	---	---	Rn.114503	AI555195	5.36	6.07	5.37	3.67	5.37	5.36	1.74	down	2.60E-01	8.95E-01	-	-
1372532_at	Pitpnm2	phosphatidylinositol transfer protein, membrane-associated 2	304474	Rn.75968	BI289477	3.44	4.21	4.67	3.61	2.97	3.33	1.74	down	1.18E-01	8.95E-01	-	-
1374935_at	---	---	---	Rn.17648	AI412099	3.68	5.24	4.34	4.42	5.05	6.19	1.74	up	3.10E-01	8.95E-01	-	-
1393369_at	---	---	---	Rn.146808	BI300502	4.08	5.68	4.05	5.74	5.05	5.41	1.74	up	2.37E-01	8.95E-01	-	-
1395991_at	---	---	---	Rn.50806	BE107556	5.41	5.24	5.28	6.23	6.07	6.03	1.74	up	5.70E-04	8.95E-01	UR	-
1394814_at	Tpr	translocated promoter region	304862	Rn.58980	BF396127	5.76	7.35	7.09	8.14	7.36	7.09	1.74	up	2.44E-01	8.95E-01	-	-
1377733_at	---	---	---	Rn.164929	AA944531	5.51	5.49	5.16	5.92	6.13	6.50	1.74	up	1.73E-02	8.95E-01	UR	-
1383199_at	---	---	---	Rn.164402	AW140820	3.69	4.25	3.38	3.58	3.69	4.64	1.74	up	2.21E-01	8.95E-01	-	-
1385490_at	LOC686841	similar to Protein EAN57	686841	Rn.119929	AW529441	2.80	2.78	2.93	5.16	2.83	2.91	1.74	up	3.55E-01	8.95E-01	-	-
1375080_at	LOC684556	similar to mitochondrial hepatocellular carcinoma-downregulated carrier prote	684556	---	BF392317	7.01	5.89	6.79	6.66	5.99	4.64	1.74	down	3.10E-01	8.95E-01	-	-
1391005_at	Fbxl4	F-box and leucine-rich repeat protein 4	313101	Rn.12566	AA997732	3.03	3.11	2.77	3.30	4.33	3.67	1.74	up	6.58E-02	8.95E-01	-	-
1389030_a_at	Src	V-src sarcoma (Schmidt-Ruppin A-2) viral oncogene homolog (avian)	83805	Rn.112600	BI282912	6.12	4.40	6.53	4.58	5.62	4.47	1.74	down	3.47E-01	8.95E-01	-	-
1390832_at	Tmcc3	transmembrane and coiled-coil domain family 3	314751	Rn.19106	BI294696	7.01	6.52	7.49	5.45	6.40	6.78	1.74	down	1.76E-01	8.95E-01	-	-
1382745_at	---	---	---	Rn.207980	BE108581	3.54	4.32	2.20	2.71	2.20	2.75	1.74	down	2.83E-01	8.95E-01	-	-
1374890_at	---	---	---	Rn.203065	AW533905	6.37	7.41	5.96	7.21	7.18	7.73	1.74	up	1.64E-01	8.95E-01	-	-
1392792_at	Taf1	TAF1 RNA polymerase II, TATA box binding protein (TBP)-associated factor	317256	Rn.99639	AI071152	2.59	3.21	2.60	3.98	2.81	3.99	1.74	up	1.45E-01	8.95E-01	-	-
1393657_at	Prcp	prolylcarboxypeptidase (angiotensinase C)	293118	Rn.8457	BI285860	2.50	2.47	2.51	2.49	4.59	2.78	1.74	up	2.92E-01	8.95E-01	-	-
1393213_at	Ccnl2	cyclin L2	298686	Rn.162156	BE098333	7.70	6.92	6.14	7.47	5.80	5.11	1.74	down	3.94E-01	8.95E-01	-	-
1367816_at	Hopx	HOP homeobox	171160	Rn.2989	NM_133621	2.60	2.54	2.76	4.84	2.56	2.89	1.74	up	3.27E-01	8.95E-01	-	-
1390647_at	Phtf2	putative homeodomain transcription factor 2	296762	Rn.18302	AI410924	4.58	6.50	6.31	7.45	5.15	7.17	1.74	up	4.49E-01	8.95E-01	-	-
1390154_at	LOC688326	similar to Interferon-alpha/beta receptor beta chain precursor (IFN-alpha-REC	686326	---	BI299822	2.89	2.94	3.25	4.11	3.08	4.27	1.74	up	1.11E-01	8.95E-01	-	-
1379842_at	Stl7l	suppression of tumorigenicity 7-like	295344	Rn.102337	H33639	6.82	4.12	2.76	5.48	4.55	6.04	1.74	up	5.65E-01	8.95E-01	-	-
1379109_at	---	---	---	Rn.208116	BE110398	4.02	3.48	2.60	4.61	4.54	3.33	1.73	up	2.48E-01	8.95E-01	-	-
1390029_at	Tmem110	transmembrane protein 110	361110	Rn.203413	AA945898	3.55	3.20	3.83	4.67	3.75	4.53	1.73	up	8.02E-02	8.95E-01	-	-
1390455_at	Abhd2	abhydrolase domain containing 2	293050	Rn.136611	AI013474	3.99	4.73	5.53	5.02	6.12	5.49	1.73	up	2.20E-01	8.95E-01	-	-
1369364_at	Atp1a4	ATPase, Na+/K+ transporting, alpha 4 polypeptide	29132	Rn.10013	NM_022848	2.70	4.69	2.78	2.70	2.50	2.60	1.73	down	2.90E-01	8.95E-01	-	-
1388089_a_at	Rnf4	ring finger protein 4	29274	Rn.205059	AY056655	7.86	7.19	7.67	7.66	5.73	6.95	1.73	down	2.53E-01	8.95E-01	-	-
1393396_at	Sfi2d3	SFI2 domain containing 3	364835	Rn.198388	AA864966	2.98	3.52	3.24	4.25	3.74	4.13	1.73	up	2.20E-02	8.95E-01	UR	-
1376212_at	Pdcd2l	programmed cell death 2-like	689637	Rn.3078	AI102437	6.15	6.42	4.45	6.22	6.96	6.22	1.73	up	2.98E-01	8.95E-01	-	-
1390372_at	---	---	---	Rn.203465	BF521975	7.02	7.52	5.95	7.35	7.92	7.60	1.73	up	1.81E-01	8.95E-01	-	-
1388777_at	Sir3	signal sequence receptor, gamma	81784	Rn.3264	BE113224	9.37	9.25	9.75	9.95	10.11	10.69	1.73	up	4.30E-02	8.95E-01	UR	-
1378457_at	---	---	---	Rn.34019	AI179450	4.96	5.18	6.12	4.76	4.50	4.63	1.73	down	9.39E-02	8.95E-01	-	-
1367727_at	Cyth2	cytohesin 2	116692	Rn.3732	NM_053911	4.94	6.37	6.09	6.29	6.80	6.68	1.73	up	1.63E-01	8.95E-01	-	-
1385375_at	---	---	---	Rn.34775	AI535212	2.82	3.32	2.57	2.82	4.70	3.58	1.73	up	2.49E-01	8.95E-01	-	-
1393439_a_at	Ankh	ankylosis, progressive homolog (mouse)	114506	Rn.211841	AI045767	7.05	4.96	3.90	4.58	4.40	4.55	1.73	down	4.41E-01	8.95E-01	-	-
1398549_at	Ccnl2	Cyclin L2	298686	Rn.162156	AI412463	3.96	5.63	3.92	4.26	3.60	3.27	1.73	down	2.80E-01	8.95E-01	-	-
1377685_at	Esco1	establishment of cohesion 1 homolog 1 (S. cerevisiae)	680014	Rn.19439	AW435161	5.56	6.61	7.52	5.35	6.18	5.78	1.73	down	2.67E-01	8.95E-01	-	-
1396755_at	---	---	---	---	BF396394	2.69	3.16	2.61	3.63	2.69	4.51	1.73	up	2.27E-01	8.95E-01	-	-
1377964_at	Tmem167b	transmembrane protein 167B	499690	Rn.220629	BM390539	4.65	5.10	4.90	6.85	4.70	5.49	1.73	up	2.84E-01	8.95E-01	-	-
1399084_at	Dhx16	DEAH (Asp-Glu-Ala-His) box polypeptide 16	294232	Rn.6832	BF405883	3.44	4.67	4.54	3.15	2.96	4.16	1.73	down	2.17E-01	8.95E-01	-	-
1393835_s_at	---	---	---	Rn.164651	AA900738	7.42	6.23	6.60	7.10	4.22	6.55	1.73	down	4.52E-01	8.95E-01	-	-
1388337_at	Np	nucleoside phosphorylase	290029	Rn.2738	AI102495	9.11	8.46	8.62	8.52	7.86	7.43	1.73	down	1.01E-01	8.95E-01	-	-
1385760_at	---	---	---	Rn.147698	BF400633	4.63	4.64	6.21	3.82	4.40	4.90	1.73	down	2.64E-01	8.95E-01	-	-
1389756_at	Melk	maternal embryonic leucine zipper kinase	362510	Rn.28232	BM390710	6.94	7.41	7.67	5.56	7.18	6.91	1.73	down	2.20E-01	8.95E-01	-	-
1390410_at	---	---	---	Rn.165204	AA863369	7.46	6.94	6.26	7.48	7.90	7.64	1.73	up	9.88E-02	8.95E-01	-	-
1390817_at	---	---	---	Rn.48849	BF394639	4.76	4.51	6.21	4.62	4.52	3.97	1.73	down	2.34E-01	8.95E-01	-	-
1392968_at	---	---	---	Rn.169992	BI300566	3.26	3.40	3.38	4.08	4.57	3.76	1.73	up	3.01E-02	8.95E-01	UR	-
1389477_at	Ranbp3	RAN binding protein 3	501281	Rn.101054	AI598440	4.53	4.74	3.92	4.67	5.83	5.06	1.73	up	1.34E-01	8.95E-01	-	-
1393218_at	RGD1304878	similar to 2410024A21Rik protein	314415	Rn.20310	AI176155	8.62	8.89	9.24	8.32	7.57	8.49	1.73	down	7.78E-02	8.95E-01	-	-
1395271_at	Rbm27	RNA binding motif protein 27	361317	Rn.218050	BF563111	5.73	4.24	5.57	4.22	4.40	4.55	1.73	down	1.75E-01	8.95E-01	-	-
1382306_at	Arih1	ariadne ubiquitin-conjugating enzyme E2 binding protein homolog 1 (Drosoph	300756	Rn.29865	AW919478	3.56	3.06	3.96	2.68	2.74	2.78	1.73	down	3.98E-02	8.95E-01	DR	-
1381259_at	Stag1	stromal antigen 1	361318	Rn.11775	BM391784	4.86	4.99	6.35	6.07	5.83	6.66	1.73	up	2.16E-01	8.95E-01	-	-
1386346_at	Tmem19	transmembrane protein 19	299800	Rn.131677	BI275715	2.49	2.76	2.50	2.49	4.72	2.91	1.73	up	3.16E-01	8.95E-01	-	-
1376580_at	Fxn	frataxin	499335	Rn.13133	BG375952	3.56	6.14	5.86	6.93	5.46	5.53	1.73	up	4.52E-01	8.95E-01	-	-
1394049_at	Dcun1d1	DCN1, defective in cullin neddylation 1, domain containing 1 (S. cerevisiae)	310324	Rn.116073	BE108839	3.80	5.72	5.85	5.36	6.08	6.30	1.73	up	3.34E-01	8.95E-01	-	-
1380808_at	Tollip	toll interacting protein	361677	Rn.137040	BE112982	5.54	5.98	5.90	5.03	4.99	5.03	1.73	down	4.42E-03	8.95E-01	DR	-
1385788_at	Ephb3	Eph receptor B3	287989	Rn.131133	AW534949	3.99	3.60	3.99	5.42	5.45	3.08	1.73	up	3.79E-01	8.95E-01	-	-
1367795_at	Ifrd1	interferon-related developmental regulator 1	29596	Rn.3723	NM_019242	8.38	9.14	8.81	9.12	9.63	9.94	1.73	up	7.28E-02	8.95E-01	-	-
1372126_at	---	---	---	Rn.17074	BI288075	5.82	6.88	6.16	6.94	7.34	6.93	1.73	up	8.15E-02	8.95E-01	-	-
1383133_at	---	---	---	Rn.18130	BI295765	7.95	7.89	7.06	8.33	8.59	8.35	1.73	up	5.83E-02	8.95E-01	-	-
1389107_at	Cgnl1	cingulin-like 1	315795	Rn.120904	AI008974	7.95	5.97	7.26	7.22	7.39	4.21	1.73	down	5.43E-01	8.95E-01	-	-
1368290_at	Cyr61	cysteine-rich, angiogenic inducer, 61	83476	Rn.22129	NM_031327	4.90	6.64	3.47	3.16	4.78	4.71	1.73	down	4.98E-01	8.95E-01	-	-
1389944_at	Tmed7	Transmembrane emp24 protein transport domain containing 7	252889	Rn.67055	AI014155	5.31	6.84	5.31	6.84	5.66	7.31	1.73	up	3.29E-01	8.95E-01	-	-
1395887_at	LOC363060	similar to RIKEN cDNA 1600029D21	363060	Rn.39346	BF283642	2.54	2.62	2.90	4.13	3.73	2.56	1.73	up	1.78E-01	8.95E-01	-	-
1394964_at	Bat2d1	BAT2 domain containing 1	360865	Rn.206334	BM389840	6.72	7.69	7.96	6.64	6.05	7.32	1.73	down	2.08E-01	8.95E-01	-	-
1384845_at	---	---	---	Rn.165282	AI176044	2.57	2.63	4.75	2.45	2.57	2.57	1.73	down	3.35E-01	8.95E-01	-	-
1383125_at	Trmt2a	TRM2 tRNA methyltransferase 2 homolog A (S. cerevisiae)	287953	Rn.60258	AW525401	7.06	5.88	6.04	4.70	5.88	6.04	1.73	down	2.35E-01	8.95E-01	-	-
1382535_at	---	---	---	Rn.203299	AI030942	2.49	2.60	2.66	3.59	3.21	3.31	1.73	up	3.15E-03	8.95E-01	UR	-
1383134_at	RGD1311612	similar to hypothetical protein FLJ12118	361184	Rn.54352	AW918808	5.94	5.35	5.20	4.20	4.87	5.05	1.73	down	8.37E-02	8.95E-01	-	-
1367890_at	Casp2	caspase 2	64314	Rn.1438	AF136231	3.59	3.36	3.28	3.45	5.41	3.72	1.72	up	2.75E-01	8.95E-01	-	-
1368589_at	Ptprj	protein tyrosine phosphatase, receptor type, J	29645	Rn.10278	NM_017269	3.93	4.67	4.48	5.79	4.57	5.08	1.72	up	1.32E-01	8.95E-01	-	-
1396175_at	RGD1560191	similar to Zinc finger protein 62 homolog (Zfp-62) (ZT3)	497894	---	BG670617	3.69	4.30	4.33	4.97	4.63	5.07	1.72	up	3.44E-02	8.95E-01	UR	-
1379366_a_at	Bspry	B-box and SPRY domain containing	64027	Rn.53996	AW529938	6.58	6.49	6.71	7.30	7.37	7.46	1.72	up	5.92E-04	8.95E-01	UR	-
1374803_at	---	---	---	Rn.166834	BG374219	5.77	5.71	4.70	3.82	5.14	4.86	1.72	down	2.14E-01	8.95E-01	-	-
1370395_at	Htt	huntingtin	29424	Rn.11193	U18650	4.04	4.39	5.17	3.20	4.01	4.03	1.72	down	1.42E-01	8.95E-01	-	-
1368002_at	Msh2	mutS homolog 2 (E. coli)	81709	Rn.3174	NM_031058	3.07	3.94	3.64	5.67	3.41	3.94	1.72	up	3.42E-01	8.95E-01	-	-
1390263_at	---	---	---	---	AI179936	3.27	3.11	3.79	2.63	2.56	2.62	1.72	down	1.88E-02	8.95E-01	DR	-
1389238_at	LOC289740	similar to PES1 protein	289740	Rn.9521	BG376577	6.77	6.36	6.89	5.85	5.74	6.07	1.72	down	1.43E-02	8.95E-01	DR	-
1374105_at	Hgd1a	zinc f hypoxia inducible domain family, member 1A	140937	Rn.2084	H31665	8.66	8.02	7.84	6.94	7.53	7.70	1.72	down	8.18E-02	8.95E-01	-	-
1392303_at	Morc2	MORC family CW-type zinc finger 2	289736	Rn.219289	AA998501	2.35	2.38	4.80	2.41	2.37	2.41	1.72	down	3.88E-01	8.95E-01	-	-
1397782_at	Ogdh	Oxoglutarate (alpha-ketoglutarate) dehydrogenase (lipoamide)	360975	Rn.45991	BE103050	4.76	2.42	2.47	2.43	2.45	2.42	1.72	down	3.67E-01	8.95E-01	-	-
1397528_at	Sfrs2ip	Splicing factor, arginine/serine-rich 2, interacting protein	312030	Rn.199124	BE112252	3.00	3.22	3.11	3.23	5.24	3.22	1.72	up	3.09E-01	8.95E-01	-	-
1373632_at	Taf9	TAF9 RNA polymerase II, TATA box binding protein (TBP)-associated factor	373541	Rn.81839	AI172064	6.31	5.90	6.39	5.35	4.80	6.11	1.72	down	1.25E-01	8.95E-01	-	-
1393719_at	---	---	---	Rn.61986	AF412036	5.71	4.21	4.23	4.15	3.45	4.21	1.72	down	2.29E-01	8.95E-01	-	-
1376239_at	Atp6v1c2	ATPase, H+ transporting, lysosomal V1 subunit C2	362802	Rn.145217	BF283053	4.08	2.97	2.89	2.39	2.61	2.59	1.72	down	1.15E-01	8.95E-01	-	-
1384472_at	Heatr5b	HEAT repeat containing 5B	362683	Rn.6551	AA926022	5.20	6.78	7.92	5.88	5.36	6.31	1.72	down	4.01E-01	8.95E-01	-	-
1388455_at	Grg10	guanine nucleotide binding protein (G protein), gamma 10	114119	Rn.3319	AA799996	6.55	6.22	7.26	5.81	5.42	6.45	1.72	down	1.41E-01	8.95E-01	-	-
1387369_at	Exoc6	exocyst complex component 6	50556	Rn.1188	NM_019277	6.10	6.54	7.29	6.02	5.51	6.05	1.72	down	1.15E-01	8.95E-01	-	-
1398573_at	Zkscan3	zinc finger with KRAB and SCAN domains 3	306977	Rn.8231	BE098868	5.72	6.08	6.43	7.15	7.21	6.21	1.72	up	1.10E-01	8.95E-01	-	-
1391759_at	---	---	---	Rn.1097	BF283873	5.95	7.14	6.77	7.44	7.33	7.44	1.72	up	9.00E-02	8.95E-01	-	-
1397767_at	---	---	---	Rn.41665	BG377356	4.26	3.07	2.83	2.70	2.50	2.62	1.72	down	1.52E-01	8.95E-01	-	-
1383308_a_at	OC690743 /// Rfwd	similar to mixed lineage kinase domain-like /// ring finger and WD repeat dom	361409 /// 690743	Rn.105677	AI071048	2.52	2.51	2.54	2.53	3.53	3.87	1.72	up	1.24E-01	8.95E-01	-	-
1369468_at	Fzd4	frizzled homolog 4 (Drosophila)	64326	Rn.48736	NM_022823	8.88	9.24	8.98	8.29	7.85	8.63	1.72	down	3.47E-02	8.95E-01	DR	-
1368308_at	Myc	myelocytomatosis oncogene	24577	Rn.12072	NM_012603	3.92	4.74	3.89	4.36	5.20	5.35	1.72	up	1.33E-01	8.95E-01	-	-
1377405_at	Ralgps2	Ral GEF with PH domain and SH3 binding motif 2	304887	Rn.53963	BM387133	4.12	3.72	4.23	3.17	2.83	3.72	1.72	down	6.05E-02	8.95E-01	-	-
1377166_at	Als2	Amyotrophic lateral sclerosis 2 (juvenile) homolog (human)	363235	Rn.6408	BI274184	5.25	5.13	5.76	5.44	3.81	4.54	1.72	down	1.99E-01	8.95E-01	-	-
1389563_at	Trappc10	trafficking protein particle complex 10	309678	Rn.46413	BF406562	4.45	6.00	5.83	6.20	6.10	6.33	1.72	up	1.91E-01	8.95E-01	-	-
1390921_at	---	---	---	Rn.3245	BG373223	5.80	5.39	6.36	3.84	5.77	5.59	1.72	down	3.11E-01	8.95E-01	-	-
1369059_at	Trpm7	transient receptor potential cation channel, subfamily M, member 7	679906	Rn.86991	NM_053705	6.58	6.90	6.35	7.25	7.57	7.35	1.72	up	1.37E-02	8.95E-01	UR	-
1373473_a_at	Nap1l1	nucleosome assembly protein 1-like 1	89825	Rn.162938	BM386384	7.33	8.40	7.55	8.46	8.00	9.17	1.72	up	1.73E-01	8.95E-01	-	-
1377422_at	Mtmr1	Myotubularin related protein 1	317296	Rn.18311	AI029466	3.69	4.35	4.00	4.88	4.92	4.58	1.72	up	2.26E-02	8.95E-01	UR	-
1390043_at	684513 /// LOC68	similar to SWI/SNF-related matrix-associated actin-dependent regulator of ch	684513 /// 685179	Rn.20004	BF389915	6.30	5.10	5.99	5.84	4.96	4.24	1.72	down	2.54E-01	8.95E-01	-	-
1390031_at	Orai1	ORAI calcium release-activated calcium modulator 1	304496	Rn.3863	BG376798	2.74	3.25	3.00	3.76	4.18	3.39	1.72	up	4.53E-02	8.95E-01	UR	-
1373609_at	Mrps21	mitochondrial ribosomal protein S21	689432	Rn.164965	AI232274	7.15	8.61	8.49	9.07	8.53	8.99	1.72	up	1.90E-01	8.95E-01	-	-
1369400_a_at	Pfkfb2	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 2	24640	Rn.44844	NM_080477	2.44	2.35	2.44	2.44	4.06	3.09	1.72	up	1.73E-01	8.95E-01	-	-
1396565_at	RGD1565616	RGD1565616	499891	Rn.6943	AI406034	3.44	3.96	4.05	4.85	4.03	4.92	1.72	up	8.54E-02	8.95E-01	-	-
1370009_at	Apoc3	apolipoprotein C-III	24207	Rn.195323	AW012501	6.69	7.47	6.98	8.18	7.79	7.51	1.72	up	5.95E-02	8.95E-01	-	-
1375708_at	Col27a1	Collagen, type XXVII, alpha 1	298101	Rn.53800	BF392901	4.99	2.64	2.65	2.65	2.65	2.64	1.72	down	3.75E-01	8.95E-01	-	-
1390877_at	---	---	---	Rn.30223	AA850798	2.52	2.78	2.74	2.72	4.00	3.66	1.72	up	1.16E-01	8.95E-01	-	-
1383205_at	Dact2	Dact2, antagonist of beta-catenin, homolog 2 (Xenopus laevis)	308212	Rn.100050	BI288833	3.62	4.07	3.99	5.52	3.50	5.00	1.72	up	2.79E-01	8.95E-01	-	-
1387546_at	Crkrs	Cdc2-related kinase, arginine/serine-rich	192350	Rn.48817	NM_138916	2.46	2.70	2.46	5.06	2.45	2.44	1.72	up	4.23E-01	8.95E-01	-	-
1382491_at	RGD1562590	similar to hypothetical protein	312365	Rn.168137	AI555806	2.39	2.53	4.59	2.39	2.41	2.38	1.72	down	3.34E-01	8.95E-01	-	-
1389105_at	Dag1	dystroglycan 1 (dystrophin-associated glycoprotein 1)	114489	Rn.36280	BG374140	4.23	4.91	5.98	4.35	3.29	5.14	1.72	down	3.51E-01	8.95E-01	-	-
1390604_s_at	Itgb3bp	integrin beta 3 binding protein (beta3-endonexin)	362548	Rn.91426	BM387863	6.66	5.61	3.63	6.41	5.63	6.21	1.72	up	4.43E-01	8.95E-01	-	-
1397744_at	---	---	---	Rn.166967	BF276183	6.11	4.55	4.87	3.70	4.50	4.99	1.72	down	2.68E-01	8.95E-01	-	-
1397894_at	---	---	---	Rn.150835	BG381542	2.67	3.61	2.50	5.37	2.55	3.20	1.72	up	4.45E-01	8.95E-01	-	-
1393961_at	---	---	---	Rn.34561	AA926088	3.82	3.18	3.22	4.17	3.57	4.81	1.72	up	1.33E-01	8.95E-01	-	-
1377469_at	---	---	---	Rn.163747	AI103161	6.58	5.50	5.74	4.90	4.93	5.65	1.72	down	1.28E-01	8.95E-01	-	-
1377922_at	Znf507	Zinc finger protein 507	292816	Rn.122338	BE111094	4.95	5.11	5.06	3.51	4.01	5.26	1.72	down	2.11E-01	8.95E-01	-	-
1367879_at	Cdk5rap3	Cdk5 regulatory subunit associated protein 3	80274	Rn.3727	NM_024488	3.15	4.69	4.16	4.45	4.87	5.01	1.72	up	1.80E-01	8.95E-01	-	-
1379309_at	Tbl1xr1	Transducin (beta)-like 1X-linked receptor 1	365755	Rn.140831	AI030742	7.04	7.15	7.05

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1368813_at	Cebpd	CCAAT/enhancer binding protein (C/EBP), delta	25695	Rn.202620	NM_013154	4.63	2.32	2.33	2.32	2.33	2.31	1.71	down	3.72E-01	8.95E-01	-	-
1377759_at	Bid	BH3 interacting domain death agonist	64625	Rn.31142	BG666928	5.36	4.34	5.34	4.07	3.24	5.41	1.70	down	3.43E-01	8.95E-01	-	-
1371772_at	Alkbh3	alkB, alkylation repair homolog 3 (E. coli)	362169	Rn.30490	AI410425	5.58	7.32	6.90	7.09	7.17	7.84	1.70	up	2.52E-01	8.95E-01	-	-
1377345_at	---	---	---	Rn.219232	AI502211	7.06	6.94	8.76	7.32	5.75	7.40	1.70	down	3.88E-01	8.95E-01	-	-
1383627_a_at	Gtf2f1	general transcription factor IIF, polypeptide 1	316123	Rn.98836	BF420770	8.42	8.58	9.06	7.75	7.36	8.63	1.70	down	1.42E-01	8.95E-01	-	-
1395339_at	Impact	imprinted and ancient	497198	Rn.190651	BG664101	2.71	2.70	2.71	3.76	3.97	2.69	1.70	up	1.24E-01	8.95E-01	-	-
1371695_at	Tpr	translocated promoter region	304862	Rn.58980	AI230732	4.68	6.07	5.92	6.23	6.53	6.21	1.70	up	1.65E-01	8.95E-01	-	-
1382143_at	Farp1	FERM, RhoGEF (Arhgef) and pleckstrin domain protein 1 (chondrocyte-derive	306183	Rn.92109	AA964898	3.72	3.72	3.87	3.72	4.88	5.00	1.70	up	1.35E-01	8.95E-01	-	-
1387108_at	Csnk2b	casein kinase 2, beta subunit	81650	Rn.137692	BF281311	6.61	7.24	5.60	7.53	6.88	7.35	1.70	up	2.12E-01	8.95E-01	-	-
1390036_at	Slc16a6	solute carrier family 16, member 6 (monocarboxylic acid transporter 7)	303772	Rn.157381	BI289867	4.06	4.09	4.67	4.92	5.17	5.03	1.70	up	2.18E-02	8.95E-01	UR	-
1374855_at	Per1	period homolog 1 (Drosophila)	287422	Rn.34433	BI279017	3.96	4.17	3.79	4.36	4.51	5.34	1.70	up	7.65E-02	8.95E-01	-	-
1384428_at	RGD1566403	similar to OTTHUMP00000040081	502228	Rn.136597	AI043872	4.56	4.59	4.59	3.45	2.91	5.08	1.70	down	3.04E-01	8.95E-01	-	-
1367913_at	Cygb	cytoglobin	170520	Rn.105938	NM_130744	5.54	4.52	3.37	3.51	4.59	3.03	1.70	down	3.80E-01	8.95E-01	-	-
1378814_at	---	---	---	Rn.209378	BF387902	2.57	2.59	4.80	2.50	2.58	1.70	1.70	down	3.57E-01	8.95E-01	-	-
1386900_at	Serp1	stress-associated endoplasmic reticulum protein 1	80881	Rn.2119	AI103695	6.90	7.52	7.48	8.06	7.82	8.33	1.70	up	3.79E-02	8.95E-01	UR	-
1372290_at	Rdbp	RD RNA-binding protein	294258	Rn.16164	BI275979	6.18	5.65	4.80	6.16	6.30	6.47	1.70	up	1.36E-01	8.95E-01	-	-
1393148_at	Gpr137b	G protein-coupled receptor 137B	289287	Rn.60453	BF542593	8.94	9.02	9.36	8.10	8.31	8.62	1.70	down	1.78E-02	8.95E-01	DR	-
1368264_at	Pex6	peroxisomal biogenesis factor 6	117265	Rn.10675	NM_057125	3.95	4.55	4.32	5.28	5.29	4.55	1.70	up	6.31E-02	8.95E-01	-	-
1371956_at	LOC683077	similar to praja1, RING-H2 motif containing	683077	Rn.190368	BG372686	7.74	7.60	7.38	6.66	6.37	7.39	1.70	down	7.62E-02	8.95E-01	-	-
1372134_at	Chchd6	coiled-coil-helix-coiled-coil-helix domain containing 6	297436	Rn.6212	AW918650	3.92	3.25	3.93	3.94	4.73	4.73	1.70	up	9.02E-02	8.95E-01	-	-
1398861_at	Nxf1	nuclear RNA export factor 1	59087	Rn.159847	AF093139	6.83	6.32	7.36	6.65	6.06	5.50	1.70	down	1.81E-01	8.95E-01	-	-
1375601_at	---	---	---	Rn.169877	BF410219	5.45	2.98	2.95	3.48	2.66	2.95	1.70	down	4.25E-01	8.95E-01	-	-
1389180_at	---	---	---	Rn.6488	AI175035	6.66	6.16	6.30	5.95	5.44	5.42	1.70	down	2.86E-02	8.95E-01	DR	-
1367498_at	Ythdf1	YTH domain family, member 1	296467	Rn.16962	AI177873	6.55	7.56	7.37	7.93	7.83	8.01	1.70	up	7.08E-02	8.95E-01	-	-
1393689_at	Ndufaf1	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, assembly factor 1	296086	Rn.49587	BE097322	6.34	6.87	5.83	5.72	4.72	6.29	1.70	down	2.36E-01	8.95E-01	-	-
1378068_at	---	---	---	---	AW529368	3.49	3.47	2.80	4.08	3.34	4.63	1.70	up	1.55E-01	8.95E-01	-	-
1372899_at	Znf775	zinc finger protein 775	312309	Rn.22174	AI124063	6.29	6.27	7.21	6.17	6.00	5.31	1.70	down	1.34E-01	8.95E-01	-	-
1367526_at	Mrps26	mitochondrial ribosomal protein S26	362216	Rn.8520	AI180224	8.44	8.38	7.29	8.81	8.66	8.93	1.70	up	1.16E-01	8.95E-01	-	-
1383154_at	684513 /// LOC68	similar to SWI/SNF-related matrix-associated actin-dependent regulator of chi 684513 /// 685179		Rn.20004	H34497	3.65	4.17	3.71	5.19	4.12	4.51	1.70	up	9.52E-02	8.95E-01	-	-
1380323_at	Stk	STE20-like kinase (yeast)	54308	Rn.33275	BE105023	5.76	5.39	5.50	3.78	5.48	5.10	1.70	down	2.22E-01	8.95E-01	-	-
1370931_at	Xrcc5	X-ray repair complementing defective repair in Chinese hamster cells 5	363247	Rn.52078	AA893188	3.08	5.31	5.24	5.51	5.23	5.17	1.70	up	3.60E-01	8.95E-01	-	-
1393146_at	---	---	---	Rn.25263	BG663116	4.07	5.33	3.78	3.37	3.59	3.94	1.70	down	2.04E-01	8.95E-01	-	-
1368588_at	Ddx52	DEAD (Asp-Glu-Ala-Asp) box polypeptide 52	85432	Rn.18605	NM_053525	3.65	4.22	6.05	3.40	4.07	4.17	1.70	down	3.75E-01	8.95E-01	-	-
1384783_at	Zfp161	zinc finger protein 161	282825	Rn.162280	BI286823	4.83	4.97	4.28	4.91	5.59	5.87	1.70	up	9.90E-02	8.95E-01	-	-
1396042_at	---	---	---	Rn.172086	BF288404	4.97	2.55	2.62	2.75	2.64	2.46	1.70	down	3.95E-01	8.95E-01	-	-
1380219_at	---	---	---	Rn.19631	BE117902	5.44	6.00	4.56	6.60	5.69	6.00	1.70	up	2.00E-01	8.95E-01	-	-
1388807_at	Carm2bp	CARM2 binding protein	362224	Rn.36418	BG380590	5.27	2.72	2.60	2.84	2.74	2.73	1.70	down	4.32E-01	8.95E-01	-	-
1378203_at	Smarce1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin,	303518	Rn.8513	BE102273	6.24	4.13	4.26	3.99	4.21	4.14	1.69	down	3.30E-01	8.95E-01	-	-
1360934_at	Ppib	peptidylprolyl isomerase B	64367	Rn.1893	NM_022536	7.56	8.43	7.52	8.89	8.00	8.90	1.69	up	1.44E-01	8.95E-01	-	-
1375672_at	---	---	---	Rn.106882	BG380279	4.70	3.90	3.70	3.32	3.15	3.55	1.69	down	8.05E-02	8.95E-01	-	-
1371258_at	Fga	fibrinogen alpha chain	361969	Rn.98848	AA875097	2.49	2.93	3.59	3.49	3.10	4.70	1.69	up	2.59E-01	8.95E-01	-	-
1387121_a_at	Ndrg2	NDRG family member 2	171114	Rn.3407	NM_133583	6.35	6.05	6.19	6.43	4.71	5.17	1.69	down	2.17E-01	8.95E-01	-	-
1372754_at	Appl2	adaptor protein, phosphotyrosine interaction, PH domain and leucine zipper c	362860	Rn.7015	BG666424	4.78	4.21	3.76	3.55	3.25	3.67	1.69	down	7.66E-02	8.95E-01	-	-
1394667_at	Bmpr2	Bone morphogenetic protein receptor, type II (serine/threonine kinase)	140590	Rn.59276	AI137474	6.07	4.35	4.36	4.35	4.10	4.05	1.69	down	2.61E-01	8.95E-01	-	-
1371479_at	Mettl7a	methyltransferase like 7A	313306	Rn.3341	AA946026	4.16	5.77	6.21	5.77	6.05	6.60	1.69	up	3.18E-01	8.95E-01	-	-
1399146_at	Dolk	dolichol kinase	311847	Rn.19644	AI576776	7.88	8.76	8.72	9.42	8.98	9.24	1.69	up	7.30E-02	8.95E-01	-	-
1390245_at	Ift122	intraflagellar transport 122 homolog (Chlamydomonas)	312651	Rn.207472	BI298090	3.42	3.30	5.70	3.71	3.10	3.33	1.69	down	3.97E-01	8.95E-01	-	-
1376419_at	---	---	---	Rn.26899	BE116226	4.63	4.63	8.32	6.04	5.56	5.46	1.69	down	5.21E-01	8.95E-01	-	-
1379332_at	---	---	---	Rn.196181	AI556426	4.53	5.95	3.66	6.26	4.69	5.46	1.69	up	4.01E-01	8.95E-01	-	-
1391450_at	Loxl2	lysyl oxidase-like 2	290350	Rn.219739	AI044651	2.44	2.43	4.73	2.44	2.45	2.44	1.69	down	3.77E-01	8.95E-01	-	-
1378106_at	Phldа2	pleckstrin homology-like domain, family A, member 2	293637	Rn.17288	AI029402	4.75	4.91	4.80	4.04	3.93	4.21	1.69	down	1.32E-03	8.95E-01	DR	-
1372327_at	Myef2	myelin expression factor 2	679712	Rn.1269	BF552877	7.85	8.43	7.64	8.68	8.93	8.58	1.69	up	4.27E-02	8.95E-01	UR	-
1388480_at	Gltp	glycolipid transfer protein	288707	Rn.4111	AI412863	2.87	3.40	2.77	3.55	4.06	3.70	1.69	up	3.84E-02	8.95E-01	UR	-
1389489_at	---	---	---	---	BE109900	4.23	3.48	3.26	5.18	3.53	4.54	1.69	up	2.51E-01	8.95E-01	-	-
1396036_at	Ralgps2	Ral GEF with PH domain and SH3 binding motif 2	304887	Rn.53963	BF525299	5.33	7.50	5.52	6.97	6.41	7.24	1.69	up	3.62E-01	8.95E-01	-	-
1384466_at	LOC493574	notch1-induced protein	493574	Rn.119606	AA875198	4.43	4.61	5.27	4.71	2.62	4.71	1.69	down	3.65E-01	8.95E-01	-	-
1382522_at	Matr3	matrin 3	29150	Rn.29774	AI169689	3.00	3.61	3.16	4.01	4.55	3.46	1.69	up	1.06E-01	8.95E-01	-	-
1393694_at	---	---	---	---	BI302319	3.33	4.81	3.32	3.00	2.52	3.67	1.69	down	2.74E-01	8.95E-01	-	-
1368247_at	Hspa1a /// Hspa1b	heat shock 70kD protein 1A /// heat shock 70kD protein 1B (mapped)	24472 /// 294254	Rn.1950	NM_031971	5.75	5.07	5.12	5.06	5.10	3.51	1.69	down	2.54E-01	8.95E-01	-	-
1397179_at	RGD1309388	similar to DIP13 alpha	290537	Rn.34413	BF544981	5.17	5.90	6.89	6.63	6.61	6.99	1.69	up	2.15E-01	8.95E-01	-	-
1376971_at	Atg10	autophagy-related 10 (S. cerevisiae)	688555	Rn.21798	AI411341	3.16	3.86	2.46	3.39	3.69	4.67	1.69	up	2.49E-01	8.95E-01	-	-
1383339_at	RGD1310358	similar to NNX3	308537	Rn.106288	BF567255	6.12	6.90	6.90	6.84	8.21	7.14	1.69	up	1.98E-01	8.95E-01	-	-
1391786_at	Hnrnph2	Heterogeneous nuclear ribonucleoprotein H2 (H')	308650	Rn.160642	BI297047	7.65	7.22	8.06	7.09	6.48	7.08	1.69	down	7.55E-02	8.95E-01	-	-
1371975_at	---	---	---	---	BG377343	5.94	4.30	4.92	4.40	4.10	4.41	1.69	down	1.97E-01	8.95E-01	-	-
1367902_at	Gng11	guanine nucleotide binding protein (G protein), gamma 11	64199	Rn.892	NM_022396	4.90	4.88	4.71	4.02	4.45	3.76	1.69	down	2.28E-02	8.95E-01	DR	-
1386784_at	Akap2	A kinase (PRKA) anchor protein 2	298024	Rn.162811	BF544958	6.22	5.15	5.88	5.38	4.83	4.76	1.69	down	1.11E-01	8.95E-01	-	-
1374840_at	RGD1564921	similar to peptidyl prolyl isomerase H	366461	Rn.129133	BG377716	6.47	5.32	7.15	4.77	4.78	5.32	1.69	down	3.78E-01	8.95E-01	-	-
1368775_at	Glot1	gonadotropin inducible ovarian transcription factor 1	171098	Rn.107259	NM_133563	3.70	3.64	3.34	3.70	5.53	3.72	1.69	up	2.88E-01	8.95E-01	-	-
1388395_at	Gbs2	GD/G1switch 2	289388	Rn.1040	AI406839	10.95	11.36	11.70	11.68	12.03	12.56	1.69	up	8.68E-02	8.95E-01	-	-
1378027_at	Pvrl3	poliovirus receptor-related 3	288124	Rn.56373	AW525315	3.99	6.10	5.74	5.88	5.98	6.23	1.69	up	3.16E-01	8.95E-01	-	-
1371509_at	Tbrg1	transforming growth factor beta regulator 1	300521	Rn.203060	BG666773	5.73	6.35	5.10	6.59	5.92	6.95	1.69	up	1.84E-01	8.95E-01	-	-
1379295_at	Gngt2	guanine nucleotide binding protein (G protein), gamma transducing activity po	690825	Rn.37315	BI281946	2.50	3.41	3.59	4.03	4.36	3.38	1.69	up	1.64E-01	8.95E-01	-	-
1376006_at	---	---	---	Rn.167525	BG373799	8.75	8.83	9.24	7.72	7.92	8.91	1.69	down	1.31E-01	8.95E-01	-	-
1367850_at	LOC498276 /// LO	Fc fragment of IgG, low affinity IIa, receptor (CD32) /// Fc gamma receptor II 191 /// 498276 /// 49		Rn.6050	NM_053843	7.73	6.16	7.09	4.76	8.66	5.30	1.69	down	5.94E-01	8.95E-01	-	-
1371055_at	Rab12	RAB12, member RAS oncogene family	25530	Rn.11021	MB3676	3.77	3.50	3.78	3.71	5.82	3.78	1.69	up	3.39E-01	8.95E-01	-	-
1383607_at	---	---	---	Rn.203772	BG377487	4.46	4.53	4.98	5.46	5.28	5.50	1.69	up	1.32E-02	8.95E-01	UR	-
1374202_at	---	---	---	Rn.204510	BM389779	3.01	4.47	5.11	4.64	5.16	5.06	1.69	up	3.05E-01	8.95E-01	-	-
1380480_at	Agpat3	1-acylglycerol-3-phosphate O-acyltransferase 3	294324	Rn.100251	AI711263	4.16	4.14	3.66	5.24	4.82	4.16	1.69	up	1.01E-01	8.95E-01	-	-
1397624_at	---	---	---	Rn.173174	BI300158	2.67	2.67	2.68	5.05	2.68	2.54	1.69	up	4.08E-01	8.95E-01	-	-
1391419_at	Ahdc1	AT hook, DNA binding motif, containing 1	362617	Rn.112088	BG376923	5.97	3.85	3.75	3.74	3.75	3.82	1.68	down	3.57E-01	8.95E-01	-	-
1384127_at	---	---	---	Rn.153603	AW917217	6.04	6.29	4.59	5.68	6.72	6.78	1.68	up	3.06E-01	8.95E-01	-	-
1374361_at	Mcat	Malonyl CoA:ACP acyltransferase (mitochondrial)	311573	Rn.23115	BI276503	3.30	3.36	3.54	3.81	5.24	3.41	1.68	up	2.51E-01	8.95E-01	-	-
1388561_at	---	---	---	Rn.98220	AI412886	4.25	3.23	3.80	3.58	2.36	3.08	1.68	down	1.78E-01	8.95E-01	-	-
1373282_at	LOC691431	similar to mitochondrial carrier protein MGC4399	691431	Rn.8763	AI406494	4.57	4.70	4.64	5.75	4.73	5.69	1.68	up	8.76E-02	8.95E-01	-	-
1373554_at	Spsb1	spl/Aryanodine receptor domain and SOCS box containing 1	313722	Rn.219023	BE349698	2.92	4.64	4.57	4.50	4.57	5.31	1.68	up	2.92E-01	8.95E-01	-	-
1396194_at	---	---	---	Rn.54305	AW434492	4.64	2.46	2.41	2.42	2.44	2.39	1.68	down	3.63E-01	8.95E-01	-	-
1369504_at	Tgfbr1	transforming growth factor, beta receptor 1	29591	Rn.44402	NM_012775	2.38	4.37	4.11	5.40	2.98	4.73	1.68	up	4.74E-01	8.95E-01	-	-
1369768_at	Hist1h1d	histone cluster 1, H1d	201097	Rn.196361	NM_133285	6.37	6.05	5.05	6.78	6.27	6.67	1.68	up	1.52E-01	8.95E-01	-	-
1376418_a_at	Iars	isoleucyl-tRNA synthetase	306804	Rn.61745	AA859497	5.88	5.82	5.96	6.27	6.90	6.75	1.68	up	1.77E-02	8.95E-01	UR	-
1393105_at	Zfp259	zinc finger protein 259	500989	Rn.102011	BF288164	3.07	4.29	3.56	4.88	3.53	4.77	1.68	up	2.50E-01	8.95E-01	-	-
1374252_at	Cep110	centrosomal protein 110kDa	311886	Rn.60629	BE108165	4.66	2.35	2.37	2.36	2.37	2.40	1.68	down	3.81E-01	8.95E-01	-	-
1372853_at	Rela	v-rel reticuloendotheliosis viral oncogene homolog A (avian)	309165	Rn.19480	BF283772	5.18	4.66	5.54	4.38	4.73	4.02	1.68	down	8.42E-02	8.95E-01	-	-
1369562_at	Hpcal1	hippocalcin-like 1	50871	Rn.102820	NM_017356	5.99	3.63	4.39	3.66	4.77	3.33	1.68	down	4.12E-01	8.95E-01	-	-
1380269_at	Fusip1	FUS interacting protein (serine-arginine rich) 1	362630	Rn.162118	AA859619	8.16	8.44	9.02	8.19	7.30	7.88	1.68	down	1.07E-01	8.95E-01	-	-
1376452_at	---	---	---	Rn.210584	BG374420	2.76	4.79	5.63	4.18	2.58	4.16	1.68	down	4.96E-01	8.95E-01	-	-
1391045_at	Dgat2	diacylglycerol O-acyltransferase homolog 2 (mouse)	252900	Rn.9523	BI277483	3.09	5.10	3.91	5.25	4.59	4.53	1.68	up	2.97E-01	8.95E-01	-	-
1391236_at	Uba6	ubiquitin-like modifier activating enzyme 6	305268	Rn.94245	BG380318	3.50	3.18	2.69	3.15	4.71	3.76	1.68	up	2.15E-01	8.95E-01	-	-
1387368_at	Mras	muscle RAS oncogene homolog	25482	Rn.10641	NM_012981	4.68	4.40	5.53	3.62	3.90	4.83	1.68	down	2.06E-01	8.95E-01	-	-
1379839_at	---	---	---	Rn.19467	BF540573	4.51	2.26	2.27	2.27	2.27	2.26	1.68	down	3.75E-01	8.95E-01	-	-
1377887_at	---	---	---	Rn.203885	AI013044	7.45	7.95	7.76	6.47	6.89	7.54	1.68	down	9.50E-02	8.95E-01	-	-
1373273_at	Prpf38a	PRP38 pre-mRNA processing factor 38 (yeast) domain containing A	298374	Rn.222053	BM384975	7.83	6.41	6.96	6.47	6.60	5.89	1.68	down	1.84E-01	8.95E-01	-	-
1371505_at	Hnrnpc	heterogeneous nuclear ribonucleoprotein C (C1/C2)	290046	Rn.101929	BG381750	7.84	7.66	8.51	7.29	7.20	7.27	1.68	down	4.42E-02	8.95E-01	DR	-
1376712_at	---	---	---	Rn.170858	AI144987	4.47	5.13	5.41	6.16	5.66	5.44	1.68	up	9.94E-02	8.95E-01	-	-
1382232_at	---	---	---	Rn.204381	AI454322	3.51	3.26	2.65	4.40	3.51	3.76	1.68	up	1.10E-01	8.95E-01	-	-
1370244_at	Ctsl1	cathepsin L1	25697	Rn.1294	AI232474	11.54	12.09	11.99	12.44	12.64	12.79	1.68	up	1.90E-02	8.95E-01	UR	-
1373206_at	Fndc3b	fibronectin type III domain containing 3B	294925	Rn.757	BI280993	4.33	3.94	5.08	5.70	4.90	5.00	1.68	up	1.48E-01	8.95E-01	-	-
1398446_at	RGD1306107	similar to chromosome 1 open reading frame 2	310640	Rn.32304	BG376030	3.03	4.24	3.65	2.74	3.02	2.91	1.68	down	1.05E-01	8.95E-01	-	-
1380812_at	Fam20b	family with sequence similarity 20, member B	304885	Rn.34667	BI290087	4.97	6.35	5.12	4.87	4.41	4.92	1.68	down	1.84E-01	8.95E-01	-	-
1397631_at	Usp8	ubiquitin specific peptidase 8	296121	Rn.52174	BE113329	2.86	3.80	3.93	3.19	2.36	2.80	1.68	down	1.46E-01	8.95E-01	-	-
1388506_at	Dsp	desmoplakin	306871	Rn.54711	AW144509	3.62	6.38	3.85	4.19	5.86	6.05	1.68	up	5.21E-01	8.95E-01	-	-
1373291_at	---	---	---	---	AI176713	4.69	3.47	3.12	3.24	2.90	2.89	1.68	down	2.00E-01	8.95E-01	-	-
1378978_a_at	Prr12	proline rich 12	361569	Rn.17162	AW520354	3.75	4.29	2.35	3.06	2.39	2.69	1.68	down	2.88E-01	8.95E-01	-	-
1391629_at	---	---	---	Rn.40729	BI290794	6.19	7.39	5.98	6.63	7.85	7.33	1.68	up	2.54E-01	8.95E-01	-	-
1398980_at	Supt16h	suppressor of Ty 16 homolog (S. cerevisiae)	305851	Rn.93187	AW253429	4.38	4.90	5.84	4.68	3.89	4.32	1.68	down	1.97E-01	8.95E-01	-	-
1397334_at	Sec14l1	SEC14-like 1 (S. cerevisiae)	360668	Rn.101656	BM385096	2.68	4.07	3.98	3.02	2.67	2.79	1.68	down	1.78E-01	8.95E-01	-	-
1379934_at	---	---	---	Rn.175619	BI285676	2.68	2.80	2.66	2.62	5.11	2.65	1.68	up	4.16E-01	8.95E-01	-	-
1390139_a_at	Obsl1	obscurin-like 1	363259	Rn.776	BE096622	2.66	3.09	4.74	2.62	2.72	2.91	1.68	down	3.08E-01	8.95E-01	-	-
1398327_at	Fermt2	fermitin family homolog 2 (Drosophila)	289992	Rn.7658	BM386598	6.51	6.78	5.72	6.92	7.41	6.93	1.68	up	1.03E-01	8.95E-01	-	-
1389350_at	Apoh	apolipoprotein H (beta-2-glycoprotein I)	287774	Rn.1824	AI180413	3.52	4.04	2.32	3.13	4.64	4.36	1.68	up	3.40E-01	8.95E-01	-	-
1390161_at	Cyyr1	Cysteine/tyrosine-rich 1	304138	Rn.1523	AA818900	3.13	2.45	2.34	4.28	2.49	3.40	1.68	up	2.81E-01	8.95E-01	-	-
1371557_at	Thap4	THAP domain containing 4	363291	Rn.13958	BI275281	6.93	6.12	5.69	6.94	7.01	7.04	1.68	up	1.09E-01	8.95E-01	-	-
1373480_at	Hspa12a	heat shock 70kDa protein 12A	307997	Rn.18598	BG670210	6.36	6.97	6.73	5.70	6.20	5.91	1.68	down	3.10E-02	8.95E-01	DR	-
1379519_at	RGD1306502	similar to hypothetical protein FLJ11193	310158	Rn.43086	AI171230	5.26	5.49	5.81	4.93	3.97	5.43	1.68	down	1.78E-01	8.95E-01	-	-
1382928_at	Pdzd3	PDZ domain containing 3	500986	Rn.54119	AI233682	7.84	7.36	7.31	6.45	7.04	6.68	1.68	down	6.75E-02	8.95E-01	-	-
1390103_at	Phf2	PHD finger protein 2	306814	Rn.166379	BE095970	6.15	7.42	6.39	7.49	7.34	7.37	1.68	up	1.30E-01	8.95E-01	-	-
1372020_at	Tom1	target of myb1 homolog (chicken)	361370	Rn.198076	BI285561	4.71	4.98	4.70	5.14	5.41	6.08	1.68	up	6.39E-02	8.95E-01	-	-
1382755_at	---	---	---	Rn.201655	AI058343	2.68	3.07	3.10	5.10	3.08	2.91	1.68	up	3.57E-01	8.95E-01	-	-
1376261_at	Bag5	BCL2-associated athanogene 5	366734	Rn.76368	BI282898	4.99	4.88	4.09	5.63	5.22	5.36	1.68	up	7.29E-02	8.95E-01	-	-
1367823_at	Timp2	TIMP metallopeptidase inhibitor 2	29543	Rn.10161	NM_021989	4.94	3.38	2.55	3.17	2.91	2.55	1.68	down	3.62E-01	8.95E-01	-	-
1382835_at	---	---	---	Rn.66516	BM387260	3.09	2.61	2.50	2.53	5.46	2.44	1.68	up	5.00E-01	8.95E-01	-	-
1379782_a_at	---	---	---	Rn.203183	AI113136	5.17	8.72	9.55	8.20	6.52	6.48	1.68	down	6.36E-01	8.95E-01	-	-
1389385_at	B9d1	B9 protein domain 1	287383	Rn.3741	BM390324	6.01	6.12	4.99	6.20	6.65	6.50	1.68	up	1.24E-01	8.95E-01	-	-
1368341_at	Polb	polymerase (DNA directed), beta	29240	Rn.9346	NM_017141	3.21	3.08	4.22	2.45	2.85	2.98	1.68	down	1.33E-01	8.95E-01	-	-
1368140_at	Wnk1	WNK lysine deficient protein kinase 1	116477	Rn.27405	NM_053794	5.03	4.92	6.51	5.39	4.32	4.51	1.68	down	2.90E-01	8.95E-01	-	-
1384584_at	---	---	---	Rn.14792	AA892774	3.32	4.67	4.84	4.87	4.71	5.49	1.68	up	2.38E-01	8.95E-01	-	-
1371828_at	RGD1310861	similar to RIKEN cDNA 1500011H22	288667	Rn.7302	BM386571	4.63	5.71	5.62	5.72	6.25	6.20	1.68	up	1.25E-01	8.95E-01	-	-
1382577_at	11-Sep	septin 11	305227	Rn.27798	AA818895	4.62	2.37	2.38	2.40	2.37	2.37	1.68	down	3.77E-01	8.95E-01	-	-
1398369_at	Akap13	A kinase (PRKA) anchor protein 13	293024	Rn.2027	AI599048	3.55	3.51	3.90	4.41	3.99	4.79	1.68	up	4.78E-02	8.95E-01

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1373888_at	Ap3b1	adaptor-related protein complex 3, beta 1 subunit	309969	Rn.11685	BE113312	6.77	5.81	6.54	5.57	5.70	5.65	1.67	down	6.61E-02	8.95E-01	-	-
1376676_a_at	Mphosph8	M-phase phosphoprotein 8	290270	Rn.42579	BI296154	5.22	6.25	7.30	5.80	4.59	6.17	1.67	down	3.91E-01	8.95E-01	-	-
1383742_at	Snx7	sorting nexin 7	310815	Rn.29845	AA997003	9.39	9.78	9.38	8.93	8.51	8.90	1.67	down	1.72E-02	8.95E-01	DR	-
1396046_at	Sema6a	sema domain, transmembrane domain (TM), and cytoplasmic domain, (sema	361324	Rn.203621	BF559983	6.44	8.25	9.78	7.85	6.33	8.07	1.67	down	5.43E-01	8.95E-01	-	-
1392835_at	Zfp68	zinc finger protein 68	304337	Rn.144939	AI705080	5.59	5.69	6.34	5.24	4.33	5.83	1.67	down	2.13E-01	8.95E-01	-	-
1395941_at	Kctd3	potassium channel tetramerisation domain containing 3	305055	Rn.19263	BF542687	4.54	4.81	7.06	5.17	4.26	4.76	1.67	down	4.31E-01	8.95E-01	-	-
1387792_at	Csnk1g2	casein kinase 1, gamma 2	85278	Rn.98151	NM_023102	4.87	4.70	4.14	4.12	3.47	3.91	1.67	down	6.60E-02	8.95E-01	-	-
1372877_at	Plod3	procollagen-lysine, 2-oxoglutarate 5-dioxygenase 3	288583	Rn.90152	BI304070	4.92	5.10	4.51	5.01	6.29	5.43	1.67	up	1.50E-01	8.95E-01	-	-
1390131_at	Srr	serine racemase	303306	Rn.220332	BE112936	5.88	6.52	3.91	5.83	6.67	6.01	1.67	up	4.23E-01	8.95E-01	-	-
1370353_at	Timm22	translocase of inner mitochondrial membrane 22 homolog (yeast)	79463	Rn.41817	AF222951	2.62	3.74	2.76	3.06	3.88	4.39	1.67	up	2.33E-01	8.95E-01	-	-
1377045_at	---	---	---	Rn.167808	BG372832	6.03	4.00	4.48	4.51	3.50	4.29	1.67	down	3.43E-01	8.95E-01	-	-
1393615_at	Depdc6	DEP domain containing 6	314979	---	AI059603	6.04	6.24	5.03	6.24	6.55	6.72	1.66	up	1.39E-01	8.95E-01	-	-
1389788_at	Morn4	MORN repeat containing 4	293950	Rn.103625	AW522732	4.54	4.84	3.71	5.67	4.53	5.09	1.66	up	1.95E-01	8.95E-01	-	-
1372928_at	---	---	---	Rn.17878	AI169749	4.32	4.33	3.77	4.80	4.26	5.57	1.66	up	1.57E-01	8.95E-01	-	-
1397644_at	Mtap	Methylthioadenosine phosphorylase	298227	Rn.202751	BI278369	7.21	6.63	5.75	7.81	6.96	7.02	1.66	up	2.19E-01	8.95E-01	-	-
1368378_at	Aldh1l1	aldehyde dehydrogenase 1 family, member L1	64392	Rn.2328	NM_022547	8.98	8.80	8.64	8.69	7.20	8.33	1.66	down	1.85E-01	8.95E-01	-	-
1388437_at	---	---	---	Rn.11888	AI103153	4.37	2.87	4.11	3.02	2.86	3.27	1.66	down	1.99E-01	8.95E-01	-	-
1385238_at	---	---	---	Rn.154682	AA926087	7.56	7.99	7.60	7.90	8.12	9.32	1.66	up	1.86E-01	8.95E-01	-	-
1368220_at	Gtf2b	general transcription factor IIB	81673	Rn.6109	NM_031041	5.15	5.52	6.77	4.42	4.97	5.84	1.66	down	3.16E-01	8.95E-01	-	-
1377911_at	RGD1561474	Similar to oxysterol-binding protein-like protein 8 isoform a	314824	Rn.18226	AI029434	7.94	9.51	9.43	7.91	8.41	8.35	1.66	down	2.43E-01	8.95E-01	-	-
1376146_at	RGD1304587	similar to RIKEN cDNA 2310033P09	303180	Rn.21630	BI282272	5.47	5.54	4.15	5.73	6.38	5.24	1.66	up	2.29E-01	8.95E-01	-	-
1374566_at	---	---	---	Rn.203869	AI237243	7.20	6.27	5.46	5.64	4.84	6.25	1.66	down	3.21E-01	8.95E-01	-	-
1383622_at	---	---	---	Rn.204933	AI228084	3.04	4.37	3.06	2.91	2.42	2.94	1.66	down	1.96E-01	8.95E-01	-	-
1397349_at	Ubxd6	UBX domain containing 6	290802	Rn.5661	BF394199	3.67	3.65	6.03	5.02	5.29	5.25	1.66	up	4.09E-01	8.95E-01	-	-
1375652_at	Ssr3	signal sequence receptor, gamma	81784	Rn.3264	BI285910	8.44	7.68	6.98	8.48	7.95	8.88	1.66	up	2.16E-01	8.95E-01	-	-
1377016_at	Creld2	cysteine-rich with EGF-like domains 2	362978	Rn.19198	BE106888	7.46	8.20	7.40	8.45	7.73	9.09	1.66	up	1.93E-01	8.95E-01	-	-
1390547_at	---	---	---	Rn.198924	BG375792	6.48	5.24	6.26	4.51	5.08	5.18	1.66	down	1.20E-01	8.95E-01	-	-
1387366_at	Il13	interleukin enhancer binding factor 3	84472	Rn.203881	NM_053412	4.78	6.72	5.10	4.21	4.83	5.37	1.66	down	3.47E-01	8.95E-01	-	-
1390171_at	Fam76a	family with sequence similarity 76, member A	362618	Rn.27338	AA924717	5.95	5.74	4.53	6.20	6.21	6.01	1.66	up	1.78E-01	8.95E-01	-	-
1391670_at	---	---	---	Rn.38378	BI295819	4.21	3.77	4.75	5.53	4.76	4.62	1.66	up	1.41E-01	8.95E-01	-	-
1382584_at	---	---	---	---	BE116720	2.99	3.61	3.60	3.59	4.89	3.93	1.66	up	1.71E-01	8.95E-01	-	-
1372739_at	Tspan31	tetraspanin 31	362890	Rn.129220	AA818865	8.07	7.91	8.35	8.16	9.23	9.15	1.66	up	1.17E-01	8.95E-01	-	-
1396811_at	Jtb	jumping translocation breakpoint	29439	Rn.91803	NM_019213	5.96	6.43	7.10	7.19	6.83	7.66	1.66	up	1.48E-01	8.95E-01	-	-
1373740_at	---	---	---	---	AA851385	5.71	6.53	6.34	5.08	5.51	5.79	1.66	down	8.67E-02	8.95E-01	-	-
1376211_a_at	Kctd6	potassium channel tetramerisation domain containing 6	305792	Rn.105101	AI235964	7.15	8.08	7.82	6.73	6.80	7.32	1.66	down	9.43E-02	8.95E-01	-	-
1398187_at	---	---	---	---	BM391924	3.75	3.88	3.17	4.67	4.57	3.77	1.66	up	1.11E-01	8.95E-01	-	-
1368097_a_at	Rtn1	reticulon 1	116644	Rn.55126	NM_053865	2.47	2.40	2.44	3.80	2.47	3.22	1.66	up	1.31E-01	8.95E-01	-	-
1372119_at	Uba5	ubiquitin-like modifier activating enzyme 5	300968	Rn.18210	AI408251	8.54	8.73	8.66	9.50	9.13	9.49	1.66	up	5.21E-03	8.95E-01	UR	-
1373630_at	Iffo1	intermediate filament family orphan 1	362437	Rn.38932	BG378832	5.57	3.72	3.43	3.48	3.45	3.60	1.66	down	3.36E-01	8.95E-01	-	-
1378043_at	RGD1563091	similar to OEF2	500011	Rn.13231	AW532890	2.51	2.47	2.62	2.51	4.78	2.51	1.66	up	3.90E-01	8.95E-01	-	-
1382763_at	LOC691921	hypothetical protein LOC691921	691921	Rn.81730	AW921300	5.79	6.15	5.04	6.74	6.86	5.58	1.66	up	2.34E-01	8.95E-01	-	-
1391578_at	RGD1307526	similar to modulator of estrogen induced transcription	315792	Rn.49121	BF397936	5.56	7.48	6.66	7.08	7.28	7.53	1.66	up	2.69E-01	8.95E-01	-	-
1383118_at	Tmem209	transmembrane protein 209	312200	Rn.72687	BI288120	2.65	4.79	3.33	2.94	2.19	3.45	1.66	down	3.74E-01	8.95E-01	-	-
1396201_at	---	---	---	---	BF543295	6.63	4.48	4.54	4.39	4.54	4.52	1.66	down	3.61E-01	8.95E-01	-	-
1370905_at	Dock9	dedicator of cytokinesis 9	259237	Rn.10431	BI291229	4.35	5.18	5.03	5.08	5.59	6.08	1.66	up	1.32E-01	8.95E-01	-	-
1373465_at	Polc1	PQ loop repeat containing 1	361352	Rn.17290	AI228284	3.76	5.00	4.63	5.48	5.06	5.03	1.66	up	1.37E-01	8.95E-01	-	-
1389490_at	Cd248	CD248 molecule, endosialin	293669	Rn.38806	BI274335	5.08	4.29	2.28	4.30	5.71	3.84	1.66	up	5.09E-01	8.95E-01	-	-
1397768_at	LOC686796	hypothetical protein LOC686796	686796	---	BI282074	3.64	3.82	2.82	4.15	4.55	3.77	1.66	up	1.26E-01	8.95E-01	-	-
1374189_at	Zfp219	zinc finger protein 219	305848	Rn.206680	BG668883	8.12	7.92	7.48	7.45	5.94	7.94	1.66	down	3.10E-01	8.95E-01	-	-
1388661_at	Mtp18	mitochondrial protein 18 kDa	289745	Rn.106244	AA943734	4.64	5.85	4.58	5.97	5.54	5.75	1.66	up	1.65E-01	8.95E-01	-	-
1395825_at	Cfdp1	Craniofacial development protein 1	292027	Rn.128746	BF284859	7.09	7.78	7.02	7.99	8.30	7.78	1.66	up	6.26E-02	8.95E-01	-	-
1375872_at	Fktn	Fukutin	362520	Rn.100220	AI144944	6.41	6.80	6.62	7.20	7.34	7.48	1.66	up	6.17E-03	8.95E-01	UR	-
1393366_at	Lemd3	LEM domain containing 3	680066	Rn.22132	BF521857	2.89	3.01	2.97	2.82	2.91	5.33	1.66	up	4.26E-01	8.95E-01	-	-
1393985_at	Prpf3	PRP3 pre-mRNA processing factor 3 homolog (S. cerevisiae)	361995	Rn.116267	AI072539	5.15	5.32	3.29	5.21	5.52	5.22	1.66	up	3.29E-01	8.95E-01	-	-
1378948_at	Pon2	paraoxonase 2	296851	Rn.1100	BG686051	6.81	7.67	7.65	7.92	7.90	8.50	1.66	up	1.03E-01	8.95E-01	-	-
1376862_at	Ube4b	ubiquitination factor E4B	298652	Rn.19289	BI296848	7.52	8.60	7.14	8.25	8.03	9.18	1.66	up	2.64E-01	8.95E-01	-	-
1383132_at	Lzic	leucine zipper and CTNNBIP1 domain containing	366507	Rn.162132	BG377939	3.56	4.01	5.93	3.67	3.07	4.57	1.66	down	4.40E-01	8.95E-01	-	-
1386258_at	Rnpc3	RNA-binding region (RNP1, RRM) containing 3	691538	Rn.17587	AA945099	5.09	5.13	3.76	3.52	3.56	4.70	1.66	down	2.86E-01	8.95E-01	-	-
1382873_at	Ctnbp2nl	CTTNBP2 N-terminal like	310760	Rn.25049	BF414250	3.99	5.18	3.91	4.72	4.99	5.55	1.66	up	2.02E-01	8.95E-01	-	-
1398975_at	Aamp	angio-associated, migratory cell protein	301512	Rn.13592	BI281948	7.95	6.15	6.24	6.14	6.11	5.90	1.66	down	2.84E-01	8.95E-01	-	-
1376149_at	---	---	---	Rn.17059	BE100200	6.72	6.41	7.70	6.24	6.06	6.33	1.66	down	1.41E-01	8.95E-01	-	-
1379415_at	---	---	---	Rn.147786	AA998194	3.50	3.11	2.31	3.75	3.86	3.50	1.66	up	1.17E-01	8.95E-01	-	-
1385422_at	Mll5	myeloid/lymphoid or mixed-lineage leukemia 5 (trithorax homolog, Drosophila	311968	Rn.106040	BF396651	4.25	5.65	4.95	3.74	3.67	5.25	1.66	down	3.29E-01	8.95E-01	-	-
1389487_at	Dnajb12	DnaJ (Hsp40) homolog, subfamily B, member 12	294513	Rn.20419	AA818949	4.77	6.42	6.69	6.77	6.71	6.59	1.66	up	2.93E-01	8.95E-01	-	-
1384283_at	Asb9	ankyrin repeat and SOCS box-containing 9	367785	Rn.22749	BI288318	4.72	2.95	4.34	2.69	3.57	3.66	1.66	down	4.24E-01	8.95E-01	-	-
1392986_at	Strn	striatin, calmodulin binding protein	29149	Rn.37469	AI227920	5.07	5.60	5.87	4.62	4.75	4.99	1.66	down	4.89E-02	8.95E-01	DR	-
1376808_at	---	---	---	Rn.21871	BG672572	8.28	7.75	8.34	7.52	7.14	7.52	1.66	down	3.16E-02	8.95E-01	DR	-
1380419_at	Tapt1	Transmembrane anterior posterior transformation 1	305386	Rn.204286	BF287246	3.38	3.53	3.85	3.42	4.70	4.82	1.66	up	1.94E-01	8.95E-01	-	-
1376731_at	---	---	---	Rn.201834	AI411331	6.28	6.65	6.78	5.54	5.93	6.06	1.66	down	2.79E-02	8.95E-01	DR	-
1372473_at	Tjp1	tight junction protein 1	292994	Rn.101871	AW434048	5.69	5.75	4.96	6.47	6.03	6.08	1.66	up	6.75E-02	8.95E-01	-	-
1387969_at	Cxcl10	chemokine (C-X-C motif) ligand 10	245920	Rn.10584	U22520	2.46	2.54	2.35	2.54	4.40	2.59	1.66	up	3.01E-01	8.95E-01	-	-
1392872_at	Clec1a	C-type lectin domain family 11, member a	29313	Rn.162423	AI576758	5.56	2.31	2.32	3.38	2.34	2.29	1.65	down	5.58E-01	8.95E-01	-	-
1371243_at	Grm8	glutamate receptor, metabotropic 8	60590	Rn.44420	Y11153	4.58	2.41	2.44	2.42	2.44	2.40	1.65	down	3.68E-01	8.95E-01	-	-
1392329_at	Homez	homeobox and leucine zipper encoding	260325	Rn.52743	BI295531	4.82	4.88	5.04	5.73	5.11	6.08	1.65	up	6.61E-02	8.95E-01	-	-
1379141_at	---	---	---	---	BF402028	2.78	2.74	2.81	2.77	5.01	2.72	1.65	up	3.91E-01	8.95E-01	-	-
1370473_a_at	Ptpn23	protein tyrosine phosphatase, non-receptor type 23	117552	Rn.54442	AF077000	5.38	3.54	5.06	4.32	3.55	3.93	1.65	down	3.01E-01	8.95E-01	-	-
1390423_at	Mycbp2	MYC binding protein 2	290447	Rn.13538	BE104245	4.58	4.65	2.71	4.59	3.88	5.64	1.65	up	4.24E-01	8.95E-01	-	-
1369816_at	Rab3a	RAB3A, member RAS oncogene family	25531	Rn.44409	NM_013018	5.34	2.83	2.74	3.03	2.84	2.86	1.65	down	4.42E-01	8.95E-01	-	-
1376221_at	Ccdc97	coiled-coil domain containing 97	292724	Rn.44186	BG373555	2.65	2.69	2.70	4.33	3.21	2.68	1.65	up	2.10E-01	8.95E-01	-	-
1379725_at	---	---	---	Rn.28951	AW920459	3.34	4.10	3.44	2.58	2.77	3.35	1.65	down	9.57E-02	8.95E-01	-	-
1386156_at	Med13	mediator complex subunit 13	303403	Rn.94023	AI639451	3.65	4.21	5.62	3.65	3.63	4.03	1.65	down	2.94E-01	8.95E-01	-	-
1372570_at	Usp30	ubiquitin specific peptidase 30	304579	Rn.162152	AI145892	3.92	4.41	3.05	4.38	4.62	4.55	1.65	up	1.48E-01	8.95E-01	-	-
1385271_at	---	---	---	Rn.148832	AI763870	2.73	3.07	2.66	2.79	4.27	3.58	1.65	up	1.79E-01	8.95E-01	-	-
1383962_at	Siva1	SIVA1, apoptosis-inducing factor	362791	Rn.23843	BI275530	2.90	3.40	2.82	3.47	4.33	3.49	1.65	up	9.78E-02	8.95E-01	-	-
1372984_at	---	---	---	Rn.176854	BI291204	2.65	2.57	2.53	4.78	2.58	2.56	1.65	up	3.81E-01	8.95E-01	-	-
1388103_at	Tmem37	transmembrane protein 37	245953	Rn.92180	AF361355	6.27	5.96	6.54	7.60	6.37	6.97	1.65	up	1.38E-01	8.95E-01	-	-
1374860_at	LOC684993	hypothetical protein LOC684993	684993	Rn.198934	AW523507	5.81	6.44	5.66	7.03	6.53	6.51	1.65	up	6.87E-02	8.95E-01	-	-
1389869_at	Sssca1	Sjogren's syndrome/scleroderma autoantigen 1 homolog (human)	689397	Rn.6896	BM390235	2.61	2.74	2.74	4.17	2.84	3.26	1.65	up	1.39E-01	8.95E-01	-	-
1380794_at	---	---	---	Rn.199807	BE106342	5.87	5.68	4.99	6.05	5.89	6.78	1.65	up	1.32E-01	8.95E-01	-	-
1388663_at	LOC687118	similar to death effector domain-containing DNA binding protein 2	687118	---	AI100783	3.52	3.31	5.33	3.21	3.33	3.45	1.65	down	3.24E-01	8.95E-01	-	-
1384388_at	Tmed9	transmembrane emp24 protein transport domain containing 9	361207	Rn.9386	H34273	3.27	3.28	3.27	3.38	3.29	5.33	1.65	up	3.38E-01	8.95E-01	-	-
1388922_at	Aip	aryl-hydrocarbon receptor-interacting protein	282827	Rn.95160	BM388677	5.86	6.11	5.38	6.75	6.68	6.09	1.65	up	7.39E-02	8.95E-01	-	-
1388577_at	---	---	---	Rn.63458	BI274650	4.50	5.13	4.12	4.90	4.87	6.15	1.65	up	2.33E-01	8.95E-01	-	-
1389510_at	Lyar	Ly1 antibody reactive homolog (mouse)	289707	Rn.137862	BE111765	3.35	3.49	3.91	2.94	2.54	3.10	1.65	down	3.86E-02	8.95E-01	DR	-
1374199_at	ip2a /// LOC68768	DIP2 disco-interacting protein 2 homolog A (Drosophila) /// similar to Disco-int	687682 /// 690211	Rn.137473	BI282130	2.69	3.53	3.58	3.42	4.06	4.48	1.65	up	1.63E-01	8.95E-01	-	-
1392806_at	---	---	---	Rn.200475	AI234807	5.00	2.97	2.96	2.74	2.96	3.07	1.65	down	3.50E-01	8.95E-01	-	-
1398517_at	---	---	---	Rn.203237	BI295779	4.41	4.44	4.60	2.62	4.42	4.62	4.58	1.65	up	3.02E-01	8.95E-01	-	-
1386921_at	Cpe	carboxypeptidase E	25669	Rn.7149	NM_013128	4.55	5.18	5.21	5.48	4.73	6.89	1.65	up	3.42E-01	8.95E-01	-	-
1370938_at	Pdxp /// Sh3bp1	pyridoxal (pyridoxine, vitamin B6) phosphatase /// SH3-domain binding protei	300067 /// 727679	Rn.9374	AI551444	5.35	3.97	5.69	4.18	4.06	4.60	1.65	down	2.55E-01	8.95E-01	-	-
1385670_at	Sdsl	serine dehydratase-like	360815	Rn.54338	BF521655	7.21	6.92	6.85	6.22	6.29	6.30	1.65	down	3.13E-03	8.95E-01	DR	-
1371098_a_at	Masp2	mannan-binding lectin serine peptidase 2	64459	Rn.45144	AA996755	2.42	2.41	4.59	2.42	2.43	2.41	1.65	down	3.75E-01	8.95E-01	-	-
1371652_at	---	---	---	Rn.14503	BF550566	4.33	3.21	3.04	3.75	5.08	3.92	1.65	up	2.82E-01	8.95E-01	-	-
1379262_at	Acot8	Acyl-CoA thioesterase 9	302640	Rn.8792	AW525789	4.16	5.67	4.98	5.21	6.58	5.19	1.65	up	3.17E-01	8.95E-01	-	-
1376894_at	Pldn	pallidin homolog (mouse)	317630	Rn.139756	AA849956	6.92	6.42	6.35	6.68	4.72	6.12	1.65	down	3.02E-01	8.95E-01	-	-
1389097_at	---	---	---	Rn.216722	BI275857	6.55	6.78	7.49	6.88	4.99	6.78	1.65	down	3.46E-01	8.95E-01	-	-
1379399_at	Ccdc1a	coiled-coil and C2 domain containing 1A	288908	Rn.21651	AI711484	5.28	3.32	3.69	3.40	3.36	3.36	1.65	down	2.96E-01	8.95E-01	-	-
1373033_at	Sft2d1	SFT2 domain containing 1	292305	Rn.81634	BI289505	5.68	6.60	5.79	6.63	6.34	7.26	1.65	up	1.42E-01	8.95E-01	-	-
1367780_at	Pttg1	pituitary tumor-transforming 1	64193	Rn.271	NM_022391	2.36	2.63	4.25	2.35	2.37	2.35	1.65	down	2.88E-01	8.95E-01	-	-
1396014_at	Timm8a2	translocase of inner mitochondrial membrane 8 homolog a2 (yeast)	680794	Rn.131975	BM384523	4.90	2.71	2.82	2.79	2.81	2.67	1.65	down	3.69E-01	8.95E-01	-	-
1383144_at	---	---	---	---	BF559410	6.02	5.51	4.44	5.08	6.50	6.56	1.65	up	3.43E-01	8.95E-01	-	-
1397392_at	---	---	---	Rn.204031	AW535120	3.16	3.53	3.54	3.78	4.07	4.54	1.65	up	4.63E-02	8.95E-01	UR	-
1394705_at	---	---	---	Rn.69463	BE117266	7.40	6.63	5.88	5.97	5.36	6.43	1.65	down	2.50E-01	8.95E-01	-	-
1393114_at	---	---	---	---	AI136864	7.08	7.07	6.96	7.31	7.97	7.99	1.65	up	3.40E-02	8.95E-01	UR	-
1369879_a_at	Tmbim6	transmembrane BAX inhibitor motif containing 6	24822	Rn.107678	NM_019381	10.10	10.12	9.43	10.00	11.62	10.18	1.65	up	2.67E-01	8.95E-01	-	-
1383355_at	Abca1	ATP-binding cassette, sub-family A (ABC1), member 1	313210	Rn.148916	AW918387	2.45	2.68	2.45	3.79	3.27	2.68	1.65	up	9.49E-02	8.95E-01	-	-
1370801_at	---	---	---	---	AF336872	6.37	4.00	4.24	4.45	4.05	3.95	1.65	down	4.02E-01	8.95E-01	-	-
1388787_at	Ube2z	ubiquitin-conjugating enzyme E2Z	303478	Rn.16992	BM383736	6.68	6.01	6.17	5.58	5.19	5.93	1.65	down	7.20E-02	8.95E-01	-	-
1392417_s_at	Trp53rk	TP53 regulating kinase	362272	Rn.19574	AI711481	6.01	7.03	4.91	7.16	6.24	6.71	1.65	up	3.41E-01	8.95E-01	-	-
1373014_at	B3galt3	beta-1,3-glucuronyltransferase 3 (glucuronosyltransferase I)	293722	Rn.2058	BE111966	3.08	4.10	5.11	4.97	4.49	5.00	1.65	up	3.02E-01	8.95E-01	-	-
1389205_at	---	---	---	Rn.6367	AI012582	2.51	2.90	3.46	5.56	2.56	2.92	1.65	up	5.04E-01	8.95E-01	-	-
1383301_at	LOC498154	hypothetical protein LOC498154	498154	Rn.11782	AI237554	2.30	2.27	2.30	2.29	3.04	3.70	1.65	up	1.50E-01	8.95E-01	-	-
1376906_at	Med1	mediator complex subunit 1	497991	Rn.4262	BM391974	3.41	4.54	3.41	5.34	3.34	4.83	1.65	up	3.66E-01	8.95E-01	-	-
1395250_at	Fbxo42	F-box protein 42	362646	Rn.162839	BM383984	2.36	2.36	4.78	2.36	2.36	2.62	1.65	down	4.25E-01	8.95E-01	-	-
1379654_at	Ckap4	cytoskeleton-associated protein 4	362859	Rn.99508	BI278813	3.39	3.20	2.13	3.29	3.30	4.30	1.65	up	2.35E-01	8.95E-01	-	-
1384423_at	LOC365090	similar to 5-nucleotidase, cytosolic II	365090	---	AW140661	7.15	7.10	5.57	5.72	5.85	6.09	1.65	down	2.48E-01	8.95E-01	-	-
1398523_a_at	Ifnar1	interferon (alpha, beta and omega) receptor 1	288264	Rn.105738	AA900618	6.35	5.58	5.25	4.87	4.99	5.17	1.65	down	9.88E-02	8.95E-01	-	-
1372939_at	Nudcd2	NudC domain containing 2	287199	Rn.3419	AI010173	6.92	6.75	6.27	7.57	7.28	7.25	1.65	up	3.10E-02	8.95E-01	UR	-
1388951_at	Mll4	myeloid/lymphoid or mixed-lineage leukemia 4	361543	Rn.57787	BI294789	3.22	2.35	4.11	2.36	2.82	2.35	1.65	down	2.48E-01	8.95E-01	-	-
1367863_at	Bnip1	BCL2/adenovirus E1B 19kDa-interacting protein 1	140932	Rn.16757	NM_080897	3.32	4.10	2.92	4.10	4.11	4.27	1.65	up	1.10E-01	8.95E-01	-	-
1367523_at	Trappc2l	trafficking protein particle complex 2-like	292074	Rn.24899	AI409145	6.26	6.35	4.56	6.41	6.39	6.52	1.65	up	2.85E-01	8.95E-01	-	-
1378241_at	---	---	---	---	AI555203	5.44	7.78	6.18	7.66	7.01	6.89	1.65	up	3.82E-01	8.95E-01	-	-
1386280_at	Mettl7b	methyltransferase like 7B	366792	Rn.145341	AA892888	9.22	8.96	9.64	8.54	8.50	8.62	1.65	down	2.26E-02	8.95E-01	DR	-
1394951_at	---	---	---	Rn.136022	BE107308	3.35	3.29	2.78	4.29	3.84	3.44	1.65	up	7.74E-02	8.95E-01	-	-
1382114_at	Tlk1	tousled-like kinase 1	311118	Rn.6114	BG379991	5.33	4.73	5.28	4.03	4.73	4.42	1.65	down	6.15E-02	8.95E-01	-	-
1373156_at	Armcx2	armadillo repeat containing, X-linked 2	367903	Rn.15754	AI385330	4.76	2.73	2.75	2.74	2.64	2.51	1.64	down	3.47E-01	8.95E-01	-	-
1376963_at	Dyrk2	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2	314862	Rn.23189	BM388710	5.53	5.98	7.30	6.05	4.99	5.62	1.64	down	3.08E-01	8.95E-01	-	-
1389341_at	Vac14	Vac14 homolog (S. cerevisiae)	307844	Rn.46386	BF408597	2.68	5.26	4.59	4.57	4.83	5.27	1.64	up	4.20E-01	8.95E-01	-	-
1387826_at	tbx /// RGD15660	pyridoxal (pyridoxine, vitamin B6) kinase /// similar to pyridoxal (pyridoxine, vit	361819 /// 83578	Rn.18815	NM_031769	7.29	7.41	5.15	8.16	7.00	6.85	1.64	up	4.43E-01	8.95E-01	-	-
1393191_at	RGD1561205	similar to RIKEN cDNA 2610200G18	500557	Rn.162108	BF554733	6.14	5.93	4.32	6.59	5.26

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1384377_at	Ddx28	DEAD (Asp-Glu-Ala-Asp) box polypeptide 28	364995	Rn.140812	BI284877	3.66	3.46	2.77	3.69	4.05	4.28	1.64	up	8.92E-02	8.95E-01	-	-
1373753_at	---	---	---	Rn.209274	BF404406	5.36	4.48	5.58	4.52	4.32	4.44	1.64	down	1.05E-01	8.95E-01	-	-
1374478_at	RGD1305347	similar to RIKEN cDNA 2610528J11	362576	Rn.1992	AA819329	8.25	8.62	8.56	7.81	7.45	8.04	1.64	down	2.72E-02	8.95E-01	DR	-
1389644_at	Wdr67	WD repeat domain 67	299949	Rn.39013	BI289857	3.27	2.86	2.69	3.47	3.04	4.43	1.64	up	1.87E-01	8.95E-01	-	-
1390967_a_at	Cpsf3l	cleavage and polyadenylation specific factor 3-like	298688	Rn.98615	AW919980	6.08	2.23	2.47	2.73	2.96	2.96	1.64	down	5.99E-01	8.95E-01	-	-
1383168_at	rCG_34418	hypothetical protein LOC688298	688298	Rn.216435	BE102209	4.02	5.53	6.63	6.25	5.90	6.16	1.64	up	4.05E-01	8.95E-01	-	-
1372386_at	LOC295194	similar to SUMO/sentrin specific protease 2	295194	Rn.196323	AW530777	5.56	3.94	5.14	3.08	5.30	4.14	1.63	down	4.27E-01	8.95E-01	-	-
1373757_at	Trafd1	TRAF type zinc finger domain containing 1	114635	Rn.16272	AW529298	7.29	7.29	5.31	7.35	7.36	7.31	1.63	up	3.42E-01	8.95E-01	-	-
1392612_at	---	---	---	Rn.203475	AW142962	9.28	9.10	8.87	7.90	8.26	8.96	1.63	down	1.02E-01	8.95E-01	-	-
1393045_at	Rock2	Rho-associated coiled-coil containing protein kinase 2	25537	Rn.88642	BF556405	6.06	6.16	6.63	5.67	4.85	6.21	1.63	down	1.76E-01	8.95E-01	-	-
1391905_at	Pwp2	PWP2 periodic tryptophan protein homolog (yeast)	690297	Rn.208019	BE108910	2.89	3.80	2.73	4.33	4.14	3.09	1.63	up	2.37E-01	8.95E-01	-	-
1371953_at	Ccng2	cyclin G2	29157	Rn.162246	AI408309	6.18	6.91	6.72	5.37	6.10	6.24	1.63	down	1.11E-01	8.95E-01	-	-
1372361_at	Ccdc22	coiled-coil domain containing 22	317381	Rn.38478	AW552931	5.98	5.93	5.96	5.49	4.96	5.29	1.63	down	1.01E-02	8.95E-01	DR	-
1397924_at	---	---	---	Rn.169405	AW523490	2.92	3.14	2.39	2.65	4.01	3.92	1.63	up	2.23E-01	8.95E-01	-	-
1390041_at	Opa3	optic atrophy 3 (human)	308409	Rn.146575	AI070399	5.06	5.55	5.28	4.76	4.22	4.79	1.63	down	3.79E-02	8.95E-01	DR	-
1369209_at	P34	p34 protein	171435	Rn.163023	NM_134398	3.81	5.98	5.89	3.46	4.31	5.80	1.63	down	5.12E-01	8.95E-01	-	-
1372937_at	---	---	---	Rn.164473	AI072601	3.26	3.39	3.37	2.82	4.99	4.33	1.63	up	3.33E-01	8.95E-01	-	-
1374533_at	Gabpb1	GA repeat binding protein, beta 1	499883	---	AI234190	4.66	5.66	6.62	5.17	3.92	5.72	1.63	down	4.14E-01	8.95E-01	-	-
1385418_at	LOC688717	similar to CG33714-PB, isoform B	688717	Rn.65910	AI502524	2.64	2.77	2.36	2.55	2.70	4.64	1.63	up	3.60E-01	8.95E-01	-	-
1386279_at	Stard4	StAR-related lipid transfer (START) domain containing 4	291699	Rn.163776	AI235655	5.11	5.44	5.75	4.38	5.14	4.65	1.63	down	7.00E-02	8.95E-01	-	-
1385268_at	Ccdc93	coiled-coil domain containing 93	304743	Rn.79004	BI289167	6.53	6.41	5.35	6.37	7.09	6.95	1.63	up	1.81E-01	8.95E-01	-	-
1372048_at	Podxl2	podocalyxin-like 2	297433	Rn.100042	BI276946	2.34	2.34	2.36	2.35	4.48	2.34	1.63	up	3.77E-01	8.95E-01	-	-
1384335_at	Bcl9l	B-cell CLL/lymphoma 9-like	300673	Rn.32447	BE111885	6.28	4.43	5.14	3.92	5.01	4.80	1.63	down	3.28E-01	8.95E-01	-	-
1388636_at	Rnf167	ring finger protein 167	360554	Rn.26488	BI280272	6.41	6.97	6.21	7.67	7.82	6.22	1.63	up	2.75E-01	8.95E-01	-	-
1383441_at	Sap30bp	SAP30 binding protein	360662	Rn.198907	BF413614	2.34	2.50	5.06	2.64	2.63	2.51	1.63	down	4.69E-01	8.95E-01	-	-
1397216_at	---	---	---	Rn.155367	BF288606	3.61	4.19	4.17	2.69	3.51	3.65	1.63	down	1.17E-01	8.95E-01	-	-
1376797_at	Carp2bp	CSRP2 binding protein	362224	Rn.36418	AA998458	5.97	7.31	6.20	7.32	6.91	7.36	1.63	up	1.82E-01	8.95E-01	-	-
1378136_at	Klf16b	kinesin family member 16B	311478	Rn.7029	BI296233	6.36	5.86	6.61	5.71	5.43	5.56	1.63	down	3.95E-02	8.95E-01	DR	-
1374128_at	---	---	---	Rn.167805	BI278569	4.45	4.17	4.89	5.58	5.40	4.65	1.63	up	1.17E-01	8.95E-01	-	-
1371765_at	Hist3h2a	histone cluster 3, H2a	64646	Rn.198869	AA850895	4.12	3.69	3.79	3.22	2.58	3.69	1.63	down	1.11E-01	8.95E-01	-	-
1373880_at	---	---	---	Rn.16384	AI408513	6.16	6.33	6.78	5.47	5.67	6.00	1.63	down	4.29E-02	8.95E-01	DR	-
1376437_at	LOC687738	similar to Der1-like domain family, member 2	687738	---	BM383834	6.37	7.26	7.30	7.69	7.67	7.70	1.63	up	8.09E-02	8.95E-01	-	-
1391098_x_at	---	---	---	Rn.13318	BE108925	3.05	4.32	3.96	5.05	3.81	4.58	1.63	up	2.48E-01	8.95E-01	-	-
1398324_at	Rpl18a	ribosomal protein L18A	290641	Rn.105821	BI279866	9.56	10.19	10.12	10.54	10.56	10.87	1.63	up	3.56E-02	8.95E-01	UR	-
1375633_at	Clic1	chloride intracellular channel 1	406864	Rn.203139	AI012221	5.70	7.23	6.09	6.97	6.84	7.32	1.63	up	2.15E-01	8.95E-01	-	-
1397872_at	---	---	---	Rn.147549	AI577099	3.24	2.24	2.50	4.69	2.50	2.90	1.63	up	3.93E-01	8.95E-01	-	-
1390515_at	---	---	---	Rn.165496	AA998383	5.60	6.08	6.34	5.29	4.60	6.01	1.63	down	2.04E-01	8.95E-01	-	-
1385117_at	---	---	---	Rn.68592	BE101831	3.70	2.45	3.24	2.35	2.58	1.63	1.63	down	1.32E-01	8.95E-01	-	-
1389015_at	Fundc2	FUN14 domain containing 2	361288	Rn.49474	AI171982	6.54	7.55	7.73	7.73	8.51	7.70	1.63	up	1.98E-01	8.95E-01	-	-
1372260_at	Rogdi	rogdi homolog (Drosophila)	287061	Rn.995	BI296304	10.18	9.00	9.19	9.16	8.58	8.52	1.63	down	1.67E-01	8.95E-01	-	-
1375524_at	Arid1a	AT rich interactive domain 1A (SWI-like)	297867	Rn.61077	AA856714	6.12	5.90	4.59	6.50	6.50	5.73	1.63	up	2.64E-01	8.95E-01	-	-
1390888_a_at	Hemk1	HemK methyltransferase family member 1	300989	Rn.37790	AI233704	3.42	4.01	3.28	4.16	3.33	5.32	1.63	up	3.20E-01	8.95E-01	-	-
1397321_at	LOC679894	similar to THO complex subunit 2 (Tho2)	679894	---	AA899866	3.50	2.45	3.50	2.45	2.45	2.43	1.63	down	1.16E-01	8.95E-01	-	-
1391583_at	Carkd	carbohydrate kinase domain containing	361185	Rn.24864	BI280377	3.41	4.08	5.29	3.68	3.36	3.84	1.63	down	2.76E-01	8.95E-01	-	-
1379940_at	---	---	---	Rn.206668	BE101968	2.33	2.31	2.33	2.32	4.44	2.32	1.63	up	3.77E-01	8.95E-01	-	-
1377650_at	---	---	---	Rn.37226	BF283610	3.75	5.20	4.17	5.19	4.87	5.17	1.63	up	1.88E-01	8.95E-01	-	-
1393997_at	RGD1564257	similar to hypothetical protein FLJ32825	500595	Rn.38213	AI556333	8.22	8.65	8.77	9.81	9.26	8.68	1.63	up	1.27E-01	8.95E-01	-	-
1372571_at	02-Mar	membrane-associated ring finger (C3HC4) 2	362849	Rn.145219	AW143187	8.75	7.66	7.42	8.37	8.84	8.73	1.63	up	1.79E-01	8.95E-01	-	-
1367779_at	Bin1	bridging integrator 1	117028	Rn.17098	NM_053959	5.11	5.02	3.89	6.05	5.07	5.02	1.63	up	2.45E-01	8.95E-01	-	-
1375739_at	Ehd4	EH-domain containing 4	192204	Rn.7379	BI395171	2.94	3.57	2.93	4.55	3.68	3.31	1.63	up	1.73E-01	8.95E-01	-	-
1383871_at	Adam9	ADAM metallopeptidase domain 9 (meltrin gamma)	290834	Rn.25221	AI071724	3.72	5.11	6.14	3.76	4.75	4.35	1.63	down	4.08E-01	8.95E-01	-	-
1392854_at	RGD1564560	similar to RCK	500988	Rn.222046	BE116127	5.44	7.94	7.62	7.92	7.38	7.80	1.63	up	4.32E-01	8.95E-01	-	-
1368881_at	Bet1	blocked early in transport 1 homolog (S. cerevisiae)	29631	Rn.3953	NM_019251	5.66	6.16	6.36	6.75	6.47	7.07	1.63	up	6.01E-02	8.95E-01	-	-
1374094_at	---	---	---	Rn.144097	BF408129	5.50	4.38	5.31	3.86	4.42	4.80	1.63	down	1.87E-01	8.95E-01	-	-
1373499_at	Gas5	growth arrest specific 5	81714	Rn.14733	BF287008	9.71	9.69	9.16	10.22	10.10	10.34	1.63	up	2.19E-02	8.95E-01	UR	-
1376879_at	Rwdd4a	RWD domain containing 4A	502084	Rn.15503	AI716916	7.39	6.97	6.99	5.87	6.55	6.82	1.63	down	8.84E-02	8.95E-01	-	-
1395696_at	RGD1306613	similar to RIKEN cDNA 1600012F09	360484	Rn.8045	BF560874	7.11	7.18	7.51	8.10	7.82	7.99	1.63	up	9.17E-03	8.95E-01	UR	-
1371913_at	Tgfbi	transforming growth factor, beta induced	116487	Rn.1046	BG378319	8.53	9.69	9.59	9.69	9.94	10.29	1.63	up	1.61E-01	8.95E-01	-	-
1391438_at	---	---	---	Rn.203065	BF283846	4.52	5.68	4.54	4.78	5.80	6.26	1.63	up	2.95E-01	8.95E-01	-	-
1370468_at	Slc13a1	solute carrier family 13 (sodium/sulfate symporters), member 1	58980	Rn.9699	AI454619	7.71	6.03	7.10	8.28	7.18	7.48	1.63	up	2.99E-01	8.95E-01	-	-
1394042_at	LOC687994	similar to 82-kD FMRP Interacting Protein	687994	---	AI011673	4.26	3.82	5.42	6.36	4.95	4.30	1.63	up	4.16E-01	8.95E-01	-	-
1389530_at	Slc35e1	solute carrier family 35, member E1	498599	Rn.132368	BI274313	4.32	5.15	3.25	4.84	4.41	4.58	1.63	up	3.39E-01	8.95E-01	-	-
1369793_a_at	Mcam	melanoma cell adhesion molecule	78967	Rn.2694	AB035507	2.49	2.44	2.54	4.61	2.49	2.48	1.63	up	3.78E-01	8.95E-01	-	-
1386061_at	Ccdc88a	coiled coil domain containing 88A	305605	Rn.163266	BF523573	3.74	3.42	5.44	3.62	3.42	3.46	1.63	down	3.29E-01	8.95E-01	-	-
1389625_at	Chchd4	coiled-coil-helix-coiled-coil-helix domain containing 4	312559	Rn.16427	BI299402	2.38	2.52	2.58	2.38	4.25	2.94	1.63	up	2.78E-01	8.95E-01	-	-
1396001_at	---	---	---	Rn.53527	BF404704	2.67	4.54	2.77	2.86	5.55	3.67	1.63	up	5.23E-01	8.95E-01	-	-
1397089_at	---	---	---	Rn.210608	BF399386	4.20	2.40	2.64	2.36	2.40	2.37	1.63	down	2.84E-01	8.95E-01	-	-
1397797_at	Tigd3	Tigger transposable element derived 3	309174	Rn.40556	BE103164	6.57	5.95	5.96	6.44	4.54	5.38	1.62	down	2.99E-01	8.95E-01	-	-
1375453_at	685233 /// LOC68	hypothetical protein LOC685233 /// hypothetical protein LOC688211	685233 /// 688211	Rn.209277	BM392052	5.09	4.51	4.27	5.50	5.52	4.93	1.62	up	8.74E-02	8.95E-01	-	-
1377197_at	---	---	---	Rn.146957	BE108892	3.56	3.25	3.78	4.95	3.72	4.02	1.62	up	1.57E-01	8.95E-01	-	-
1394783_at	Dcun1d1	DCN1, defective in cullin neddylation 1, domain containing 1 (S. cerevisiae)	310324	Rn.116073	BF564151	7.56	8.03	6.59	7.80	8.00	8.48	1.62	up	2.11E-01	8.95E-01	-	-
1398504_at	---	---	---	Rn.209933	BF391867	3.13	3.16	2.87	3.13	5.10	3.02	1.62	up	3.63E-01	8.95E-01	-	-
1382707_at	Rps6ka3	ribosomal protein S6 kinase polypeptide 3	501560	Rn.204789	BM386762	4.45	5.41	4.39	5.63	5.00	5.72	1.62	up	1.57E-01	8.95E-01	-	-
1368332_at	Gbp2	guanylate binding protein 2	171164	Rn.25736	NM_133624	5.32	2.40	2.42	3.20	2.44	2.40	1.62	down	5.25E-01	8.95E-01	-	-
1393881_at	Narg1	NMDA receptor regulated 1	310399	Rn.12587	AW527638	7.38	6.37	6.60	6.77	4.74	6.75	1.62	down	3.98E-01	8.95E-01	-	-
1382691_at	Sf3b1	Splicing factor 3b, subunit 1	84486	Rn.198843	AI234943	3.03	2.93	3.04	5.10	2.98	3.01	1.62	up	3.77E-01	8.95E-01	-	-
1376767_at	Gpr116	G protein-coupled receptor 116	245977	Rn.25073	BF542425	2.98	3.02	4.25	2.63	6.76	2.96	1.62	up	6.41E-01	8.95E-01	-	-
1373054_at	Cdw92	CDW92 antigen	85254	Rn.97686	AA801076	5.48	6.13	4.70	6.54	5.23	6.62	1.62	up	3.16E-01	8.95E-01	-	-
1370249_at	Tapo	translocator protein	24230	Rn.1820	AI008680	4.79	4.74	5.16	4.51	7.50	4.77	1.62	up	5.10E-01	8.95E-01	-	-
1388360_at	Npepps	aminopeptidase puromycin sensitive	50558	Rn.12214	BE110600	5.25	6.09	5.93	5.51	4.16	5.51	1.62	down	2.51E-01	8.95E-01	-	-
1381902_at	Znf292	zinc finger protein 292	50552	Rn.106753	BI116321	6.74	8.25	7.40	7.96	8.23	8.29	1.62	up	1.93E-01	8.95E-01	-	-
1396749_at	---	---	---	Rn.50886	BE104663	4.12	2.48	2.96	2.49	2.50	2.47	1.62	down	2.24E-01	8.95E-01	-	-
1372638_at	Arhgef7	Rho guanine nucleotide exchange factor (GEF7)	114559	Rn.146763	BG371454	2.18	3.82	5.56	3.01	3.22	3.24	1.62	down	5.15E-01	8.95E-01	-	-
1377653_at	LOC366669	similar to mKIAA1011 protein	366669	Rn.50877	BI293195	7.99	7.75	8.69	7.99	6.50	7.86	1.62	down	2.76E-01	8.95E-01	-	-
1388190_at	Apob	apolipoprotein B (including Ag(x) antigen)	54225	Rn.33815	BF396597	2.34	2.33	2.36	2.32	2.33	4.46	1.62	up	3.83E-01	8.95E-01	-	-
1368852_at	Dnaja1	DnaJ (Hsp40) homolog, subfamily A, member 1	64627	Rn.6456	NM_022934	8.85	8.63	9.22	8.07	8.23	8.32	1.62	down	2.01E-02	8.95E-01	DR	-
1389068_at	Wipi2	WD repeat domain, phosphoinositide interacting 2	288498	Rn.163194	BI288819	5.22	4.93	4.73	4.45	3.63	4.70	1.62	down	1.19E-01	8.95E-01	-	-
1388667_at	Man2a1	mannosidase, alpha, class 2A, member 1	25478	Rn.163804	AI178793	7.33	7.95	6.98	7.62	8.07	8.67	1.62	up	1.70E-01	8.95E-01	-	-
1368700_at	Plcl1	phospholipase C-like 1	84587	Rn.10684	NM_053456	5.93	4.05	3.61	3.71	3.76	4.02	1.62	down	3.86E-01	8.95E-01	-	-
1381447_at	RGD1311517	similar to RIKEN cDNA 9430015G10	313775	Rn.83717	BF418759	2.56	3.89	2.94	2.92	2.85	5.71	1.62	up	5.32E-01	8.95E-01	-	-
1371033_at	RT1-Bb	RT1 class II, locus Bb	309622	Rn.202964	AI715202	6.01	2.61	4.16	4.29	2.75	3.65	1.62	down	5.54E-01	8.95E-01	-	-
1372943_at	LOC497952	similar to Ubiquitin-associated protein 2-like	497952	Rn.197327	AI072985	6.88	6.12	6.17	5.75	5.55	5.79	1.62	down	5.24E-02	8.95E-01	-	-
1371906_at	---	---	---	---	BF288092	4.16	4.62	4.20	4.94	5.00	5.12	1.62	up	1.17E-02	8.95E-01	UR	-
1376834_at	---	---	---	---	AI407992	3.11	3.97	2.93	3.20	4.12	4.78	1.62	up	2.82E-01	8.95E-01	-	-
1373327_at	Tfeb	transcription factor EB	316214	Rn.22098	BI112887	3.71	4.61	4.22	5.14	4.77	4.72	1.62	up	7.67E-02	8.95E-01	-	-
1371360_at	Ndrg1	N-myc downstream regulated gene 1	299923	Rn.153992	BM384099	10.47	10.65	10.69	9.70	10.28	9.74	1.62	down	2.55E-02	8.95E-01	DR	-
1377480_at	Bud13	BUD13 homolog (S. cerevisiae)	300687	Rn.102777	BF387366	4.12	5.53	6.91	4.24	5.03	5.21	1.62	down	4.63E-01	8.95E-01	-	-
1393613_at	Zfp462	zinc finger protein 462	362522	Rn.23557	BE117871	3.81	2.72	3.90	4.21	4.50	3.80	1.62	up	1.83E-01	8.95E-01	-	-
1372062_at	Cinp	cyclin-dependent kinase 2-interacting protein	299334	Rn.1799	BF394161	5.74	4.55	5.35	6.60	5.07	6.04	1.62	up	2.89E-01	8.95E-01	-	-
1389344_at	Usp39	ubiquitin specific peptidase 39	297336	Rn.50051	BE109258	5.58	5.96	5.91	5.90	7.25	6.39	1.62	up	1.67E-01	8.95E-01	-	-
1381988_at	---	---	---	Rn.203053	AI029833	4.32	6.49	2.37	5.28	5.05	4.94	1.62	up	5.93E-01	8.95E-01	-	-
1373428_at	Brms1	breast cancer metastasis-suppressor 1	293668	Rn.2839	AA851241	5.88	5.41	5.47	4.67	4.68	5.33	1.62	down	5.75E-02	8.95E-01	-	-
1382929_at	Leng8	leukocyte receptor cluster (LRC) member 9	292596	Rn.92802	BF386243	3.31	3.15	4.65	2.86	3.14	3.02	1.62	down	2.25E-01	8.95E-01	-	-
1379078_at	---	---	---	Rn.207679	BE105838	3.78	3.84	4.14	4.82	5.64	3.38	1.62	up	3.59E-01	8.95E-01	-	-
1393070_at	Scrn2	secernin 2	360612	Rn.15274	BE118406	3.38	4.11	4.72	4.65	5.94	3.70	1.62	up	4.10E-01	8.95E-01	-	-
1374600_at	Hist1h4b	histone cluster 1, H4b	84627	Rn.1659	BM86836	6.79	7.47	6.95	6.50	6.75	6.88	1.62	down	1.03E-01	8.95E-01	-	-
1369219_at	Tgfbr3	transforming growth factor, beta receptor III	29610	Rn.9953	NM_017256	4.96	5.11	4.73	4.43	3.93	4.35	1.62	down	2.07E-02	8.95E-01	DR	-
1392557_at	---	---	---	Rn.23854	BF389151	5.46	4.93	2.49	5.35	4.70	4.92	1.62	up	4.99E-01	8.95E-01	-	-
1374844_at	---	---	---	Rn.203474	BF284573	8.65	7.90	7.79	7.79	7.54	6.93	1.62	down	1.37E-01	8.95E-01	-	-
1370955_at	Adam10	ADAM metalloppeptidase domain 10	29650	Rn.42924	BI300565	4.69	4.24	4.99	4.22	3.39	4.23	1.62	down	1.23E-01	8.95E-01	-	-
1384104_at	---	---	---	Rn.134649	BE115892	2.84	3.14	2.82	3.27	4.34	3.27	1.62	up	1.36E-01	8.95E-01	-	-
1382924_at	Pank1	pantothenate kinase 1	294088	Rn.6581	AA850195	9.15	9.40	9.90	8.80	8.61	8.96	1.62	down	4.69E-02	8.95E-01	DR	-
1372116_at	Mrps2	mitochondrial ribosomal protein S2	362094	Rn.48907	AI008855	8.67	8.84	9.97	7.92	8.62	8.87	1.62	down	2.36E-01	8.95E-01	-	-
1377769_at	Ap1s1	adaptor-related protein complex 1, sigma 1 subunit	360785	Rn.11795	AA955775	4.23	4.70	5.13	3.09	3.75	5.15	1.62	down	3.53E-01	8.95E-01	-	-
1375867_at	Zbtb4	zinc finger and BTB domain containing 4	287441	Rn.15836	AW524493	5.57	6.58	6.45	6.74	7.05	6.87	1.62	up	1.03E-01	8.95E-01	-	-
1383680_at	Tmem132a	transmembrane protein 132A	338474	Rn.160719	BG376339	2.77	2.60	2.67	3.30	3.58	3.25	1.62	up	3.70E-03	8.95E-01	UR	-
1372964_at	---	---	---	Rn.86982	BI294751	4.84	6.81	6.43	6.76	6.00	7.39	1.62	up	3.93E-01	8.95E-01	-	-
1368176_at	Rara	retinoic acid receptor, alpha	24705	Rn.91057	NM_031528	5.26	3.13	2.94	3.20	2.90	3.14	1.62	down	4.08E-01	8.95E-01	-	-
1372958_at	Otub1	OTU domain, ubiquitin aldehyde binding 1	293705	Rn.9218	BE111986	7.21	6.96	7.34	6.61	6.17	6.66	1.62	down	2.23E-02	8.95E-01	DR	-
1383126_at	Akt1	V-akt murine thymoma viral oncogene homolog 1	24185	Rn.11422	AA998057	4.30	4.43	5.08	5.77	4.43	5.68	1.62	up	2.35E-01	8.95E-01	-	-
1384702_at	---	---	---	Rn.165625	AI231062	6.29	4.82	5.51	5.55	4.34	4.65	1.62	down	2.81E-01	8.95E-01	-	-
1384233_at	---	---	---	---	BE107090	4.44	2.36	2.38	2.37	2.38	2.35	1.62	down	3.73E-01	8.95E-01	-	-
1375644_at	---	---	---	Rn.203841	AI170561	5.15	6.02	4.61	5.78	5.80	6.27	1.62	up	1.91E-01	8.95E-01	-	-
1388792_at	Gadd45g	growth arrest and DNA-damage-inducible, gamma	291005	Rn.16950	AI599423	3.43	5.48	4.98	4.48	5.86	5.62	1.62	up	4.09E-01	8.95E-01	-	-
1392407_at	---	---	---	Rn.131539	AI012031	4.39	2.33	2.34	2.33	2.34	2.32	1.62	down	3.70E-01	8.95E-01	-	-
1392466_at	Tmem135	transmembrane protein 135	293098	Rn.19940	BF416266	2.88	2.94	2.89	4.62	2.88	3.29	1.62	up	2.58E-01	8.95E-01	-	-
1367845_at	Nefm	neurofilament, medium polypeptide	24588	Rn.10971	NM_017029	5.88	6.66	5.28	4.83	5.87	5.04	1.62	down	2.47E-01	8.95E-01	-	-
1394881_at	Fam81a	family with sequence similarity 81, member A	315789	Rn.163030	AI578410	4.21	5.85	4.53	4.74	6.72	5.20	1.62	up	4.25E-01	8.95E-01	-	-
1381405_at	---	---	---	Rn.53534	BF412149	6.05	6.40	5.70	6.38	6.76	7.09	1.61	up	7.53E-02	8.95E-01	-	-
1374428_at	Klf3b	kinesin family member 3B	296284	Rn.41581	BI300933	5.64	6.96	6.34	6.86	6.53	7.61	1.61	up	2.37E-01	8.95E-01	-	-
1374299_at	Dhx9	DEAH (Asp-Glu-Ala-His) box polypeptide 9	304859	Rn.107359	BF398414	6.72	7.49	7.25	7.34	8.22	7.97	1.61	up	1.17E-01	8.95E-01	-	-
1373044_at	RGD1565840	similar to Dendritic cell protein GA17	295975	Rn.3390	BI285403	7.87	8.41	8.15	8.23	9.15	9.12	1.61	up	1.11E-01	8.95E-01	-	-
1386252_at	---	---	---	Rn.54041	BE349825	3.07	3.29	4.50	3.06	2.42	3.32	1.61	down	2.52E-01	8.95E-01	-	-
1377679_at	Nucks1	nuclear casein kinase and cyclin-dependent kinase substrate 1	64709	Rn.21324	AI599187	7.14	7.89	8.72	7.70	7.98	8.16	1.61	up	1.33E-01	8.95E-01	-	-
1389149_at	Eya3	Eyes absent homolog 3 (Drosophila)	313027	Rn.164239	BM389321	4.94	5.71	5.50	4.74	4.56	4.78	1.61	down	4.45E-02	8.95E-01	DR	-
1377902_a_at	Rad52	RAD52 homolog (S. cerevisiae)	297561	Rn.8154	AA893822	2.95	3.51	4.56	3.02	2.98	2.95	1.61	down	2.18E-01	8.95E-01	-	-
1374501_at	---	---	---	Rn.211867	BF550209	7.98	7.37	8.44	6.73	7.42	7.57	1.61	down	1.62E-01	8.95E-01	-	-
1378896_at	Slc30a2	solute carrier family 30 (zinc transporter), member 2	25362	Rn.11135	BI277879	2.85	2.81	2.92	4.73	2.94	2.99	1.61	up	3.05E-01	8.95E-01	-	-
1395651_at	---	---	---	Rn.199371	AI511118	5.26	3.88	3.38	3.93	3.16	3.35	1.61	down	3.19E-01	8.95E-01	-	-
1375003_at	Serpinb6a	serine (or cysteine) peptidase inhibitor, clade B, member 6a	291085	Rn.12754	AA997359	4.64	4.39	4.19	4.87	5.06	5.36	1.61	up	2

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)				
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG MTC
1383491_at	Aen	apoptosis enhancing nuclease	361594	Rn.46887	BM391709	4.67	4.87	6.67	4.89	4.17	5.09	1.61	down	3.79E-01	8.95E-01	- -
1391210_at	---	---	---	Rn.28872	AI175259	2.58	3.13	2.51	2.88	2.56	4.84	1.61	up	4.07E-01	8.95E-01	- -
1392385_at	Ncoa3	Nuclear receptor coactivator 3	84584	Rn.20691	BF398583	6.48	6.48	4.26	5.85	6.38	5.04	1.61	up	4.43E-01	8.95E-01	- -
1386090_at	---	---	---	---	BF289454	2.24	3.39	3.22	3.06	4.63	3.21	1.61	up	3.27E-01	8.95E-01	- -
1395914_at	Csnk1d	casein kinase 1, delta	64462	Rn.8046	AA684862	8.24	4.44	2.79	4.14	4.49	4.80	1.61	down	6.95E-01	9.06E-01	- -
1387259_at	Cdh2	cadherin 2	83501	Rn.23200	AF097593	6.56	8.63	7.84	8.84	7.66	8.59	1.61	up	3.84E-01	8.95E-01	- -
1387864_at	Kidins220	Kinase D-interacting substrate 220	116478	Rn.21470	AI169232	7.05	6.95	6.44	7.37	7.77	7.36	1.61	up	4.21E-02	8.95E-01	UR -
1393078_at	Narg1	NMDA receptor regulated 1	310399	Rn.12587	BG671648	2.64	2.59	4.59	2.59	2.61	2.58	1.61	down	3.58E-01	8.95E-01	- -
1390972_at	Tprkb	Tp53rk binding protein	297411	Rn.203015	BI281729	3.20	3.98	3.89	4.91	3.84	4.38	1.61	up	1.60E-01	8.95E-01	- -
1386938_at	Anpep	alanyl (membrane) aminopeptidase	81641	Rn.11132	NM_001012	10.65	11.30	11.46	10.39	10.31	10.66	1.61	down	6.33E-02	8.95E-01	- -
1387000_at	Gorasp1	golgi reassembly stacking protein 1	56082	Rn.144458	NM_019385	5.63	5.47	4.96	3.89	5.01	5.11	1.61	down	1.95E-01	8.95E-01	- -
1396238_at	Galnt14	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltrar	313878	Rn.24642	AI763990	6.99	6.75	7.30	6.52	6.22	6.25	1.61	down	2.13E-02	8.95E-01	DR -
1369197_at	Apaf1	apoptotic peptidase activating factor 1	78963	Rn.64522	AF218388	4.75	2.58	2.60	2.58	2.59	2.71	1.61	down	3.98E-01	8.95E-01	- -
1382278_at	---	---	---	Rn.21549	BI278180	3.93	3.25	2.58	2.76	2.49	2.46	1.61	down	1.64E-01	8.95E-01	- -
1391594_at	---	---	---	Rn.55842	BI295733	6.72	7.61	6.83	6.55	5.64	6.92	1.61	down	2.23E-01	8.95E-01	- -
1392744_at	Atg7	ATG7 autophagy related 7 homolog (S. cerevisiae)	312647	Rn.162765	AI179130	5.08	3.20	3.21	3.20	3.21	3.02	1.61	down	3.37E-01	8.95E-01	- -
1393165_at	Tmem206	transmembrane protein 206	305070	Rn.18267	BG377584	5.42	6.35	6.71	6.66	7.36	6.51	1.61	up	2.15E-01	8.95E-01	- -
1393713_at	Gmds	GDP-mannose 4, 6-dehydratase	291095	Rn.212995	BM389780	6.20	5.01	3.21	5.48	5.07	5.91	1.61	up	4.91E-01	8.95E-01	- -
1378029_at	---	---	---	Rn.6440	AI233769	3.98	3.63	3.71	4.12	4.32	4.93	1.61	up	6.30E-02	8.95E-01	- -
1394842_at	Tmem19	transmembrane protein 19	299800	Rn.131677	BF289172	3.16	3.95	3.66	4.26	3.95	4.61	1.61	up	8.31E-02	8.95E-01	- -
1396261_at	Fam168a	family with sequence similarity 168, member A	361614	Rn.137163	BF542635	3.38	3.38	3.54	2.51	2.32	3.42	1.61	down	1.18E-01	8.95E-01	- -
1383519_at	Hk2	Hexokinase 2	25059	Rn.91375	BI294137	3.29	3.45	2.65	3.26	4.94	3.23	1.60	up	3.29E-01	8.95E-01	- -
1386888_at	Eif4ebp1	eukaryotic translation initiation factor 4E binding protein 1	116636	Rn.11161	NM_053857	2.71	2.71	2.71	3.02	2.71	4.45	1.60	up	2.72E-01	8.95E-01	- -
1383514_a_at	Narg1	NMDA receptor regulated 1	310399	Rn.12587	BG671648	5.15	6.05	6.12	5.03	4.59	5.65	1.60	down	1.95E-01	8.95E-01	- -
1382258_at	Rgnef	Rho-guanine nucleotide exchange factor	361882	Rn.33912	AW521384	7.09	7.57	8.17	7.22	7.51	6.05	1.60	down	2.78E-01	8.95E-01	- -
1381391_at	MGC95210	hypothetical LOC287798	287798	Rn.43287	BI288583	5.60	4.99	5.34	4.41	4.48	4.99	1.60	down	5.43E-02	8.95E-01	- -
1377873_at	---	---	---	Rn.199227	BF415139	8.75	6.75	7.59	7.59	6.68	6.77	1.60	down	3.53E-01	8.95E-01	- -
1382372_at	---	---	---	Rn.174710	AA858521	6.43	6.17	5.36	4.20	6.64	5.08	1.60	down	4.33E-01	8.95E-01	- -
1378740_at	Rasal2	RAS protein activator like 2	304893	Rn.66627	AI577567	2.54	4.31	3.70	3.69	3.53	5.37	1.60	up	4.32E-01	8.95E-01	- -
1370591_at	Rfc1	replication factor C (activator 1) 1	89809	Rn.103272	AF059678	5.42	4.37	5.20	4.22	4.38	4.35	1.60	down	1.04E-01	8.95E-01	- -
1393065_at	RGD1562582	similar to KIAA0406-like protein	499935	Rn.48856	BI276770	6.48	6.78	6.84	5.20	6.51	6.34	1.60	down	1.84E-01	8.95E-01	- -
1367674_at	Pitpnb	phosphatidylinositol transfer protein, beta	114561	Rn.2399	NM_053742	7.37	7.21	7.34	8.13	8.36	7.47	1.60	up	6.57E-02	8.95E-01	- -
1395311_at	Icmt	isoprenylcysteine carboxyl methyltransferase	170818	Rn.48709	BI293227	4.47	6.22	4.73	5.40	6.06	6.00	1.60	up	3.08E-01	8.95E-01	- -
1379401_a_at	Fbxo33	F-box protein 33	314157	Rn.222042	AW916372	3.21	3.79	3.94	2.85	2.97	3.07	1.60	down	4.25E-02	8.95E-01	DR -
1389804_at	Relt	RELT tumor necrosis factor receptor	361615	Rn.16770	BF392605	2.24	2.23	2.24	2.23	4.29	2.23	1.60	up	3.77E-01	8.95E-01	- -
1373514_at	LOC688296	similar to chromosome 17 open reading frame 27	688296	---	AA899109	3.40	3.39	3.56	3.89	4.96	3.54	1.60	up	1.89E-01	8.95E-01	- -
1390193_at	---	---	---	Rn.30123	BF389884	5.47	4.67	5.59	5.77	5.73	6.28	1.60	up	1.15E-01	8.95E-01	- -
1374147_at	Zgpat	zinc finger, CCCH-type with G patch domain	296478	Rn.8219	BF420306	3.08	3.02	3.77	2.52	2.73	2.57	1.60	down	5.26E-02	8.95E-01	- -
1396409_at	Dtnb	dystrobrevin, beta	362715	Rn.61275	BE113690	5.02	2.77	2.95	3.14	2.98	2.57	1.60	down	4.10E-01	8.95E-01	- -
1373045_at	Kctd13	potassium channel tetramerisation domain containing 13	293497	Rn.103144	AI235230	2.40	2.72	2.73	3.06	3.49	3.34	1.60	up	1.45E-02	8.95E-01	UR -
1376991_at	---	---	---	Rn.25269	BE095620	3.81	5.14	4.12	4.70	5.36	5.06	1.60	up	2.02E-01	8.95E-01	- -
1396185_at	Rbm17	RNA binding motif protein 17	291295	Rn.20694	BF566807	3.20	3.20	6.13	4.01	3.26	3.23	1.60	down	5.37E-01	8.95E-01	- -
1380030_at	Znf593	zinc finger protein 593	298546	Rn.147537	AW523520	4.21	4.63	4.04	5.79	4.50	4.64	1.60	up	2.00E-01	8.95E-01	- -
1383406_at	---	---	---	Rn.1961	BE103634	2.36	2.35	4.50	2.36	2.46	2.35	1.60	down	3.95E-01	8.95E-01	- -
1386908_at	Glrx1	glutaredoxin 1 (thioltransferase)	64445	Rn.1484	NM_022278	4.26	4.99	4.53	3.58	3.80	4.35	1.60	down	9.57E-02	8.95E-01	- -
1386253_at	Med4	Mediator complex subunit 4	306030	Rn.114469	AA800290	5.17	4.37	3.46	4.67	5.28	5.09	1.60	up	2.66E-01	8.95E-01	- -
1367475_at	Cdc42	cell division cycle 42 (GTP binding protein)	64465	Rn.60067	AI227695	7.92	7.83	7.74	7.51	6.53	7.41	1.60	down	9.86E-02	8.95E-01	- -
1377280_at	Abcf3	ATP-binding cassette, sub-family F (GCN20), member 3	287982	Rn.98647	BF390831	4.74	5.51	4.84	6.53	5.55	5.06	1.60	up	2.42E-01	8.95E-01	- -
1376446_at	Visa	virus-induced signaling adapter	311430	Rn.34996	BE099060	3.22	3.21	2.12	3.78	3.22	3.59	1.60	up	1.65E-01	8.95E-01	- -
1383158_at	Agfg1	ArfGAP with FG repeats 1	363266	Rn.3734	AI575747	5.61	5.65	6.56	5.32	5.40	5.06	1.60	down	1.08E-01	8.95E-01	- -
1371391_at	---	---	---	---	BM390196	4.14	4.20	5.10	5.20	4.48	5.81	1.60	up	2.40E-01	8.95E-01	- -
1379911_at	Dapk1	death associated protein kinase 1	306722	Rn.23108	BI281823	2.52	2.50	4.54	2.51	2.52	2.49	1.60	down	3.71E-01	8.95E-01	- -
1369499_at	Tyms	thymidylate synthetase	29261	Rn.162284	NM_019179	6.34	4.79	5.02	3.93	5.32	4.86	1.60	down	3.43E-01	8.95E-01	- -
1374254_a_at	Tmem205	transmembrane protein 205	300441	Rn.13486	BM386220	5.38	5.50	5.93	6.53	5.91	6.41	1.60	up	5.56E-02	8.95E-01	- -
1391416_at	Ankrd17	ankyrin repeat domain 17	362521	Rn.8442	BE117829	6.88	6.78	5.03	7.17	6.04	6.52	1.60	up	3.23E-01	8.95E-01	- -
1367759_at	H1f0	H1 histone family, member 0	24437	Rn.3129	NM_012578	5.71	6.32	6.47	6.94	6.64	6.96	1.60	up	5.60E-02	8.95E-01	- -
1377793_at	---	---	---	---	BF407551	6.81	5.04	5.39	5.28	5.09	4.84	1.60	down	2.91E-01	8.95E-01	- -
1372587_at	Emcn	endomucin	295490	Rn.8542	AI172271	4.11	4.43	3.26	3.02	3.25	3.50	1.60	down	1.47E-01	8.95E-01	- -
1374160_at	Tmcc2	transmembrane and coiled-coil domain family 2	305095	Rn.106120	BE111296	2.28	2.27	2.28	4.10	2.28	2.49	1.60	up	3.03E-01	8.95E-01	- -
1374771_at	---	---	---	Rn.199303	BM388859	3.30	3.75	3.68	2.90	2.56	3.24	1.60	down	4.93E-02	8.95E-01	DR -
1373083_at	Ppapdc2	phosphatidic acid phosphatase type 2 domain containing 2	619549	Rn.7335	AW915681	7.94	8.16	8.45	8.53	8.92	9.13	1.60	up	4.10E-02	8.95E-01	UR -
1382561_at	---	---	---	---	BF285103	5.55	4.72	4.69	4.43	4.21	4.28	1.60	down	7.90E-02	8.95E-01	- -
1372102_at	Ncor1	nuclear receptor co-repressor 1	54299	Rn.24948	AA848674	3.84	5.17	4.73	6.25	4.77	4.75	1.60	up	3.44E-01	8.95E-01	- -
1395386_at	---	---	---	Rn.202997	AF411881	3.32	4.47	3.97	4.52	4.51	4.77	1.60	up	1.20E-01	8.95E-01	- -
1380496_at	Ube4a	ubiquitination factor E4A	315608	Rn.102204	BF543485	4.86	4.37	3.84	6.00	4.68	4.43	1.60	up	2.99E-01	8.95E-01	- -
1373123_at	Rmi1	RMI1, RecQ mediated genome instability 1, homolog (S. cerevisiae)	306734	Rn.22107	BG372671	5.38	6.25	6.95	5.52	4.28	6.74	1.60	down	4.66E-01	8.95E-01	- -
1375138_at	Timp3	TIMP metallopeptidase inhibitor 3	25358	Rn.19163	AA893169	10.11	10.00	9.99	9.52	9.52	9.03	1.60	down	1.60E-02	8.95E-01	DR -
1372440_at	Serpine2	serine (or cysteine) peptidase inhibitor, clade E, member 2	29366	Rn.2271	BI275818	2.76	2.71	2.80	3.68	4.16	2.46	1.60	up	2.52E-01	8.95E-01	- -
1379831_at	Utp6	UTP6, small subunit (SSU) processome component, homolog (yeast)	360574	Rn.145147	AW252506	4.49	4.09	4.22	3.43	3.57	3.78	1.60	down	1.21E-02	8.95E-01	DR -
1373933_at	Rapgef2	Rap guanine nucleotide exchange factor (GEF) 2	310533	Rn.23121	BF407276	5.09	6.02	5.53	4.34	4.86	5.42	1.60	down	1.77E-01	8.95E-01	- -
1393178_at	Slc25a44	solute carrier family 25, member 44	365841	Rn.18145	BF551322	4.88	4.51	4.67	5.23	5.38	5.47	1.60	up	6.07E-03	8.95E-01	UR -
1368270_at	Apobec1	apolipoprotein B mRNA editing enzyme, catalytic polypeptide 1	25393	Rn.10002	NM_012907	3.77	3.96	2.46	3.94	4.32	3.95	1.60	up	2.39E-01	8.95E-01	- -
1380435_at	Shoc2	soc-2 (suppressor of clear) homolog (C. elegans)	309548	Rn.214772	AI112329	5.29	4.91	3.28	2.85	3.90	4.70	1.60	down	4.56E-01	8.95E-01	- -
1382428_at	Tasp1	taspase, threonine aspartase 1	311468	Rn.22314	AA925658	3.15	3.53	2.94	4.65	3.15	3.84	1.60	up	2.22E-01	8.95E-01	- -
1394304_at	Slc33a1	Solute carrier family 33 (acetyl-CoA transporter), member 1	64018	Rn.95276	BF556357	6.69	7.99	7.42	7.89	7.66	8.58	1.60	up	2.20E-01	8.95E-01	- -
1392764_at	---	---	---	Rn.202407	BE115434	2.70	2.95	2.99	3.64	3.55	3.49	1.60	up	2.50E-03	8.95E-01	UR -
1392056_at	---	---	---	Rn.211141	BF406061	2.82	3.44	3.47	4.99	4.02	2.75	1.60	up	3.79E-01	8.95E-01	- -
1398757_at	Npnm1	nucleophosmin (nucleolar phosphoprotein B23, numatrin)	25498	Rn.54537	NM_012992	8.76	9.22	8.84	9.44	9.53	9.87	1.60	up	2.50E-02	8.95E-01	UR -
1393104_at	Dtwd2	DTW domain containing 2	361326	Rn.16239	BI292315	3.72	2.68	4.16	2.65	2.71	3.18	1.60	down	2.23E-01	8.95E-01	- -
1385420_at	Dvl3	dishevelled, dsh homolog 3 (Drosophila)	303811	Rn.219497	BF390548	2.81	3.07	3.12	3.16	4.80	3.07	1.60	up	3.03E-01	8.95E-01	- -
1381283_at	---	---	---	Rn.162186	BE105217	4.56	2.52	2.53	2.53	2.55	2.52	1.60	down	3.77E-01	8.95E-01	- -
1378236_at	Lrrc16a	leucine rich repeat containing 16A	306941	Rn.40387	BE100650	4.14	4.32	3.27	5.21	4.45	4.09	1.60	up	2.19E-01	8.95E-01	- -
1385644_at	Rnf121	ring finger protein 121	308871	Rn.20943	AI058291	2.42	3.74	3.31	3.30	4.11	4.08	1.60	up	2.25E-01	8.95E-01	- -
1379785_at	---	---	---	Rn.52251	BI275894	5.73	7.88	6.96	7.07	7.76	7.76	1.60	up	3.68E-01	8.95E-01	- -
1368035_a_at	Ptprf	protein tyrosine phosphatase, receptor type, F	360406	Rn.11386	X83505	4.50	7.14	4.94	6.20	6.41	6.00	1.60	up	4.59E-01	8.95E-01	- -
1383415_at	---	---	---	Rn.203201	AW531415	3.75	3.45	2.99	3.59	4.42	4.21	1.60	up	1.13E-01	8.95E-01	- -
1389639_at	RGD1565350	similar to Shb protein	362513	Rn.84084	BF283302	4.74	6.17	4.77	6.03	5.46	6.21	1.60	up	2.67E-01	8.95E-01	- -
1368136_at	Tmpo	thymopoietin	25359	Rn.202955	AI044110	3.30	5.20	4.50	4.85	4.55	5.62	1.60	up	3.50E-01	8.95E-01	- -
1383898_at	Fam3d	family with sequence similarity 3, member D	289949	Rn.38497	AA900127	2.42	2.47	4.35	2.41	2.42	2.39	1.60	down	3.48E-01	8.95E-01	- -
1378773_at	---	---	---	---	BG372744	4.48	4.71	4.08	4.21	3.77	3.27	1.60	down	1.08E-01	8.95E-01	- -
1382357_at	---	---	---	---	AI713784	5.77	5.61	4.22	5.74	6.08	5.81	1.60	up	2.50E-01	8.95E-01	- -
1384620_at	---	---	---	Rn.100422	AI716355	4.82	4.06	2.99	3.06	3.71	3.09	1.59	down	3.05E-01	8.95E-01	- -
1385892_at	---	---	---	Rn.166561	AI716355	4.82	4.06	2.99	3.06	3.71	3.09	1.59	down	3.05E-01	8.95E-01	- -
1376641_at	Thoc1	THO complex 1	291797	Rn.167008	AA800322	5.31	4.83	3.74	6.27	4.48	5.15	1.59	up	3.91E-01	8.95E-01	- -
1373502_at	Dym	dymeclin	291433	Rn.202648	BM384228	7.03	6.96	5.64	7.32	7.56	6.77	1.59	up	2.58E-01	8.95E-01	- -
1392043_at	---	---	---	Rn.59303	BM389188	3.83	4.81	3.80	5.46	3.77	5.23	1.59	up	3.42E-01	8.95E-01	- -
1389860_at	Rkhd2	Ring finger and KH domain containing 2	307271	Rn.205298	BE116206	3.90	4.14	3.92	4.30	5.36	4.32	1.59	up	1.34E-01	8.95E-01	- -
1387900_at	Cdipt	CDP-diacylglycerol--inositol 3-phosphatidyltransferase (phosphatidylinositol s	192260	Rn.10598	D82928	4.81	5.69	5.40	6.28	5.49	6.15	1.59	up	1.33E-01	8.95E-01	- -
1383302_at	Dnajb1	DnaJ (Hsp40) homolog, subfamily B, member 1	361384	Rn.128947	BM384926	2.57	3.40	3.33	2.66	4.47	4.19	1.59	up	3.40E-01	8.95E-01	- -
1384214_a_at	---	---	---	Rn.221935	AI045459	5.91	4.52	7.14	6.09	3.83	5.63	1.59	down	5.47E-01	8.95E-01	- -
1389053_at	Rmnd1	Required for meiotic nuclear division 1 homolog (S. cerevisiae)	292268	Rn.207169	AI171280	7.08	6.19	6.46	6.61	5.20	5.90	1.59	down	2.39E-01	8.95E-01	- -
1379987_at	RGD1304595	similar to RIKEN cDNA 6330416G13 gene	298104	Rn.15144	BE100570	6.69	6.24	7.76	5.42	7.29	5.97	1.59	down	4.01E-01	8.95E-01	- -
1386897_at	Prmt1	protein arginine methyltransferase 1	60421	Rn.5870	NM_024363	6.90	7.52	8.09	7.30	7.46	7.76	1.59	up	1.99E-01	8.95E-01	- -
1378608_at	---	---	---	---	BF417283	3.71	2.85	3.88	2.98	2.71	2.72	1.59	down	1.11E-01	8.95E-01	- -
1381025_at	---	---	---	---	BF410266	3.79	3.92	2.79	5.17	3.59	3.75	1.59	up	3.37E-01	8.95E-01	- -
1389346_at	Adnp	activity-dependent neuroprotector homeobox	64622	Rn.48777	BI274136	4.98	5.91	4.77	5.64	5.68	6.34	1.59	up	1.85E-01	8.95E-01	- -
1383050_at	Prr6	proline rich 6	501702	Rn.3337	AW523199	3.83	4.98	2.70	2.79	3.15	3.56	1.59	down	3.88E-01	8.95E-01	- -
1382922_at	Pabpn1	Poly(A) binding protein, nuclear 1	116697	Rn.39199	BG375109	5.14	4.66	3.48	4.15	4.42	2.70	1.59	down	4.07E-01	8.95E-01	- -
1394605_at	RGD1566149	similar to CDNA sequence BC017647	497960	Rn.19152	AI409909	6.39	6.42	5.45	6.43	4.64	7.22	1.59	up	5.94E-01	8.95E-01	- -
1392644_s_at	LOC498662	similar to RIKEN cDNA 2610019F03	498662	Rn.11716	AA864146	6.59	7.92	7.95	7.27	6.01	7.16	1.59	down	3.29E-01	8.95E-01	- -
1378565_at	LOC366300	hypothetical LOC366300	366300	Rn.203101	AW435439	8.71	9.06	8.41	9.38	9.48	9.32	1.59	up	2.65E-02	8.95E-01	UR -
1371714_at	Srpk1	SFRS protein kinase 1	361811	Rn.2688	BG378760	3.17	3.45	3.47	4.02	2.93	5.15	1.59	up	3.58E-01	8.95E-01	- -
1387188_at	Slc17a1	solute carrier family 17 (sodium phosphate), member 1	171080	Rn.11150	NM_133554	7.46	7.58	7.41	7.73	8.19	8.55	1.59	up	5.03E-02	8.95E-01	- -
1397583_at	---	---	---	Rn.153894	BF394946	3.74	3.79	3.67	3.76	5.70	3.76	1.59	up	3.60E-01	8.95E-01	- -
1382400_at	Rlf	rearranged L-myc fusion	313566	Rn.50631	BE104395	2.83	2.69	2.70	2.68	4.43	3.12	1.59	up	2.73E-01	8.95E-01	- -
1387301_at	Fgf1	fibroblast growth factor 1	25317	Rn.88013	NM_012846	4.12	4.95	5.27	3.90	3.99	4.43	1.59	down	1.51E-01	8.95E-01	- -
1391463_at	Ddx58	DEAD (Asp-Glu-Ala-Asp) box polypeptide 58	297989	Rn.38642	AI575284	4.49	6.36	7.23	5.24	5.99	4.85	1.59	down	4.87E-01	8.95E-01	- -
1385253_at	RGD1304610	similar to DNA segment, Chr 14, ERATO Doi 436, expressed	305831	Rn.47301	AW529791	5.06	4.58	4.08	4.98	3.74	3.74	1.59	down	3.58E-01	8.95E-01	- -
1373053_at	---	---	---	---	AI169620	8.47	7.66	7.63	7.70	6.99	7.05	1.59	down	1.33E-01	8.95E-01	- -
1383531_at	---	---	---	---	AA801061	4.51	5.74	7.32	4.81	5.18	5.57	1.59	down	4.70E-01	8.95E-01	- -
1390818_at	---	---	---	Rn.165756	BF288088	3.89	4.97	3.75	3.70	5.82	5.10	1.59	up	4.11E-01	8.95E-01	- -
1374557_at	Gpr177	G protein-coupled receptor 177	362065	Rn.103639	BF394235	2.72	3.38	3.88	4.04	3.98	3.97	1.59	up	1.17E-01	8.95E-01	- -
1391714_at	Plag1	pleiomorphic adenoma gene 1	297804	Rn.39161	BI290063	2.31	2.30	2.32	4.33	2.31	2.30	1.59	up	3.77E-01	8.95E-01	- -
1369083_at	Cirbp	cold inducible RNA binding protein	81825	Rn.28931	NM_031147	3.33	5.90	3.08	4.60	5.56	4.15	1.59	up	5.38E-01	8.95E-01	- -
1397756_at	RGD1563701	similar to BC068281 protein	500623	---	AI549567	3.31	3.31	3.14	3.61	5.26	2.89	1.59	up	3.96E-01	8.95E-01	- -
1379467_at	---	---	---	Rn.2564	BF284065	7.40	7.23	6.89	6.93	5.89	6.69	1.59	down	1.27E-01	8.95E-01	- -
1370583_s_at	Abcb1a /// Abcb1b	ATP-binding cassette, sub-family B (MDR/TAP), member 1A /// ATP-binding c	170913 /// 24646	Rn.144554	AY082609	3.08	3.55	3.15	4.41	3.81	3.56	1.59	up	8.25E-02	8.95E-01	- -
1378307_at	---	---	---	Rn.35024	AI412126	3.64	3.63	4.62	3.08	3.64	3.16	1.59	down	1.46E-01	8.95E-01	- -
1372043_at	Mrto4	mRNA turnover 4 homolog (S. cerevisiae)	298586	Rn.219376	BI282363	6.03	7.59	7.16	6.82	7.95	8.01	1.59	up	3.32E-01	8.95E-01	- -
1371696_at	Gpr56	G protein-coupled receptor 56	280326	Rn.1677	AI412938	8.31	7.90	7.36	8.63	8.16	8.78	1.59	up	1.13E-01	8.95E-01	- -
1388718_at	Tmod1	tropomodulin 1	25566	Rn.1646	AI104913	5.54	4.44	6.07	4.60	4.74	4.71	1.59	down	2.37E-01	8.95E-01	- -
1383788_at	---	---	---	---	AI453887	2.57	5.14	2.39	2.86	2.56	2.67	1.59	down	4.96E-01	8.95E-01	- -
1389557_at	Tex261	testis expressed 261	297392	Rn.198161	BM384037	5.31	4.57	4.50	5.27	5.45	5.66	1.59	up	7.76E-02	8.95E-01	- -
1379028_at	Spag7	sperm associated antigen 7	303260	Rn.219156	BE116950	6.87	6.99	6.16	5.89	6.07	6.06	1.59	down	6.59E-02	8.95E-01	- -
1368967_at	Eif2b3	eukaryotic translation initiation factor 2B, subunit 3 gamma	171145	Rn.10577	NM_133609	3.42	3.76	3.66	4.44	4.17	4.24	1.59	up	7.02E-03	8.95E-01	UR -
1386971_at	Ppp1r10	protein phosphatase 1, regulatory subunit 10	65045	Rn.37758	NM_022951	4.51	3.35	3.30	2.92	3.15	3.10	1.59	down	1.71E-01	8.95E-01	- -
1385581_at	---	---	---	Rn.165449	BF551187	6.23	6.48	5.76	5.45	5.73	5.29	1.59	down	5.40E-02	8.95E-01	- -
1398628_at	Gba3	glucosidase, beta, acid 3 (cytosolic)	289687	Rn.19324	AI059960	9.09	8.31	8.87	8.31	7.91	8.04	1.59	down	6.28E-02	8.95E-01	- -
1390721_at	---	---	---	Rn.16373	AA817700	3.81	3.80	3.30	4.33	3.82	4.77	1.59	up	1.07E-01	8.95E-01	- -
1384589_at	Spata2L	spermatogenesis associated 2-like	498963	Rn.91547	BF401982	4.41	3.15	2.88	2.69	2.83	2.91	1.59	down	2.34E-01	8.95E-01	- -
1369876_at	Dync2h1	dynein cytoplasmic 2 heavy chain 1	65209	Rn.44896	NM_023024	3.27	4.00	5.50	4.06	3.25	3.46	1.59	down	3.95E-01

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1395408_at	Nostrin	nitric oxide synthase trafficker	311111	Rn.39383	AI058709	4.56	4.97	6.00	3.31	4.99	5.24	1.58	down	4.23E-01	8.95E-01	-	-
1390558_at	Stau2	staufen, RNA binding protein, homolog 2 (Drosophila)	171500	Rn.73714	AI502229	5.55	4.36	5.63	6.21	5.85	5.46	1.58	up	2.27E-01	8.95E-01	-	-
1372299_at	Nasp	nuclear autoantigenic sperm protein (histone-binding)	298441	Rn.48344	AI137618	5.77	6.77	6.51	6.21	4.73	6.12	1.58	down	3.08E-01	8.95E-01	-	-
1370607_a_at	Nrg1	neuregulin 1	112400	Rn.37438	U02323	4.45	2.37	2.41	2.37	2.41	2.47	1.58	down	3.92E-01	8.95E-01	-	-
1387655_at	Cxcl12	chemokine (C-X-C motif) ligand 12 (stromal cell-derived factor 1)	24772	Rn.54439	AF189724	6.07	6.31	4.82	6.75	6.71	5.72	1.58	up	3.13E-01	8.95E-01	-	-
1388915_at	---	---	---	Rn.834	BI295753	2.49	2.70	2.88	2.78	4.42	2.84	1.58	up	2.93E-01	8.95E-01	-	-
1389699_at	LOC684903	similar to Probable ATP-dependent RNA helicase DHX34 (DEAH box protein	684903	---	AW433598	4.01	2.78	3.70	2.88	2.78	2.85	1.58	down	1.49E-01	8.95E-01	-	-
1371898_at	Kcnk5	potassium channel, subfamily K, member 5	364241	Rn.23969	BI287946	7.44	5.40	6.83	7.55	7.23	6.87	1.58	up	3.59E-01	8.95E-01	-	-
1371766_at	---	---	---	Rn.4018	BE113242	3.69	3.13	2.63	3.87	3.42	4.15	1.58	up	1.51E-01	8.95E-01	-	-
1393164_at	Mrps27	mitochondrial ribosomal protein S27	361883	Rn.203126	AI137642	4.37	2.40	2.44	2.39	2.44	2.42	1.58	down	3.68E-01	8.95E-01	-	-
1367939_at	Rbp1	retinol binding protein 1, cellular	25056	Rn.902	NM_012733	7.95	6.44	7.03	6.70	6.11	6.64	1.58	down	2.41E-01	8.95E-01	-	-
1367474_at	LOC685144	similar to SEC24 related gene family, member C	685144	Rn.122667	AI231320	8.48	8.40	8.16	9.09	8.50	9.43	1.58	up	8.36E-02	8.95E-01	-	-
1391577_at	Pgam5	phosphoglycerate mutase family member 5	288731	Rn.23489	BI293450	7.20	7.11	7.96	6.83	6.67	6.79	1.58	down	7.44E-02	8.95E-01	-	-
1387234_at	Acgp1	alpha-2-glycoprotein 1, zinc-binding	25294	Rn.5007	NM_012826	4.54	6.92	4.93	6.07	5.91	6.39	1.58	up	4.29E-01	8.95E-01	-	-
1392862_at	---	---	---	Rn.24818	AA859389	6.36	7.66	6.60	7.27	7.17	8.16	1.58	up	2.65E-01	8.95E-01	-	-
1398876_at	Abcf1	ATP-binding cassette, sub-family F (GCN20), member 1	85493	Rn.14350	BG380494	5.55	7.12	6.68	6.93	7.17	7.23	1.58	up	2.40E-01	8.95E-01	-	-
1375438_at	Gosr2	golgi SNAP receptor complex member 2	64154	Rn.13518	AA864687	7.25	7.13	7.50	8.13	7.88	7.84	1.58	up	9.93E-03	8.95E-01	UR	-
1376242_at	---	---	---	Rn.38126	BF402365	4.78	4.49	3.39	4.66	5.36	4.62	1.58	up	2.48E-01	8.95E-01	-	-
1384005_at	Dr1	down-regulator of transcription 1	289881	Rn.6666	BG662895	4.34	5.50	5.69	4.63	4.15	4.77	1.58	down	2.29E-01	8.95E-01	-	-
1373100_at	LOC499779	similar to RIKEN cDNA 2900010J23	499779	Rn.30992	BI288811	7.24	9.05	6.51	8.04	8.02	8.72	1.58	up	4.52E-01	8.95E-01	-	-
1393424_at	---	---	---	Rn.16847	BF407028	2.71	2.81	2.85	2.86	3.54	3.95	1.58	up	1.11E-01	8.95E-01	-	-
1373127_at	---	---	---	Rn.199181	BM383645	8.04	7.21	7.14	6.70	6.20	7.52	1.58	down	2.42E-01	8.95E-01	-	-
1372553_at	MGC94199	similar to RIKEN cDNA 2610301B20; EST AI428449	362483	Rn.7569	AI233205	7.31	5.89	5.79	5.42	5.36	6.24	1.58	down	3.10E-01	8.95E-01	-	-
1371733_at	Ari8a	ADP-ribosylation factor-like 8A	498234	Rn.138927	BG867965	4.50	5.57	6.40	6.01	5.68	6.75	1.58	up	3.60E-01	8.95E-01	-	-
1391338_at	---	---	---	Rn.168349	AI603449	3.93	3.92	3.99	4.50	5.18	4.12	1.58	up	1.01E-01	8.95E-01	-	-
1377096_at	Mtfmt	mitochondrial methionyl-tRNA formyltransferase	315763	Rn.34645	AW251803	6.78	6.96	4.77	7.46	6.24	6.78	1.58	up	4.50E-01	8.95E-01	-	-
1371552_at	---	---	---	Rn.41520	BF400684	6.90	4.88	5.45	5.42	5.40	4.45	1.58	down	3.89E-01	8.95E-01	-	-
1375642_at	Ube2b	ubiquitin-conjugating enzyme E2B, RAD6 homology (S. cerevisiae)	81816	Rn.20766	AA892795	9.06	9.42	9.53	8.72	8.54	8.78	1.58	down	1.54E-02	8.95E-01	DR	-
1388125_a_at	Klc1	kinesin light chain 1	171041	Rn.106230	AI576961	5.87	6.62	4.22	6.98	6.76	4.93	1.58	up	5.32E-01	8.95E-01	-	-
1387195_at	St14	suppression of tumorigenicity 14 (colon carcinoma)	114093	Rn.49170	AB049189	3.30	2.67	4.81	2.46	3.12	3.22	1.58	down	3.89E-01	8.95E-01	-	-
1375423_at	LOC689959	hypothetical protein LOC689959	689959	Rn.9433	BE098181	4.77	5.49	5.36	6.07	5.56	5.95	1.58	up	7.23E-02	8.95E-01	-	-
1398309_at	Pigl	phosphatidylinositol glycan anchor biosynthesis, class L	192263	Rn.10774	D88364	4.25	5.65	3.78	5.21	4.71	5.72	1.58	up	3.58E-01	8.95E-01	-	-
1369640_at	Gja1	gap junction protein, alpha 1	24392	Rn.10346	BG378227	2.68	2.64	2.66	4.04	3.28	2.63	1.58	up	1.82E-01	8.95E-01	-	-
1380221_at	Nsd1	Nuclear receptor binding SET domain protein 1	306764	Rn.19435	BE116223	3.74	4.46	2.58	4.49	3.75	4.51	1.58	up	3.39E-01	8.95E-01	-	-
1374633_at	---	---	---	Rn.23149	BF284700	5.37	4.59	4.99	5.82	5.49	5.61	1.58	up	5.60E-02	8.95E-01	-	-
1369631_at	BC088250 /// Myo	similar to unconventional myosin Myr2 I heavy chain /// myosin IC	65261 /// 686250	Rn.55135	NM_023092	4.22	4.95	4.13	3.85	3.41	4.08	1.58	down	1.15E-01	8.95E-01	-	-
1391055_at	Snx5	Sorting nexin 5	296199	Rn.86151	AA866467	7.58	7.12	6.15	7.64	7.26	7.92	1.58	up	2.30E-01	8.95E-01	-	-
1378314_at	---	---	---	Rn.165017	AA856277	2.73	2.68	2.64	2.85	4.11	3.05	1.58	up	1.68E-01	8.95E-01	-	-
1368092_at	Fah	fumarylacetoacetate hydrolase	29383	Rn.9195	NM_017181	10.65	10.92	10.70	10.60	12.70	10.94	1.57	up	3.75E-01	8.95E-01	-	-
1370945_at	Sec16a	SEC16 homolog A (S. cerevisiae)	114089	Rn.199218	BF282728	3.71	4.92	4.54	4.30	3.70	3.20	1.57	down	2.43E-01	8.95E-01	-	-
1390655_at	---	---	---	---	BF402663	5.48	5.40	7.00	4.71	5.14	6.06	1.57	down	3.74E-01	8.95E-01	-	-
1369239_at	Clcn5	chloride channel 5	25749	Rn.10337	NM_017106	3.81	6.13	4.60	3.57	4.30	4.70	1.57	down	4.36E-01	8.95E-01	-	-
1374120_at	Slc45a4	solute carrier family 45, member 4	315054	Rn.33421	BI296223	2.84	3.10	2.85	4.29	3.30	3.16	1.57	up	1.47E-01	8.95E-01	-	-
1382286_at	Slc12a6	solute carrier family 12, member 6	691209	Rn.13442	AA965275	2.98	2.60	4.09	2.64	2.47	2.60	1.57	down	2.21E-01	8.95E-01	-	-
1389128_at	Wdfy3	WD repeat and FYVE domain containing 3	305164	Rn.57981	AI146179	6.45	7.66	8.01	6.82	6.35	6.99	1.57	down	2.69E-01	8.95E-01	-	-
1368821_at	Fstl1	follistatin-like 1	79210	Rn.95652	BI290885	5.49	4.50	4.64	4.49	4.31	3.86	1.57	down	1.45E-01	8.95E-01	-	-
1395409_at	Ppp2r4	protein phosphatase 2A activator, regulatory subunit 4	362102	Rn.24600	BF522283	4.31	3.36	3.06	2.55	3.12	3.10	1.57	down	1.93E-01	8.95E-01	-	-
1386574_at	---	---	---	Rn.18516	BF546904	2.70	3.87	2.15	2.89	4.14	3.65	1.57	up	3.54E-01	8.95E-01	-	-
1389161_at	---	---	---	Rn.8238	AW144193	2.42	3.01	3.76	2.40	2.42	2.41	1.57	down	1.67E-01	8.95E-01	-	-
1372199_at	Pink1	PTEN induced putative kinase 1	298575	Rn.219286	AI233191	7.45	8.03	7.80	7.09	6.77	7.45	1.57	down	6.61E-02	8.95E-01	-	-
1390178_at	Srprb	signal recognition particle receptor, B subunit	300985	Rn.138078	BM387756	7.25	7.79	7.66	8.08	7.86	8.71	1.57	up	9.58E-02	8.95E-01	-	-
1375519_at	LOC287167	globin, alpha	287167	Rn.163132	AI237401	3.69	3.25	3.06	2.70	2.70	2.63	1.57	down	2.49E-02	8.95E-01	DR	-
1397052_at	Rbbp6	retinoblastoma binding protein 6	308968	Rn.95305	BF408911	6.56	7.11	4.66	5.70	4.93	5.74	1.57	down	4.53E-01	8.95E-01	-	-
1392643_at	Rab5b	RAB5B, member RAS oncogene family	288779	Rn.3305	BF407212	6.38	4.87	4.91	4.86	4.48	4.85	1.57	down	2.71E-01	8.95E-01	-	-
1387913_at	Cyp24v1	cytochrome P450, family 2, subfamily d, polypeptide 4	171522	Rn.26060	U48220	3.68	5.17	3.67	3.36	3.54	3.66	1.57	down	2.66E-01	8.95E-01	-	-
1383614_at	Nuak2	NUAK family, SNF1-like kinase, 2	289419	Rn.16922	BI295051	9.62	10.09	9.14	9.19	9.12	8.58	1.57	down	1.24E-01	8.95E-01	-	-
1368322_at	Sod3	superoxide dismutase 3, extracellular	25352	Rn.10358	NM_012880	8.98	8.56	8.49	9.02	9.29	9.67	1.57	up	5.40E-02	8.95E-01	-	-
1379008_at	---	---	---	---	BE104149	2.58	2.96	2.61	3.61	3.22	3.29	1.57	up	1.88E-02	8.95E-01	UR	-
1370991_at	Cml3	camello-like 3	113892	Rn.198165	AF187814	10.23	9.51	9.32	9.53	8.49	9.07	1.57	down	1.85E-01	8.95E-01	-	-
1388130_at	Zyx	zyxin	114636	Rn.107363	AA943537	5.86	6.63	5.11	6.29	3.81	5.55	1.57	down	4.88E-01	8.95E-01	-	-
1395359_at	---	---	---	---	BF559566	5.85	5.43	6.37	5.44	4.96	5.29	1.57	down	1.01E-01	8.95E-01	-	-
1384041_at	---	---	---	Rn.165282	BG671630	2.34	2.33	4.30	2.34	2.33	2.33	1.57	down	3.74E-01	8.95E-01	-	-
1372423_at	Perp	PERP, TP53 apoptosis effector	292949	Rn.101762	BI286396	10.04	10.48	10.28	10.89	10.78	11.09	1.57	up	1.36E-02	8.95E-01	UR	-
1389127_at	---	---	---	Rn.202991	BF552908	7.46	5.14	5.82	5.48	5.35	5.63	1.57	down	4.01E-01	8.95E-01	-	-
1384301_at	---	---	---	Rn.3665	BE113571	3.95	3.39	3.04	2.93	3.06	2.42	1.57	down	1.18E-01	8.95E-01	-	-
1374560_at	Prrc1	proline-rich coiled-coil 1	291444	Rn.22764	AI137296	3.95	4.44	3.64	4.95	4.20	4.84	1.57	up	1.19E-01	8.95E-01	-	-
1382267_at	Fjx1	four jointed box 1 (Drosophila)	366140	Rn.93503	BF390450	6.88	8.00	7.18	6.43	6.86	6.81	1.57	down	1.45E-01	8.95E-01	-	-
1373570_at	Npepl1	aminopeptidase-like 1	311671	Rn.8518	AI411240	4.71	5.84	5.62	6.38	5.42	6.33	1.57	up	2.33E-01	8.95E-01	-	-
1372055_at	Prex1	Phosphatidylinositol-3,4,5-trisphosphate-dependent Rac exchange factor 1	311647	Rn.14163	AI060225	4.32	2.36	2.37	2.37	2.38	2.35	1.57	down	3.73E-01	8.95E-01	-	-
1386874_at	Rps15	ribosomal protein S15	29285	Rn.3391	NM_017151	9.25	9.64	9.49	9.67	10.52	10.14	1.57	up	7.35E-02	8.95E-01	-	-
1383917_at	Abi3	ABI family, member 3	303476	Rn.95169	BE110730	5.56	2.94	2.81	3.51	2.95	2.89	1.57	down	5.16E-01	8.95E-01	-	-
1382805_at	LOC360570	similar to myosin XVIIIa	360570	Rn.106278	BF281984	6.79	5.38	4.26	6.41	6.00	5.98	1.57	up	4.30E-01	8.95E-01	-	-
1379101_at	Dhx36	DEAH (Asp-Glu-Ala-His) box polypeptide 36	310461	Rn.2744	BE114021	4.17	5.17	5.03	5.19	5.89	5.24	1.57	up	1.66E-01	8.95E-01	-	-
1384296_at	---	---	---	---	AI136388	3.86	3.69	3.13	3.82	4.35	4.46	1.57	up	9.22E-02	8.95E-01	-	-
1395413_at	Lrp6	Low density lipoprotein receptor-related protein 6	312781	Rn.32960	BE116600	2.36	2.95	2.38	3.91	2.32	3.42	1.57	up	2.69E-01	8.95E-01	-	-
1370067_at	Me1	malic enzyme 1, NADP(+)-dependent, cytosolic	24552	Rn.3519	NM_012600	9.02	9.12	9.73	9.22	8.13	8.57	1.57	down	1.67E-01	8.95E-01	-	-
1367751_at	Dpm2	dolichyl-phosphate mannosyltransferase polypeptide 2, regulatory subunit	29640	Rn.167749	NM_019252	4.72	4.48	4.57	5.00	5.96	4.76	1.57	up	1.57E-01	8.95E-01	-	-
1398995_at	Uimc1	ubiquitin interaction motif containing 1	290997	Rn.103261	BM389233	4.76	4.59	4.67	4.54	3.17	4.36	1.57	down	2.05E-01	8.95E-01	-	-
1374750_at	---	---	---	Rn.6257	AI172313	3.26	4.49	3.91	4.02	4.64	4.96	1.57	up	2.21E-01	8.95E-01	-	-
1370986_s_at	---	---	---	---	AW535280	5.26	3.16	2.99	3.53	2.96	2.96	1.57	down	4.37E-01	8.95E-01	-	-
1394939_at	Ppm1k	protein phosphatase 1K (PP2C domain containing)	312381	Rn.164392	BE116933	6.08	8.95	8.69	8.48	8.06	9.13	1.57	up	5.38E-01	8.95E-01	-	-
1389922_at	---	---	---	---	AA891362	7.63	7.18	7.46	6.24	7.26	6.82	1.57	down	1.12E-01	8.95E-01	-	-
1395298_at	Ubp1	upstream binding protein 1 (LBP-1a)	301038	Rn.15705	AI070708	5.03	5.88	6.59	5.92	4.45	5.17	1.57	down	3.51E-01	8.95E-01	-	-
1389316_at	Usp9x	ubiquitin specific peptidase 9, X-linked	363445	Rn.7273	AW914946	8.71	8.38	7.88	7.94	6.68	8.40	1.57	down	3.15E-01	8.95E-01	-	-
1392908_at	Akirin1	akirin 1	595134	Rn.3674	BG381166	8.49	7.65	8.95	7.69	7.29	8.15	1.57	down	2.25E-01	8.95E-01	-	-
1387375_at	Khk	ketohexokinase	25659	Rn.33324	NM_031855	9.69	10.59	10.57	9.78	9.49	9.63	1.57	down	1.04E-01	8.95E-01	-	-
1377643_at	Hoxd10	homeo box D10	303991	Rn.12766	BI291489	3.03	2.57	2.73	4.20	3.19	2.89	1.57	up	1.96E-01	8.95E-01	-	-
1393179_at	---	---	---	Rn.203900	BF553172	2.59	2.65	3.15	4.02	2.56	3.76	1.57	up	2.51E-01	8.95E-01	-	-
1389993_at	Wdr33	WD repeat domain 33	307524	Rn.22892	BI296095	7.08	6.90	6.91	6.18	6.20	6.56	1.57	down	9.20E-03	8.95E-01	DR	-
1370505_at	Adprh	ADP-ribosylarginine hydrolase	25371	Rn.13315	M86341	3.21	2.72	2.97	2.94	4.51	3.40	1.57	up	2.53E-01	8.95E-01	-	-
1370386_at	Ruvbl1	RuvB-like 1 (E. coli)	65137	Rn.86410	AB002406	4.12	5.86	4.13	4.92	5.10	6.02	1.57	up	3.88E-01	8.95E-01	-	-
1370754_at	Impact	imprinted and ancient	497198	Rn.190851	AA858090	5.26	5.36	4.64	6.75	4.43	6.02	1.57	up	4.20E-01	8.95E-01	-	-
1373200_at	Eef1e1	eukaryotic translation elongation factor 1 epsilon 1	291057	Rn.98308	AI600237	7.73	7.39	8.00	7.10	6.84	7.23	1.57	down	3.69E-02	8.95E-01	DR	-
1379267_a_at	---	---	---	Rn.8316	AA924312	5.74	6.48	6.52	7.34	7.05	6.30	1.57	up	1.82E-01	8.95E-01	-	-
1395371_at	Suds3	suppressor of defective silencing 3 homolog (S. cerevisiae)	360819	Rn.98280	AA957790	3.12	3.11	4.88	3.04	3.05	3.09	1.57	down	3.32E-01	8.95E-01	-	-
1367806_at	Gls	glutaminase	24398	Rn.5762	AI577681	6.54	4.70	4.67	4.32	4.70	4.95	1.57	down	3.71E-01	8.95E-01	-	-
1371813_at	Hirip3	HIRA interacting protein 3	361650	Rn.12594	BI275598	3.28	3.97	3.29	3.76	4.33	4.40	1.57	up	1.01E-01	8.95E-01	-	-
1396349_at	---	---	---	Rn.160454	BE099657	3.06	3.50	2.83	4.25	3.34	3.74	1.57	up	1.18E-01	8.95E-01	-	-
1370164_at	Hadha	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/en	170670	Rn.3340	AA800240	9.31	9.62	9.11	8.89	8.29	8.92	1.57	down	6.19E-02	8.95E-01	-	-
1393643_at	Rcn1	reticulocalbin 1, EF-hand calcium binding domain	362182	Rn.103345	AI112962	8.06	6.98	6.93	8.39	6.92	8.60	1.57	up	3.70E-01	8.95E-01	-	-
1397234_at	Gpatch1	G patch domain containing 1	292810	Rn.64293	AI598507	3.22	3.36	3.17	4.20	3.41	4.10	1.57	up	6.26E-02	8.95E-01	-	-
1390892_at	Depdc1b	DEP domain containing 1B	310074	Rn.14993	AA899893	2.55	6.04	3.14	2.40	3.13	4.25	1.57	down	6.19E-01	8.95E-01	-	-
1386296_at	08-Sep	septin 8	303135	Rn.23507	AI639205	2.71	2.70	2.49	3.46	2.67	3.71	1.57	up	1.13E-01	8.95E-01	-	-
1367478_at	Htra2	HtrA serine peptidase 2	297376	Rn.107325	AI600136	4.97	5.54	6.42	5.37	4.02	5.60	1.57	down	3.73E-01	8.95E-01	-	-
1389460_at	---	---	---	Rn.16928	AI231787	3.18	3.89	3.44	2.96	4.51	4.98	1.57	up	3.72E-01	8.95E-01	-	-
1376890_at	G4	G4 protein	406868	Rn.205352	BE117326	5.39	6.37	5.64	6.58	6.08	6.68	1.57	up	1.37E-01	8.95E-01	-	-
1374819_at	---	---	---	Rn.16845	AI599945	3.40	3.87	5.16	3.38	2.50	4.61	1.57	down	4.67E-01	8.95E-01	-	-
1382104_at	Wdr33	WD repeat domain 33	307524	Rn.22892	AI113277	4.38	3.70	3.66	3.04	3.50	3.26	1.57	down	7.36E-02	8.95E-01	-	-
1394790_at	Clcn6	chloride channel 6	295586	Rn.7226	AW921911	6.71	7.46	6.92	6.26	6.18	6.70	1.57	down	7.81E-02	8.95E-01	-	-
1374027_at	---	---	---	Rn.20480	AI072143	4.23	4.92	5.82	5.41	6.08	5.42	1.57	up	2.73E-01	8.95E-01	-	-
1369318_at	Fhit	fragile histidine triad gene	60398	Rn.45598	NM_021774	4.87	4.69	4.81	4.19	4.21	4.04	1.57	down	1.01E-03	8.95E-01	DR	-
1374851_at	Med29	mediator complex subunit 29	292751	Rn.23452	BG376202	7.38	5.97	5.97	5.75	5.72	5.91	1.57	down	2.42E-01	8.95E-01	-	-
1373047_at	Prkci	Rnb6	361308	Rn.1388	BF284699	6.16	7.51	6.10	7.53	7.05	7.12	1.57	up	2.53E-01	8.95E-01	-	-
1372995_at	Prkd2	protein kinase D2	292658	Rn.15035	AI703715	4.52	2.48	2.51	2.46	2.67	2.44	1.57	down	3.94E-01	8.95E-01	-	-
1391228_at	Rsph1	radial spoke head 1 homolog (Chlamydomonas)	361818	Rn.14627	BE106353	2.67	2.63	2.80	3.70	3.64	2.70	1.57	up	1.20E-01	8.95E-01	-	-
1388391_at	Slc35e3	solute carrier family 35, member E3	362883	Rn.21084	AI411981	5.19	5.56	4.99	6.04	5.77	5.87	1.57	up	2.41E-02	8.95E-01	UR	-
1383893_at	Atp6v1g3	ATPase, H+ transporting, lysosomal V1 subunit G3	289407	Rn.14804	AW140864	10.15	8.45	7.57	9.19	8.99	8.04	1.57	down	6.37E-01	8.95E-01	-	-
1370351_at	Tdrd7	tudor domain containing 7	85425	Rn.16138	AB030644	4.67	4.86	4.80	4.61	6.49	5.17	1.57	up	3.12E-01	8.95E-01	-	-
1368331_at	Ctbs	chitobiase, di-N-acetyl-	81652	Rn.11199	NM_031023	6.10	7.75	8.73	7.79	8.52	8.21	1.57	up	4.63E-01	8.95E-01	-	-
1379472_at	Naa1	NAD synthetase 1	353255	Rn.22886	AI220666	7.79	5.62	6.43	6.58	5.39	5.93	1.56	down	4.21E-01	8.95E-01	-	-
1374804_at	Gnl2	guanine nucleotide binding protein-like 2 (nucleolar)	362593	Rn.18964	AI060050	5.89	6.32	6.63	6.52	7.11	7.15	1.56	up	9.33E-02	8.95E-01	-	-
1372076_at	Hbxip	hepatitis B virus x interacting protein	295357	Rn.3763	BI294704	10.47	10.36	10.76	9.73	9.95	9.97	1.56	down	1.10E-02	8.95E-01	DR	-
1398770_at	Rpl36al	ribosomal protein L36a-like	81769	Rn.112597	NM_031105	9.68	10.24	10.23	10.60	10.34	11.14	1.56	up	9.88E-02	8.95E-01	-	-
1377785_at	Dhx40	DEAH (Asp-Glu-Ala-His) box polypeptide 40	287595	Rn.29182	BI275330	7.96	6.36	6.82	6.73	5.74	6.73	1.56	down	3.27E-01	8.95E-01	-	-
1392522_at	Nus1	nuclear undecaprenyl pyrophosphate synthase 1 homolog (S. cerevisiae)	294400	Rn.23082	AA925790	6.89	6.68	7.26	5.05	7.23	6.61	1.56	down	3.89E-01	8.95E-01	-	-
1371961_at	Pld3	phospholipase D family, member 3	361527	Rn.128036	BF287282	3.66	3.58	5.06	3.64	3.35	3.38	1.56	down	2.58E-01	8.95E-01	-	-
1391977_at	---	---	---	Rn.16789	AA819560	4.40	2.50	2.55	2.51	2.52	2.48	1.56	down	3.61E-01	8.95E-01	-	-
1395768_at	---	---	---	Rn.203355	BG378085	6.13	3.00	5.06	3.93	4.47	3.86	1.56	down	5.30E-01	8.95E-01	-	-
1389129_at	2ecr2 /// Rab11fip2	2,4-dienoyl CoA reductase 2, peroxisomal /// RAB11 family interacting protein	303002 /// 64461	Rn.17377	BF282876	9.94	9.50	10.13	9.65	9.00	8.98	1.56	down	9.05E-02	8.95E-01	-	-
1390469_at	---	---	---	Rn.161078	BF397709	2.93	3.98	3.42	4.24	4.08	3.96	1.56	up	1.09E-01	8.95E-01	-	-
1390200_at	Fkbp15	FK506 binding protein 15	362528	Rn.162820	BM388794	6.23	5.22	3.81	5.02	7.14	5.03	1.56	up	5.52E-01	8.95E-01	-	-
1395192_at	Orc3l	origin recognition complex, subunit 3-like (yeast)	313138	Rn.162803	BF392026	3.20	4.23	4.35	5.17	4.32	4.22	1.56	up	2.45E-01	8.95E-01	-	-
1381403_at	Me2	malic enzyme 2, NAD(+)-dependent, mitochondrial	307270	Rn.16233	AI575071	3.37	4.23	5.31	3.70	3.59	3.69	1.56	down	3.17E-01	8.95E-01	-	-
1397660_at	B3galt6	beta 1,3-galactosyltransferase-like	689765	Rn.49884	BE109588	2.56	2.53	4.51	2.55	2.55	2.55	1.56	down	3.82E-01	8.95E-01	-	-
1378646_at	Ythdf3	YTH domain family, member 3	361920	Rn.4014	AW525661	4.63	4.98	5.88	4.43	4.51	4.62	1.56	down	1.62E-01	8.95E-01	-	-
1386064_at	---	---	---	Rn.165284	AI501693	5.13	6.07	5.07	5.90	5.96	6.34	1.56	up	1.42E-01	8.95E-01	-	-
1397947_at	Utrn	utrophin	25600	Rn.9901	AW530193	2.36	2.35	2.36	4.30	2.36	2.35	1.56	up	3.78E-01	8.95E-01	-	-
1384204_at	---	---	---	Rn.164171	BG379466	6.04	5.72	5.62	6.28	6.58	6.45	1.56	up	1.37E-02	8.95E-01	UR	-
1392054_at	Pbrm1	polybromo 1	306254	Rn.19314	AW532414	7.58	7.18	7.92	7.28	6.01	7.45	1.56	down	2.68

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1376138_at	---	---	---	---	BI289557	4.12	2.61	2.71	2.41	2.44	2.67	1.56	down	2.64E-01	8.95E-01	-	-
1376524_at	Ddi2	hypothetical protein Ddi2	360863	Rn.8478	BG378747	3.31	4.15	3.71	3.75	5.60	3.74	1.56	up	3.90E-01	8.95E-01	-	-
1375348_at	Enah	Enabled homolog (Drosophila)	360891	Rn.163240	AW531648	2.91	2.91	2.47	4.40	2.91	2.91	1.56	up	2.84E-01	8.95E-01	-	-
1367625_at	Rpl10	ribosomal protein L10	81764	Rn.102157	NM_031100	10.06	10.56	10.55	10.74	10.87	11.49	1.56	up	8.88E-02	8.95E-01	-	-
1382744_at	Zkscan3	zinc finger with KRAB and SCAN domains 3	306977	Rn.8231	H33694	6.34	4.90	4.93	4.64	4.64	4.97	1.56	down	2.60E-01	8.95E-01	-	-
1379587_at	Rdh5	retinol dehydrogenase 5	366791	Rn.119479	AI717097	6.18	6.35	7.60	5.72	6.32	6.17	1.56	down	2.56E-01	8.95E-01	-	-
1388309_at	Hmga1	high mobility group AT-hook 1	117062	Rn.83614	BG378885	2.47	3.18	2.01	4.04	2.94	2.60	1.56	up	3.12E-01	8.95E-01	-	-
1391534_at	Elovl2	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 2	498728	Rn.105402	BG666735	5.51	5.04	5.89	3.83	5.32	5.37	1.56	down	3.17E-01	8.95E-01	-	-
1378568_a_at	RGD1306228	similar to chromosome 14 open reading frame 138	362748	Rn.154714	BM389379	5.88	5.84	5.42	5.87	7.01	6.19	1.56	up	1.60E-01	8.95E-01	-	-
1382368_at	Trove2	TROVE domain family, member 2	304833	Rn.146598	AA964575	4.15	3.87	3.21	3.82	4.97	4.36	1.56	up	2.13E-01	8.95E-01	-	-
1390445_at	LOC688133	similar to mbt domain containing 1	688133	---	BE114154	6.82	5.46	3.42	4.92	3.36	5.50	1.56	down	6.16E-01	8.95E-01	-	-
1374098_at	Egfl8	EGF-like-domain, multiple 8	406166	Rn.146030	AW530272	3.30	2.71	2.79	4.80	3.00	2.91	1.56	up	3.78E-01	8.95E-01	-	-
1393097_at	Rprd1a	Regulation of nuclear pre-mRNA domain containing 1A	291736	Rn.162287	AI709802	6.79	5.72	4.90	6.85	6.46	6.02	1.56	up	3.48E-01	8.95E-01	-	-
1389419_at	---	---	---	Rn.23543	BI296079	6.45	5.75	6.19	6.63	6.73	6.94	1.56	up	4.56E-02	8.95E-01	UR	-
1371691_at	Rarres2	retinoic acid receptor responder (tazarotene induced) 2	297073	Rn.28532	BI282993	5.33	4.86	4.49	5.75	5.85	5.00	1.56	up	1.54E-01	8.95E-01	-	-
1372458_at	Setd8	SET domain containing (lysine methyltransferase) 8	689820	Rn.8879	AI235220	4.29	5.29	3.94	6.14	4.59	4.70	1.56	up	3.76E-01	8.95E-01	-	-
1368992_a_at	Sfrs5	splicing factor, arginine/serine-rich 5	29667	Rn.54448	AI104005	9.04	10.15	8.94	10.39	9.79	9.87	1.56	up	2.13E-01	8.95E-01	-	-
1380108_at	Wbp1	WW domain binding protein 1	297381	Rn.219265	BI289053	7.04	7.22	7.70	6.86	6.73	6.47	1.56	down	5.04E-02	8.95E-01	-	-
1392547_at	MGC105649	hypothetical LOC302884	302884	Rn.106101	AI716211	4.30	2.42	2.44	2.41	2.43	2.41	1.56	down	3.65E-01	8.95E-01	-	-
1373026_at	Spc24	SPC24, NDC80 kinetochore complex component, homolog (S. cerevisiae)	363028	Rn.162084	BI303598	2.36	3.54	5.82	4.21	4.23	5.21	1.56	up	5.83E-01	8.95E-01	-	-
1393276_at	Med31	mediator complex subunit 31	287473	Rn.20884	BF418487	8.58	8.66	9.62	8.51	7.98	8.45	1.56	down	1.64E-01	8.95E-01	-	-
1376317_at	Orc6l	origin recognition complex, subunit 6 like (yeast)	291927	Rn.41300	BI282917	4.48	2.39	2.41	2.40	2.59	2.39	1.56	down	4.12E-01	8.95E-01	-	-
1380268_at	---	---	---	---	AA956352	6.27	6.76	6.23	6.89	7.54	6.75	1.56	up	9.88E-02	8.95E-01	-	-
1398375_at	---	---	---	---	BM392144	2.56	3.10	2.97	3.16	4.41	2.97	1.55	up	2.56E-01	8.95E-01	-	-
1371447_at	Plac8	placenta-specific 8	360914	Rn.2649	BG378630	8.72	8.91	9.82	8.48	8.72	8.34	1.55	down	1.49E-01	8.95E-01	-	-
1383996_at	---	---	---	Rn.139210	BI281608	3.69	3.81	3.71	4.02	4.03	5.08	1.55	up	1.47E-01	8.95E-01	-	-
1371867_at	---	---	---	Rn.2914	BI210836	5.24	7.15	5.02	6.96	6.03	6.32	1.55	up	4.32E-01	8.95E-01	-	-
1389142_at	Sqrdl	sulfide quinone reductase-like (yeast)	691966	Rn.1416	AI013361	3.85	4.18	2.73	3.72	3.93	5.02	1.55	up	3.47E-01	8.95E-01	-	-
1379084_at	Wdr22	WD repeat domain 22	314273	Rn.47944	AW533710	3.89	4.01	4.01	4.17	5.11	4.54	1.55	up	8.30E-02	8.95E-01	-	-
1380835_at	Isg20l2	interferon stimulated exonuclease gene 20-like 2	361977	Rn.56954	BF389476	3.94	3.40	4.40	3.43	2.52	3.88	1.55	down	2.66E-01	8.95E-01	-	-
1389452_at	Zdhhc8	zinc finger, DHHC-type containing 8	303796	Rn.17261	AW528458	2.66	2.54	2.50	2.69	4.26	2.65	1.55	up	2.96E-01	8.95E-01	-	-
1384658_at	---	---	---	Rn.146788	AW530445	4.27	2.35	2.36	2.35	2.36	2.36	1.55	down	3.74E-01	8.95E-01	-	-
1382811_at	---	---	---	Rn.164134	AA891721	4.10	5.48	5.23	5.39	5.94	5.39	1.55	up	2.40E-01	8.95E-01	-	-
1388024_s_at	Tor1ap1	torsin A interacting protein 1	246314	Rn.11373	U20286	4.80	5.16	4.44	4.12	3.32	4.87	1.55	down	2.71E-01	8.95E-01	-	-
1374570_at	Agpat2	1-acylglycerol-3-phosphate O-acyltransferase 2 (lysophosphatidic acid acyltra	311821	Rn.55456	AI012474	3.71	3.87	3.04	3.72	3.88	4.93	1.55	up	2.36E-01	8.95E-01	-	-
1371907_at	Arl6ip4	ADP-ribosylation-like factor 6 interacting protein 4	288656	Rn.105729	BE101624	6.12	7.31	7.11	7.48	7.41	7.56	1.55	up	1.62E-01	8.95E-01	-	-
1367997_at	Clpb	ClpB caseinolytic peptidase B homolog (E. coli)	65041	Rn.37542	NM_022947	6.87	6.84	6.56	6.09	5.70	6.58	1.55	down	8.08E-02	8.95E-01	-	-
1372902_at	Alg12	asparagine-linked glycosylation 12 homolog (yeast, alpha-1,6-mannosyltransf	315212	Rn.30142	BI289084	4.76	4.04	4.06	4.82	4.71	5.24	1.55	up	9.00E-02	8.95E-01	-	-
1381967_at	Rbm39	RNA binding motif protein 39	362251	Rn.8555	BE114972	6.07	6.17	5.26	6.18	6.91	6.32	1.55	up	1.57E-01	8.95E-01	-	-
1370290_at	Tubb5	tubulin, beta 5	29214	Rn.2458	BI285440	5.34	5.10	4.23	5.49	5.40	5.68	1.55	up	1.40E-01	8.95E-01	-	-
1382346_at	---	---	---	Rn.13650	BF281960	2.41	2.44	2.46	2.44	4.34	2.44	1.55	up	3.71E-01	8.95E-01	-	-
1373840_at	Nudt9	nudix (nucleoside diphosphate linked moiety X)-type motif 9	305149	Rn.22103	BM384191	7.45	7.80	6.34	8.17	7.22	8.11	1.55	up	3.02E-01	8.95E-01	-	-
1386045_at	---	---	---	---	AA893205	4.67	5.29	5.49	4.05	4.58	4.91	1.55	down	1.45E-01	8.95E-01	-	-
1394721_at	Baz2a	bromodomain adjacent to zinc finger domain, 2A	304601	Rn.11607	BF412697	4.32	5.71	5.98	4.52	4.86	4.72	1.55	down	2.91E-01	8.95E-01	-	-
1372895_at	RGD1309676	similar to RIKEN cDNA 5730469M10	361118	Rn.13520	AI169367	7.93	7.19	8.78	8.04	7.76	8.01	1.55	up	1.41E-01	8.95E-01	-	-
1386880_at	Acaa2	acetyl-Coenzyme A acyltransferase 2	170465	Rn.3786	NM_130433	8.81	8.95	9.71	10.21	9.52	9.65	1.55	up	1.43E-01	8.95E-01	-	-
1371601_at	Man1b1	mannosidase, alpha, class 1B, member 1	499751	Rn.86273	BE107520	5.96	4.91	4.29	4.01	3.93	5.32	1.55	down	3.93E-01	8.95E-01	-	-
1397356_at	---	---	---	---	AI234957	4.39	3.04	2.51	2.50	2.51	3.04	1.55	down	3.41E-01	8.95E-01	-	-
1375374_at	---	---	---	---	BF400606	3.02	3.02	3.02	4.93	3.02	3.01	1.55	up	3.77E-01	8.95E-01	-	-
1393506_at	---	---	---	Rn.12460	BF558068	2.55	2.53	2.80	2.54	4.91	2.33	1.55	up	4.88E-01	8.95E-01	-	-
1388736_at	Ccdc43	coiled-coil domain containing 43	360637	Rn.13165	AI175383	5.61	5.31	3.52	5.63	5.20	5.52	1.55	up	3.95E-01	8.95E-01	-	-
1378479_at	Cln3	ceroid-lipofuscinosis, neuronal 3	293485	Rn.102386	BI285912	3.71	3.80	3.30	3.22	2.39	3.31	1.55	down	1.29E-01	8.95E-01	-	-
1392025_x_at	---	---	---	---	BI303277	7.52	7.58	7.95	7.39	6.44	7.32	1.55	down	1.29E-01	8.95E-01	-	-
1388981_at	LOC503165	similar to ADP-ribosylation factor GTPase-activating protein 3 (ARF GAP 3)	503165	Rn.161999	AI104127	7.10	7.55	6.42	7.33	7.84	7.80	1.55	up	1.61E-01	8.95E-01	-	-
1380306_at	---	---	---	Rn.54177	AW435415	2.42	2.41	2.43	4.34	2.42	2.40	1.55	up	3.79E-01	8.95E-01	-	-
1376229_at	Foxo3	Forkhead box O3	294515	Rn.24593	BF419138	2.36	3.29	2.31	2.97	3.93	2.96	1.55	up	2.33E-01	8.95E-01	-	-
1381147_at	---	---	---	---	BF409065	4.48	2.57	2.64	2.59	2.62	2.56	1.55	down	3.69E-01	8.95E-01	-	-
1381411_at	---	---	---	Rn.204116	AI548328	4.22	5.57	4.03	5.73	5.84	4.15	1.55	up	4.35E-01	8.95E-01	-	-
1375668_at	---	---	---	---	AW525189	2.43	2.38	4.64	2.79	2.38	2.37	1.55	down	4.52E-01	8.95E-01	-	-
1377737_at	Nipa2	non imprinted in Prader-Willi/Angelman syndrome 2 homolog (human)	308667	Rn.2757	BE098874	6.97	4.71	5.50	4.57	5.58	5.13	1.55	down	4.31E-01	8.95E-01	-	-
1381008_at	---	---	---	Rn.147275	BF390077	3.52	3.46	3.57	3.33	5.12	4.00	1.55	up	2.93E-01	8.95E-01	-	-
1373355_at	---	---	---	---	BI289014	6.76	7.42	7.00	7.48	7.35	8.24	1.55	up	1.35E-01	8.95E-01	-	-
1375637_at	RGD1311122	similar to RIKEN cDNA 1110003E01	364154	Rn.2533	AI010441	9.74	9.88	10.25	10.64	10.42	10.70	1.55	up	2.25E-02	8.95E-01	UR	-
1368159_at	Abcb6	ATP-binding cassette, sub-family B (MDR/TAP), member 6	140669	Rn.54408	NM_080582	6.55	6.08	7.46	6.30	5.57	6.33	1.55	down	2.53E-01	8.95E-01	-	-
1397921_at	---	---	---	---	AW535104	2.53	2.52	2.56	2.52	4.14	2.84	1.55	up	2.70E-01	8.95E-01	-	-
1395913_at	Acbd4	Acyl-Coenzyme A binding domain containing 4	303577	Rn.18284	AI136400	7.30	7.02	6.58	7.16	5.69	6.15	1.55	down	2.61E-01	8.95E-01	-	-
1395830_at	---	---	---	Rn.206741	AI003256	3.56	3.55	3.58	2.36	3.62	2.82	1.55	down	1.60E-01	8.95E-01	-	-
1382536_at	Dhfr	dihydrofolate reductase	24312	Rn.24681	AI712541	6.21	7.12	5.99	5.43	5.81	6.18	1.55	down	1.97E-01	8.95E-01	-	-
1393729_at	Nelo2	neuropilin (NRP) and tolloid (TLL)-like 2	307757	Rn.147057	BE112114	4.46	4.96	5.70	4.30	4.57	4.35	1.55	down	1.62E-01	8.95E-01	-	-
1398498_at	---	---	---	Rn.204153	BE119823	2.73	2.73	2.73	3.84	2.72	3.52	1.55	up	1.31E-01	8.95E-01	-	-
1375604_at	---	---	---	Rn.164976	AI059443	3.50	3.21	3.13	4.03	3.51	4.19	1.55	up	5.34E-02	8.95E-01	-	-
1395149_at	Tshz1	teashirt zinc finger homeobox 1	307217	Rn.205514	BE115914	3.60	3.52	4.38	4.36	5.29	3.75	1.55	up	2.95E-01	8.95E-01	-	-
1373693_at	Gprc5c	G protein-coupled receptor, family C, group 5, member C	287805	Rn.3658	BF414143	5.71	5.41	5.26	4.30	5.32	4.87	1.55	down	1.21E-01	8.95E-01	-	-
1368215_at	Tpp1	tripeptidyl peptidase I	83534	Rn.162472	NM_031357	6.45	7.28	7.59	7.72	8.22	7.26	1.55	up	2.24E-01	8.95E-01	-	-
1384397_x_at	Crb3	crumbs homolog 3 (Drosophila)	301112	Rn.14560	AI072527	5.55	5.43	4.67	4.54	4.67	4.56	1.55	down	8.69E-02	8.95E-01	-	-
1379715_at	RGD1307882	similar to CG9346-PA	315903	Rn.30126	BE115506	6.89	8.09	7.35	7.93	8.49	7.81	1.55	up	1.98E-01	8.95E-01	-	-
1373624_at	---	---	---	Rn.7899	AA945713	5.97	6.85	7.60	5.96	6.01	6.55	1.55	down	2.81E-01	8.95E-01	-	-
1382918_at	LOC685001	Similar to MIR-interacting saposin-like protein precursor (Transmembrane pro	685001	Rn.147475	AA956561	6.18	8.30	6.22	7.64	7.13	7.82	1.55	up	4.35E-01	8.95E-01	-	-
1374473_at	Ppp1r15b	protein phosphatase 1, regulatory (inhibitor) subunit 15b	304799	Rn.78049	BI282910	8.35	8.55	8.42	9.11	8.80	9.30	1.55	up	1.59E-02	8.95E-01	UR	-
1386073_at	Psmd14	Proteasome (prosome, macropain) 26S subunit, non-ATPase, 14	311078	Rn.161794	BG662631	6.12	6.58	6.10	5.46	5.09	6.35	1.55	down	1.95E-01	8.95E-01	-	-
1371347_at	Tmem50b	transmembrane protein 50B	360698	Rn.992	BI279371	4.50	4.68	5.07	4.56	3.61	4.19	1.55	down	1.22E-01	8.95E-01	-	-
1380412_at	Elac1	elaC homolog 1 (E. coli)	307604	Rn.37959	AI411098	5.15	4.18	4.40	5.23	5.03	5.36	1.55	up	1.12E-01	8.95E-01	-	-
1387352_at	Src	v-src sarcoma (Schmidt-Ruppin A-2) viral oncogene homolog (avian)	83805	Rn.112600	AI175966	3.54	3.03	3.21	2.60	2.83	2.46	1.55	down	2.74E-02	8.95E-01	DR	-
1370855_at	Cst3	cystatin C	25307	Rn.106351	BG666933	8.32	8.73	7.89	8.75	9.42	8.66	1.55	up	1.38E-01	8.95E-01	-	-
1374405_at	Hnrnpa3	heterogeneous nuclear ribonucleoprotein A3	362152	Rn.107690	AI233336	4.47	5.58	4.49	5.00	5.36	6.06	1.55	up	2.62E-01	8.95E-01	-	-
1375449_at	---	---	---	Rn.204836	BI296717	3.13	3.34	3.98	3.13	2.34	3.09	1.55	down	1.58E-01	8.95E-01	-	-
1384385_at	---	---	---	Rn.154696	AI060176	2.78	4.60	4.21	4.05	4.10	5.32	1.55	up	4.15E-01	8.95E-01	-	-
1387893_at	C1s	complement component 1, s subcomponent	192262	Rn.4037	D88250	5.09	4.90	5.83	5.10	5.06	3.77	1.55	down	2.94E-01	8.95E-01	-	-
1371817_at	Isyna1	inositol-3-phosphate synthase 1	299651	Rn.98850	BI285489	4.09	3.65	4.33	3.94	2.59	3.65	1.55	down	2.40E-01	8.95E-01	-	-
1370792_at	Mapre1	microtubule-associated protein, RP/EB family, member 1	114764	Rn.7652	U75920	4.81	5.09	6.15	4.36	4.12	5.69	1.55	down	3.78E-01	8.95E-01	-	-
1380596_at	---	---	---	Rn.205340	BE098869	6.46	5.04	5.53	5.76	6.36	6.79	1.55	up	2.86E-01	8.95E-01	-	-
1398105_at	---	---	---	---	AI548809	4.59	2.74	2.34	2.39	2.33	3.07	1.55	down	4.40E-01	8.95E-01	-	-
1392953_at	Ptpla	protein tyrosine phosphatase-like (proline instead of catalytic arginine), membt	680115	Rn.38334	BI296250	2.90	2.89	4.60	2.97	2.37	3.17	1.55	down	3.66E-01	8.95E-01	-	-
1390201_at	Rap1a	RAP1A, member of RAS oncogene family	295347	Rn.106321	AA943817	3.09	3.98	4.01	4.01	4.08	4.88	1.55	up	2.00E-01	8.95E-01	-	-
1385217_at	---	---	---	Rn.212850	BM385870	5.83	4.89	4.92	4.14	4.13	5.48	1.55	down	3.12E-01	8.95E-01	-	-
1389303_at	Mif4gd	MIF4G domain containing	360659	Rn.198913	AI411019	4.73	4.21	4.14	4.07	3.08	4.04	1.55	down	1.67E-01	8.95E-01	-	-
1390418_at	Actr1b	ARP1 actin-related protein 1 homolog B (yeast)	316333	Rn.24317	AW251888	4.67	4.55	5.59	4.43	3.89	4.60	1.55	down	1.83E-01	8.95E-01	-	-
1371924_at	Olfml3	olfactomedin-like 3	310743	Rn.106761	BI274355	4.20	2.51	2.82	2.54	2.58	2.53	1.55	down	2.93E-01	8.95E-01	-	-
1395759_at	---	---	---	Rn.177284	AI556251	5.43	3.80	3.64	3.69	3.33	3.98	1.55	down	3.56E-01	8.95E-01	-	-
1392663_at	RGD1305500	similar to hypothetical protein FLJ13188	308004	Rn.24232	AI179925	3.30	3.98	4.87	2.86	4.16	3.24	1.55	down	3.53E-01	8.95E-01	-	-
1377684_at	Rars2	arginyl-tRNA synthetase 2, mitochondrial	297969	Rn.105643	BE118562	3.89	5.00	4.22	4.56	5.30	5.14	1.55	up	1.92E-01	8.95E-01	-	-
1387783_a_at	/// RGD15623	acetyl-Coenzyme A acyltransferase 1 /// similar to 3-ketoacyl-CoA thiolase B,	24157 /// 501072	Rn.8913	NM_012489	6.95	7.18	7.41	6.60	6.58	6.47	1.55	down	1.05E-02	8.95E-01	DR	-
1371716_at	684513 /// LOC68	similar to SWI/SNF-related matrix-associated actin-dependent regulator of chr	684513 /// 685178	Rn.20024	BE107610	7.13	7.05	6.65	6.74	5.66	6.55	1.55	down	1.60E-01	8.95E-01	-	-
1391437_at	Gltpd1	glycolipid transfer protein domain containing 1	313771	Rn.3197	AA874995	3.64	3.00	5.88	3.43	3.43	3.79	1.54	down	5.16E-01	8.95E-01	-	-
1398418_at	Rasl10b	RAS-like, family 10, member B	303382	Rn.8804	BF392904	2.45	2.91	4.27	2.55	2.76	2.45	1.54	down	3.19E-01	8.95E-01	-	-
1399015_at	---	---	---	Rn.163919	BI281753	6.54	5.81	5.93	6.42	5.92	7.83	1.54	up	3.64E-01	8.95E-01	-	-
1371735_at	---	---	---	Rn.113924	AI105202	6.18	6.24	6.47	6.48	7.16	7.13	1.54	up	5.88E-02	8.95E-01	-	-
1373808_at	---	---	---	Rn.148060	BI279573	7.12	7.18	6.68	6.56	5.43	7.11	1.54	down	2.94E-01	8.95E-01	-	-
1380030_at	---	---	---	Rn.199439	AI502367	3.35	3.90	4.02	3.50	4.87	4.78	1.54	up	2.68E-01	8.95E-01	-	-
1383300_at	St3gal6	ST3 beta-galactoside alpha-2,3-sialyltransferase 6	304023	Rn.32316	BF522030	5.80	7.04	6.10	6.81	6.39	7.62	1.54	up	2.94E-01	8.95E-01	-	-
1382859_at	Rif1	RAP1 interacting factor homolog (yeast)	295602	Rn.20916	AI043754	3.46	5.15	5.24	3.96	3.71	4.30	1.54	down	3.58E-01	8.95E-01	-	-
1384029_at	Xpa	xeroderma pigmentosum, complementation group A	298074	Rn.12469	BF554085	5.31	5.62	6.02	5.86	6.56	6.42	1.54	up	1.01E-01	8.95E-01	-	-
1376709_at	RGD1564799	similar to transmembrane 4 superfamily member 10	501569	Rn.16447	BG373822	4.98	3.24	4.54	4.12	3.87	4.88	1.54	down	3.86E-01	8.95E-01	-	-
1389256_at	---	---	---	Rn.1630	BG381256	4.44	5.93	7.29	6.52	6.64	6.38	1.54	up	4.90E-01	8.95E-01	-	-
1367681_at	Cd151	CD151 molecule (Raph blood group)	64315	Rn.1465	NM_022523	7.50	7.48	7.56	7.78	8.33	8.30	1.54	up	2.56E-02	8.95E-01	UR	-
1381816_at	RGD1309804	similar to hypothetical protein FLJ11218	361751	Rn.15885	BE119617	6.81	7.25	7.18	6.15	6.33	6.88	1.54	down	7.38E-02	8.95E-01	-	-
1388399_at	Mast2	microtubule associated serine/threonine kinase 2	313819	Rn.11677	BE116597	4.39	4.69	5.50	4.64	3.61	4.45	1.54	down	2.45E-01	8.95E-01	-	-
1378178_at	Smc6l1	SMC6 structural maintenance of chromosomes 6-like 1 (yeast)	313961	Rn.7047	AA850777	4.52	6.08	6.08	4.60	3.81	6.39	1.54	down	5.35E-01	8.95E-01	-	-
1368600_at	Slc26a1	solute carrier family 26 (sulfate transporter), member 1	64076	Rn.10016	NM_022287	10.27	9.43	10.58	9.60	9.35	9.45	1.54	down	1.49E-01	8.95E-01	-	-
1371941_at	RGD1310230	similar to RIKEN cDNA 5230400G24	301563	Rn.93479	AI411390	7.30	7.85	7.35	7.96	8.15	8.26	1.54	up	3.27E-02	8.95E-01	UR	-
1380148_at	---	---	---	Rn.199098	BE118688	5.48	4.81	2.72	5.05	4.58	5.26	1.54	up	5.05E-01	8.95E-01	-	-
1389874_at	Zrsr1	zinc finger (CCCH type), RNA binding motif and serine/arginine rich 1	498425	Rn.204453	BF404554	5.33	4.05	3.36	3.70	3.47	3.69	1.54	down	3.44E-01	8.95E-01	-	-
1384896_at	---	---	---	Rn.12536	AA997660	5.99	4.76	4.27	5.25	3.21	4.68	1.54	down	4.75E-01	8.95E-01	-	-
1370312_at	Spon1	spondin 1, extracellular matrix protein	64456	Rn.7546	M89469	4.96	6.83	5.66	6.55	6.42	6.36	1.54	up	3.17E-01	8.95E-01	-	-
1388339_at	Pea15a	phosphoprotein enriched in astrocytes 15A	364052	Rn.155339	BE112895	5.89	6.51	4.37	4.51	5.07	5.31	1.54	down	4.08E-01	8.95E-01	-	-
1388595_at	Dhx30	DEAH (Asp-Glu-Ala-His) box polypeptide 30	367172	Rn.163034	AI102995	7.27	7.68	7.34	7.08	6.46	6.88	1.54	down	4.79E-02	8.95E-01	DR	-
1374498_at	---	---	---	Rn.204137	AW916866	6.09	6.18	5.56	6.65	6.79	6.28	1.54	up	6.36E-02	8.95E-01	-	-
1378267_at	---	---	---	Rn.18915	AI058581	2.33	4.18	2.33	2.32	2.33	2.31	1.54	down	3.67E-01	8.95E-01	-	-
1368667_at	P2rx3	purinergic receptor P2X, ligand-gated ion channel, 3	81739	Rn.10388	NM_031075	2.31	2.33	4.17	2.30	2.32	2.32	1.54	down	3.69E-01	8.95E-01	-	-
1384794_at	---	---	---	Rn.170969	BE106136	5.25	4.34	5.33	4.65	3.06	5.32	1.54	down	4.46E-01	8.95E-01	-	-
1384172_at	RGD1310474	similar to KIAA0423	314169	Rn.144424	BF398262	3.90	3.52	4.00	4.02	4.28	4.99	1.54	up	1.28E-01	8.95E-01	-	-
1372941_at	Pdrg1	p53 and DNA damage regulated 1	296278	Rn.101752	BI273897	4.51	4.39	5.33	4.48	3.42	4.46	1.54	down	2.44E-01	8.95E-01	-	-
1397419_at	Mpp6	Membrane protein, palmitoylated 6 (MAGUK p55 subfamily member 6)	362359	Rn.49289	AI101314	6.22	6.51	7.08	5.93	5.67	6.34	1.54	down	1.23E-01	8.95E-01	-	-
1396109_at	Antxr1	anthrax toxin receptor 1	362393	Rn.41192	R47022	2.33	2.32	2.34	2.33	4.19	2.34	1.54	up	3.71E-01	8.95E-01	-	-
1372373_at	Wdr13	WD repeat domain 13	317370	Rn.107767	AI713206	4.27	6.77	6.93	6.97	6.46	6.41	1.54	up	5.18E-01	8.95E-01	-	-
1394585_at	---	---	---	Rn.205012	BE116089	2.63	2.90	2.77	4.59	2.75	2.82	1.54	up	3.61E-01	8.95E-01	-	-
1385487_at	Lsm1	LSM1 homolog, U6 small nuclear RNA associated (S. cerevisiae)	364624	Rn.128606	AW530957	5.66	6.85	7.56	7.57	7.37	7.01	1.54	up	3.41E-01	8.95E-01	-	-
1371341_at	Snrpd2	small nuclear ribonucleoprotein D2	680309	Rn.145735	BG372885	9.28	9.27	8.57	9.70	9.45	9.84	1.54	up	7.

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)				
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG MTC
1379980_at	---	---	---	Rn.165777	BM386302	4.41	6.08	4.65	5.59	5.59	5.82	1.54	up	3.05E-01	8.95E-01	- -
1367922_at	Adam17	ADAM metallopeptidase domain 17	57027	Rn.144585	NM_020306	4.06	4.01	3.36	3.88	5.27	4.14	1.54	up	2.70E-01	8.95E-01	- -
1391514_at	---	---	---	Rn.147659	AI575440	4.51	4.23	5.75	4.19	4.21	4.24	1.54	down	2.57E-01	8.95E-01	- -
1374092_at	Wwtr1	WW domain containing transcription regulator 1	295062	Rn.9622	BM392093	6.01	6.86	7.27	6.00	6.00	6.27	1.54	down	1.81E-01	8.95E-01	- -
1376882_at	---	---	---	Rn.28469	BF398580	4.95	5.08	4.58	4.83	5.94	5.69	1.54	up	1.68E-01	8.95E-01	- -
1395199_at	Eif3j	eukaryotic translation initiation factor 3, subunit J	691947	Rn.162681	AA998946	7.24	8.09	8.54	8.71	8.46	8.55	1.54	up	1.86E-01	8.95E-01	- -
1373158_at	Gpr146	G protein-coupled receptor 146	498153	Rn.41446	AI170446	4.76	4.51	3.58	3.71	5.98	5.02	1.54	up	4.56E-01	8.95E-01	- -
1383117_at	Pxmp4	peroxisomal membrane protein 4	282634	Rn.7752	AI232414	7.89	8.78	8.20	9.17	8.71	8.84	1.54	up	1.06E-01	8.95E-01	- -
1387926_at	Sc5dl	sterol-C5-desaturase (ERG3 delta-5-desaturase homolog, S. cerevisiae)-like	114100	Rn.18741	AB052846	4.97	6.73	5.13	5.77	5.50	7.41	1.53	up	4.92E-01	8.95E-01	- -
1394458_at	---	---	---	Rn.159722	BF291026	9.59	7.87	8.99	8.65	7.87	8.06	1.53	down	3.28E-01	8.95E-01	- -
1391867_at	---	---	---	---	BI293159	4.62	2.76	2.78	2.81	2.74	2.75	1.53	down	3.73E-01	8.95E-01	- -
1398713_at	---	---	---	Rn.151560	BI279821	11.24	11.38	10.86	11.90	11.34	12.09	1.53	up	8.64E-02	8.95E-01	- -
1385851_at	---	---	---	Rn.15526	AA925441	2.33	3.23	2.34	2.70	2.33	4.74	1.53	up	4.86E-01	8.95E-01	- -
1387440_at	Ireb2	iron responsive element binding protein 2	64831	Rn.10132	NM_022863	7.79	6.40	6.54	6.42	5.39	7.06	1.53	down	4.01E-01	8.95E-01	- -
1382445_at	Mxra7	matrix-remodelling associated 7	690599	Rn.203783	BF408094	4.99	6.89	5.93	5.96	6.94	6.77	1.53	up	3.80E-01	8.95E-01	- -
1381366_at	RGD1562310	similar to hypothetical protein FLJ21415	498188	Rn.146520	BE109426	2.40	3.52	3.80	2.75	2.41	2.72	1.53	down	2.35E-01	8.95E-01	- -
1373758_at	Flad1	flavin adenine dinucleotide synthetase	751787	Rn.202488	AI171855	4.77	5.93	5.93	6.38	6.25	5.85	1.53	up	2.13E-01	8.95E-01	- -
1369775_at	Nucks1	nuclear casein kinase and cyclin-dependent kinase substrate 1	64709	Rn.21324	NM_022799	8.26	8.49	7.45	8.59	8.57	8.89	1.53	up	1.36E-01	8.95E-01	- -
1385660_at	Smek1	SMEK homolog 1, suppressor of mek1 (Dictyostelium)	314388	Rn.22873	AA924079	5.42	6.21	5.59	5.91	6.87	6.28	1.53	up	1.69E-01	8.95E-01	- -
1371101_at	Ryk	receptor-like tyrosine kinase	140585	Rn.11796	AB073721	3.48	4.82	3.57	5.23	3.63	4.85	1.53	up	3.95E-01	8.95E-01	- -
1390068_at	RGD1562136	Similar to D1Ertd622e protein	501195	Rn.165553	AA899954	4.81	6.24	5.94	5.50	7.07	6.27	1.53	up	3.82E-01	8.95E-01	- -
1379482_at	Tm6sf1	transmembrane 6 superfamily member 1	361600	Rn.219352	BI283829	3.67	2.52	3.19	2.53	2.54	2.47	1.53	down	1.40E-01	8.95E-01	- -
1389709_at	LOC499900	similar to Zinc finger protein 133	499900	Rn.117293	AI146063	3.77	3.79	3.30	3.76	3.50	5.45	1.53	up	3.84E-01	8.95E-01	- -
1378579_at	---	---	---	Rn.59786	BF394125	2.57	2.76	4.79	2.56	2.61	3.10	1.53	down	4.48E-01	8.95E-01	- -
1393484_at	---	---	---	---	AI715391	2.43	2.42	2.44	4.26	2.44	2.44	1.53	up	3.69E-01	8.95E-01	- -
1389446_at	---	---	---	---	AI576586	8.99	9.58	9.02	9.79	9.74	9.91	1.53	up	3.55E-02	8.95E-01	UR -
1382567_at	---	---	---	Rn.165812	AI073639	4.67	3.09	3.27	3.10	2.90	3.20	1.53	down	2.92E-01	8.95E-01	- -
1381478_at	---	---	---	Rn.210899	BF403155	3.88	3.82	3.56	3.77	3.10	2.55	1.53	down	1.67E-01	8.95E-01	- -
1386794_at	---	---	---	---	BF544968	4.80	5.72	5.75	6.06	6.66	5.40	1.53	up	2.68E-01	8.95E-01	- -
1384227_at	Ptprk	protein tyrosine phosphatase, receptor type, K, extracellular region	360302	Rn.216454	AI044031	8.69	9.40	8.50	9.41	9.40	9.62	1.53	up	9.46E-02	8.95E-01	- -
1383175_a_at	RGD1306959	similar to C11orf17 protein	361624	Rn.106344	BF561368	4.26	5.68	4.02	4.56	5.67	5.57	1.53	up	3.81E-01	8.95E-01	- -
1396024_at	Sptlc1	serine palmitoyltransferase, long chain base subunit 1	361213	Rn.18996	AW916358	5.27	2.68	3.46	3.45	2.58	3.54	1.53	down	4.99E-01	8.95E-01	- -
1397757_at	---	---	---	Rn.12638	AW523345	3.73	4.96	6.27	5.36	3.91	3.84	1.53	down	5.25E-01	8.95E-01	- -
1392893_a_at	---	---	---	Rn.105786	AA926239	7.76	6.89	5.60	7.25	7.32	7.32	1.53	up	3.80E-01	8.95E-01	- -
1386954_at	Ak2	adenylate kinase 2	24184	Rn.3421	NM_030986	7.99	7.11	7.02	6.75	6.36	7.17	1.53	down	1.87E-01	8.95E-01	- -
1398224_at	---	---	---	Rn.210046	BF393183	2.48	2.45	2.50	4.30	2.53	2.44	1.53	up	3.68E-01	8.95E-01	- -
1391445_at	---	---	---	Rn.13674	AI009603	3.40	4.56	5.44	4.11	3.30	4.14	1.53	down	3.99E-01	8.95E-01	- -
1380339_at	Agtpbp1	ATP/GTP binding protein 1	290986	Rn.33035	AW520369	5.01	5.08	5.10	4.86	3.88	4.61	1.53	down	1.05E-01	8.95E-01	- -
1371858_at	Ap1s1	adaptor-related protein complex 1, sigma 1 subunit	360785	Rn.11795	BM385719	6.16	6.07	6.31	5.35	5.89	5.45	1.53	down	2.71E-02	8.95E-01	DR -
1388422_at	Lims2	LIM and senescent cell antigen like domains 2	361303	Rn.115282	BI275904	6.11	4.04	4.04	4.53	4.09	3.73	1.53	down	4.46E-01	8.95E-01	- -
1380116_at	---	---	---	Rn.177340	AI146098	5.65	6.35	5.73	6.41	6.53	6.83	1.53	up	5.52E-02	8.95E-01	- -
1371019_at	Trib1	tribbles homolog 1 (Drosophila)	78969	Rn.204391	BM387324	2.33	2.36	2.37	3.85	2.33	2.73	1.53	up	2.47E-01	8.95E-01	- -
1392590_at	Arhgap24	Rho GTPase activating protein 24	305156	Rn.24657	BG377201	10.53	10.37	9.93	10.11	9.03	9.85	1.53	down	1.72E-01	8.95E-01	- -
1375024_at	Tyw3	tRNA-yW synthesizing protein 3 homolog (S. cerevisiae)	499731	Rn.43835	AI410356	5.39	6.97	4.67	6.52	6.17	6.18	1.53	up	4.23E-01	8.95E-01	- -
1379154_at	---	---	---	Rn.208657	BE119212	2.44	2.51	3.57	2.48	3.22	2.53	1.53	up	1.28E-01	8.95E-01	- -
1389764_at	Dmap1	DNA methyltransferase 1-associated protein 1	298447	Rn.22845	BG377235	7.09	5.47	6.14	5.58	5.12	6.17	1.53	down	3.35E-01	8.95E-01	- -
1368779_a_at	Gucy1b2	guanylate cyclase 1, soluble, beta 2	25206	Rn.10933	NM_012770	7.32	8.67	9.39	7.45	8.00	8.09	1.53	down	3.91E-01	8.95E-01	- -
1385437_at	Cad	carbamoyl-phosphate synthetase 2, aspartate transcarbamylase, and dihydro	24240	Rn.19416	BG376590	3.90	4.54	5.55	7.49	4.49	4.85	1.53	up	6.47E-01	8.95E-01	- -
1376112_a_at	Nutf2	nuclear transport factor 2	291981	Rn.107980	AI231712	6.47	7.41	5.66	6.89	7.15	7.35	1.53	up	3.05E-01	8.95E-01	- -
1389321_at	---	---	---	Rn.19306	BI292917	4.29	5.00	4.13	5.28	4.01	5.97	1.53	up	3.87E-01	8.95E-01	- -
1384242_at	---	---	---	Rn.173115	BI303239	4.14	3.02	4.37	3.02	3.16	3.50	1.53	down	2.37E-01	8.95E-01	- -
1374586_at	Arl15	ADP-ribosylation factor-like 15	689079	Rn.32026	AI103993	5.22	4.55	5.52	4.80	4.20	4.45	1.53	down	1.43E-01	8.95E-01	- -
1380343_at	Thada	thyroid adenoma associated	313865	Rn.18157	BM390523	3.81	4.15	6.48	3.75	4.07	4.78	1.53	down	5.31E-01	8.95E-01	- -
1396579_at	Dhx32	DEAH (Asp-Glu-Ala-His) box polypeptide 32	361667	Rn.162500	BG666347	2.92	3.05	4.99	2.91	2.88	3.33	1.53	down	4.22E-01	8.95E-01	- -
1391840_at	Raph9	radial spoke head 9 homolog (Chlamydomonas)	316238	Rn.98420	BE108137	2.88	3.95	2.99	4.36	3.22	4.07	1.53	up	2.74E-01	8.95E-01	- -
1389849_at	Tmem42	transmembrane protein 42	363171	Rn.161976	BE111831	2.43	2.77	3.93	4.68	2.72	3.57	1.53	up	4.49E-01	8.95E-01	- -
1377102_at	Tmem63a	transmembrane protein 63a	289318	Rn.19355	BI288335	6.88	6.28	5.35	6.45	7.04	6.87	1.53	up	2.70E-01	8.95E-01	- -
1383062_at	---	---	---	Rn.203210	BE106102	4.85	5.68	5.58	5.69	6.48	5.79	1.53	up	1.65E-01	8.95E-01	- -
1382316_at	Hira	HIR histone cell cycle regulation defective homolog A (S. cerevisiae)	363849	Rn.14920	BE118866	2.98	4.96	4.91	4.80	4.66	5.22	1.53	up	4.16E-01	8.95E-01	- -
1390546_at	---	---	---	Rn.15292	BI289684	2.70	3.44	3.90	3.71	4.16	4.01	1.53	up	1.76E-01	8.95E-01	- -
1398233_at	---	---	---	Rn.160315	BE095550	3.20	3.14	2.50	3.79	3.48	3.40	1.53	up	7.25E-02	8.95E-01	- -
1380852_at	RGD1305844	hypothetical LOC294883	294883	Rn.24012	AI112346	4.49	2.46	2.46	2.45	2.45	2.67	1.53	down	4.22E-01	8.95E-01	- -
1394808_at	Tm9sf4	transmembrane 9 superfamily protein member 4	296279	Rn.98601	AW531925	7.24	6.58	5.96	5.62	6.13	6.20	1.53	down	2.12E-01	8.95E-01	- -
1380568_a_at	---	---	---	---	AI575274	5.35	5.75	4.30	6.55	5.35	5.33	1.53	up	3.60E-01	8.95E-01	- -
1382879_at	Eif2c1	Eukaryotic translation initiation factor 2C, 1	313594	Rn.62413	AA874815	3.19	3.60	4.78	3.40	3.19	3.15	1.53	down	2.73E-01	8.95E-01	- -
1372934_at	RGD1307392	similar to 1700019E19Rik protein	299209	Rn.25150	AI104146	5.68	5.50	5.90	5.67	3.77	5.82	1.53	down	4.14E-01	8.95E-01	- -
1371476_at	Copa4	COP9 constitutive photomorphogenic homolog subunit 4 (Arabidopsis)	360915	Rn.7506	AI411531	6.88	7.89	7.27	8.07	7.57	8.24	1.53	up	1.62E-01	8.95E-01	- -
1383910_at	---	---	---	Rn.34845	BF398220	6.06	6.44	6.80	6.10	5.25	6.12	1.53	down	1.62E-01	8.95E-01	- -
1372263_at	LOC296637	similar to HLA-B associated transcript-2 isoform a	296637	Rn.98457	BF396485	5.07	4.26	5.28	3.91	4.31	4.57	1.53	down	1.69E-01	8.95E-01	- -
1380216_at	Pip5k3	phosphatidylinositol-3-phosphate/phosphatidylinositol 5-kinase, type III	316457	Rn.27739	BE098860	5.14	4.84	4.58	4.27	4.43	4.03	1.53	down	3.74E-02	8.95E-01	DR -
1396252_at	---	---	---	---	BE117174	5.61	4.58	3.41	6.45	4.49	4.48	1.53	up	5.41E-01	8.95E-01	- -
1367739_at	Cox8b	cytochrome c oxidase, subunit 8B	25250	Rn.10325	NM_012786	4.42	2.70	3.70	5.44	4.24	2.96	1.53	up	5.23E-01	8.95E-01	- -
1388883_at	Pold4	polymerase (DNA-directed), delta 4	361698	Rn.104646	BF281976	6.36	6.53	8.09	6.04	6.41	6.70	1.53	down	3.53E-01	8.95E-01	- -
1397565_at	---	---	---	Rn.203566	BI296579	2.27	2.26	4.18	2.35	2.27	2.25	1.53	down	3.94E-01	8.95E-01	- -
1398807_at	Ormdl2	ORM1-like 2 (S. cerevisiae)	288783	Rn.106721	BI296182	7.47	7.89	7.02	8.05	7.90	8.27	1.53	up	8.82E-02	8.95E-01	- -
1368355_at	Myo5b	myosin Vb	25132	Rn.10640	NM_017083	5.78	6.16	5.89	6.13	6.72	6.81	1.53	up	6.43E-02	8.95E-01	- -
1371171_at	RT1-Aw2	RT1 class Ib, locus Aw2	24737	Rn.116787	M10094	4.85	3.35	3.37	3.04	3.35	3.35	1.53	down	2.97E-01	8.95E-01	- -
1389551_at	Lactb2	lactamase, beta 2	297768	Rn.1263	AI008160	10.52	10.60	10.97	9.80	10.08	10.38	1.53	down	4.94E-02	8.95E-01	DR -
1388239_at	Per3	period homolog 3 (Drosophila)	78962	Rn.63521	AF311875	2.86	2.67	2.87	3.94	3.46	2.84	1.53	up	1.34E-01	8.95E-01	- -
1398608_at	Cenpl	centromere protein L	289150	Rn.3322	BG371578	3.05	3.44	3.43	3.03	4.70	4.02	1.53	up	2.93E-01	8.95E-01	- -
1394566_at	RGD1305500	similar to hypothetical protein FLJ13188	308004	Rn.24232	AI549119	4.35	6.74	6.78	6.98	6.24	6.48	1.53	up	5.04E-01	8.95E-01	- -
1390743_at	---	---	---	Rn.60798	BF405616	2.35	2.34	2.36	2.34	3.99	2.54	1.53	up	3.06E-01	8.95E-01	- -
1370377_at	Cyp2d1 /// Cyp2d5	cytochrome P450, family 2, subfamily d, polypeptide 1 /// cytochrome P450, fa	266684 /// 286963	Rn.91133	M25143	8.22	9.47	8.96	8.32	7.95	8.55	1.53	down	2.05E-01	8.95E-01	- -
1388924_at	Angptl4	angiopoietin-like 4	362850	Rn.119611	AA818262	2.90	2.87	4.68	2.87	2.89	2.87	1.53	down	3.65E-01	8.95E-01	- -
1395155_at	Exoc5	exocyst complex component 5	60627	Rn.44430	BF386083	2.75	2.91	4.48	2.76	2.83	2.71	1.52	down	3.33E-01	8.95E-01	- -
1395745_at	---	---	---	Rn.166667	AI113308	5.60	5.08	4.43	5.50	5.95	5.48	1.52	up	1.77E-01	8.95E-01	- -
1371385_at	Psmg1	proteasome (prosome, macropain) assembly chaperone 1	288236	Rn.82972	BF407158	6.78	7.26	6.12	7.02	7.19	7.78	1.52	up	2.06E-01	8.95E-01	- -
1377353_a_at	Tnfsf13	tumor necrosis factor (ligand) superfamily, member 13	287437	Rn.19955	AA800814	5.44	4.61	5.05	6.28	5.13	5.52	1.52	up	2.17E-01	8.95E-01	- -
1371365_at	Ube2s	ubiquitin-conjugating enzyme E2S	292588	Rn.120398	BI279788	4.49	4.37	5.27	6.58	4.96	4.42	1.52	up	4.37E-01	8.95E-01	- -
1395463_at	---	---	---	Rn.41371	BE099121	3.11	3.78	4.28	3.11	3.11	3.13	1.52	down	1.47E-01	8.95E-01	- -
1374286_at	---	---	---	Rn.8901	AA998636	6.37	5.85	7.05	6.00	5.38	6.06	1.52	down	2.13E-01	8.95E-01	- -
1379638_at	---	---	---	Rn.57215	BF401654	2.51	2.50	4.35	2.50	2.54	2.50	1.52	down	3.78E-01	8.95E-01	- -
1382281_at	---	---	---	Rn.204394	BI296136	3.76	3.59	3.61	4.03	4.84	3.92	1.52	up	1.09E-01	8.95E-01	- -
1388819_at	Scamp1	secretory carrier membrane protein 1	29521	Rn.20374	BM386698	3.60	4.80	4.77	4.54	5.29	5.15	1.52	up	2.54E-01	8.95E-01	- -
1393184_at	---	---	---	Rn.164335	BF420805	7.38	6.46	6.73	5.66	6.71	6.38	1.52	down	2.15E-01	8.95E-01	- -
1373521_at	Sh3tc2	SH3 domain and tetratricopeptide repeats 2	307393	Rn.24687	BF283122	4.81	6.31	4.69	5.52	5.45	6.66	1.52	up	4.06E-01	8.95E-01	- -
1370806_at	Retsat	retinol saturase (all trans retinol 13,14 reductase)	246298	Rn.55275	AF465614	10.10	10.41	10.97	9.66	9.72	10.28	1.52	down	1.30E-01	8.95E-01	- -
1378804_at	---	---	---	Rn.207370	BE098265	2.80	2.77	2.80	2.84	4.60	2.75	1.52	up	3.70E-01	8.95E-01	- -
1392816_at	RGD1311164	similar to DNA segment, Chr 6, Wayne State University 163, expressed	297607	Rn.125921	BI304039	6.48	4.80	4.60	4.60	4.63	4.83	1.52	down	3.70E-01	8.95E-01	- -
1390345_at	---	---	---	---	BG375523	5.17	4.51	5.23	4.69	2.76	2.64	1.52	down	6.14E-01	8.95E-01	- -
1373909_at	LOC689176	similar to transmembrane protein 64	689176	---	AI175507	2.71	3.98	2.42	3.68	3.66	3.59	1.52	up	2.75E-01	8.95E-01	- -
1393734_at	Fxc1	Fractured callus expressed transcript 1	84384	Rn.13451	AA997025	2.81	3.13	4.18	4.72	4.50	2.71	1.52	up	4.69E-01	8.95E-01	- -
1389450_at	C360830 /// Wbsc	similar to Putative methyltransferase WBSCR22 (Williams-Beuren syndrome	360830 /// 368084	Rn.163205	BF392737	5.23	4.87	5.14	5.54	6.30	5.22	1.52	up	1.46E-01	8.95E-01	- -
1383223_at	Ubl3	ubiquitin-like 3	363869	Rn.12128	BG672206	8.04	8.41	7.54	8.44	8.28	9.08	1.52	up	1.59E-01	8.95E-01	- -
1393896_at	Lamc3	laminin gamma 3	311862	Rn.205670	AI716974	3.49	4.20	2.97	2.94	2.97	2.93	1.52	down	1.63E-01	8.95E-01	- -
1375538_at	Vcl	Vcl	305879	Rn.164613	AI230737	7.09	6.06	6.12	5.95	5.55	5.94	1.52	down	1.67E-01	8.95E-01	- -
1370534_at	Acvr1c	activin A receptor, type IC	245921	Rn.10580	U35025	2.71	3.38	3.04	2.94	4.89	3.12	1.52	up	4.05E-01	8.95E-01	- -
1393257_at	Cugbp1	CUG triplet repeat, RNA binding protein 1	362160	Rn.203134	BI293905	7.70	7.91	8.79	7.42	7.23	7.92	1.52	down	1.96E-01	8.95E-01	- -
1387861_at	Aes	amino-terminal enhancer of split	29466	Rn.11495	BI274118	9.15	9.85	8.83	10.17	9.85	9.63	1.52	up	1.46E-01	8.95E-01	- -
1388175_at	Clcnkb	chloride channel Kb	79430	Rn.10339	Z30663	5.20	4.03	4.01	4.48	4.51	4.42	1.52	down	4.88E-01	8.95E-01	- -
1382146_at	Tspan6	tetraspanin 6	302313	Rn.22880	BF412968	3.03	3.34	3.50	4.75	3.60	3.34	1.52	up	2.54E-01	8.95E-01	- -
1387998_at	Exoc8	exocyst complex component 8	245709	Rn.10901	AF032669	5.70	4.45	3.70	3.95	6.73	5.00	1.52	up	5.77E-01	8.95E-01	- -
1374115_at	Mzf1	myeloid zinc finger 1	361508	Rn.205285	BG380595	2.56	2.55	2.69	4.58	2.55	2.48	1.52	up	4.29E-01	8.95E-01	- -
1376131_a_at	Pelp1	proline, glutamic acid and leucine rich protein 1	360552	Rn.11628	AW535500	5.86	5.55	4.40	5.72	6.43	5.48	1.52	up	3.14E-01	8.95E-01	- -
1375926_at	---	---	---	Rn.22507	BG372589	5.25	4.17	4.11	4.27	4.08	3.37	1.52	down	2.58E-01	8.95E-01	- -
1395191_at	---	---	---	Rn.210742	BF401203	4.78	2.37	2.44	2.93	2.38	2.47	1.52	down	4.95E-01	8.95E-01	- -
1378110_at	---	---	---	Rn.164440	AI412190	5.39	5.36	5.87	5.78	6.33	6.32	1.52	up	6.96E-02	8.95E-01	- -
1393468_at	Mrps2	mitochondrial ribosomal protein S2	362094	Rn.48907	BF556423	6.94	6.73	6.88	6.22	6.56	5.95	1.52	down	3.15E-02	8.95E-01	DR -
1387146_a_at	Ednrb	endothelin receptor type B	50672	Rn.11412	X57764	2.87	3.72	2.58	5.17	3.17	2.65	1.52	up	5.12E-01	8.95E-01	- -
1374460_at	Cops7a	COP9 constitutive photomorphogenic homolog subunit 7A (Arabidopsis)	312710	Rn.154027	BM386508	6.78	6.45	6.20	5.92	5.57	6.13	1.52	down	6.10E-02	8.95E-01	- -
1376363_at	Actr10	Actin-related protein 10 homolog (S. cerevisiae)	299121	Rn.36338	AI233337	5.60	5.57	5.97	4.48	5.79	5.06	1.52	down	2.06E-01	8.95E-01	- -
1387623_at	Stc1	stanniocalcin 1	81801	Rn.10647	NM_031123	4.18	2.39	2.39	2.36	2.44	2.35	1.52	down	3.68E-01	8.95E-01	- -
1394742_at	---	---	---	Rn.170057	AW534107	3.71	2.90	3.68	2.80	2.80	2.87	1.52	down	8.42E-02	8.95E-01	- -
1382097_at	RGD1310754	similar to G2	311264	---	AI145591	2.78	3.57	3.39	2.34	2.35	3.24	1.52	down	1.89E-01	8.95E-01	- -
1383111_at	---	---	---	Rn.220664	AI058895	10.26	9.93	9.92	9.77	9.30	9.23	1.52	down	4.10E-02	8.95E-01	DR -
1373770_at	---	---	---	---	AI105345	6.39	6.37	8.77	6.50	6.61	6.61	1.52	down	4.90E-01	8.95E-01	- -
1399074_at	Cdc16	CDC16 cell division cycle 16 homolog (S. cerevisiae)	290875	Rn.66098	BI279569	5.33	6.56	5.58	6.53	5.71	7.04	1.52	up	3.24E-01	8.95E-01	- -
1394318_at	Arpp-19	cyclic AMP phosphoprotein	60336	Rn.112577	AW918228	2.96	3.41	2.53	3.24	3.63	3.84	1.52	up	1.22E-01	8.95E-01	- -
1377871_at	---	---	---	Rn.14788	AI103528	5.07	4.71	5.40	5.09	5.85	6.05	1.52	up	1.64E-01	8.95E-01	- -
1371349_at	Col6a1	collagen, type VI, alpha 1	294337	Rn.107165	AI598402	3.96	3.22	4.43	3.26	3.27	3.28	1.52	down	1.62E-01	8.95E-01	- -
1397574_at	---	---	---	Rn.51254	BF563598	4.75	4.07	3.81	4.06	5.01	5.37	1.52	up	2.78E-01	8.95E-01	- -
1393101_at	Kdm2b	lysine (K)-specific demethylase 2B	304495	Rn.32641	BM385838	2.94	3.78	3.08	3.66	3.67	4.29	1.52	up	1.42E-01	8.95E-01	- -
1383066_at	---	---	---	---	BG379237	2.63	2.57	3.04	2.64	4.71	2.71	1.52	up	4.33E-01	8.95E-01	- -
1372470_at	Arvcf	armadillo repeat gene deleted in velo-cardio-facial syndrome	303798	Rn.201779	BI294809	2.74	3.06	3.94	2.75	2.45	2.74	1.52	down	1.80E-01	8.95E-01	- -
1384644_at	---	---	---	Rn.23865	AI169061	2.80	2.48	2.59	3.89	2.70	3.09	1.52	up	1.74E-01	8.95E-01	- -
1382643_at	Snx16	sorting nexin 16	64088	Rn.64585	BE102993	4.99	4.23	4.93	3.92	4.41	4.01	1.52	down	1.01E-01	8.95E-01	- -
1371187_a_at	LOC685132	hypothetical protein LOC685132	685132	Rn.198329	AI407888	6.07	6.02	6.19	5.15	5.68	5.63	1.52	down	2.60E-02	8.95E-01	DR -
1380297_at	---	---	---	---	AW915533	8.31	8.02	6.16	7.95	8.26	8.10	1.52	up	4.26E-01	8.95E-01	- -
1389753_at	Brp16	brain protein 16	315094	Rn.17102	AA892305	4.11	4.86	4.72	5.25	4.56	5.70	1.52	up	2.08E-01	8.95E-01	- -
1388629_at	Impdh2	IMP (inosine monophosphate) dehydrogenase 2	301005	Rn.8093	BF281270	5.26	5.71	4.52	6.52	4.74	6.05	1.52	up	3.96E-01	8.95E-01	- -
1380620_at	---	---	---	Rn.208066	BF405053	3.29	3.86	4.25	3.28	3.21	3.10	1.52	down	1.01E-01	8.95E-01	- -
1388568_at	Eif3d	eukaryotic translation initiation factor 3, subunit D	362952	Rn.3463	AA891553	8.52	9.16	9.00	9.51	9.37	9.61	1.52	up	4.21E-02	8.95E-01	UR -
1390077_

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1388557_at	C7 /// Tubb2c	complement component 7 /// tubulin, beta 2c	117517 /// 296554	Rn.33787	BF284922	8.24	7.90	7.54	8.97	8.62	7.89	1.51	up	1.88E-01	8.95E-01	-	-
1391056_at	---	---	---	Rn.16371	AA817695	5.11	5.67	5.82	5.03	5.15	4.62	1.51	down	8.92E-02	8.95E-01	-	-
1382594_at	---	---	---	Rn.166650	AI113090	7.34	8.81	8.67	8.73	8.32	8.56	1.51	up	3.70E-01	8.95E-01	-	-
1389940_at	Tmed2	transmembrane emp24 domain trafficking protein 2	65165	Rn.1022	AI178934	7.09	7.25	6.83	7.37	7.61	7.99	1.51	up	5.14E-02	8.95E-01	-	-
1372090_at	Max	MYC associated factor X	60661	Rn.4210	AI231566	7.47	7.44	9.00	7.33	7.26	7.52	1.51	down	3.15E-01	8.95E-01	-	-
1368140_at	Rab13	RAB13, member RAS oncogene family	81756	Rn.9819	AW253722	5.66	5.86	5.68	6.79	6.45	5.76	1.51	up	1.26E-01	8.95E-01	-	-
1393666_at	---	---	---	Rn.170771	BE101321	3.83	4.18	3.63	3.24	3.29	3.32	1.51	down	2.12E-02	8.95E-01	DR	-
1387184_at	Axin2	axin2	29134	Rn.162212	NM_024355	4.21	5.54	2.37	2.92	4.49	2.92	1.51	down	6.01E-01	8.95E-01	-	-
1383146_at	RGD1562629	similar to neurobeachin	361948	---	BM388077	3.56	3.49	2.96	2.53	2.74	2.94	1.51	down	5.56E-02	8.95E-01	-	-
1372665_at	Psat1	phosphoserine aminotransferase 1	293820	Rn.100813	AI230228	11.08	11.29	10.78	11.63	11.62	11.69	1.51	up	1.56E-02	8.95E-01	UR	-
1378050_at	Hars2l	histidyl-tRNA synthetase 2-like	307491	Rn.139312	AI058960	5.21	5.06	4.53	4.88	5.70	6.01	1.51	up	2.06E-01	8.95E-01	-	-
1382911_at	---	---	---	---	BE105150	8.74	9.84	10.14	9.17	8.67	9.10	1.51	down	2.57E-01	8.95E-01	-	-
1394293_at	Immp1l	IMP1 inner mitochondrial membrane peptidase-like (S. cerevisiae)	691145	Rn.6180	BG864873	6.73	5.50	6.23	6.41	4.34	5.91	1.51	down	4.53E-01	8.95E-01	-	-
1390164_at	---	---	---	Rn.23225	BE099850	5.95	7.27	6.62	6.41	5.01	6.64	1.51	down	4.01E-01	8.95E-01	-	-
1368253_at	Gamt	guanidinoacetate N-methyltransferase	25257	Rn.33890	NM_012793	9.13	9.52	9.76	8.86	9.04	8.71	1.51	down	4.48E-02	8.95E-01	DR	-
1369289_at	Hnf4a	hepatocyte nuclear factor 4, alpha	25735	Rn.44442	NM_022180	8.44	8.98	8.03	9.09	8.96	9.19	1.51	up	1.03E-01	8.95E-01	-	-
1390591_at	Slc17a3	solute carrier family 17 (sodium phosphate), member 3	266730	Rn.16357	AI169163	9.39	9.62	9.53	10.00	9.96	10.37	1.51	up	1.54E-02	8.95E-01	UR	-
1381780_at	---	---	---	Rn.164649	AA900704	5.54	2.64	2.89	4.26	4.23	4.37	1.51	up	5.55E-01	8.95E-01	-	-
1383327_at	Pdcd4	programmed cell death 4	64031	Rn.206228	AI576297	5.94	7.33	7.59	7.69	7.90	7.06	1.51	up	3.66E-01	8.95E-01	-	-
1373142_at	Ghitm	Growth hormone inducible transmembrane protein	290596	Rn.98375	AA858928	8.34	8.08	7.27	8.49	8.06	8.94	1.51	up	2.18E-01	8.95E-01	-	-
1375565_at	Timm22	translocase of inner mitochondrial membrane 22 homolog (yeast)	79463	Rn.41817	BF420723	2.75	2.57	2.67	3.23	3.85	2.69	1.51	up	1.55E-02	8.95E-01	UR	-
1367482_at	Anapc11	anaphase promoting complex subunit 11 homolog (yeast)	498030	Rn.3964	AI172459	3.54	4.22	3.56	3.76	4.38	4.97	1.51	up	2.23E-01	8.95E-01	-	-
1398496_at	---	---	---	Rn.164919	BF390696	5.57	5.21	5.17	4.18	4.50	5.49	1.51	down	2.22E-01	8.95E-01	-	-
1371979_at	Eif3e	eukaryotic translation initiation factor 3, subunit E	299872	Rn.98547	AI237620	9.66	10.12	9.66	10.12	10.42	10.68	1.51	up	5.45E-02	8.95E-01	-	-
1389972_at	---	---	---	Rn.216579	AA943681	2.61	2.62	2.23	4.01	2.62	2.62	1.51	up	2.81E-01	8.95E-01	-	-
1383933_at	RGD1308772	Similar to KIAA0564 protein	290381	Rn.12947	AI136714	7.43	8.59	8.24	6.44	7.99	8.04	1.51	down	3.95E-01	8.95E-01	-	-
1374068_at	Vps39	vacuolar protein sorting 39 homolog (S. cerevisiae)	362199	Rn.1508	BG673672	4.93	5.93	6.05	5.45	3.91	5.76	1.51	down	4.24E-01	8.95E-01	-	-
1393280_at	Ly86	lymphocyte antigen 86	291359	Rn.3176	AA874924	2.45	2.43	2.49	2.44	4.29	2.43	1.51	up	3.90E-01	8.95E-01	-	-
1389431_at	Prkdc	protein kinase, DNA activated, catalytic polypeptide	360748	Rn.24110	BF400782	6.49	5.08	3.10	4.01	3.95	4.91	1.51	down	5.94E-01	8.95E-01	-	-
1370803_at	Zwint	ZW10 interactor	257644	Rn.163272	AF439397	9.12	9.00	9.03	8.23	8.37	8.76	1.51	down	2.18E-02	8.95E-01	DR	-
1384523_at	Pms1	PMS1 postmeiotic segregation increased 1 (S. cerevisiae)	494322	Rn.47845	BF400964	5.23	2.85	3.17	3.18	2.89	3.39	1.51	down	4.76E-01	8.95E-01	-	-
1371926_at	---	---	---	Rn.203436	AI171807	7.25	7.71	6.52	7.98	7.32	7.97	1.51	up	2.19E-01	8.95E-01	-	-
1374060_at	---	---	---	Rn.28354	AI411374	2.83	2.83	4.31	2.87	2.80	2.51	1.51	down	3.02E-01	8.95E-01	-	-
1376753_at	Fpgt	fucose-1-phosphate guanylyltransferase	310935	Rn.7364	BE105571	3.01	4.78	4.74	3.02	3.79	3.93	1.51	down	4.11E-01	8.95E-01	-	-
1374689_at	Pi4kb	phosphatidylinositol 4-kinase, catalytic, beta	81747	Rn.14991	AI102103	6.70	5.72	6.74	5.53	6.23	5.61	1.51	down	2.12E-01	8.95E-01	-	-
1391170_at	Setd5	SET domain containing 5	297514	Rn.49964	BE115521	6.48	6.34	4.41	6.06	5.97	6.99	1.51	up	4.67E-01	8.95E-01	-	-
1369039_at	Pi4kb	phosphatidylinositol 4-kinase, catalytic, beta	81747	Rn.14991	NM_031083	5.29	6.22	5.17	6.28	6.15	6.05	1.51	up	1.53E-01	8.95E-01	-	-
1376843_at	Bmpr2	bone morphogenetic protein receptor, type II (serine/threonine kinase)	140590	Rn.59270	BE118651	4.65	5.37	4.31	5.33	5.67	5.12	1.51	up	1.67E-01	8.95E-01	-	-
1369698_at	Abcc3	ATP-binding cassette, sub-family C (CFTR/MRP), member 3	140668	Rn.205054	AF072816	5.28	5.75	5.34	6.09	6.12	5.94	1.51	up	2.03E-02	8.95E-01	UR	-
1372212_at	LOC293589	putative GTP-binding protein	293589	Rn.219298	BI285445	5.09	5.10	4.59	5.43	5.96	5.18	1.51	up	1.07E-01	8.95E-01	-	-
1367634_at	Rpl31	ribosomal protein L31	84298	Rn.1101	NM_022506	11.53	11.66	11.44	11.68	12.73	12.01	1.51	up	1.33E-01	8.95E-01	-	-
1371637_at	Hp1bp3	heterochromatin protein 1, binding protein 3	313647	Rn.92942	AI411691	7.91	8.27	8.40	7.73	7.34	7.72	1.51	down	3.88E-02	8.95E-01	DR	-
1393367_at	Pnkp	polynucleotide kinase 3'-phosphatase	308576	Rn.45061	AW520745	5.45	4.55	6.23	5.14	4.47	4.84	1.51	down	3.18E-01	8.95E-01	-	-
1399019_at	Abhd4	abhydrolase domain containing 4	364380	Rn.1831	AI407868	6.74	5.43	4.48	6.32	5.60	6.52	1.51	up	4.50E-01	8.95E-01	-	-
1368403_at	Rbl2	retinoblastoma-like 2	81758	Rn.1020	NM_031094	6.69	7.27	7.07	7.56	7.44	7.81	1.51	up	4.19E-02	8.95E-01	UR	-
1367453_at	Cdc37	cell division cycle 37 homolog (S. cerevisiae)	114562	Rn.17982	NM_053743	6.59	5.84	4.32	6.69	5.64	6.20	1.51	up	4.63E-01	8.95E-01	-	-
1393911_at	---	---	---	Rn.35396	AI502300	4.10	2.32	2.33	2.32	2.33	2.32	1.51	down	3.71E-01	8.95E-01	-	-
1370675_at	Trpv1	transient receptor potential cation channel, subfamily V, member 1	83810	Rn.3073	AF158248	5.44	7.99	8.17	7.80	7.57	8.02	1.51	up	5.40E-01	8.95E-01	-	-
1379377_at	Gdap2	ganglioside-induced differentiation-associated-protein 2	362004	Rn.24196	BG371655	4.41	4.76	5.39	4.14	4.29	4.35	1.51	down	1.13E-01	8.95E-01	-	-
1385704_at	Tns1	tensin 1	301509	Rn.3793	AI071148	8.89	8.32	9.08	9.23	9.65	9.20	1.51	up	9.26E-02	8.95E-01	-	-
1396337_at	---	---	---	---	AW529811	3.23	3.05	3.09	2.64	5.43	3.09	1.51	up	5.31E-01	8.95E-01	-	-
1372987_at	---	---	---	Rn.38688	BF393934	5.24	3.05	2.83	3.25	2.93	3.15	1.51	down	4.87E-01	8.95E-01	-	-
1395744_at	---	---	---	Rn.165750	BF291140	6.87	7.92	7.44	7.72	8.13	8.17	1.51	up	1.52E-01	8.95E-01	-	-
1388889_at	Ermp1	endoplasmic reticulum metallopeptidase 1	373544	Rn.99609	AI598417	5.44	5.80	6.50	5.23	5.02	5.71	1.51	down	1.87E-01	8.95E-01	-	-
1395628_at	---	---	---	Rn.207029	AW434310	4.12	2.51	2.63	2.45	2.55	2.47	1.51	down	3.18E-01	8.95E-01	-	-
1370959_at	Col3a1	collagen, type III, alpha 1	84032	Rn.3247	BI275716	7.02	6.03	4.08	7.08	6.14	5.69	1.51	up	5.68E-01	8.95E-01	-	-
1374801_at	---	---	---	Rn.6793	AW915643	2.30	2.30	2.30	2.29	4.10	2.29	1.51	up	3.81E-01	8.95E-01	-	-
1384681_at	Frmd4b	FERM domain containing 4B	252858	Rn.41044	AI715014	5.83	6.14	4.18	5.90	6.02	6.02	1.51	up	3.85E-01	8.95E-01	-	-
1389305_at	Anxa4	annexin A4	79124	Rn.19270	BM385237	7.90	8.12	7.94	7.24	7.65	7.29	1.51	down	1.47E-02	8.95E-01	DR	-
1368882_at	St6galnac3	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosamini	29758	Rn.88072	NM_019123	5.98	6.10	6.40	7.04	6.61	6.61	1.51	up	3.67E-02	8.95E-01	UR	-
1375996_at	01-Sep	septin 1	293507	Rn.68675	AA894262	2.72	3.92	3.75	4.09	4.08	4.00	1.51	up	1.88E-01	8.95E-01	-	-
1378245_at	Fam81a	family with sequence similarity 81, member A	315789	Rn.163030	BF563206	6.23	6.48	7.63	5.48	6.52	6.57	1.51	down	3.48E-01	8.95E-01	-	-
1385274_at	Pcdhb19	protocadherin beta 19	548106	Rn.172273	AW526381	4.05	2.54	2.44	2.38	2.44	2.43	1.51	down	3.19E-01	8.95E-01	-	-
1372749_at	---	---	---	Rn.164775	AI009786	3.64	3.72	3.65	5.05	3.29	4.46	1.51	up	3.15E-01	8.95E-01	-	-
1388743_at	---	---	---	Rn.43522	BI297291	3.27	3.25	2.75	3.17	3.87	4.00	1.51	up	1.27E-01	8.95E-01	-	-
1393631_at	---	---	---	Rn.221957	AW527492	5.16	2.70	2.96	3.46	2.81	2.77	1.51	down	5.06E-01	8.95E-01	-	-
1382318_at	---	---	---	Rn.43928	AA964856	7.21	6.95	7.03	7.04	5.77	6.62	1.51	down	1.95E-01	8.95E-01	-	-
1392923_at	---	---	---	Rn.220861	H34314	4.94	5.54	4.94	4.94	3.86	4.85	1.51	down	2.12E-01	8.95E-01	-	-
1373393_at	Ext1	exostoses (multiple) 1	299907	Rn.106323	BM384468	3.92	4.82	4.76	5.15	5.10	5.03	1.51	up	1.14E-01	8.95E-01	-	-
1389382_at	Mkrn2	makorin, ring finger protein, 2	297525	Rn.129070	BI277034	3.16	4.34	3.25	4.04	4.43	4.05	1.51	up	2.13E-01	8.95E-01	-	-
1388253_at	Scd	Stearoyl-CoA desaturase (delta-9-desaturase)	83792	Rn.83595	M15114	2.93	3.65	2.92	4.06	3.00	4.23	1.51	up	2.64E-01	8.95E-01	-	-
1371439_at	Epb4.1	erythrocyte membrane protein band 4.1	313052	Rn.203205	AA894008	8.89	8.35	8.80	8.66	7.34	8.25	1.51	down	2.36E-01	8.95E-01	-	-
1388729_at	Rras	Harvey rat sarcoma virus oncogene, subgroup R	361568	Rn.71224	BF282474	3.45	5.72	4.16	5.39	4.47	5.24	1.51	up	4.62E-01	8.95E-01	-	-
1372061_at	Rabepk	Rab9 effector protein with kelch motifs	296649	Rn.39139	BG381287	6.72	6.37	4.82	6.22	6.64	6.82	1.51	up	3.85E-01	8.95E-01	-	-
1374029_at	---	---	---	---	AI226596	2.62	3.49	3.48	2.61	2.58	2.61	1.51	down	1.09E-01	8.95E-01	-	-
1373171_at	Ccdc21	coiled-coil domain containing 21	362622	Rn.20146	BI294854	4.05	2.33	2.30	2.30	2.32	2.29	1.51	down	3.65E-01	8.95E-01	-	-
1382717_at	Fam168a	family with sequence similarity 168, member A	361614	Rn.137163	BF386949	3.48	4.63	6.26	5.41	2.99	4.18	1.51	down	6.09E-01	8.95E-01	-	-
1372535_at	LOC366431	similar to RIKEN cDNA 2210012G02	366431	Rn.17312	AI410203	5.73	3.08	2.36	3.08	3.12	3.19	1.51	down	5.95E-01	8.95E-01	-	-
1376653_at	Phtf1	putative homeodomain transcription factor 1	252962	Rn.22952	BE106772	3.51	4.50	4.76	3.44	3.34	4.22	1.51	down	2.78E-01	8.95E-01	-	-
1385527_at	Usp7	ubiquitin specific peptidase 7 (herpes virus-associated)	360471	Rn.72721	AA955194	4.46	3.99	3.38	3.32	3.42	3.31	1.51	down	1.31E-01	8.95E-01	-	-
1383769_at	---	---	---	Rn.222010	BF398206	5.10	6.12	5.56	5.68	6.20	6.68	1.51	up	2.24E-01	8.95E-01	-	-
1373261_at	---	---	---	Rn.156297	BF388657	4.87	4.61	4.87	5.29	5.02	5.81	1.51	up	7.43E-02	8.95E-01	-	-
1378484_at	Rasl12	RAS-like, family 12	315762	Rn.147874	BI279720	3.17	2.68	2.54	2.99	2.71	4.46	1.51	up	3.63E-01	8.95E-01	-	-
1388609_at	Ddi2	DNA-damage inducible protein 2	313668	Rn.144389	AI406723	3.56	3.65	3.65	4.62	4.16	3.86	1.51	up	5.61E-02	8.95E-01	-	-
1368438_at	Pde10a	phosphodiesterase 10A	63885	Rn.44869	NM_022236	4.52	2.77	2.74	2.77	2.77	2.71	1.51	down	3.72E-01	8.95E-01	-	-
1393314_at	---	---	---	Rn.216741	BI289840	8.05	7.77	7.06	6.28	7.37	7.45	1.51	down	2.84E-01	8.95E-01	-	-
1367640_at	Rps12	ribosomal protein S12	65139	Rn.8400	NM_031709	9.56	10.02	9.77	10.09	10.35	10.68	1.51	up	5.41E-02	8.95E-01	-	-
1372761_at	---	---	---	Rn.22957	AI228076	6.68	5.28	5.81	5.75	5.04	5.21	1.51	down	2.70E-01	8.95E-01	-	-
1394653_at	---	---	---	Rn.33652	BM387172	3.81	2.74	2.36	2.43	2.36	2.35	1.51	down	2.45E-01	8.95E-01	-	-
1387498_a_at	Fgfr1	Fibroblast growth factor receptor 1	79114	Rn.207203	S54008	4.10	6.51	6.76	5.04	4.19	6.37	1.51	down	6.06E-01	8.95E-01	-	-
1369968_at	Ptn	pleiotrophin	24924	Rn.1653	NM_017086	4.85	2.91	3.49	3.37	3.49	2.63	1.51	down	4.06E-01	8.95E-01	-	-
1377259_at	---	---	---	Rn.52511	BE116379	4.10	2.31	2.32	2.32	2.33	2.31	1.51	down	3.77E-01	8.95E-01	-	-
1395886_at	Actr3	ARP3 actin-related protein 3 homolog (yeast)	81732	Rn.103326	H31273	7.65	8.62	8.67	7.85	7.42	7.90	1.51	down	1.83E-01	8.95E-01	-	-
1374795_at	---	---	---	Rn.199123	AA891859	7.17	5.72	6.22	5.67	5.18	6.50	1.51	down	3.62E-01	8.95E-01	-	-
1398875_at	Polr3k	polymerase (RNA) III (DNA directed) polypeptide K, 12.3 kDa	366277	Rn.92563	AI105044	5.75	6.24	5.38	6.86	6.21	6.07	1.51	up	1.67E-01	8.95E-01	-	-
1372420_at	Mpv17l2	MPV17 mitochondrial membrane protein-like 2	299645	Rn.160899	AI408084	6.46	6.89	5.98	6.81	7.11	7.18	1.51	up	1.09E-01	8.95E-01	-	-
1370283_at	Hspa5	heat shock protein 5	25617	Rn.11088	M14050	10.64	10.74	10.77	11.27	10.95	11.70	1.51	up	5.65E-02	8.95E-01	-	-
1391661_at	Gk	glycerol kinase	79223	Rn.153497	AA945076	9.86	8.13	7.52	7.84	7.66	8.24	1.51	down	4.60E-01	8.95E-01	-	-
1392928_at	RGD1305721	similar to RIKEN cDNA 2810055F11	314214	Rn.105727	AA891693	8.83	7.38	7.56	7.52	7.57	6.91	1.51	down	3.05E-01	8.95E-01	-	-
1371787_at	---	---	---	Rn.203194	AI231686	2.67	4.17	3.42	4.11	4.34	3.59	1.50	up	2.91E-01	8.95E-01	-	-
1390085_at	---	---	---	---	BF406291	2.86	2.62	4.12	2.61	2.66	2.55	1.50	down	2.75E-01	8.95E-01	-	-
1367499_at	Slc35c1	solute carrier family 35, member C1	311204	Rn.3950	BM390900	3.57	3.77	3.47	4.66	3.45	4.46	1.50	up	2.01E-01	8.95E-01	-	-
1396465_at	Mtmr3	myotubularin related protein 3	305482	Rn.8338	AI407842	4.33	6.27	6.42	4.12	5.73	5.41	1.50	down	5.18E-01	8.95E-01	-	-
1373412_at	Nt5c3	5'-nucleotidase, cytosolic III	312373	Rn.36789	AI409146	6.27	6.69	5.73	6.54	6.56	7.35	1.50	up	2.01E-01	8.95E-01	-	-
1372763_at	Nus1	nuclear undecaprenyl pyrophosphate synthase 1 homolog (S. cerevisiae)	294400	Rn.23082	AI407545	7.31	7.25	6.73	7.68	7.33	8.05	1.50	up	9.95E-02	8.95E-01	-	-
1385474_at	Znf294	zinc finger protein 294	288308	Rn.44204	BF416362	4.12	3.95	5.19	4.63	3.77	4.10	1.50	down	4.83E-01	8.95E-01	-	-
1377189_at	RGD1307390	similar to BC282485_1	292680	Rn.34772	BI295093	3.63	2.61	3.15	2.65	2.66	2.31	1.50	down	1.35E-01	8.95E-01	-	-
1371401_at	Rnf5	ring finger protein 5	407784	Rn.136937	BI278836	8.91	8.70	9.08	8.47	8.42	8.02	1.50	down	3.20E-02	8.95E-01	DR	-
1372100_at	Tmem50a	transmembrane protein 50A	298552	Rn.957	BI283746	6.04	6.16	5.94	4.67	5.76	5.93	1.50	down	2.14E-01	8.95E-01	-	-
1383790_at	LOC690745	MOCO sulphurase C-terminal domain containing-like	690745	Rn.26676	BF550303	2.40	2.40	2.40	4.17	2.42	2.39	1.50	up	3.75E-01	8.95E-01	-	-
1388544_at	Bpgm	2,3-bisphosphoglycerate mutase	296973	Rn.204528	BI294941	6.74	7.93	7.35	8.41	7.20	8.18	1.50	up	3.09E-01	8.95E-01	-	-
1391377_at	---	---	---	---	BM387935	3.24	2.49	2.51	4.83	2.64	2.53	1.50	up	4.97E-01	8.95E-01	-	-
1379134_at	---	---	---	---	BE099532	2.28	2.27	4.05	2.28	2.31	2.25	1.50	down	3.78E-01	8.95E-01	-	-
1368509_at	Bbs2	Bardet-Biedl syndrome 2 homolog (human)	113948	Rn.15987	NM_053618	8.85	8.72	7.99	7.76	8.38	7.66	1.50	down	1.67E-01	8.95E-01	-	-
1397217_at	---	---	---	Rn.211213	BF408757	5.05	3.57	2.27	3.18	2.97	2.98	1.50	down	5.06E-01	8.95E-01	-	-
1367645_at	Rps17	ribosomal protein S17	29286	Rn.6920	NM_017152	11.23	10.76	10.36	11.39	11.40	11.31	1.50	up	7.96E-02	8.95E-01	-	-
1393632_at	C1qtnf7	C1q and tumor necrosis factor related protein 7	305423	Rn.35540	AI501709	2.48	2.46	2.49	4.25	2.49	2.46	1.50	up	3.76E-01	8.95E-01	-	-
1371469_at	Chp	calcium binding protein p22	64152	Rn.11041	BM958511	6.96	6.97	8.21	6.77	6.53	7.08	1.50	down	2.57E-01	8.95E-01	-	-
1376970_at	RGD1308722	similar to RIKEN cDNA A130042E20; open reading frame 57	361822	Rn.41811	AW530127	2.57	2.56	4.32	2.55	2.57	2.56	1.50	down	3.71E-01	8.95E-01	-	-
1387673_a_at	Anxa6	Annexin A6	79125	Rn.204053	BI285568	6.68	7.28	4.98	6.85	7.42	6.43	1.50	up	4.73E-01	8.95E-01	-	-
1370823_at	Bambi	BMP and activin membrane-bound inhibitor, homolog (Xenopus laevis)	83837	Rn.25267	AF387513	7.13	7.22	6.93	6.25	6.34	6.93	1.50	down	6.24E-02	8.95E-01	-	-
1369966_a_at	Rps24	ribosomal protein S24	81776	Rn.979	BG375811	9.66	10.36	10.07	10.40	10.48	10.98	1.50	up	9.76E-02	8.95E-01	-	-
1367567_at	Rpl6	ribosomal protein L6	117042	Rn.2680	NM_053971	9.50	9.82	9.35	9.99	9.92	10.51	1.50	up	6.39E-02	8.95E-01	-	-
1376990_at	---	---	---	Rn.205409	BE118704	3.35	3.46	4.14	2.85	3.58	2.76	1.50	down	1.76E-01	8.95E-01	-	-
1373553_at	Top3b	topoisomerase (DNA) III beta	287930	Rn.23773	AI233765	2.52	2.51	2.50	2.51	4.28	2.50	1.50	up	3.75E-01	8.95E-01	-	-
1377875_at	---	---	---	Rn.17760	BF400747	6.09	6.07	5.43	6.81	5.91	6.64	1.50	up	1.70E-01	8.95E-01	-	-
1390114_at	Mpzl1	myelin protein zero-like 1	360871	Rn.8087	BM384017	3.57	3.22	2.48	2.60	2.46	2.44	1.50	down	1.45E-01	8.95E-01	-	-
1384118_at	Zfp329	zinc finger protein 329	308361	Rn.100854	AA956308	4.76	2.90	5.57	4.65	2.54	4.28	1.50	down	5.96E-01	8.95E-01	-	-
1369738_s_at	Crem	cAMP responsive element modulator	25620	Rn.10251	NM_017334	2.72	3.15	4.25	3.16	2.69	2.51	1.50	down	3.03E-01	8.95E-01	-	-
1395536_at	---	---	---	Rn.177645	BG673248	2.71	4.57	2.74	2.71	2.81	2.74	1.50	down	3.92E-01	8.95E-01	-	-
1382161_at	Mphosph10	M-phase phosphoprotein 10 (U3 small nucleolar ribonucleoprotein)	293828	Rn.103228	AA817668	6.01	6.30	6.12	5.20	5.43	6.03	1.50	down	8.64E-02	8.95E-01	-	-
1394953_at	Spred1	sprouty-related, EVH1 domain containing 1	296072	Rn.202884	BF388068	3.46	3.28	4.37	3.08	2.99	3.28	1.50	down	1.68E-01	8.95E-01	-	-
1374574_at	RGD1310552	similar to hypothetical protein MGC38960	300836	Rn.23973	AI547611	5.31	6.30	5.37	5.03	4.95	5.24	1.50	down	1.51E-01	8.95E-01	-	-
1379286_at	Rnf152	ring finger protein 152	293561	Rn.169056	BM383184	9.05	7.59	7.87	7.17	7.61	7.98	1.50	down	3.06E-01	8.95E-01	-	-
1394433_at	Katnal1	katanin p60 subunit A-like 1	288449	Rn.208215	BF408149	2.61	2.39	2.40	3.33	3.26	2.56	1.50	up	8.59E-02	8.95E-01	-	-
1368926_at	Acsl5	acyl-CoA synthetase long-chain family member 5	94340	Rn.105862	NM_053607	6.64	7.14	6.76	6.50	8.03	7.77	1.50	up	3.01E-01	8.95E-01	-	-
1392397_at	---	---	---	Rn.206192	BF389365	3.85	4.14	3.73	4.81	3.91	4.76	1.50	up	1.39E-01	8.95E-01	-	-
1380310_at	Zfand1	zinc finger, AN1-type domain 1	361917	Rn.19319	AI059937	4.42	5.59	3.53	4.87	4.91	5.51	1.50	up	4.06E-01	8.95E-01	-	-
1393501_at	---	---	---	Rn.163899	AI043579	7.26	6.66	4.56	7.87	7.20	5.18	1.50	up	6.37E-01	8.95E-01	-	-
1381644_at	---	---	---	Rn.170556	BE121056	7.67	6.27	5.66	6.85	4.25	6.75	1.50	down	6.02E-01	8.95E-01	-	-
1383011_at

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1392351_at	Fpgt	fucose-1-phosphate guanylyltransferase	310935	Rn.7364	BI288242	3.60	3.67	2.62	3.86	4.22	3.56	1.50	up	2.09E-01	8.95E-01	-	-
1388198_at	Nup1	nucleoporin like 1	245922	Rn.11099	AF000899	3.76	3.80	3.81	5.54	3.80	3.77	1.50	up	3.77E-01	8.95E-01	-	-
1372112_at	RGD1304579	similar to 9230105E10Rik protein	308906	Rn.12117	AA945761	3.35	3.76	2.57	4.65	3.29	3.50	1.50	up	3.48E-01	8.95E-01	-	-
1381960_at	Ropn1l	ropporin 1-like	685646	Rn.198580	BI288014	5.86	7.15	5.98	6.25	6.71	7.78	1.50	up	3.95E-01	8.95E-01	-	-
1369476_at	Efnb1	ephrin B1	25186	Rn.44398	NM_017089	4.89	5.54	3.98	6.05	4.00	6.11	1.50	up	5.20E-01	8.95E-01	-	-
1388956_at	Xpo5	exportin 5	363194	Rn.19170	BI285945	4.79	4.64	5.59	4.37	4.60	4.30	1.50	down	1.31E-01	8.95E-01	-	-
1372010_at	Mapkapk5	mitogen-activated protein kinase-activated protein kinase 5	498183	Rn.17463	BF283797	6.77	6.80	7.33	6.71	5.40	7.04	1.50	down	3.35E-01	8.95E-01	-	-
1393527_at	---	---	---	Rn.166801	AI501914	6.53	5.64	5.46	6.55	6.43	6.40	1.50	up	1.55E-01	8.95E-01	-	-
1393457_at	---	---	---	Rn.203935	BI289669	4.61	4.62	7.50	6.21	4.17	4.60	1.50	down	6.38E-01	8.95E-01	-	-
1380186_at	---	---	---	Rn.199318	AI101272	7.53	6.05	6.22	5.94	5.89	6.22	1.50	down	2.91E-01	8.95E-01	-	-
1387456_at	Stau2	staufen, RNA binding protein, homolog 2 (Drosophila)	171500	Rn.73714	NM_134466	2.44	2.42	2.43	3.40	2.63	3.01	1.50	up	6.04E-02	8.95E-01	-	-
1390388_at	Fech	ferrochelatase	361338	Rn.92711	BF283951	7.18	7.29	6.73	5.71	6.93	6.82	1.50	down	2.43E-01	8.95E-01	-	-
1388730_at	Cdo42ep4	CDC42 effector protein (Rho GTPase binding) 4	303653	Rn.8595	AI407903	4.57	4.40	2.63	3.61	5.23	4.49	1.50	up	4.97E-01	8.95E-01	-	-
1378117_at	---	---	---	Rn.153226	BF396289	3.65	5.50	6.10	5.59	5.85	5.55	1.50	up	4.79E-01	8.95E-01	-	-
1389273_at	Atg4b	ATG4 autophagy related 4 homolog B (S. cerevisiae)	316640	Rn.163086	BG374362	5.14	3.39	2.85	3.38	3.11	3.14	1.50	down	4.52E-01	8.95E-01	-	-
1397959_at	Ubn2	ubinuclein 2	312248	Rn.205186	AW534218	4.87	5.54	5.00	5.51	5.78	5.86	1.50	up	6.55E-02	8.95E-01	-	-
1378127_at	Cul2	cullin 2	361258	Rn.2970	BF420355	5.67	3.16	4.09	3.48	3.84	3.86	1.50	down	4.79E-01	8.95E-01	-	-
1374223_at	---	---	---	Rn.19635	BG371547	3.04	3.79	3.53	3.56	4.53	4.01	1.50	up	1.80E-01	8.95E-01	-	-
1394196_at	---	---	---	---	AA956971	5.95	5.86	7.48	5.91	5.61	6.04	1.50	down	3.44E-01	8.95E-01	-	-
1397590_at	Myo1b	myosin Ib	117057	Rn.36339	AA859098	2.56	3.41	2.63	3.38	4.56	2.41	1.49	up	4.41E-01	8.95E-01	-	-
1376076_at	---	---	---	---	BI282296	2.43	2.51	2.89	3.15	2.86	3.56	1.49	up	7.97E-02	8.95E-01	-	-
1394630_at	---	---	---	Rn.203534	BE114809	4.44	2.82	2.95	3.15	2.83	2.49	1.49	down	3.54E-01	8.95E-01	-	-
1376049_at	---	---	---	Rn.85735	AA925805	5.79	4.11	5.60	4.18	4.74	4.84	1.49	down	3.67E-01	8.95E-01	-	-
1373971_at	Lpcat4	lysophosphatidylcholine acyltransferase 4	296048	Rn.24844	BE115322	3.28	3.70	3.67	3.19	2.51	3.22	1.49	down	9.80E-02	8.95E-01	-	-
1378007_at	RGD1306148	similar to KIAA0368	313196	Rn.154631	BE103359	2.58	2.57	2.63	3.02	2.63	3.86	1.49	up	1.87E-01	8.95E-01	-	-
1383052_a_at	Zfp91	zinc finger protein 91	246282	Rn.1772	BE112093	4.50	6.25	4.51	4.87	4.22	4.43	1.49	down	3.99E-01	8.95E-01	-	-
1373138_at	Rps16	ribosomal protein S16	140655	Rn.29791	BG666872	9.70	10.00	9.68	10.03	10.44	10.64	1.49	up	4.82E-02	8.95E-01	-	-
1377781_at	---	---	---	Rn.22265	AA899278	5.06	4.83	4.99	5.70	5.31	5.61	1.49	up	1.35E-02	8.95E-01	-	-
1380490_at	---	---	---	Rn.216619	AW434884	4.73	7.61	8.76	7.81	8.01	7.01	1.49	up	6.64E-01	8.99E-01	-	-
1377424_at	Dut	Deoxyuridine triphosphatase	497778	Rn.6102	AI712672	6.62	6.95	7.88	6.78	5.69	7.24	1.49	down	3.86E-01	8.95E-01	-	-
1397834_at	Rdh13	retinol dehydrogenase 13 (all-trans/9-cis)	361504	Rn.2371	BI294052	3.40	2.79	3.25	4.59	3.35	3.24	1.49	up	2.85E-01	8.95E-01	-	-
1383553_at	Nlrx1	NLR family member X1	315599	Rn.12444	BE097591	3.77	4.89	4.05	4.65	4.54	5.26	1.49	up	2.23E-01	8.95E-01	-	-
1368989_at	Timp3	TIMP metallopeptidase inhibitor 3	25358	Rn.119634	NM_012886	9.94	9.27	8.74	9.20	9.01	8.00	1.49	down	3.19E-01	8.95E-01	-	-
1368595_at	Mmp24	matrix metallopeptidase 24	83513	Rn.3117	NM_031757	3.47	4.63	4.47	4.29	4.97	5.04	1.49	up	2.55E-01	8.95E-01	-	-
1393698_at	Dido1	death inducer-obliterator 1	362286	Rn.219449	BE106785	5.86	5.18	5.18	5.18	5.19	4.11	1.49	down	2.42E-01	8.95E-01	-	-
1393100_at	RGD1305089	similar to 1110008L16Rik protein	299050	Rn.35652	AI071493	4.66	4.64	3.44	3.93	5.10	5.45	1.49	up	3.97E-01	8.95E-01	-	-
1376248_at	Sulf2b1	sulfotransferase family, cytosolic, 2B, member 1	292915	Rn.100606	BM390571	2.68	2.64	2.71	2.83	3.30	3.63	1.49	up	6.79E-02	8.95E-01	-	-
1398407_at	Tnfaip8	tumor necrosis factor, alpha-induced protein 8	307428	Rn.116157	AA801395	7.12	7.31	8.21	6.83	6.56	7.53	1.49	down	2.64E-01	8.95E-01	-	-
1368356_a_at	Erap1	endoplasmic reticulum aminopeptidase 1	80897	Rn.22516	NM_030836	6.79	5.66	5.78	6.58	6.85	6.54	1.49	up	1.93E-01	8.95E-01	-	-
1374480_at	Daam1	dishevelled associated activator of morphogenesis 1	314212	Rn.92012	BE107255	7.05	6.35	5.84	5.95	4.70	6.86	1.49	down	4.65E-01	8.95E-01	-	-
1395349_at	---	---	---	Rn.26899	BF561061	3.36	3.59	4.30	3.43	2.70	3.40	1.49	down	1.94E-01	8.95E-01	-	-
1375532_at	---	---	---	Rn.220010	AI008792	9.83	10.41	10.41	9.49	9.61	9.82	1.49	down	5.68E-02	8.95E-01	-	-
1389085_at	---	---	---	Rn.161242	BI296359	5.32	5.38	5.96	5.15	7.01	6.23	1.49	up	3.73E-01	8.95E-01	-	-
1374839_at	Spg7	spastic paraplegia 7 homolog (human)	353231	Rn.16437	BE329255	7.43	7.98	7.88	7.20	6.66	7.69	1.49	down	1.66E-01	8.95E-01	-	-
1386818_at	---	---	---	Rn.164405	AA848601	4.32	4.51	4.52	5.46	4.30	5.32	1.49	up	1.93E-01	8.95E-01	-	-
1386701_at	---	---	---	Rn.156229	BF565038	3.80	4.03	2.91	5.02	3.69	3.76	1.49	up	3.51E-01	8.95E-01	-	-
1393012_at	RGD1560636	similar to novel protein	305467	Rn.163258	BI294441	4.55	4.90	3.59	4.05	3.90	3.36	1.49	down	2.63E-01	8.95E-01	-	-
1392378_at	Klhdc3	kelch domain containing 3	363192	Rn.203058	BF410753	2.45	2.43	2.61	4.38	2.46	2.39	1.49	up	4.27E-01	8.95E-01	-	-
1381135_at	---	---	---	Rn.204447	AW533560	5.57	5.10	5.35	5.03	6.97	5.76	1.49	up	3.78E-01	8.95E-01	-	-
1372110_at	---	---	---	Rn.163253	BE113148	6.61	6.95	6.56	5.57	6.31	6.52	1.49	down	1.41E-01	8.95E-01	-	-
1381840_at	---	---	---	Rn.210877	BF402893	3.69	2.87	2.45	2.44	2.45	2.40	1.49	down	1.88E-01	8.95E-01	-	-
1388813_at	Arf2	ADP-ribosylation factor 2	79119	Rn.62175	BE112160	6.90	6.84	6.88	5.84	6.32	6.72	1.49	down	8.67E-02	8.95E-01	-	-
1380651_at	Rnf6	ring finger protein (C3H2C3 type) 6	304271	Rn.53030	BI296352	7.56	7.29	6.69	7.58	7.67	8.02	1.49	up	1.18E-01	8.95E-01	-	-
1394101_at	---	---	---	Rn.199305	BE109260	6.20	4.78	5.43	4.20	5.27	5.21	1.49	down	3.44E-01	8.95E-01	-	-
1379046_at	Mlec	malectin	304543	Rn.162140	BI290140	6.68	8.42	5.79	7.79	6.47	8.36	1.49	up	5.78E-01	8.95E-01	-	-
1384237_at	Pex10	peroxisome biogenesis factor 10	680424	Rn.111	BF420822	5.74	6.71	6.22	6.73	6.78	6.88	1.49	up	1.12E-01	8.95E-01	-	-
1383206_at	Cog3	component of oligomeric golgi complex 3	361073	Rn.163311	AA955098	6.15	7.57	7.50	7.84	6.88	8.24	1.49	up	4.02E-01	8.95E-01	-	-
1385595_at	Kln	antigenic determinant of rec-A protein	689197	Rn.53701	BE114414	6.26	6.02	5.59	6.17	4.38	6.58	1.49	down	3.62E-01	8.95E-01	-	-
1397452_at	---	---	---	Rn.21208	AI112776	3.40	3.36	3.39	3.79	3.39	4.71	1.49	up	2.13E-01	8.95E-01	-	-
1381126_at	Srgap2	SLIT-ROBO Rho GTPase activating protein 2	360840	Rn.220450	BE099652	2.62	2.58	4.51	2.62	2.77	2.59	1.49	down	4.19E-01	8.95E-01	-	-
1381652_at	Ankrd32	ankyrin repeat domain 32	362811	Rn.8972	BF396587	2.47	2.51	2.49	4.21	2.56	2.43	1.49	up	3.72E-01	8.95E-01	-	-
1372918_at	LOC100174909	hypothetical LOC100174909	100174909	Rn.18836	BM385785	4.01	4.00	3.52	3.81	4.63	4.82	1.49	up	1.76E-01	8.95E-01	-	-
1383316_at	Hddc2	HD domain containing 2	361462	Rn.60559	BF409313	3.16	4.37	4.49	4.86	4.40	4.48	1.49	up	2.68E-01	8.95E-01	-	-
1390466_at	---	---	---	Rn.47783	AW531623	4.86	5.57	6.16	6.23	5.86	6.23	1.49	up	2.20E-01	8.95E-01	-	-
1368848_at	Lman1	lectin, mannose-binding, 1	116666	Rn.25734	NM_053886	5.86	5.93	5.87	5.92	6.46	7.00	1.49	up	1.39E-01	8.95E-01	-	-
1390710_x_at	Sorl1	sortilin-related receptor, LDLR class A repeats-containing	300652	Rn.92871	AA850618	5.58	5.83	4.78	5.98	5.83	6.11	1.49	up	1.52E-01	8.95E-01	-	-
1395228_at	---	---	---	Rn.190650	AI044273	6.91	6.35	6.17	6.12	5.32	6.26	1.49	down	1.93E-01	8.95E-01	-	-
1378551_at	Cyp20a1	cytochrome P450, family 20, subfamily A, polypeptide 1	316435	Rn.101629	BE118606	7.91	8.79	7.94	8.60	8.70	9.06	1.49	up	1.45E-01	8.95E-01	-	-
1385475_a_at	Stra6	stimulated by retinoic acid gene 6	363071	Rn.12735	AI030451	3.15	3.78	2.69	2.61	2.71	2.56	1.49	down	1.46E-01	8.95E-01	-	-
1382524_at	Zbtb20	zinc finger and BTB domain containing 20	288105	Rn.168502	AA850361	7.50	8.12	7.34	7.06	6.54	7.63	1.49	down	2.19E-01	8.95E-01	-	-
1392841_at	---	---	---	Rn.37544	AA891751	3.65	3.53	3.41	4.80	3.66	3.85	1.49	up	1.84E-01	8.95E-01	-	-
1386550_at	Ikzf5	IKAROS family zinc finger 5	309031	Rn.21942	BF563739	2.66	2.58	2.50	4.13	2.50	2.83	1.49	up	3.13E-01	8.95E-01	-	-
1375887_at	---	---	---	Rn.7439	BI282089	6.66	6.70	7.70	5.91	6.51	6.91	1.49	down	2.70E-01	8.95E-01	-	-
1397547_at	Ikbkb	Inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase beta	84351	Rn.19222	BF407913	2.47	2.46	2.48	2.46	4.11	2.55	1.49	up	3.45E-01	8.95E-01	-	-
1368466_a_at	Odf2	outer dense fiber of sperm tails 2	29479	Rn.91211	NM_017213	5.25	6.31	4.61	5.90	5.85	6.15	1.49	up	3.18E-01	8.95E-01	-	-
1398617_at	---	---	---	Rn.144605	BE098167	5.06	5.10	5.19	5.08	5.53	6.45	1.49	up	2.30E-01	8.95E-01	-	-
1384124_at	---	---	---	Rn.148509	AW534915	3.00	3.38	4.06	3.26	4.57	4.32	1.49	up	3.21E-01	8.95E-01	-	-
1376371_at	---	---	---	Rn.161063	AW434139	4.42	2.71	2.71	2.70	2.71	2.71	1.49	down	3.72E-01	8.95E-01	-	-
1384278_x_at	Ccdc34	coiled-coil domain containing 34	362187	Rn.18453	BG377047	5.11	5.59	3.54	5.30	5.36	5.29	1.49	up	4.07E-01	8.95E-01	-	-
1374963_s_at	---	---	---	---	BI290604	7.86	9.63	8.64	8.90	9.31	9.64	1.49	up	3.60E-01	8.95E-01	-	-
1391580_at	---	---	---	Rn.202696	AI234123	2.80	2.89	2.53	2.90	3.62	3.43	1.49	up	7.66E-02	8.95E-01	-	-
1372861_at	Pip5k1c	phosphatidylinositol-4-phosphate 5-kinase, type I, gamma	314641	Rn.2928	BG380713	5.02	4.13	3.99	5.09	5.35	4.42	1.49	up	2.49E-01	8.95E-01	-	-
1391730_at	---	---	---	Rn.162024	AW433989	3.86	4.39	4.21	3.43	3.45	3.86	1.49	down	5.45E-02	8.95E-01	-	-
1396000_at	---	---	---	Rn.147147	AI704583	6.08	6.87	6.33	7.23	6.83	6.93	1.49	up	9.44E-02	8.95E-01	-	-
1379941_at	RGD1560364	similar to vacuolar protein sorting 13C protein	363087	Rn.21609	BM384685	2.88	2.52	2.93	4.18	3.02	2.84	1.49	up	2.63E-01	8.95E-01	-	-
1374069_at	Rab11a	RAB11a, member RAS oncogene family	81830	Rn.1016	BE118560	6.55	6.37	7.00	6.49	5.52	6.19	1.49	down	1.70E-01	8.95E-01	-	-
1367718_at	Chkb	choline kinase beta	29367	Rn.1302	NM_017177	4.98	3.00	2.88	2.96	3.01	3.17	1.49	down	4.50E-01	8.95E-01	-	-
1388086_a_at	Rest	RE1-silencing transcription factor	83618	Rn.10879	AF037203	5.30	6.44	3.31	6.20	4.16	6.40	1.49	up	6.48E-01	8.96E-01	-	-
1388390_at	Eif3h	eukaryotic translation initiation factor 3, subunit H	299899	Rn.129213	AI231784	9.78	10.29	9.21	10.21	10.34	10.44	1.49	up	1.47E-01	8.95E-01	-	-
1393912_at	---	---	---	Rn.168745	AI548154	2.33	2.33	2.34	2.33	4.06	2.33	1.49	up	3.77E-01	8.95E-01	-	-
1379650_at	Pdzd8	PDZ domain containing 8	308000	Rn.24878	AI231443	5.96	6.39	5.03	6.06	6.93	6.10	1.49	up	3.11E-01	8.95E-01	-	-
1383771_at	Usp48	ubiquitin specific peptidase 48	289584	Rn.18609	BF545879	4.21	3.53	5.50	3.52	4.48	3.51	1.49	down	4.37E-01	8.95E-01	-	-
1391800_at	Hsd17b14	hydroxysteroid (17-beta) dehydrogenase 14	891018	Rn.212885	BF543501	4.57	4.84	2.82	4.66	3.89	5.39	1.49	up	4.97E-01	8.95E-01	-	-
1386606_at	Mrpl37	Mitochondrial ribosomal protein L37	56281	Rn.3445	AA848353	3.31	5.49	4.98	4.54	5.72	5.23	1.49	up	4.85E-01	8.95E-01	-	-
1377663_at	Rnd3	Rho family GTPase 3	295588	Rn.25153	AI598323	5.23	5.81	6.34	6.14	4.56	4.97	1.49	down	3.75E-01	8.95E-01	-	-
1392993_at	Fam130b1	family with sequence similarity 13, member B1	291694	Rn.25218	BI665293	5.58	7.89	8.28	6.29	7.67	8.07	1.49	down	5.91E-01	8.95E-01	-	-
1374958_at	Adpgk	ADP-dependent glucokinase	315722	Rn.66171	AA819640	3.85	4.61	4.62	3.47	3.33	4.56	1.49	down	2.87E-01	8.95E-01	-	-
1373093_at	Errfi1	ERBB receptor feedback inhibitor 1	310739	Rn.100336	AI169756	10.92	9.93	10.79	11.25	10.78	11.32	1.49	up	1.84E-01	8.95E-01	-	-
1372472_at	LOC679221	similar to Microtubule-associated protein RP/EB family member 2 (APC-bindi	679221	---	AA856614	4.37	4.09	4.96	5.20	5.06	4.88	1.49	up	1.04E-01	8.95E-01	-	-
1372186_at	Ncaph2	non-SMC condensin II complex, subunit H2	301491	Rn.4227	BM392171	3.54	3.94	3.38	3.24	2.81	3.10	1.49	down	5.27E-02	8.95E-01	-	-
1379433_at	Plk3c2a	phosphoinositide-3-kinase, class 2, alpha polypeptide	361632	Rn.60820	AI059449	5.55	6.29	4.44	5.41	5.59	7.00	1.49	up	4.82E-01	8.95E-01	-	-
1396195_at	Ankrd13a	ankyrin repeat domain 13a	360823	Rn.3722	BF550130	5.08	6.36	6.28	3.79	6.08	6.14	1.49	down	5.51E-01	8.95E-01	-	-
1384573_at	Papola	poly (A) polymerase alpha	314417	Rn.3455	BE108853	7.73	9.03	7.79	8.62	8.66	8.99	1.49	up	2.65E-01	8.95E-01	-	-
1375850_at	---	---	---	Rn.203200	BG371810	7.11	5.79	2.63	6.24	6.70	4.30	1.49	up	7.26E-01	9.13E-01	-	-
1382485_at	---	---	---	Rn.20948	BF285608	2.49	2.49	4.19	2.47	2.50	2.49	1.49	down	3.72E-01	8.95E-01	-	-
1371688_at	Tram1	translocation associated membrane protein 1	312903	Rn.104193	AI178493	7.95	7.91	7.66	8.12	8.20	8.91	1.49	up	1.01E-01	8.95E-01	-	-
1376737_at	LOC690243	hypothetical protein LOC690243	690243	Rn.198535	BE110674	6.97	6.79	5.52	7.14	6.91	6.94	1.49	up	2.85E-01	8.95E-01	-	-
1388515_at	---	---	---	Rn.6571	BE112952	6.34	6.27	4.74	6.45	5.87	6.75	1.49	up	3.81E-01	8.95E-01	-	-
1397735_at	Bpil3	bactericidal/permeability-increasing protein-like 3	311558	Rn.55818	BF289741	3.77	2.79	2.45	2.44	2.46	2.41	1.48	down	2.23E-01	8.95E-01	-	-
1393029_at	---	---	---	Rn.22432	BF410771	7.22	6.34	5.33	7.12	7.02	6.46	1.48	up	3.83E-01	8.95E-01	-	-
1387619_at	Crebbp	CREB binding protein	54244	Rn.108128	NM_133381	3.79	3.10	2.85	2.78	2.63	2.62	1.48	down	1.15E-01	8.95E-01	-	-
1384040_at	Cep290	centrosomal protein 290	314787	Rn.162935	BE121108	4.14	4.36	3.63	3.35	3.59	3.48	1.48	down	6.72E-02	8.95E-01	-	-
1368158_at	Scfd1	sec1 family domain containing 1	54350	Rn.10761	NM_019364	5.72	5.97	6.25	6.27	6.43	6.95	1.48	up	9.13E-02	8.95E-01	-	-
1384248_at	---	---	---	Rn.146542	AI072686	4.14	2.46	2.55	2.48	2.49	2.48	1.48	down	3.56E-01	8.95E-01	-	-
1389190_at	Lzts2	leucine zipper, putative tumor suppressor 2	365468	Rn.23951	BM392076	4.25	2.58	2.42	2.64	2.32	2.59	1.48	down	3.93E-01	8.95E-01	-	-
1373078_at	Ahcyl2	S-adenosylhomocysteine hydrolase-like 2	312192	Rn.8222	AI409271	6.47	4.94	6.22	5.22	5.37	5.34	1.48	down	2.99E-01	8.95E-01	-	-
1383028_at	LOC315970	similar to CDV-3B	315970	Rn.8104	BE120656	8.58	8.71	8.47	9.00	8.86	9.60	1.48	up	7.43E-02	8.95E-01	-	-
1369459_at	Pip4k2b	phosphatidylinositol-5-phosphate 4-kinase, type II, beta	89812	Rn.30025	NM_053550	2.52	2.70	2.70	3.97	2.53	3.13	1.48	up	2.48E-01	8.95E-01	-	-
1374579_at	RGD1560873	similar to RIKEN cDNA E230015L20 gene	306238	---	BF281860	6.93	6.03	5.97	5.49	5.04	6.69	1.48	down	3.84E-01	8.95E-01	-	-
1392895_at	---	---	---	Rn.216496	BE101114	4.61	5.04	4.55	5.43	5.01	5.47	1.48	up	5.63E-02	8.95E-01	-	-
1381748_at	Raph1	Ras association (RalGDS/AF-6) and pleckstrin homology domains 1	363239	Rn.16844	BM383697	4.83	2.98	3.00	2.99	3.01	3.10	1.48	down	4.07E-01	8.95E-01	-	-
1370656_a_at	Homer1	homer homolog 1 (Drosophila)	29546	Rn.37500	AF093267	6.55	6.67	5.58	6.83	6.68	6.99	1.48	up	1.84E-01	8.95E-01	-	-
1383238_at	Qtrt1	queuine tRNA-ribosyltransferase 1	64016	Rn.53858	AI060136	3.01	3.60	2.85	3.57	4.06	3.53	1.48	up	1.17E-01	8.95E-01	-	-
1395361_at	Dut	Deoxyuridine triphosphatase	497778	Rn.6102	AW142913	2.61	2.60	2.62	2.52	3.89	3.12	1.48	up	2.25E-01	8.95E-01	-	-
1376497_a_at	Mettl1d1	methyltransferase 11 domain containing 1	305845	Rn.8815	BI274096	3.07	3.28	2.37	2.33	2.35	2.33	1.48	down	1.09E-01	8.95E-01	-	-
1377796_at	Fzd5	Frizzled homolog 5 (Drosophila)	317674	Rn.24792	AI234226	3.36	3.27	5.91	3.56	3.06	4.21	1.48	down	5.73E-01	8.95E-01	-	-
1382332_at	Stag2	stromal antigen 2	313304	Rn.29288	AI549167	5.96	6.13	6.91	5.10	6.13	6.07	1.48	down	2.70E-01	8.95E-01	-	-
1388517_at	Mrpl40	mitochondrial ribosomal protein L40	287962	Rn.3831	AI599474	5.32	6.67	6.25	6.79	6.30	6.86	1.48	up	2.64E-01	8.95E-01	-	-
1386922_at	Car2	carbonic anhydrase II	54231	Rn.26083	AI408948	7.50	8.10	8.03	6.94	7.76	7.21	1.48	down	1.39E-01	8.95E-01	-	-
1383616_at	Il10rb	interleukin 10 receptor, beta	304091	Rn.22261	AA997562	6.29	8.20	8.27	7.94	7.90	8.63	1.48	up	4.56E-01	8.95E-01	-	-
1377461_at	LOC680485	hypothetical protein LOC680485	680485	Rn.25200	AI409983	2.45	2.44	2.46	2.43	3.84	2.79	1.48	up	2.51E-01	8.95E-01	-	-
1382736_at	---	---	---	Rn.199574	AI407047	4.18	4.13	4.49	4.99	4.48	5.03	1.48	up	5.34E-02	8.95E-01	-	-
1380802_at	Snx8	sorting nexin 8	288504	Rn.19565	BM384243	3.06	3.48	4.04	4.90	2.92	4.47	1.48	up	4.42E-01	8.95E-01	-	-
1383389_at	Zer1	zer-1 homolog (C. elegans)	311842	Rn.23384	BM389790	5.41	4.44	4.81	4.67	4.21	4.07	1.48	down	1.67E-01	8.95E-01	-	-
1389453_at	Rdm1	RAD52 motif 1	287726	Rn.22736	AA818364	5.14	6.29	5.64	4.83	4.48	6.07	1.48	down	3.87E-01	8.95E-01	-	-
1382017_at	---	---	---	Rn.164833	AI012949	2.41	2.41	2.42	4.02	2.49	2.43	1.48	up	3.38E-01	8.95E-01	-	-
1368010_at	Ptpn6	protein tyrosine phosphatase, non-receptor type 6	116689	Rn.18985	NM_053908	3.03	4.07	3.88	4.72	3.86	4.10	1.48	up	2.39E-01	8.95E-01	-	-
1381356_at	Fam63b	family with sequence similarity 63, member B	363089	Rn.15746	AI639262	4.07	2.38	2.41	2.40	2.39	2.36	1.48	down	3.67E-01	8.95E-01	-	-
1390213_at	---	---	---	Rn.38416	BF388763	5.67	6.71	7.23	7.26	6.67	7.38	1.48	up	3.27E-01	8.95E-01	-	-
1376068_at	Prr12	Proline rich 12	361569	Rn.17162	BF283674	3.33	4.06	3.32	4.42	3.41	4.59	1.48	up	2.70E-01	8.95E-01	-	-
1370437_at	Nup1	nucleoporin like 1	245922	Rn.11099	U63839	5.35	4.63	5.34	4.54	4.47	4.60	1.48	down	7.59E-02	8.95E-01	-	-
1382009_at	Chd1	chromodomain helicase DN

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1373689_at	---	---	---	Rn.160502	BG379711	3.22	3.55	3.81	3.24	5.49	3.54	1.48	up	4.80E-01	8.95E-01	-	-
1388886_at	Rbm25	RNA binding motif protein 25	366693	Rn.95285	BM392240	4.87	6.18	5.66	5.83	3.47	5.73	1.48	down	5.47E-01	8.95E-01	-	-
1378104_at	RGD1307465	similar to RIKEN cDNA 8430406I07	296200	Rn.23965	AI105459	4.48	3.66	4.66	3.66	3.79	3.86	1.48	down	1.45E-01	8.95E-01	-	-
1378570_at	---	---	---	Rn.6539	AA849985	3.75	4.23	5.02	3.59	3.55	4.17	1.48	down	2.52E-01	8.95E-01	-	-
1370615_at	LOC286989	UDP-glucuronosyltransferase	286989	Rn.11131	U27518	5.72	3.99	4.63	5.08	3.81	3.77	1.48	down	4.44E-01	8.95E-01	-	-
1373133_at	Arl8b	ADP-ribosylation factor-like 8B	500282	Rn.6283	BF410786	7.80	8.50	8.59	8.61	9.14	8.83	1.48	up	1.27E-01	8.95E-01	-	-
1372969_at	Fbxl3	F-box and leucine-rich repeat protein 3	306129	Rn.36356	BI289651	6.50	7.68	7.22	6.62	6.37	6.72	1.48	down	1.92E-01	8.95E-01	-	-
1373736_at	---	---	---	Rn.13717	AI178446	5.28	6.50	6.46	6.94	6.16	6.83	1.48	up	2.98E-01	8.95E-01	-	-
1388532_at	RGD1310571	similar to hypothetical protein	361301	Rn.54973	AI599496	2.53	3.05	3.01	2.66	3.99	3.63	1.48	up	2.61E-01	8.95E-01	-	-
1374638_at	Pex13	peroxisomal biogenesis factor 13	305581	Rn.218543	AI010951	8.24	8.06	8.38	7.46	7.58	7.96	1.48	down	3.24E-02	8.95E-01	-	-
1387382_at	Hmmt	histamine N-methyltransferase	81676	Rn.13145	NM_031044	9.98	10.91	10.52	9.80	9.61	10.32	1.48	down	1.76E-01	8.95E-01	-	-
1374285_at	---	---	---	Rn.203820	AW531275	6.34	5.66	5.27	6.81	6.31	5.83	1.48	up	2.55E-01	8.95E-01	-	-
1377865_at	---	---	---	Rn.7900	AI411393	3.63	3.57	4.88	4.96	4.32	4.49	1.48	up	2.98E-01	8.95E-01	-	-
1397874_at	Lsm11	LSM11, U7 small nuclear RNA associated	501688	Rn.40966	AI548493	3.83	2.52	2.62	3.24	4.17	3.24	1.48	up	3.43E-01	8.95E-01	-	-
1373887_at	Sf3b1	splicing factor 3b, subunit 1	84486	Rn.198843	BF523561	5.16	5.44	5.23	6.17	5.61	5.74	1.48	up	4.01E-02	8.95E-01	-	-
1377427_at	Ptpn14	Protein tyrosine phosphatase, non-receptor type 14	305064	Rn.61099	BE104739	3.35	3.58	2.58	2.60	2.59	2.63	1.48	down	1.35E-01	8.95E-01	-	-
1375705_at	---	---	---	Rn.164619	AI103622	7.97	8.09	7.34	8.27	8.48	8.32	1.48	up	8.22E-02	8.95E-01	-	-
1392514_at	Bxdc1	brix domain containing 1	294436	Rn.25279	BE095565	5.42	5.72	7.00	6.95	5.96	6.91	1.48	up	3.91E-01	8.95E-01	-	-
1382186_a_at	Gpatch4	G patch domain containing 4	295228	Rn.20166	AI136314	3.59	5.74	6.32	4.83	6.68	5.83	1.48	up	6.01E-01	8.95E-01	-	-
1388851_at	Hspa9	heat shock protein 9	291671	Rn.7535	BI282281	8.47	9.14	9.43	9.19	9.50	10.02	1.48	up	2.08E-01	8.95E-01	-	-
1393032_x_at	Rab5	RAB, member RAS oncogene family-like 5	288585	Rn.36074	BI290033	4.32	3.83	3.48	4.68	4.09	4.55	1.48	up	1.37E-01	8.95E-01	-	-
1373244_at	Tmub2	transmembrane and ubiquitin-like domain containing 2	303567	Rn.143886	AI412948	4.49	5.39	5.40	5.23	5.40	6.34	1.48	up	2.88E-01	8.95E-01	-	-
1383077_at	Bsdc1	BSD domain containing 1	297890	Rn.3404	BI287209	8.00	7.97	7.97	7.84	6.63	7.79	1.48	down	2.27E-01	8.95E-01	-	-
1368928_at	Trim3	tripartite motif-containing 3	83616	Rn.203982	NM_031786	3.42	2.66	2.77	2.46	2.34	2.37	1.48	down	7.79E-02	8.95E-01	-	-
1396444_at	Mrpl12	mitochondrial ribosomal protein L12	303746	Rn.105932	BF524934	4.71	5.71	5.83	6.36	5.71	5.86	1.48	up	2.39E-01	8.95E-01	-	-
1371749_at	RGD1306001	similar to 2210021J22Rik protein	362975	Rn.3452	AI169439	5.33	5.32	5.33	5.33	6.61	5.73	1.48	up	2.12E-01	8.95E-01	-	-
1374155_at	---	---	---	Rn.33247	BF410502	4.38	2.91	2.68	2.80	2.61	2.88	1.48	down	3.57E-01	8.95E-01	-	-
1377032_at	---	---	---	Rn.166390	AI103506	3.48	3.47	3.64	3.57	5.16	3.54	1.48	up	3.55E-01	8.95E-01	-	-
1375345_at	Cnpy2	canopy 2 homolog (zebrafish)	685814	Rn.40568	AW919569	6.96	7.44	8.00	7.44	8.22	8.42	1.48	up	2.57E-01	8.95E-01	-	-
1371991_at	RGD1311249	Similar to RIKEN cDNA B230312A22	298201	Rn.63818	AA894318	5.95	6.11	8.13	7.09	5.11	6.31	1.48	down	5.70E-01	8.95E-01	-	-
1379558_at	LOC680222	similar to zinc finger protein 748 isoform 2	680222	---	AA957033	7.19	8.11	8.10	7.82	5.88	8.02	1.48	down	4.94E-01	8.95E-01	-	-
1398354_at	Ctnnal1	catenin (cadherin associated protein), alpha-like 1	298019	Rn.33021	AI555457	3.03	3.92	4.19	4.06	4.57	4.19	1.48	up	2.17E-01	8.95E-01	-	-
1383027_at	---	---	---	Rn.164622	AA900262	2.51	2.47	2.51	2.47	4.26	2.45	1.48	up	4.05E-01	8.95E-01	-	-
1374562_at	RGD1311429	similar to KIAA1267 protein	360642	Rn.24932	AI177115	7.27	6.53	7.19	8.80	6.15	6.36	1.47	down	1.40E-01	8.95E-01	-	-
1383679_at	Rnf31	ring finger protein 31	364386	Rn.138034	BF411972	3.36	3.17	2.66	4.00	3.22	3.65	1.47	up	1.45E-01	8.95E-01	-	-
1370890_at	Actr3	ARP3 actin-related protein 3 homolog (yeast)	81732	Rn.103326	BI292004	8.93	8.48	8.98	8.26	8.06	8.39	1.47	down	3.92E-02	8.95E-01	-	-
1392352_at	---	---	---	Rn.147865	AW521481	3.13	3.32	3.57	4.81	3.52	3.36	1.47	up	3.04E-01	8.95E-01	-	-
1379062_at	LOC100151767	hypothetical LOC100151767	100151767	Rn.159880	BI291230	7.50	8.31	7.43	8.42	7.69	8.90	1.47	up	3.00E-01	8.95E-01	-	-
1388444_at	Ubxn4	UBX domain protein 4	304766	Rn.2022	BI291633	8.25	8.57	8.21	8.83	8.72	9.17	1.47	up	3.33E-02	8.95E-01	-	-
1378776_at	Pou6f1	POU class 6 homeobox 1	116545	Rn.44845	BE097103	2.54	2.55	2.45	3.32	2.46	3.44	1.47	up	1.45E-01	8.95E-01	-	-
1378216_at	---	---	---	Rn.203997	BM387900	5.19	6.49	5.21	6.52	6.33	5.72	1.47	up	3.21E-01	8.95E-01	-	-
1388303_at	Rpl26	ribosomal protein L26	287417	Rn.144702	AI598536	11.19	11.33	11.10	11.57	11.65	12.09	1.47	up	3.37E-02	8.95E-01	-	-
1371410_at	RGD1564058	similar to cDNA sequence BC056474	288925	Rn.98317	AI599071	5.77	5.47	4.36	5.92	5.46	5.90	1.47	up	2.84E-01	8.95E-01	-	-
1389193_at	Sorcs2	sortilin-related VPS10 domain containing receptor 2	305438	Rn.41133	BM388083	3.09	4.36	4.27	3.26	3.48	3.30	1.47	down	2.50E-01	8.95E-01	-	-
1381871_at	---	---	---	Rn.201838	BM383359	7.28	6.62	5.06	7.10	6.95	6.58	1.47	up	4.53E-01	8.95E-01	-	-
1384438_at	---	---	---	---	AA924634	6.20	7.50	7.30	7.62	7.68	7.38	1.47	up	2.49E-01	8.95E-01	-	-
1396279_at	Atp6ap2	ATPase, H+ transporting, lysosomal accessory protein 2	302526	Rn.12944	BG663051	7.29	7.26	4.90	7.49	6.46	7.18	1.47	up	5.46E-01	8.95E-01	-	-
1398609_at	Ubox5	U-box domain containing 5	296161	Rn.16485	BI288829	3.64	3.77	3.14	4.06	4.15	4.01	1.47	up	4.53E-02	8.95E-01	-	-
1375656_at	Tecpr1	tectonin beta-propeller repeat containing 1	304285	Rn.162096	AI717725	5.84	4.01	3.62	3.79	3.80	4.20	1.47	down	4.66E-01	8.95E-01	-	-
1394438_at	Actr1a	ARP1 actin-related protein 1 homolog A, centractin alpha (yeast)	294010	Rn.32312	BI294346	4.63	5.73	5.80	6.16	5.80	5.88	1.47	up	2.30E-01	8.95E-01	-	-
1386229_at	---	---	---	Rn.129730	AA998453	2.58	2.49	2.55	3.28	3.12	2.88	1.47	up	9.34E-03	8.95E-01	-	-
1374561_at	RGD1309634	hypothetical LOC305452	305452	Rn.7798	AW523899	5.90	6.79	5.91	6.97	6.68	6.63	1.47	up	1.48E-01	8.95E-01	-	-
1382831_at	Dusp18	dual specificity phosphatase 18	305477	Rn.19584	AI071054	2.32	3.08	2.33	2.40	3.85	3.14	1.47	up	3.16E-01	8.95E-01	-	-
1388063_a_at	Pfkfb2	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 2	24640	Rn.44844	AB040532	2.43	4.23	3.28	2.43	2.96	2.88	1.47	down	3.64E-01	8.95E-01	-	-
1385401_at	---	---	---	---	BI290381	4.32	3.04	4.60	4.45	5.13	4.06	1.47	up	3.83E-01	8.95E-01	-	-
1378721_at	---	---	---	Rn.205762	AI547942	2.54	2.52	2.54	2.80	3.97	2.51	1.47	up	2.79E-01	8.95E-01	-	-
1384675_at	Apeg3	antisense paternally expressed gene 3	619476	Rn.49740	AI029113	5.18	5.96	4.77	5.82	6.59	5.18	1.47	up	3.55E-01	8.95E-01	-	-
1388965_at	Ppp2r5e	protein phosphatase 2, regulatory subunit B', epsilon isoform	299147	Rn.24394	AI144683	6.65	6.12	7.40	5.85	6.11	6.55	1.47	down	2.58E-01	8.95E-01	-	-
1398749_at	Rpl4	ribosomal protein L4	64302	Rn.1133	NM_022510	10.03	10.46	9.91	10.56	10.52	10.99	1.47	up	6.81E-02	8.95E-01	-	-
1370643_a_at	Kalrn	kalirin, RhoGEF kinase	84009	Rn.87882	AF230644	2.37	2.48	2.48	3.99	2.35	2.66	1.47	up	3.29E-01	8.95E-01	-	-
1367832_at	Lypla1	lysophospholipase 1	25514	Rn.3594	NM_013006	9.23	9.10	9.75	8.82	8.73	8.86	1.47	down	5.04E-02	8.95E-01	-	-
1380993_at	Fam20b	family with sequence similarity 20, member B	304885	Rn.34667	AI496057	7.71	8.69	8.61	7.91	7.40	8.02	1.47	down	2.04E-01	8.95E-01	-	-
1380464_at	---	---	---	Rn.139089	AI145031	4.29	2.85	3.35	2.84	2.93	3.05	1.47	down	2.59E-01	8.95E-01	-	-
1372256_at	Crip	cysteine-rich intestinal protein	691657	Rn.8405	BF550246	4.40	6.12	2.51	4.42	2.97	3.96	1.47	down	6.47E-01	8.95E-01	-	-
1389493_at	Ankb1	ankyrin repeat and BTB (POZ) domain containing 1	297432	Rn.40721	AI411278	4.62	5.15	4.08	5.13	5.15	5.23	1.47	up	1.49E-01	8.95E-01	-	-
1397991_at	---	---	---	Rn.199968	BF409291	3.90	2.67	2.47	2.47	2.46	2.44	1.47	down	2.80E-01	8.95E-01	-	-
1393059_at	Zpf799	zinc finger protein 799	494339	Rn.24086	AI137360	2.57	3.29	3.47	5.01	2.46	3.53	1.47	up	5.19E-01	8.95E-01	-	-
1373938_at	Wdr24	WD repeat domain 24	360497	Rn.20330	BF284753	5.85	5.04	4.07	4.86	3.36	5.07	1.47	down	4.95E-01	8.95E-01	-	-
1372926_at	Timp3	TIMP metallopeptidase inhibitor 3	25350	Rn.119634	AI009159	9.65	9.55	9.92	9.38	9.36	8.71	1.47	down	8.50E-02	8.95E-01	-	-
1388271_at	Mt2A	metallothionein 2A	689415	Rn.115549	BM383531	11.70	11.22	11.31	11.05	10.50	11.00	1.47	down	7.11E-02	8.95E-01	-	-
1393239_at	Mtfr1	Mitochondrial fission regulator 1	311403	Rn.14754	BI296413	7.40	8.13	8.75	7.40	7.38	7.82	1.47	down	2.52E-01	8.95E-01	-	-
1376615_at	Tead3	TEA domain family member 3	294299	Rn.198098	BI289650	6.79	4.17	4.88	3.81	5.33	5.04	1.47	down	5.73E-01	8.95E-01	-	-
1370089_at	Ppargc1a	peroxisome proliferator-activated receptor gamma, coactivator 1 alpha	83516	Rn.19172	NM_031347	6.89	6.13	7.22	6.15	5.98	6.43	1.47	down	1.87E-01	8.95E-01	-	-
1396298_at	---	---	---	Rn.176549	BI298052	5.99	2.90	4.32	4.53	2.72	4.29	1.47	down	6.27E-01	8.95E-01	-	-
1375556_at	Tbx2	T-box 2	303398	Rn.38282	AI602844	3.99	2.91	2.72	2.67	2.68	2.61	1.47	down	2.29E-01	8.95E-01	-	-
1380827_at	RGD1307890	similar to C1orf25	304851	Rn.16683	AA819867	4.24	4.82	5.44	3.32	5.34	4.17	1.47	up	4.59E-01	8.95E-01	-	-
1399158_a_at	Npm1	nucleophosmin (nucleolar phosphoprotein B23, numatrin)	25498	Rn.54537	J04943	11.86	11.63	11.22	12.00	12.15	12.21	1.47	up	4.74E-02	8.95E-01	-	-
1377617_at	Pura	purine rich element binding protein A	307498	Rn.41055	BF550438	4.95	6.29	6.84	5.64	7.36	6.75	1.47	up	5.01E-01	8.95E-01	-	-
1375760_at	---	---	---	Rn.165692	AI070270	5.65	5.45	4.32	6.08	5.61	5.50	1.47	up	2.89E-01	8.95E-01	-	-
1376298_at	Upf3b	UPF3 regulator of nonsense transcripts homolog B (yeast)	313449	Rn.29454	AW525099	4.94	5.25	3.80	5.44	5.42	4.80	1.47	up	3.18E-01	8.95E-01	-	-
1373950_at	Znf496	zinc finger protein 496	287361	Rn.13860	AI598911	4.47	6.57	6.90	5.58	7.57	6.45	1.47	up	5.91E-01	8.95E-01	-	-
1370592_at	Keg1	kidney expressed gene 1	171179	Rn.22745	AB019693	4.50	5.41	5.20	6.22	5.25	5.31	1.47	up	2.55E-01	8.95E-01	-	-
1398871_at	Rpl17	ribosomal protein L17	291434	Rn.34429	BG671311	11.15	11.54	11.30	11.74	11.77	12.15	1.47	up	3.34E-02	8.95E-01	-	-
1382791_at	---	---	---	Rn.16246	AI716238	2.72	3.53	4.58	3.46	4.97	4.08	1.47	up	4.67E-01	8.95E-01	-	-
1374549_at	Rbm4b	RNA binding motif protein 4B	474154	Rn.203522	AI317860	4.24	4.55	4.03	3.90	3.24	4.00	1.47	down	1.20E-01	8.95E-01	-	-
1367750_at	Prpsap1	phosphoribosyl pyrophosphate synthetase-associated protein 1	64390	Rn.2290	NM_022545	5.01	6.75	6.63	6.93	6.39	6.74	1.47	up	3.93E-01	8.95E-01	-	-
1373792_at	Actr1b	ARP1 actin-related protein 1 homolog B (yeast)	316333	Rn.24317	AI228348	7.40	8.31	7.83	8.28	8.42	8.52	1.47	up	1.11E-01	8.95E-01	-	-
1390508_at	---	---	---	Rn.1589	BI284393	5.66	5.65	3.94	6.02	5.46	5.44	1.47	up	4.09E-01	8.95E-01	-	-
1386006_at	Larp7	La ribonucleoprotein domain family, member 7	686883	Rn.168323	AA866456	6.32	5.62	5.73	6.43	3.07	6.49	1.47	down	6.54E-01	8.97E-01	-	-
1373764_at	Zfml	zinc finger, matrin-like	312491	Rn.15272	AI235272	9.07	8.95	9.16	8.45	8.35	8.71	1.47	down	1.04E-02	8.95E-01	-	-
1381985_at	Tia1	TIA1 cytotoxic granule-associated RNA binding protein	312510	Rn.198158	AI412335	2.34	2.30	2.32	2.36	3.94	2.33	1.47	up	3.55E-01	8.95E-01	-	-
1379730_at	Atp6v1h	ATPase, H+ transporting, lysosomal V1 subunit H	297797	Rn.21454	AA942681	6.43	6.39	6.59	5.54	5.46	6.74	1.47	down	2.56E-01	8.95E-01	-	-
1372994_at	Fance	Fanconi anemia, complementation group E	309643	Rn.2861	AA875278	2.87	2.96	3.02	3.96	3.57	2.99	1.47	up	1.23E-01	8.95E-01	-	-
1376781_at	---	---	---	Rn.204749	BI286116	6.88	6.26	6.48	6.15	6.07	5.73	1.47	down	6.63E-02	8.95E-01	-	-
1373186_at	Slain2	SLAIN motif family, member 2	305310	Rn.23030	AI176617	5.34	5.56	6.05	6.49	5.63	6.49	1.47	up	1.95E-01	8.95E-01	-	-
1377283_at	Hps4	Hermansky-Pudlak syndrome 4 homolog (human)	304555	Rn.18930	BI274486	4.28	4.50	6.39	3.89	4.07	5.54	1.47	down	5.49E-01	8.95E-01	-	-
1376591_a_at	Tmem179b	transmembrane protein 179B	690263	Rn.103195	AA800172	3.69	3.82	3.25	4.22	4.11	4.09	1.47	up	3.54E-02	8.95E-01	-	-
1374379_at	---	---	---	Rn.45931	BF396810	2.72	2.70	2.68	4.14	2.96	2.67	1.47	up	2.84E-01	8.95E-01	-	-
1387646_a_at	Max	MYC associated factor X	60661	Rn.4210	NM_022210	7.21	9.24	8.46	8.71	8.49	8.38	1.47	up	4.41E-01	8.95E-01	-	-
1382914_at	---	---	---	Rn.15266	AA924097	3.73	4.75	5.19	5.14	4.77	5.43	1.47	up	3.05E-01	8.95E-01	-	-
1388424_at	Eif3j	eukaryotic translation initiation factor 3, subunit J	691947	Rn.162681	AI407015	7.90	8.49	7.95	8.50	8.68	8.83	1.47	up	5.90E-02	8.95E-01	-	-
1388403_at	Idh2	isocitrate dehydrogenase 2 (NADP+), mitochondrial	361596	Rn.3490	AI172491	11.32	10.13	10.66	10.29	10.20	9.97	1.47	down	1.96E-01	8.95E-01	-	-
1372533_at	Edem1	ER degradation enhancer, mannosidase alpha-like 1	297504	Rn.8162	AI176790	7.59	7.13	6.91	7.34	7.51	8.44	1.47	up	2.35E-01	8.95E-01	-	-
1367720_at	Alad	aminolevulinate, delta-, dehydratase	25374	Rn.3941	NM_012899	6.69	6.77	6.91	6.25	6.34	6.12	1.47	down	3.50E-03	8.95E-01	-	-
1371853_at	Mrpl42	mitochondrial ribosomal protein L42	299743	Rn.11	AI176602	9.00	8.92	9.28	8.34	8.46	8.74	1.47	down	2.66E-02	8.95E-01	-	-
1398531_at	---	---	---	Rn.15770	AI058947	4.42	5.78	5.28	5.40	5.17	6.56	1.47	up	3.98E-01	8.95E-01	-	-
1376878_at	RGD1559896	similar to RIKEN cDNA 2310022B05	498967	Rn.6137	AI103552	5.13	4.61	4.65	4.62	4.53	3.58	1.47	down	2.11E-01	8.95E-01	-	-
1385158_at	Chmp1b	chromatin modifying protein 1B	689364	Rn.39132	BI301125	6.11	5.62	7.03	6.18	7.06	7.18	1.47	up	3.46E-01	8.95E-01	-	-
1386643_at	Fem1b	feminization 1 homolog b (C. elegans)	315745	Rn.219320	BF552914	4.99	5.21	5.69	5.73	6.44	5.39	1.47	up	2.10E-01	8.95E-01	-	-
1398066_at	EUBR1	EUBR1	313858	Rn.37755	AI556149	2.53	2.49	2.54	4.30	2.50	2.42	1.47	up	4.19E-01	8.95E-01	-	-
1374695_at	Cbx1	chromobox homolog 1 (HP1 beta homolog Drosophila)	360609	Rn.32816	BF564593	7.87	7.73	9.46	7.88	7.69	7.84	1.47	down	3.77E-01	8.95E-01	-	-
1380610_at	---	---	---	Rn.169276	AI406521	7.08	7.58	7.23	7.50	7.69	8.37	1.47	up	1.40E-01	8.95E-01	-	-
1393905_at	Fam149a	family with sequence similarity 149, member A	361153	Rn.201721	AA962978	9.22	8.96	7.03	8.04	7.63	7.88	1.47	down	4.75E-01	8.95E-01	-	-
1388899_at	---	---	---	Rn.25434	BE098818	2.97	3.52	2.72	2.68	2.61	2.26	1.47	down	1.11E-01	8.95E-01	-	-
1389143_at	Pik3ca	Phosphatidylinositol 3-kinase, catalytic, alpha polypeptide	170911	Rn.44193	BF288139	5.75	5.85	6.74	5.66	4.74	6.27	1.47	down	3.67E-01	8.95E-01	-	-
1398401_at	Tdrd3	tudor domain containing 3	306066	Rn.18991	AI412183	7.10	6.48	6.37	5.56	6.37	6.36	1.47	down	1.90E-01	8.95E-01	-	-
1378162_at	---	---	---	Rn.165888	AI045884	2.39	2.37	2.43	2.55	3.94	2.36	1.47	up	3.28E-01	8.95E-01	-	-
1377624_at	Glpbp10	GTP-binding protein 10 (putative)	312054	Rn.139851	BI303922	4.96	6.90	5.13	6.50	5.71	6.44	1.47	up	4.54E-01	8.95E-01	-	-
1390661_at	---	---	---	Rn.203846	BE115928	3.93	3.56	6.69	4.48	3.18	4.85	1.47	down	6.44E-01	8.95E-01	-	-
1369788_s_at	Jun	Jun oncogene	24516	Rn.9374	NM_021835	6.40	6.14	7.45	6.62	7.22	7.80	1.47	up	3.55E-01	8.95E-01	-	-
1386125_at	Hoxb4	homeo box B4	497988	Rn.209614	BF389738	6.65	5.83	6.59	5.76	5.52	6.13	1.47	down	1.59E-01	8.95E-01	-	-
1373883_at	Cdadc1	cytidine and dCMP deaminase domain containing 1	361052	Rn.76647	BE102485	4.96	6.01	5.30	5.07	5.90	6.95	1.47	up	4.28E-01	8.95E-01	-	-
1396180_at	Lrrc16a	leucine rich repeat containing 16A	306941	Rn.40387	AA997691	2.94	4.10	2.95	2.93	2.66	2.74	1.47	down	2.34E-01	8.95E-01	-	-
1391893_at	Clp1	cleavage and polyadenylation factor I subunit, homolog (S. cerevisiae)	311166	Rn.144332	AI501557	2.35	2.34	2.39	2.44	3.51	2.79	1.47	up	1.56E-01	8.95E-01	-	-
1368195_at	Hspbap1	Hspb associated protein 1	171460	Rn.37915	NM_134419	5.62	4.48	4.00	4.08	4.45	3.93	1.47	down	3.34E-01	8.95E-01	-	-
1383573_at	Tshz1	teashirt zinc finger homeobox 1	307217	Rn.205514	BE117444	6.30	5.71	6.76	5.45	5.48	6.17	1.47	down	2.24E-01	8.95E-01	-	-
1373306_at	Slc25a44	solute carrier family 25, member 44	365841	Rn.18145	BM386212	7.25	7.03	7.42	6.41	6.60	7.03	1.47	down	6.33E-02	8.95E-01	-	-
1379498_at	---	---	---	Rn.48269	AW534136	4.92	4.74	2.40	4.74	4.82	4.16	1.47	up	5.46E-01	8.95E-01	-	-
1369967_at	Cs	citrate synthase	170587	Rn.66581	NM_130755	6.59	6.37	6.23	5.59	5.70	6.25	1.47	down	7.42E-02	8.95E-01	-	-
1388176_at	Cml5	cameloid-like 5	114020	Rn.205673	AI710047	9.17	8.76	9.25	10.16	8.93	9.75	1.47	up	2.30E-01	8.95E-01	-	-
1368866_at	Eif2c2	eukaryotic translation initiation factor 2C, 2	59117	Rn.35512	BF281131	2.46	2.38	4.79	2.71	2.38	2.89	1.47	down	5.30E-01	8.95E-01	-	-
1398054_at	306556 /// RGD15	similar to hypothetical protein A530094D01 /// similar to OTTHUMP00000028784	498144 /// 360825	Rn.138867	BF393118	2.34	2.33	3.99	2.33	2.34	2.33	1.47	down	3.73E-01	8.95E-01	-	-
1375951_at	Thbd	thrombomodulin	83580	Rn.88295	AA818521	2.59	2.37	3.82	2.37	2.39	2.36	1.47	down	2.88E-01	8.95E-01	-	-
1385423_at	Immt	inner membrane protein, mitochondrial	312444	Rn.47124	AW521399	9.27	8.37	8.01	8.05	7.41	8.54	1.47	down	3.31E-01	8.95E-01	-	-
1378890_at	---	---	---	Rn.33007	BF408090	2.50	2.50	2.53	2.47	2.52	4.19	1.47	up	3.85E-01	8.95E-01	-	-
1369130_at	Rasgrp1	RAS guanyl releasing protein 1 (calcium and DAG-regulated)	29434	Rn.162685	AF081196	4.01	2.43	2.43	2.41	2.42	2.39	1.47	down	3.53E-01	8.95E-01	-	-
1386856_a_at	Samd4b	sterile alpha motif domain containing 4B	308475	Rn.40291	AA859633	6.06	5.82	4.46	4.64	5.78	5.59	1.47	up	4.05E-01	8.95E-01	-	-
1379438_at	Smarcad1	SWI/SNF-related, matrix-associated actin-dependent regulator of chromatin,	312398	Rn.7758	AA944576	5.32	4.59	6.08	5.19	3.98	5.16	1.47	down	4.01E-01	8.95E-01	-	-
1393492_at	---	---	---	Rn.199822	BE107812	4.90	6.26	5.66	6.18	5.69	6.60	1.47	up	3.08E-01	8

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1374145_at	Pih1d1	PIH1 domain containing 1	292898	Rn.155172	BF414252	2.85	4.63	2.84	3.85	3.76	4.34	1.46	up	4.29E-01	8.95E-01	-	-
1382265_at	Gcap14	granule cell antiserum positive 14	306306	Rn.96252	AI070061	9.22	9.06	8.84	8.03	7.91	9.54	1.46	down	3.66E-01	8.95E-01	-	-
1381989_at	---	---	---	---	BI280114	6.14	6.99	7.01	7.01	7.54	7.24	1.46	up	1.67E-01	8.95E-01	-	-
1368578_at	Hsd3b1	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase	360348	Rn.128814	NM_017265	3.35	4.07	5.10	2.84	3.51	4.53	1.46	down	4.83E-01	8.95E-01	-	-
1388799_at	Klhl7	kelch-like 7 (Drosophila)	362303	Rn.8854	BG374559	6.88	6.74	7.14	6.11	5.83	7.17	1.46	down	2.67E-01	8.95E-01	-	-
1382310_at	RGD1563296	similar to component of oligomeric golgi complex 5 isoform 1	314030	---	AA849263	4.08	4.83	4.64	4.85	5.25	5.10	1.46	up	9.67E-02	8.95E-01	-	-
1380015_at	---	---	---	Rn.210673	BF404338	3.78	3.09	2.62	3.80	2.59	4.74	1.46	up	4.83E-01	8.95E-01	-	-
1379814_at	---	---	---	Rn.14694	AW532796	6.65	5.60	5.90	5.88	5.51	5.12	1.46	down	2.22E-01	8.95E-01	-	-
1367946_at	Pdlim1	PDZ and LIM domain 1	54133	Rn.11170	NM_017365	2.99	4.27	3.01	4.68	3.42	3.81	1.46	up	3.88E-01	8.95E-01	-	-
1368772_at	Lsm8	LSM8 homolog, U8 small nuclear RNA associated (S. cerevisiae)	296913	Rn.14059	AI770716	6.99	8.06	8.31	8.10	8.35	8.57	1.46	up	2.70E-01	8.95E-01	-	-
1390592_at	LOC688018	Similar to SH3-domain binding protein 3	688018	Rn.162688	BM389412	4.33	6.64	6.02	6.30	5.80	6.54	1.46	up	4.93E-01	8.95E-01	-	-
1374185_at	Txndc11	thioredoxin domain containing 11	302899	Rn.54595	AI232819	5.21	5.69	5.18	5.83	5.70	6.19	1.46	up	6.85E-02	8.95E-01	-	-
1379685_at	Sfrs15	splicing factor, arginine/serine-rich 15	245924	Rn.101886	AI502753	5.77	6.71	6.19	6.62	6.58	7.12	1.46	up	1.69E-01	8.95E-01	-	-
1393274_at	RGD1311578	similar to PRO1853 homolog	298748	Rn.27740	AI059798	2.42	3.24	3.17	2.39	2.40	2.39	1.46	down	1.06E-01	8.95E-01	-	-
1377899_at	RGD1304982	similar to RIKEN cDNA 2810025M15	289138	Rn.198952	BF419886	8.63	8.89	8.44	8.08	7.98	8.26	1.46	down	2.49E-02	8.95E-01	-	-
1380728_at	---	---	---	Rn.217555	BE118404	4.74	4.63	3.98	5.34	4.79	4.86	1.46	up	1.39E-01	8.95E-01	-	-
1393140_at	Zc3h12a	zinc finger CCCH type containing 12A	313587	Rn.93819	AI574699	4.35	2.72	2.76	2.73	2.74	2.71	1.46	down	3.67E-01	8.95E-01	-	-
1396197_at	Zdhhc5	Zinc finger, DHHC-type containing 5	362156	Rn.4240	BF547499	7.13	5.51	5.94	6.08	5.44	5.42	1.46	down	3.60E-01	8.95E-01	-	-
1393806_at	Mansc1	MANSC domain containing 1	690606	Rn.155646	BE107400	4.02	4.15	2.75	3.89	2.70	2.69	1.46	down	4.13E-01	8.95E-01	-	-
1372044_at	RGD1310348	similar to Ser/Thr-rich protein T10 in DGCR region	360738	Rn.101776	AI410321	4.71	4.89	3.29	5.28	4.19	5.06	1.46	up	4.18E-01	8.95E-01	-	-
1387772_at	Eif4a2	Eukaryotic translation initiation factor 4A2	303831	Rn.143972	BF558764	8.70	9.72	8.25	8.85	8.44	7.75	1.46	down	3.68E-01	8.95E-01	-	-
1371506_at	---	---	---	Rn.163645	AA891207	5.83	6.03	5.07	5.99	6.17	6.40	1.46	up	1.58E-01	8.95E-01	-	-
1372357_at	---	---	---	Rn.1185	BI281833	4.34	3.90	4.08	5.12	4.88	3.95	1.46	up	2.24E-01	8.95E-01	-	-
1370003_at	Eef2	eukaryotic translation elongation factor 2	29565	Rn.55145	NM_017245	9.92	10.11	9.68	10.47	10.22	10.66	1.46	up	3.77E-02	8.95E-01	-	-
1382142_at	---	---	---	Rn.3724	AI029975	2.81	2.59	2.62	3.18	3.36	3.12	1.46	up	5.50E-03	8.95E-01	-	-
1377328_at	---	---	---	---	BI290012	3.54	2.45	3.79	2.46	2.47	3.22	1.46	down	3.22E-01	8.95E-01	-	-
1374403_at	---	---	---	---	H35017	4.31	4.60	4.86	5.38	5.29	4.74	1.46	up	1.00E-01	8.95E-01	-	-
1375194_at	---	---	---	Rn.12107	AI231460	3.29	3.95	3.80	3.00	5.36	4.32	1.46	up	4.85E-01	8.95E-01	-	-
1389520_at	Wdr1	WD repeat domain 1	360950	Rn.3168	BI285874	5.60	6.15	6.05	5.42	5.28	5.47	1.46	down	3.67E-02	8.95E-01	-	-
1384323_at	Psmc6	proteasome (prosome, macropain) 26S subunit, ATPase, 6	289990	Rn.103233	BF418369	8.36	8.60	8.91	7.27	8.41	8.55	1.46	down	2.78E-01	8.95E-01	-	-
1374715_at	Wdr70	WD repeat domain 70	294783	Rn.17260	BE097245	4.37	5.53	3.58	4.52	4.95	5.65	1.46	up	4.53E-01	8.95E-01	-	-
1389011_at	Nsmce2	non-SMC element 2, MMS21 homolog (S. cerevisiae)	299957	Rn.203454	BG374333	6.07	6.75	5.01	6.14	6.05	7.26	1.46	up	4.42E-01	8.95E-01	-	-
1394086_at	Senp7	SUMO1/sentrin specific protease 7	288167	Rn.162010	AI069981	3.74	5.26	5.96	5.15	5.52	5.92	1.46	up	4.74E-01	8.95E-01	-	-
1394626_at	Hmbox1	homeobox containing 1	365968	Rn.137881	AW557544	3.20	3.42	3.37	4.15	3.48	3.99	1.46	up	6.37E-02	8.95E-01	-	-
1385811_at	Hira	HIR histone cell cycle regulation defective homolog A (S. cerevisiae)	363849	Rn.14920	BF555598	4.12	2.48	2.51	2.49	2.50	2.48	1.46	down	3.71E-01	8.95E-01	-	-
1385678_at	Polk	polymerase (DNA directed) kappa	171525	Rn.92419	BG372536	2.75	3.32	3.70	2.60	2.76	2.78	1.46	down	1.25E-01	8.95E-01	-	-
1387941_s_at	Pla2g6	phospholipase A2, group VI (cytosolic, calcium-independent)	360426	Rn.44692	U51898	5.51	6.69	6.01	5.52	5.53	5.52	1.46	down	1.86E-01	8.95E-01	-	-
1374822_at	---	---	---	Rn.203181	BE118465	4.74	4.52	5.00	4.47	4.19	3.98	1.46	down	5.11E-02	8.95E-01	-	-
1375597_at	---	---	---	Rn.211310	BI300655	2.69	2.68	2.74	2.80	4.24	2.71	1.46	up	3.34E-01	8.95E-01	-	-
1368867_at	Eif2c2	eukaryotic translation initiation factor 2C, 2	59117	Rn.35512	BF281131	3.52	3.80	3.21	5.56	3.33	3.27	1.46	up	5.20E-01	8.95E-01	-	-
1374817_at	---	---	---	Rn.19071	BE103235	3.27	4.43	3.28	3.30	4.26	5.05	1.46	up	4.40E-01	8.95E-01	-	-
1380229_at	Maff	v-maf musculoaponeurotic fibrosarcoma oncogene homolog F (avian)	366960	Rn.31639	AW530004	3.21	5.13	5.79	4.46	3.08	4.96	1.46	down	5.99E-01	8.95E-01	-	-
1391791_at	Acer2	alkaline ceramidase 2	313339	Rn.6387	AI137826	4.77	3.30	3.12	3.09	3.39	3.08	1.46	down	3.62E-01	8.95E-01	-	-
1383311_at	Mtmr11	Myotubularin related protein 11	689613	Rn.103871	AI716026	5.22	4.46	4.24	5.82	4.61	5.12	1.46	up	3.01E-01	8.95E-01	-	-
1395164_at	---	---	---	---	AI549495	4.74	3.58	3.85	3.74	3.75	3.04	1.46	down	2.65E-01	8.95E-01	-	-
1393836_at	Mitf	microphthalmia-associated transcription factor	25094	Rn.207359	BE097933	3.32	3.18	3.60	3.87	4.35	3.52	1.46	up	1.14E-01	8.95E-01	-	-
1377728_at	RGD1565641	RGD1565641	499567	Rn.145579	BI280802	8.63	9.31	8.51	9.13	9.39	9.57	1.46	up	1.24E-01	8.95E-01	-	-
1398374_at	Lrrc57	leucine rich repeat containing 57	311346	Rn.101996	BE101274	6.54	6.23	5.74	5.85	6.29	6.01	1.46	up	5.77E-01	8.95E-01	-	-
1376984_at	---	---	---	Rn.199135	AW915048	4.05	5.10	2.98	4.07	4.82	4.87	1.46	up	4.58E-01	8.95E-01	-	-
1385922_at	LOC296637	Similar to HLA-B associated transcript-2 isoform a	296637	Rn.98457	AW443347	5.17	4.03	5.49	4.22	4.42	4.42	1.46	down	2.93E-01	8.95E-01	-	-
1377648_at	Fam120b	family with sequence similarity 120B	308218	Rn.2664	BF414047	4.76	4.81	5.44	4.76	3.70	4.91	1.46	down	2.81E-01	8.95E-01	-	-
1372953_at	Ncald	neurocalcin delta	553106	Rn.13744	AI101330	7.01	7.64	7.39	6.41	7.03	6.97	1.46	down	1.13E-01	8.95E-01	-	-
1393322_at	Taf15	TAF15 RNA polymerase II, TATA box binding protein (TBP)-associated factor	287571	Rn.72554	AI556910	6.81	8.40	6.41	7.68	7.52	8.06	1.46	up	4.35E-01	8.95E-01	-	-
1373568_at	---	---	---	Rn.92595	AI172222	5.99	5.71	7.17	6.87	6.85	6.78	1.46	up	2.91E-01	8.95E-01	-	-
1373204_at	Tmem176a	transmembrane protein 176A	297077	Rn.17071	BM388911	3.51	4.08	2.75	4.16	3.56	4.26	1.46	up	2.88E-01	8.95E-01	-	-
1371883_at	Mmd	monocyte to macrophage differentiation-associated	303439	Rn.163163	BG376037	4.24	2.56	2.61	2.85	2.52	2.41	1.46	down	3.93E-01	8.95E-01	-	-
1374418_at	Tmem188	transmembrane protein 188	291914	Rn.101963	BF289188	7.15	7.55	7.34	7.56	7.90	8.20	1.46	up	6.74E-02	8.95E-01	-	-
1370489_a_at	Ptcb4	phospholipase C, beta 4	25031	Rn.6158	U57836	5.34	4.25	4.98	5.72	5.86	6.46	1.46	up	2.99E-01	8.95E-01	-	-
1388371_at	Prkcsh	protein kinase C substrate 80K-H	300445	Rn.104417	AI008784	7.31	8.17	7.66	8.23	8.14	8.40	1.46	up	1.03E-01	8.95E-01	-	-
1374945_at	Trmt61a	tRNA methyltransferase 61 homolog A (S. cerevisiae)	314462	Rn.54722	BI281827	4.52	3.85	3.48	4.27	4.38	4.83	1.46	up	1.94E-01	8.95E-01	-	-
1387823_at	Pitrg1	pleiotropic regulator 1, PRL1 homolog (Arabidopsis)	60376	Rn.44181	NM_021757	6.65	6.64	5.56	6.43	7.53	6.52	1.46	up	3.40E-01	8.95E-01	-	-
1375662_at	---	---	---	Rn.199192	BI291391	7.84	8.85	8.20	9.05	8.36	9.11	1.46	up	2.26E-01	8.95E-01	-	-
1370341_at	Eno2	enolase 2, gamma, neuronal	24334	Rn.10828	AF019973	2.48	2.43	2.46	2.46	4.02	2.52	1.46	up	3.48E-01	8.95E-01	-	-
1375486_at	LOC680025	similar to nuclear RNA export factor 2	680025	Rn.101740	BI296423	2.53	2.86	2.55	3.09	2.66	3.82	1.46	up	2.02E-01	8.95E-01	-	-
1367861_at	Evl	Ena/Vasp-like	79115	Rn.28912	NM_024147	6.75	4.69	5.34	7.02	5.53	5.85	1.46	up	5.14E-01	8.95E-01	-	-
1373575_at	Fcer1g	Fc fragment of IgE, high affinity I, receptor for; gamma polypeptide	25441	Rn.201810	BE111722	6.94	6.44	6.70	7.56	8.01	6.13	1.46	up	4.05E-01	8.95E-01	-	-
1378480_at	---	---	---	Rn.166811	BI282157	2.45	4.16	2.47	2.45	2.46	2.54	1.46	down	3.94E-01	8.95E-01	-	-
1395894_at	Api5	apoptosis inhibitor 5	362170	Rn.103083	H34636	6.58	6.90	7.83	6.51	6.54	6.62	1.46	down	2.23E-01	8.95E-01	-	-
1379684_at	---	---	---	Rn.204705	BG380889	2.46	2.47	2.47	2.47	3.32	3.23	1.46	up	1.14E-01	8.95E-01	-	-
1377501_at	Zfp317	zinc finger protein 317	500950	Rn.159405	BM383704	5.82	5.06	3.16	4.56	6.56	4.55	1.46	up	6.28E-01	8.95E-01	-	-
1387158_at	Mep1b	meprin 1 beta	25727	Rn.3520	NM_013183	8.77	9.79	9.69	10.06	9.48	10.34	1.46	up	2.56E-01	8.95E-01	-	-
1376061_at	RGD1564036	similar to RIKEN cDNA 3010026O09	497895	Rn.12839	AW525033	2.93	2.58	2.96	2.90	3.69	3.51	1.46	up	1.12E-01	8.95E-01	-	-
1392533_at	Nars2	asparaginyl-tRNA synthetase 2 (mitochondrial)(putative)	293128	Rn.161855	AI176888	5.46	4.51	5.61	4.78	4.80	4.38	1.46	down	2.16E-01	8.95E-01	-	-
1385408_at	Mga	MAX gene associated	499874	Rn.78917	BI288589	5.56	4.52	6.31	3.92	5.45	5.38	1.46	down	4.93E-01	8.95E-01	-	-
1388749_at	Rmnd5a	required for meiotic nuclear division 5 homolog A (S. cerevisiae)	312439	Rn.11791	BI278823	7.42	6.67	6.94	6.63	6.68	7.10	1.46	down	3.14E-01	8.95E-01	-	-
1392216_at	---	---	---	Rn.205552	BF403731	2.37	3.21	3.14	4.09	3.44	2.81	1.46	up	3.02E-01	8.95E-01	-	-
1388027_a_at	Rtn4	reticulon 4	83765	Rn.1348	AF051335	6.38	6.13	5.86	6.92	6.97	6.10	1.46	up	1.66E-01	8.95E-01	-	-
1378140_at	Axl11	ADP-ribosylation factor-like 11	364396	Rn.23090	BI296317	2.32	2.31	3.95	2.32	2.34	2.31	1.46	down	3.77E-01	8.95E-01	-	-
1375506_at	Adck5	aarF domain containing kinase 5	362943	Rn.145222	BG376675	7.46	7.00	5.92	6.71	6.41	5.64	1.46	down	3.85E-01	8.95E-01	-	-
1376176_at	Mast3	microtubule associated serine/threonine kinase 3	688540	Rn.155444	AI145586	4.91	4.82	5.41	4.52	3.62	5.38	1.46	down	3.74E-01	8.95E-01	-	-
1386615_at	Chst2	carbohydrate sulfotransferase 2	367145	Rn.95986	BG665096	9.63	8.87	9.02	8.48	8.42	9.01	1.45	down	1.44E-01	8.95E-01	-	-
1389744_at	---	---	---	---	AW527194	7.07	7.67	7.99	7.08	6.80	7.23	1.45	down	1.44E-01	8.95E-01	-	-
1399044_at	Zfp91	Zinc finger protein 91	246282	Rn.1772	AA819804	5.49	6.82	6.80	6.51	7.06	7.17	1.45	up	3.28E-01	8.95E-01	-	-
1369718_at	Ssr3	signal sequence receptor, gamma	81784	Rn.3264	NM_031120	5.35	5.40	4.91	5.03	5.38	6.87	1.45	up	4.07E-01	8.95E-01	-	-
1384239_at	LOC680133	similar to TBC1 domain family, member 8	680133	Rn.205305	AA818474	3.02	3.18	2.88	2.97	4.80	2.94	1.45	up	4.32E-01	8.95E-01	-	-
1374664_at	Znf787	zinc finger protein 787	365176	Rn.23427	AI235511	6.68	6.38	6.52	6.12	4.84	5.99	1.45	down	3.26E-01	8.95E-01	-	-
1398535_at	Hbs1l	Hbs1-like (S. cerevisiae)	293408	Rn.98198	AA998579	7.80	8.14	7.79	7.26	7.56	7.29	1.45	down	2.25E-02	8.95E-01	-	-
1386973_a_at	Mapk8ip1	mitogen-activated protein kinase 8 interacting protein 1	116457	Rn.44266	NM_053777	6.42	7.05	7.06	7.29	7.52	7.34	1.45	up	7.14E-02	8.95E-01	-	-
1371547_at	---	---	---	---	BI282112	8.45	8.74	8.51	8.34	7.51	8.23	1.45	down	1.23E-01	8.95E-01	-	-
1387762_s_at	Jund	Jun D proto-oncogene	24518	Rn.46225	NM_138875	5.33	4.76	5.32	4.94	4.96	3.89	1.45	down	2.49E-01	8.95E-01	-	-
1398027_at	---	---	---	Rn.210965	BF405186	5.21	3.62	3.37	3.76	3.41	3.41	1.45	down	4.08E-01	8.95E-01	-	-
1391566_at	---	---	---	Rn.53954	AA818977	3.92	2.30	2.32	2.31	2.31	2.30	1.45	down	3.71E-01	8.95E-01	-	-
1373962_at	Usp32	ubiquitin specific protease 32	303394	Rn.16359	AI178556	4.32	5.84	6.19	4.91	6.89	6.17	1.45	up	5.44E-01	8.95E-01	-	-
1372299_at	Cdkn1c	cyclin-dependent kinase inhibitor 1C (P57)	246060	Rn.162507	AI013919	2.38	2.35	2.37	2.36	4.02	2.34	1.45	up	3.88E-01	8.95E-01	-	-
1384359_at	---	---	---	Rn.173430	BF407520	2.48	2.46	4.59	2.53	2.47	2.91	1.45	down	4.94E-01	8.95E-01	-	-
1393946_at	Fusip1	PET interacting protein (serine-arginine rich) 1	362630	Rn.162118	BG377118	4.95	4.93	5.72	4.57	4.81	4.60	1.45	down	1.16E-01	8.95E-01	-	-
1389779_at	Sh2d4a	SH2 domain containing 4A	306376	Rn.137349	AA800626	4.58	3.49	3.64	4.13	3.94	5.27	1.45	up	3.70E-01	8.95E-01	-	-
1378736_at	---	---	---	Rn.66088	BF391862	4.38	2.86	2.91	2.90	2.89	2.74	1.45	down	3.41E-01	8.95E-01	-	-
1382765_at	ap271 /// LOC6919	ap271 /// LOC691918 ribosomal protein 27 like /// similar to Centrosomal protein of 27 kDa (Cep27	292105	Rn.162678	AA998645	6.34	6.96	8.08	5.93	7.05	6.78	1.45	down	4.28E-01	8.95E-01	-	-
1372030_at	Zfyve21	zinc finger, FYVE domain containing 21	362789	Rn.2468	BI283114	4.74	5.55	5.46	5.78	6.05	5.55	1.45	up	1.40E-01	8.95E-01	-	-
1373296_a_at	RGD1311634	similar to RIKEN cDNA 3200002M19	293155	Rn.6268	AA800001	7.32	7.71	7.99	6.97	6.89	7.54	1.45	down	1.28E-01	8.95E-01	-	-
1394761_at	---	---	---	Rn.52342	BE114260	5.20	6.91	5.03	5.48	6.79	6.49	1.45	up	4.94E-01	8.95E-01	-	-
1368470_at	Ggh	gamma-glutamyl hydrolase	25455	Rn.10269	NM_012960	9.24	10.19	9.94	8.41	9.67	9.67	1.45	down	3.49E-01	8.95E-01	-	-
1376796_at	Rab14	RAB14, member RAS oncogene family	94197	Rn.6008	BG372452	6.19	7.65	6.91	6.30	5.66	7.16	1.45	down	4.22E-01	8.95E-01	-	-
1372133_at	Rras2	related RAS viral (r-ras) oncogene homolog 2	365355	Rn.3271	AA955287	9.00	8.08	8.67	8.11	7.79	8.23	1.45	down	1.45E-01	8.95E-01	-	-
1370045_at	Polg	polymerase (DNA directed), gamma	85472	Rn.19327	AW435444	5.26	6.58	5.76	6.91	6.20	6.10	1.45	up	3.53E-01	8.95E-01	-	-
1375136_at	---	---	---	---	AA946053	6.05	6.84	6.88	5.83	8.30	7.25	1.45	up	5.20E-01	8.95E-01	-	-
1373990_at	C361914 /// Slc7a	similar to solute carrier family 7 (cationic amino acid transporter, y+ system),	294881 /// 361914	Rn.34357	AI411935	9.12	11.91	11.59	11.10	11.40	11.73	1.45	up	5.82E-01	8.95E-01	-	-
1388490_at	Bap1	BRCA1 associated protein-1 (ubiquitin carboxy-terminal hydrolase)	306257	Rn.3382	AI104451	6.97	8.38	7.19	8.11	7.86	8.19	1.45	up	2.96E-01	8.95E-01	-	-
1386440_at	Galnt2	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltran	292090	Rn.14472	AI711250	2.37	2.36	3.98	2.36	2.37	2.35	1.45	down	3.73E-01	8.95E-01	-	-
1367717_at	Rps27	ribosomal protein S27	94266	Rn.153914	NM_053597	11.39	11.55	11.31	11.77	11.89	12.21	1.45	up	2.22E-02	8.95E-01	-	-
1373593_at	Rnaseh1	ribonuclease H1	298933	Rn.13139	BM390974	5.17	5.60	5.37	6.39	5.76	5.59	1.45	up	1.19E-01	8.95E-01	-	-
1393034_at	RGD1565584	similar to tyrosine kinase-associated leucine zipper protein LAZIpII	293112	Rn.35776	BI282899	4.97	5.21	5.02	5.21	5.55	6.07	1.45	up	1.08E-01	8.95E-01	-	-
1374357_at	Cdc9111	CDC91 cell division cycle 91-like 1 (S. cerevisiae)	353304	Rn.40981	AI713763	5.20	5.69	4.48	4.94	5.72	6.32	1.45	up	3.67E-01	8.95E-01	-	-
1374184_at	RGD1306000	similar to CG8043-PA	363611	Rn.214947	BF405027	7.58	8.72	8.80	7.74	7.57	8.18	1.45	down	2.81E-01	8.95E-01	-	-
1384066_at	RGD1307621	hypothetical LOC314168	314168	Rn.93945	AW921699	4.06	2.38	2.35	2.39	2.36	2.43	1.45	down	3.94E-01	8.95E-01	-	-
1384279_at	Fam117b	family with sequence similarity 117, member B	362326	Rn.8073	BI275378	2.53	4.12	2.58	2.34	3.02	2.25	1.45	down	4.02E-01	8.95E-01	-	-
1394492_at	RGD1563482	similar to hypothetical protein FLJ38663	498179	Rn.64119	AW525164	4.81	4.55	4.15	5.07	4.44	5.62	1.45	up	2.41E-01	8.95E-01	-	-
1378726_at	Alkbh4	alkB, alkylation repair homolog 4 (E. coli)	288587	Rn.136729	AI556485	3.77	4.04	5.06	5.24	4.62	4.61	1.45	up	2.93E-01	8.95E-01	-	-
1377086_at	C1qtnf3	C1q and tumor necrosis factor related protein 3	294806	Rn.16507	AI233530	5.00	7.06	5.80	4.61	5.90	5.73	1.45	down	4.98E-01	8.95E-01	-	-
1392992_at	---	---	---	Rn.216494	BF395999	4.60	3.55	4.64	3.21	3.59	4.37	1.45	down	3.38E-01	8.95E-01	-	-
1388119_at	Hnrnpa3	heterogeneous nuclear ribonucleoprotein A3	362152	Rn.107690	BM392140	8.31	8.17	7.96	8.60	8.48	8.97	1.45	up	3.95E-02	8.95E-01	-	-
1378238_at	Anapc1	anaphase promoting complex subunit 1	311412	Rn.8	AI598720	2.79	2.83	2.85	2.83	2.79	4.45	1.45	up	3.81E-01	8.95E-01	-	-
1372920_at	Prodh	proline dehydrogenase	680409	Rn.153570	AI411345	5.83	5.67	4.23	5.29	4.22	4.61	1.45	down	4.17E-01	8.95E-01	-	-
1383901_at	---	---	---	Rn.13721	BI287446	5.65	6.96	5.53	6.81	6.24	6.70	1.45	up	3.33E-01	8.95E-01	-	-
1376839_at	---	---	---	Rn.3062	AA866321	6.84	5.95	6.80	6.13	5.73	6.11	1.45	down	1.66E-01	8.95E-01	-	-
1379326_at	RGD1305679	similar to 9530008L14Rik protein	361228	Rn.16893	AI169837	7.01	6.24	6.69	6.22	5.45	6.65	1.45	down	2.67E-01	8.95E-01	-	-
1394090_at	---	---	---	Rn.6418	BF290383	3.89	4.90	2.24	2.55	5.25	4.84	1.45	up	6.62E-01	8.98E-01	-	-
1382943_at	Pcdhga5 /// Pcdh	protocadherin gamma subfamily A, 1 /// protocadherin gamma subfamily A, 10	364244 /// 364845	Rn.8628	BE097805	7.03	6.31	7.03	6.81	5.35	6.59	1.45	down	3.53E-01	8.95E-01	-	-
1386440_at	Galnt2	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltran	292090	Rn.14472	AI711250	2.37	2.36	3.98	2.36	2.37	2.35	1.45	down	3.73E-01	8.95E-01	-	-
1393981_at	RGD1310474	similar to KIAA0423	314169	Rn.144424	BF567629	3.67	3.12	4.88	3.15	3.52	3.39	1.45	down	3.70E-01	8.95E-01	-	-
1379959_at	Wrb	tryptophan rich basic protein	288233	Rn.103351	BI280216	6.30	4.78	4.99	5.47	6.32	5.88	1.45	up	3.72E-01	8.95E-01	-	-
1367810_at	Slc6a8	solute carrier family 6 (neurotransmitter transporter, creatine), member 8	50690	Rn.10336	NM_017348	7.36	7.11	7.21	8.39	7.52	7.38	1.45	up	1.74E-01	8.95E-01	-	-
1367618_a_at	Gnb2l1	guanine nucleotide binding protein (G protein), beta polypeptide 2 like 1	83427	Rn.55487	NM_130734	9.55	9.98	9.85	10.27	10.14	10.58	1.45	up	4.11E-02	8.95E-01	-	-
1383279_at	Rcbtb2	regulator of chromosome condensation (RCC1) and BTB (POZ) domain conta	290363	Rn.125257	BE119554	7.00	5.44	7.59	7.08	5.61	5.72	1.45	down	5.37E-01	8.95E-01	-	-
1373852_at	Srd5a3	steroid 5 alpha-reductase 3	305291	Rn.819	AA859922	3.02	3.02	3.17	4.85	3.02	2.94	1.45	up	4.39E-01	8.95E-01	-	-
1392221_at	---	---	---	Rn.208272	BE114215	2.44	2.41	2.44	2.61	2.45	3.84	1.45	up	2.87E-01	8.95

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1394636_at	---	---	---	Rn.177629	BM385501	3.23	3.23	3.18	3.22	3.25	4.78	1.45	up	3.59E-01	8.95E-01	-	-
1377607_at	Map3k3	mitogen activated protein kinase kinase kinase 3	303604	Rn.72680	BM385631	3.89	4.56	3.52	4.01	5.49	4.07	1.45	up	4.04E-01	8.95E-01	-	-
1377856_at	---	---	---	Rn.8961	BE1130045	2.51	2.39	3.78	2.25	2.43	2.42	1.45	down	2.99E-01	8.95E-01	-	-
1383228_at	---	---	---	---	AA875288	5.27	6.02	6.00	6.84	6.03	6.02	1.45	up	2.21E-01	8.95E-01	-	-
1376353_at	Actr5	ARP5 actin-related protein 5 homolog (yeast)	362258	Rn.219470	BI289883	2.46	2.52	2.44	2.44	3.83	2.75	1.45	up	2.74E-01	8.95E-01	-	-
1374968_at	Eif2c1	eukaryotic translation initiation factor 2C, 1	313594	Rn.62413	AI599930	4.09	6.04	4.64	5.64	4.60	6.13	1.45	up	5.10E-01	8.95E-01	-	-
1396264_at	---	---	---	Rn.205358	BF397752	2.58	2.58	4.17	2.58	2.59	2.57	1.45	down	3.72E-01	8.95E-01	-	-
1386965_at	Lpl	lipoprotein lipase	24539	Rn.3834	NM_012598	3.75	2.94	2.52	2.50	2.62	2.49	1.45	down	2.18E-01	8.95E-01	-	-
1383420_at	Lace1	lactation elevated 1	502479	Rn.24314	BM390554	7.77	8.08	7.75	7.60	6.73	7.67	1.45	down	1.72E-01	8.95E-01	-	-
1385824_at	Cep350	centrosomal protein 350kDa	246304	Rn.56823	BF388819	3.70	3.87	5.47	4.57	5.34	4.73	1.45	up	4.33E-01	8.95E-01	-	-
1398884_at	Ube2g1	ubiquitin-conjugating enzyme E2G 1 (UBC7 homolog, C. elegans)	64631	Rn.163149	BM389287	8.03	6.96	7.54	6.83	7.31	6.79	1.45	down	2.07E-01	8.95E-01	-	-
1379229_at	---	---	---	---	AI501127	6.15	6.37	4.39	5.57	4.39	5.36	1.45	down	5.04E-01	8.95E-01	-	-
1394436_at	Spag9	sperm associated antigen 9	360600	Rn.24583	BF560163	7.83	9.18	8.48	9.22	8.51	9.35	1.45	up	3.20E-01	8.95E-01	-	-
1392767_at	---	---	---	Rn.167938	AI502349	4.65	5.97	5.52	5.21	6.60	5.92	1.45	up	3.94E-01	8.95E-01	-	-
1390347_at	---	---	---	Rn.26656	AW535909	2.43	2.40	3.86	2.38	2.37	2.35	1.45	down	3.33E-01	8.95E-01	-	-
1373523_at	Fcgr3a	Fc fragment of IgG, low affinity IIIa, receptor	304966	Rn.23977	AI011757	2.64	2.69	2.64	2.73	4.18	2.65	1.45	up	3.47E-01	8.95E-01	-	-
1390024_at	---	---	---	Rn.95653	AI237685	6.29	6.96	7.37	7.13	7.37	7.72	1.45	up	2.12E-01	8.95E-01	-	-
1376616_at	---	---	---	Rn.203090	BF551036	7.50	7.80	8.94	6.79	7.82	8.04	1.44	down	4.16E-01	8.95E-01	-	-
1395642_at	Nol9	nucleolar protein 9	313744	Rn.162134	BG372596	5.02	4.65	4.79	4.56	4.04	4.27	1.44	down	4.49E-02	8.95E-01	-	-
1393242_at	RGD1310922	similar to chromosome 16 open reading frame 33; minus -99 protein	287170	Rn.106760	BE104107	8.22	7.76	7.88	6.80	7.23	8.23	1.44	down	3.00E-01	8.95E-01	-	-
1383605_at	360919 /// LOC68	similar to alpha-fetoprotein /// similar to Alpha-fetoprotein precursor (Alpha-fet	360919 /// 684913	Rn.30321	BE119842	8.37	10.08	9.69	9.80	9.90	10.03	1.44	up	3.66E-01	8.95E-01	-	-
1392782_at	---	---	---	Rn.166423	AI071197	2.70	2.68	2.40	3.80	2.86	2.71	1.44	up	2.08E-01	8.95E-01	-	-
1391211_at	Atp11c	Atpase, class VI, type 11C	317599	Rn.105357	AI144936	5.16	5.24	5.04	5.25	6.20	5.59	1.44	up	1.34E-01	8.95E-01	-	-
1372583_at	---	---	---	Rn.13877	AI009094	4.15	3.13	2.98	3.64	2.56	2.48	1.44	down	3.70E-01	8.95E-01	-	-
1372196_at	Ncor2	nuclear receptor co-repressor 2	360801	Rn.113362	BI284203	4.62	4.72	4.48	3.30	4.26	4.66	1.44	down	2.63E-01	8.95E-01	-	-
1370363_at	Ces3	carboxylesterase 3	113902	Rn.2549	L46791	7.28	8.08	7.55	7.53	8.32	8.65	1.44	up	2.60E-01	8.95E-01	-	-
1378215_at	Glyd2	GIY-YIG domain containing 2	293489	Rn.30339	BI291205	2.89	2.87	4.45	2.92	2.86	2.84	1.44	down	3.69E-01	8.95E-01	-	-
1392184_at	---	---	---	Rn.212013	BI298049	8.84	9.13	8.08	8.96	9.10	9.58	1.44	up	2.20E-01	8.95E-01	-	-
1374057_at	Hoxd9	Homeo box D9	689999	Rn.13330	AI177143	9.17	8.21	7.91	7.95	8.23	7.52	1.44	down	2.86E-01	8.95E-01	-	-
1379272_at	Paip1	Poly(A) binding protein interacting protein 1	365684	Rn.222035	AA963084	5.67	5.04	6.19	5.84	6.46	6.18	1.44	up	2.34E-01	8.95E-01	-	-
1373101_at	Plgk /// Ubp33	phosphatidylinositol glycan, class K /// ubiquitin specific peptidase 33	295543 /// 310960	Rn.17350	AI236743	6.25	6.86	6.94	6.95	7.37	7.32	1.44	up	1.04E-01	8.95E-01	-	-
1375271_at	Nek9	NIMA (never in mitosis gene a)- related kinase 9	299204	Rn.102369	BE118382	5.19	3.82	3.92	3.30	3.94	4.11	1.44	down	3.52E-01	8.95E-01	-	-
1377250_at	RGD1310799	similar to RIKEN cDNA A930008G19	309060	Rn.12282	AI407325	3.95	3.64	3.14	4.10	3.82	4.39	1.44	up	1.41E-01	8.95E-01	-	-
1394488_at	---	---	---	Rn.169433	AW524157	2.41	2.40	2.30	2.40	3.80	2.50	1.44	up	3.07E-01	8.95E-01	-	-
1372580_at	Madd	MAP-kinase activating death domain	94193	Rn.90117	BF283599	7.43	6.87	6.24	7.31	7.12	7.70	1.44	up	2.41E-01	8.95E-01	-	-
1395763_at	---	---	---	Rn.170858	BE101696	2.71	2.85	2.87	3.99	3.20	2.82	1.44	up	2.02E-01	8.95E-01	-	-
1372155_at	Trim28	tripartite motif-containing 28	116698	Rn.19494	BI283697	4.74	6.54	5.78	5.88	6.88	5.89	1.44	up	4.40E-01	8.95E-01	-	-
1395264_at	Rif1	RAP1 interacting factor homolog (yeast)	295602	Rn.20919	BF543757	5.03	6.15	5.06	5.74	5.98	6.10	1.44	up	2.39E-01	8.95E-01	-	-
1385496_at	Ccdc127	coiled-coil domain containing 127	308060	Rn.21666	AI043653	6.27	4.69	4.81	5.97	3.94	4.27	1.44	down	5.48E-01	8.95E-01	-	-
1379104_at	---	---	---	Rn.154941	BF400861	3.85	4.21	4.94	4.58	5.65	4.36	1.44	up	3.60E-01	8.95E-01	-	-
1385553_at	684506 /// LOC68	similar to SMP3 mannosyltransferase /// similar to nuclear cap binding protein	684506 /// 689116	Rn.204538	AI136699	6.24	5.27	5.90	5.30	4.98	5.55	1.44	down	1.80E-01	8.95E-01	-	-
1383929_at	---	---	---	Rn.7599	AI230265	4.82	5.08	5.23	4.82	3.46	5.26	1.44	down	3.95E-01	8.95E-01	-	-
1391480_at	---	---	---	Rn.26807	BI296013	3.17	3.86	3.57	3.68	3.78	4.73	1.44	up	2.46E-01	8.95E-01	-	-
1380044_at	Pfkfb2	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 2	24640	Rn.44844	L27084	4.31	4.63	4.66	3.23	4.03	4.74	1.44	down	3.06E-01	8.95E-01	-	-
1381905_at	---	---	---	Rn.24527	AI230826	4.55	4.31	2.81	3.05	2.55	4.47	1.44	down	5.41E-01	8.95E-01	-	-
1386008_at	Polr3f	polymerase (RNA) III (DNA directed) polypeptide F, 39 kDa	311487	Rn.22329	AW914833	5.50	5.69	4.36	6.11	5.10	5.92	1.44	up	3.66E-01	8.95E-01	-	-
1367580_at	Rpl10a	ribosomal protein L10A	81729	Rn.2262	NM_031065	9.43	9.87	9.29	9.79	9.95	10.43	1.44	up	1.13E-01	8.95E-01	-	-
1392475_at	Atf6	activating transcription factor 6	304962	Rn.15235	BE104169	4.66	5.26	4.82	5.47	5.25	5.61	1.44	up	6.37E-02	8.95E-01	-	-
1387258_a_at	Pcmt1	protein-L-isoaspartate (D-aspartate) O-methyltransferase 1	25604	Rn.86985	D11475	5.79	5.76	6.45	6.47	6.46	6.65	1.44	up	8.58E-02	8.95E-01	-	-
1389784_at	Pogz	pogo transposable element with ZNF domain	310658	Rn.103975	AI177507	5.22	5.53	4.61	5.21	6.53	5.19	1.44	up	3.88E-01	8.95E-01	-	-
1373290_at	Ezh2	enhancer of zeste homolog 2 (Drosophila)	312299	Rn.9027	AI012781	3.65	3.25	3.11	3.72	4.49	3.38	1.44	up	2.24E-01	8.95E-01	-	-
1369167_at	Gfra2	GDNF family receptor alpha 2	25136	Rn.90137	NM_012750	2.55	2.37	2.35	2.37	4.14	2.34	1.44	up	4.28E-01	8.95E-01	-	-
1385828_at	---	---	---	Rn.217037	BF559433	3.70	4.50	4.72	4.93	4.99	4.57	1.44	up	1.91E-01	8.95E-01	-	-
1372363_at	Ir2h /// RGD15659	polymerase (RNA) II (DNA directed) polypeptide H /// similar to polymerase (R	291795 /// 498109	Rn.9160	BF404414	7.33	7.95	6.84	7.62	7.81	8.28	1.44	up	2.33E-01	8.95E-01	-	-
1368219_at	Clcn2	chloride channel 2	29232	Rn.11073	NM_017137	3.48	4.87	4.69	4.12	4.93	5.58	1.44	up	4.34E-01	8.95E-01	-	-
1380032_at	Slain2	SLAIN motif family, member 2	305310	Rn.23030	BF407634	6.29	6.02	5.66	6.22	6.84	6.50	1.44	up	1.08E-01	8.95E-01	-	-
1383226_at	Zfx	zinc finger protein X-linked	367832	Rn.218078	BI293943	4.27	4.30	4.42	4.19	3.37	3.84	1.44	down	9.64E-02	8.95E-01	-	-
1389583_at	Tmem82	transmembrane protein 82	298605	Rn.104972	BF282712	6.97	7.34	6.20	7.06	7.01	8.04	1.44	up	3.30E-01	8.95E-01	-	-
1382165_at	Smndc1	survival motor neuron domain containing 1	287768	Rn.103854	BI288396	6.83	7.11	6.79	6.78	5.99	6.39	1.44	down	1.01E-01	8.95E-01	-	-
1389796_at	---	---	---	Rn.50018	BI298018	2.55	2.53	2.57	2.56	2.58	4.09	1.44	up	3.57E-01	8.95E-01	-	-
1388858_at	Map2k3	mitogen activated protein kinase kinase 3	303200	Rn.100064	BI283843	4.90	4.23	4.77	4.95	5.68	4.85	1.44	up	1.86E-01	8.95E-01	-	-
1398944_at	Acin1	apoptotic chromatin condensation inducer 1	303584	Rn.97147	BE116857	6.76	5.60	4.99	5.17	4.98	5.62	1.44	down	3.94E-01	8.95E-01	-	-
1370807_at	Tmem49	transmembrane protein 49	192129	Rn.109048	AF411216	5.61	6.71	4.71	6.37	5.75	6.49	1.44	up	4.44E-01	8.95E-01	-	-
1388542_at	OC292282 /// Use	similar to USE1-like protein (Hematopoietic stem/progenitor cells protein MDS	290627 /// 292282	Rn.201293	BI283120	9.67	10.20	9.36	10.10	10.30	10.41	1.44	up	1.14E-01	8.95E-01	-	-
1372413_at	Mcrs1	microsphere protein 1	300227	Rn.2727	BI278600	4.64	4.75	4.78	4.25	3.87	4.48	1.44	down	4.53E-02	8.95E-01	-	-
1384023_at	Spin2a	spindlin family, member 2A	317395	Rn.203523	AI229556	3.89	3.10	2.76	2.61	2.75	2.81	1.44	down	1.96E-01	8.95E-01	-	-
1375436_at	Naprt1	nicotinate phosphoribosyltransferase domain containing 1	315085	Rn.22665	BF416417	8.77	8.71	8.50	8.22	8.03	8.14	1.44	down	6.01E-03	8.95E-01	-	-
1385903_at	---	---	---	Rn.202361	BI303933	8.69	6.65	7.31	6.78	7.30	6.98	1.44	down	4.43E-01	8.95E-01	-	-
1373858_at	---	---	---	Rn.163726	BE109064	5.57	5.01	4.45	3.91	4.29	5.25	1.44	down	3.63E-01	8.95E-01	-	-
1382497_at	---	---	---	Rn.163725	AA875457	3.32	2.91	2.64	2.42	2.31	2.56	1.44	down	6.65E-02	8.95E-01	-	-
1392410_at	RGD1561678	similar to mKIAA0978 protein	311553	Rn.199307	AI603414	2.49	2.84	4.55	2.79	2.78	2.74	1.44	down	4.55E-01	8.95E-01	-	-
1390163_at	RGD1563863	similar to expressed sequence AI553587	498418	Rn.25205	BF282174	2.49	2.53	4.04	2.64	2.53	2.32	1.44	down	3.69E-01	8.95E-01	-	-
1388579_at	Slc25a42	solute carrier family 25, member 42	689414	Rn.17455	AI176841	3.27	3.02	2.86	3.60	3.14	3.99	1.44	up	1.28E-01	8.95E-01	-	-
1371579_at	LOC680782	similar to signal peptidase complex subunit 3 homolog	680782	Rn.29528	AI012456	8.19	8.69	8.83	9.01	8.67	9.61	1.44	up	1.93E-01	8.95E-01	-	-
1393217_at	Abcg311	ATP-binding cassette, sub-family G (WHITE), member 3-like 1	289453	Rn.160591	BF282804	5.76	4.24	3.91	4.66	3.41	4.27	1.44	down	4.83E-01	8.95E-01	-	-
1393915_at	Lpcat3	lysophosphatidylcholine acyltransferase 3	362434	Rn.19543	BE128627	5.72	4.12	4.22	4.45	6.06	5.13	1.44	up	4.93E-01	8.95E-01	-	-
1371359_at	Mlf2	myeloid leukemia factor 2	312709	Rn.3678	BG381670	7.42	7.49	8.24	7.44	7.14	6.98	1.44	down	1.49E-01	8.95E-01	-	-
1390838_at	Satb2	SATB homeobox 2	501145	Rn.219670	BE115823	5.78	7.05	7.14	6.18	5.72	6.50	1.44	down	3.50E-01	8.95E-01	-	-
1371382_at	Flna	filamin, alpha	293860	Rn.4213	BI283080	5.48	4.62	3.23	6.05	4.30	4.55	1.44	up	5.71E-01	8.95E-01	-	-
1368576_at	Alx1	ALX homeobox 1	25401	Rn.9282	NM_012921	2.38	2.37	2.39	2.38	3.96	2.37	1.44	up	3.78E-01	8.95E-01	-	-
1387152_at	Nrbf2	nuclear receptor binding factor 2	58839	Rn.44867	NM_022186	2.41	3.90	3.91	3.92	3.91	3.97	1.44	up	3.53E-01	8.95E-01	-	-
1385508_x_at	---	---	---	Rn.131357	AA962944	5.58	4.55	5.42	4.50	4.52	4.96	1.44	down	2.13E-01	8.95E-01	-	-
1372822_at	---	---	---	Rn.129500	BI287226	7.48	6.87	6.79	7.44	7.59	7.67	1.44	up	8.19E-02	8.95E-01	-	-
1371515_at	Elof1	elongation factor 1 homolog (S. cerevisiae)	691193	Rn.814	AI100773	8.58	8.71	7.64	8.70	8.86	8.95	1.44	up	2.03E-01	8.95E-01	-	-
1390882_at	Heyl	hairy/enhancer-of-split related with YRPW motif-like	313575	Rn.22252	AI101924	3.46	3.97	3.53	3.52	5.42	3.59	1.44	up	4.61E-01	8.95E-01	-	-
1396815_at	---	---	---	Rn.199600	AW251438	2.33	2.33	2.36	2.37	3.23	2.98	1.44	up	1.10E-01	8.95E-01	-	-
1369013_a_at	Mrpl17	mitochondrial ribosomal protein L17	171061	Rn.40354	AI103095	8.49	7.92	8.16	7.78	7.75	7.47	1.44	down	5.44E-02	8.95E-01	-	-
1387967_at	Spink1	serine peptidase inhibitor, Kazal type 1	266602	Rn.144683	M27883	9.63	8.64	9.75	9.59	9.28	7.59	1.44	down	5.03E-01	8.95E-01	-	-
1387347_at	Igfbp5	insulin-like growth factor binding protein 5	25285	Rn.1593	BE113270	6.51	5.73	4.23	5.51	5.22	4.16	1.44	down	5.41E-01	8.95E-01	-	-
1389319_at	Ergic1	endoplasmic reticulum-golgi intermediate compartment (ERGIC) 1	287177	Rn.98517	AA800719	6.65	7.07	7.44	6.31	6.39	6.88	1.44	down	1.45E-01	8.95E-01	-	-
1368040_at	Synj2bp	synaptojanin 2 binding protein	64531	Rn.6258	BF284821	6.14	7.37	7.65	7.75	7.24	7.74	1.44	up	3.49E-01	8.95E-01	-	-
1389191_at	Vps36	vacuolar protein sorting 36 homolog (S. cerevisiae)	290851	Rn.12707	AA858649	6.68	6.59	5.86	7.21	6.72	6.76	1.44	up	1.60E-01	8.95E-01	-	-
1387402_at	Myh9	myosin, heavy chain 9, non-muscle	25745	Rn.11385	NM_013194	4.33	5.63	4.59	6.18	4.77	5.18	1.44	up	4.15E-01	8.95E-01	-	-
1391145_at	---	---	---	Rn.16850	BE112120	4.27	5.02	5.36	5.29	5.08	5.85	1.44	up	2.57E-01	8.95E-01	-	-
1375940_a_at	RGD1311154	similar to hypothetical protein FLJ12242	300317	Rn.198231	BF396656	7.82	6.87	6.87	7.36	6.71	5.92	1.44	down	3.74E-01	8.95E-01	-	-
1374348_at	Ofcd7b	OTU domain containing 7B	310977	Rn.199225	BG373082	4.52	5.61	6.81	5.13	4.63	5.61	1.44	down	5.07E-01	8.95E-01	-	-
1390135_at	RGD1311595	Similar to KIAA2026 protein	309307	Rn.96138	AI044718	2.66	2.54	2.53	3.63	3.10	2.57	1.44	up	1.65E-01	8.95E-01	-	-
1389439_at	---	---	---	---	AI172618	3.94	4.52	3.95	4.52	4.44	5.02	1.44	up	1.21E-01	8.95E-01	-	-
1367950_at	Slc22a5	solute carrier family 22 (organic cation/carnitine transporter), member 5	29726	Rn.8844	NM_019269	8.20	7.13	8.52	7.13	7.63	7.53	1.44	down	3.07E-01	8.95E-01	-	-
1390370_at	---	---	---	Rn.208819	BF402582	2.78	2.93	2.84	2.99	4.35	2.78	1.44	up	3.50E-01	8.95E-01	-	-
1369024_at	Rabep2	rabaptin, RAB GTPase binding effector protein 2	80754	Rn.3228	NM_030585	3.19	3.35	3.98	2.53	2.48	3.94	1.44	down	3.84E-01	8.95E-01	-	-
1389200_at	Bysl	bystin-like	359727	Rn.185236	AA851296	5.93	6.40	4.08	5.62	6.03	6.33	1.44	up	5.18E-01	8.95E-01	-	-
1382574_at	---	---	---	---	AI176776	7.09	7.00	8.32	7.08	7.45	7.44	1.44	up	1.24E-01	8.95E-01	-	-
1379160_at	---	---	---	Rn.26603	BF399572	5.19	6.26	5.14	4.48	4.61	5.93	1.44	down	4.24E-01	8.95E-01	-	-
1368082_at	Slc4a2	solute carrier family 4 (anion exchanger), member 2	24780	Rn.9860	NM_017048	5.24	5.95	5.65	5.16	4.97	5.15	1.44	down	7.10E-02	8.95E-01	-	-
1374047_at	RGD1311805	similar to RIKEN cDNA 2400010D15	291784	Rn.35239	BM390427	3.61	3.60	3.10	3.91	3.48	4.48	1.44	up	1.93E-01	8.95E-01	-	-
1393401_at	---	---	---	---	BE109323	4.23	2.46	2.51	2.56	2.61	2.47	1.44	down	4.21E-01	8.95E-01	-	-
1380735_at	---	---	---	Rn.199752	BM385424	3.28	3.52	3.48	3.38	4.78	3.69	1.44	up	2.93E-01	8.95E-01	-	-
1393612_a_at	Depdc7	DEP domain containing 7	295971	Rn.97407	AI059270	4.17	4.89	5.29	4.66	3.55	4.57	1.44	down	3.40E-01	8.95E-01	-	-
1390866_at	---	---	---	Rn.146252	AI188981	6.70	6.26	6.80	5.34	6.30	6.55	1.44	down	2.67E-01	8.95E-01	-	-
1368436_at	Nudc	nuclear distribution gene C homolog (Aspergillus)	29648	Rn.10413	NM_017271	7.67	8.10	7.81	8.63	8.13	8.39	1.44	up	5.33E-02	8.95E-01	-	-
1373932_at	---	---	---	Rn.166089	BE098739	4.42	3.12	3.31	3.27	3.14	2.87	1.44	down	2.84E-01	8.95E-01	-	-
1368522_at	Mrs2	MRS2 magnesium homeostasis factor homolog (S. cerevisiae)	79032	Rn.33647	AF288290	5.50	4.23	4.03	3.84	3.92	4.44	1.44	down	3.52E-01	8.95E-01	-	-
1375549_at	---	---	---	Rn.168987	AI407719	7.99	7.91	9.59	9.65	8.28	9.13	1.44	up	4.84E-01	8.95E-01	-	-
1370548_at	Slc16a10	solute carrier family 16 (monocarboxylic acid transporters), member 10	170566	Rn.21992	AB047324	2.76	3.85	3.87	2.76	2.74	3.42	1.44	down	2.94E-01	8.95E-01	-	-
1384136_at	Osbpl3	oxysterol binding protein-like 3	362360	Rn.205820	BI291045	3.60	4.61	5.86	5.46	4.50	5.68	1.44	up	5.23E-01	8.95E-01	-	-
1379739_at	---	---	---	Rn.25349	BF408431	2.51	2.34	2.36	2.70	2.36	3.73	1.44	up	2.77E-01	8.95E-01	-	-
1387549_at	Ndst1	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 1	29633	Rn.9705	NM_024361	3.29	4.47	2.76	2.84	3.06	3.05	1.44	down	3.64E-01	8.95E-01	-	-
1387101_at	Acsl4	acyl-CoA synthetase long-chain family member 4	113976	Rn.87821	NM_053623	7.13	7.81	8.15	8.05	8.12	8.47	1.44	up	1.84E-01	8.95E-01	-	-
1387135_at	Adam15	a disintegrin and metalloprotease domain 15 (metargidin)	57025	Rn.162607	NM_020308	5.61	6.81	4.97	6.18	5.83	6.94	1.44	up	4.53E-01	8.95E-01	-	-
1371305_at	Rpl8	ribosomal protein L8	26962	Rn.127774	AI409193	9.04	10.16	9.71	10.18	9.81	10.47	1.44	up	2.38E-01	8.95E-01	-	-
1376119_at	Thada	thyroid adenoma associated	313865	Rn.18157	BE100155	4.74	6.32	7.08	5.99	6.39	7.32	1.44	up	5.48E-01	8.95E-01	-	-
1376489_at	Sos2	son of sevenless homolog 2 (Drosophila)	85384	Rn.4226	BF397919	7.27	6.73	8.09	6.74	6.98	6.80	1.44	down	2.63E-01	8.95E-01	-	-
1368339_at	S100g	S100 calcium binding protein G	24249	Rn.9974	NM_012521	4.93	3.51	5.29	4.33	4.27	3.57	1.44	down	4.31E-01	8.95E-01	-	-
1392588_at	Ripk5	receptor interacting protein kinase 5	304791	Rn.32539	BG664535	4.72	4.64	3.74	2.95	3.91	4.68	1.44	down	4.28E-01	8.95E-01	-	-
1387892_at	Tubb5	tubulin, beta 5	29214	Rn.2458	BI285440	3.02	3.87	3.67	3.84	3.93	4.55	1.44	up	2.23E-01	8.95E-01	-	-
1373330_at	LOC690323	similar to Myosin-15 (Myosin XV) (Unconventional myosin-15)	690323	Rn.198905	AI406704	4.35	3.67	4.68	4.35	3.34	3.46	1.44	down	2.99E-01	8.95E-01	-	-
1375122_at	Yaf2	YY1 associated factor 2	690262	Rn.7352	AI233235	5.07	5.72	5.30	6.08	5.32	6.24	1.43	up	2.03E-01	8.95E-01	-	-
1392281_at	---	---	---	---	BF394581	2.51	4.02	2.49	2.47	2.51	2.49	1.43	down	3.83E-01	8.95E-01	-	-
1393234_at	LOC687105	hypothetical protein LOC687105	687105	Rn.216416	BI285850	3.45	4.18	6.01	4.98	5.90	4.33	1.43	up	5.89E-01	8.95E-01	-	-
1396716_at	Rab23	RAB23, member RAS oncogene family	367242	Rn.24441	BF415919	2.97	5.26	4.77	4.26	5.64	4.67	1.43	up	5.54E-01	8.95E-01	-	-
1375201_at	---	---	---	---	AA946483	4.62	5.23	5.40	5.94	5.78	5.09	1.43	up	2.14E-01	8.95E-01	-	-
1382126_at	Ncor1	Nuclear receptor co-repressor 1	54299	Rn.24948	AW528959	6.28	6.21	4.94	6.60	6.13	6.25	1.43	up	3.18E-01	8.95E-01	-	-
1372634_at	Adprhl2	ADP-ribosylhydrolase like 2	362600	Rn.1834	AI009334	7.01	6.19	7.28	6.60	6.39	5.93	1.43	down	2.47E-01	8.95E-01	-	-
1384948_at	---	---	---	---	AI113157	6.70	7.28	7.82	6.48	6.48	7.28	1.43	down	2.81E-01	8.95E-01	-	-
1384390_at	LOC681740	similar to jumonji protein	681740	---	BI278808	4.25	4.27	4.38	4.99	5.47	4.00	1.43	up	2.98E-01	8.95E-01	-	-
1385546_at	Iqwd1	IQ motif and WD repeats 1	289181	Rn.3917	AA998195	5.09	5.28	3.69	5.21	4.02	5.40	1.43	up	5.56E-01	8.95E-01	-	-
1376268_at	---	---	---	Rn.203433	BM387435	5.45	5.72	5.84	6.41	5.74	6.42	1.43	up	1.08E-01	8.95E-01	-	-
1398706_at	---	---	---	Rn.101847	BI294633	2.70	2.76	2.82	2.77	3.72	3.35	1.43	up	1.36E-01	8.95E-01	-	-
1398384_at	Exosc9	exosome component 9	294975	R

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)				REG	MTC
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval		
1378190_at	---	---	---	Rn.203411	AA945871	2.86	3.43	6.12	3.34	3.35	4.17	1.43	down	6.45E-01	8.95E-01	-	-
1383440_at	/// LOC690471	1-aminocyclopropane-1-carboxylate synthase homolog (Arabidopsis)(non-fun	311218	/// 690470	Rn.101707	BF418459	4.53	3.40	3.93	4.69	3.96	4.77	1.43	up	2.83E-01	8.95E-01	-	-
1393306_at	Cul5	Cullin 5	64624		Rn.163001	BF561475	7.98	7.76	7.81	8.65	8.17	8.28	1.43	up	3.27E-02	8.95E-01	-	-
1397813_at	---	---	---	---	---	AW915896	2.77	4.20	3.59	2.73	2.70	3.57	1.43	down	3.62E-01	8.95E-01	-	-
1377064_at	Dusp6	dual specificity phosphatase 6	116663	Rn.4313	AI602811	7.40	7.89	8.17	7.53	9.05	8.43	1.43	up	3.56E-01	8.95E-01	-	-
1368450_at	Myo5a	myosin Va	25017	Rn.44865	NM_022178	6.39	7.16	6.60	5.79	6.02	6.80	1.43	down	2.46E-01	8.95E-01	-	-
1388022_a_at	Dnm1	dynamin 1-like	114114	Rn.216851	AF132727	5.96	5.86	5.47	5.70	4.40	5.64	1.43	down	3.16E-01	8.95E-01	-	-
1383253_at	---	---	---	Rn.164489	AI179795	8.95	9.93	9.50	9.85	9.99	10.09	1.43	up	1.51E-01	8.95E-01	-	-
1371186_at	Itga6	integrin, alpha 6	114517	Rn.161799	AA855091	5.82	6.30	5.90	4.80	5.84	5.83	1.43	down	2.38E-01	8.95E-01	-	-
1371892_at	Atpaf2	ATP synthase mitochondrial F1 complex assembly factor 2	303190	Rn.2167	BI274283	5.74	5.88	5.61	6.20	6.64	5.95	1.43	up	7.54E-02	8.95E-01	-	-
1393153_at	---	---	---	Rn.64095	BG663023	5.75	6.02	4.91	5.91	5.98	6.34	1.43	up	2.22E-01	8.95E-01	-	-
1369298_at	Aqp6	aquaporin 6, kidney specific	29170	Rn.48667	NM_022181	3.11	3.06	2.99	2.44	2.61	2.57	1.43	down	1.15E-03	8.95E-01	-	-
1376129_at	---	---	---	Rn.220024	BE108174	4.83	4.27	3.54	5.18	4.07	4.94	1.43	up	3.63E-01	8.95E-01	-	-
1375178_at	Akt1	V-akt murine thymoma viral oncogene homolog 1	24185	Rn.1422	BE111601	3.10	4.87	3.66	3.10	3.48	3.50	1.43	down	3.91E-01	8.95E-01	-	-
1374729_at	---	---	---	Rn.219255	BM385616	4.14	3.08	3.78	3.25	3.19	3.02	1.43	down	1.83E-01	8.95E-01	-	-
1391802_at	---	---	---	Rn.13873	BE107950	3.70	3.16	2.77	3.39	4.08	3.70	1.43	up	1.97E-01	8.95E-01	-	-
1375172_at	Rfwd2	Ring finger and WD repeat domain 2	360860	Rn.8617	AA850517	5.09	3.98	3.79	3.81	3.74	3.77	1.43	down	2.75E-01	8.95E-01	-	-
1375221_at	Txndc13	thioredoxin domain containing 13	296182	Rn.12542	BE109676	6.86	5.71	5.80	6.50	6.92	6.50	1.43	up	2.62E-01	8.95E-01	-	-
1382578_at	---	---	---	Rn.89365	AI178173	5.02	4.09	4.46	3.22	3.75	5.05	1.43	down	4.43E-01	8.95E-01	-	-
1367683_at	Kpna2	karyopherin (importin) alpha 2	85245	Rn.2949	NM_053483	6.87	7.66	7.27	6.35	7.07	6.83	1.43	down	1.74E-01	8.95E-01	-	-
1388127_at	Cyp4v3	cytochrome P450, family 4, subfamily v, polypeptide 3	---	266761	Rn.201722	AI170346	2.51	2.46	2.44	2.45	3.60	2.91	1.43	up	2.00E-01	8.95E-01	-	-
1391723_at	---	---	---	---	Rn.164573	BI291869	5.30	5.02	6.72	5.24	5.10	5.16	1.43	down	3.83E-01	8.95E-01	-	-
1367671_at	Pcna	proliferating cell nuclear antigen	25737	Rn.223	NM_022381	7.82	8.33	8.03	7.17	7.82	7.65	1.43	down	1.03E-01	8.95E-01	-	-
1390268_at	Rab35	RAB35, member RAS oncogene family	288700	Rn.18008	AI013484	3.67	3.77	3.43	3.87	4.20	4.33	1.43	up	3.80E-02	8.95E-01	-	-
1380174_at	---	---	---	Rn.205080	BE116115	2.54	2.56	2.57	2.56	3.75	2.90	1.43	up	2.17E-01	8.95E-01	-	-
1374546_at	---	---	---	Rn.163289	AW918040	4.34	5.91	5.54	5.90	5.29	6.13	1.43	up	3.92E-01	8.95E-01	-	-
1383237_at	---	---	---	Rn.14672	BE098240	2.39	2.63	2.66	2.98	2.75	3.50	1.43	up	9.58E-02	8.95E-01	-	-
1382995_at	---	---	---	Rn.209801	AA859669	2.90	2.41	2.41	4.46	2.43	2.39	1.43	up	5.05E-01	8.95E-01	-	-
1383547_at	Pnpla6	patatin-like phospholipase domain containing 6	360753	Rn.113214	AI137593	4.08	4.79	4.19	4.23	3.41	3.88	1.43	down	1.89E-01	8.95E-01	-	-
1392875_at	Fbxl4	F-box and leucine-rich repeat protein 4	313101	Rn.12566	AA964134	2.50	2.51	4.14	2.50	2.61	2.49	1.43	down	3.99E-01	8.95E-01	-	-
1370336_at	Osgin1	oxidative stress induced growth inhibitor 1	171493	Rn.15599	AY081218	10.59	11.06	10.23	10.09	10.01	10.23	1.43	down	1.06E-01	8.95E-01	-	-
1374874_at	RGD1561042	similar to RIKEN cDNA 5730509K17 gene	498386	---	AI410818	4.56	2.92	3.63	3.27	3.04	3.24	1.43	down	3.44E-01	8.95E-01	-	-
1398987_at	Supl4h1	suppressor of Ty 4 homolog 1 (S. cerevisiae)	287608	Rn.7906	AW141261	9.79	9.85	9.47	10.11	10.12	10.42	1.43	up	2.96E-02	8.95E-01	-	-
1388442_at	Canx	calnexin	29144	Rn.1762	AA848326	7.11	7.87	7.00	7.50	7.72	8.31	1.43	up	2.33E-01	8.95E-01	-	-
1376874_a_at	Ap4b1	adaptor-related protein complex 4, beta 1 subunit	310746	Rn.8746	BF560100	4.48	4.35	5.27	4.41	3.66	4.50	1.43	down	2.59E-01	8.95E-01	-	-
1376649_at	Snf1lk2	SNF1-like kinase 2	315649	---	AI111965	7.40	7.31	6.75	7.31	7.95	7.75	1.43	up	1.38E-01	8.95E-01	-	-
1375163_at	Rab11b	RAB11B, member RAS oncogene family	79434	Rn.124832	BI275870	8.43	7.94	8.03	7.73	7.74	7.38	1.43	down	5.61E-02	8.95E-01	-	-
1386321_s_at	Trib3	tribbles homolog 3 (Drosophila)	246273	Rn.22325	H31287	2.91	2.80	3.15	3.15	3.74	3.53	1.43	up	6.29E-02	8.95E-01	-	-
1394388_at	LOC100125371	hypothetical LOC100125371	100125371	Rn.34289	AA858844	4.07	4.86	5.22	4.63	3.71	4.28	1.43	down	3.01E-01	8.95E-01	-	-
1390587_x_at	---	---	---	---	---	AW525862	8.04	8.65	7.96	7.35	7.49	8.27	1.43	down	2.28E-01	8.95E-01	-	-
1374385_at	Pdlp1	poly(rC) binding protein 1	500242	Rn.1267	AI009789	8.47	8.34	8.19	7.90	7.36	8.20	1.43	down	1.19E-01	8.95E-01	-	-
1374746_at	---	---	---	Rn.3690	AA891922	7.84	7.79	7.14	7.38	8.44	8.49	1.43	up	2.94E-01	8.95E-01	-	-
1367510_at	Txndc15	thioredoxin domain containing 15	307180	Rn.4142	BG381690	6.08	6.98	6.67	7.11	6.97	7.19	1.43	up	1.32E-01	8.95E-01	-	-
1378586_at	Cish	cytokine inducible SH2-containing protein	83681	Rn.14523	BI291842	3.18	3.17	5.18	3.43	5.00	4.84	1.43	up	5.65E-01	8.95E-01	-	-
1377674_at	RGD1560612	similar to PHF21A protein	362166	Rn.203706	AI408930	6.39	6.45	6.19	7.67	6.71	6.19	1.43	up	3.10E-01	8.95E-01	-	-
1384855_at	RGD1562658	similar to RIKEN cDNA 1700009P17	498278	Rn.7902	AA964289	2.43	2.42	2.43	2.50	2.53	3.79	1.43	up	2.95E-01	8.95E-01	-	-
1367560_at	Arbp	acidic ribosomal phosphoprotein P0	64205	Rn.1079	NM_022402	10.44	10.91	10.54	11.01	11.12	11.30	1.43	up	3.47E-02	8.95E-01	-	-
1394565_at	Copz1	coatomer protein complex, subunit zeta 1	315345	Rn.159796	BI406339	8.10	8.09	7.31	8.35	8.29	8.40	1.43	up	1.24E-01	8.95E-01	-	-
1373180_at	---	---	---	Rn.17029	AI227919	9.62	9.41	9.14	8.63	8.80	9.21	1.43	down	8.18E-02	8.95E-01	-	-
1397313_at	Phrc2	proline-rich nuclear receptor coactivator 2	100125373	Rn.118788	AI716841	8.88	8.35	7.64	7.83	7.13	8.38	1.43	down	3.71E-01	8.95E-01	-	-
1371674_at	Klhdc3	kelch domain containing 3	363192	Rn.203058	AA894104	4.67	5.19	4.71	6.56	4.71	4.85	1.43	up	4.53E-01	8.95E-01	-	-
1373168_at	LOC288913	similar to LEYDIG CELL TUMOR 10 KD PROTEIN	288913	Rn.11148	BG380214	5.77	5.69	5.71	6.90	5.77	6.04	1.43	up	2.06E-01	8.95E-01	-	-
1383282_at	Thap11	THAP domain containing 11	307806	Rn.2823	BF543075	4.47	4.84	5.50	5.32	6.23	4.79	1.43	up	3.79E-01	8.95E-01	-	-
1371344_at	Rpl27a	ribosomal protein L27a	293418	Rn.2722	AI177054	10.90	11.10	10.91	11.27	11.48	11.70	1.43	up	2.07E-02	8.95E-01	-	-
1389188_at	Gpr108	G protein-coupled receptor 108	316136	Rn.203125	BE111778	3.84	4.27	4.16	5.18	4.20	4.43	1.43	up	1.88E-01	8.95E-01	-	-
1383611_at	---	---	---	Rn.23997	AI145497	6.47	7.05	6.79	7.55	7.03	7.26	1.43	up	8.63E-02	8.95E-01	-	-
1375272_at	---	---	---	Rn.93583	BE113423	5.08	4.43	3.86	3.98	3.77	4.08	1.43	down	2.32E-01	8.95E-01	-	-
1372779_at	B3gnt2	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 2	305571	Rn.1978	BG373352	8.08	8.05	8.50	8.49	8.95	8.73	1.43	up	5.83E-02	8.95E-01	-	-
1373649_at	687381 /// LOC69	similar to COX10 homolog, cytochrome c oxidase assembly protein, heme A:	687381	/// 691853	Rn.76594	AI453889	5.91	5.92	3.40	4.85	3.84	4.99	1.43	down	6.05E-01	8.95E-01	-	-
1392374_at	---	---	---	---	Rn.209623	BF389797	2.37	2.36	3.90	2.37	2.38	2.36	1.43	down	3.72E-01	8.95E-01	-	-
1384690_at	---	---	---	---	Rn.204110	AI071329	2.59	2.37	2.37	4.15	2.37	2.35	1.43	up	4.43E-01	8.95E-01	-	-
1382441_at	Arid1b	AT rich interactive domain 1B (Swi1 like)	282546	Rn.22598	AI556402	7.84	7.40	7.20	8.30	7.74	7.93	1.43	up	1.13E-01	8.95E-01	-	-
1390035_at	LOC305076	similar to hypothetical protein MGC29875; novel putative protein similar to YIL	305076	Rn.23222	BI297073	5.26	4.88	4.30	4.50	4.19	4.20	1.43	down	1.58E-01	8.95E-01	-	-
1389381_at	Sqstm1	sequestosome 1	113894	Rn.107103	AI411586	6.19	6.88	7.61	7.54	7.60	7.08	1.43	up	3.11E-01	8.95E-01	-	-
1371510_at	Hcfc1r1	host cell factor C1 regulator 1 (XPO1-dependent)	287097	Rn.1003	AA944494	7.80	8.51	7.05	8.39	8.19	8.32	1.43	up	2.95E-01	8.95E-01	-	-
1371132_a_at	Ank3	ankyrin 3, epithelial	361833	Rn.220009	AJ428573	5.25	6.92	6.97	5.98	6.61	8.09	1.43	up	5.77E-01	8.95E-01	-	-
1381476_at	---	---	---	Rn.134531	BF416405	3.24	3.08	5.77	2.86	3.24	4.44	1.43	down	6.33E-01	8.95E-01	-	-
1383508_at	RGD1309403	similar to hypothetical protein FLJ12661	310417	Rn.38949	AW528853	2.67	2.59	2.32	2.67	3.57	2.88	1.43	up	1.56E-01	8.95E-01	-	-
1383328_x_at	Pdcd4	programmed cell death 4	64031	Rn.206229	AI576297	6.50	7.60	7.87	7.95	8.19	7.37	1.43	up	3.52E-01	8.95E-01	-	-
1398788_at	Pdia3	protein disulfide isomerase family A, member 3	29468	Rn.11527	NM_017319	10.26	10.43	9.82	10.52	10.40	11.12	1.43	up	1.52E-01	8.95E-01	-	-
1367940_at	Cxcr7	chemokine (C-X-C motif) receptor 7	84348	Rn.12959	NM_053352	6.79	5.30	6.70	7.42	7.35	5.56	1.43	up	5.46E-01	8.95E-01	-	-
1393244_at	Nploc4	Nuclear protein localization 4 homolog (S. cerevisiae)	140639	Rn.144645	AW435274	4.31	4.86	4.96	4.31	5.88	5.48	1.43	up	3.74E-01	8.95E-01	-	-
1392165_at	Ing2	inhibitor of growth family, member 2	290744	Rn.20482	AI071247	6.56	6.81	6.99	7.18	7.33	7.38	1.43	up	2.04E-02	8.95E-01	-	-
1381119_at	Ttc1	tetratricopeptide repeat domain 1	287208	Rn.81253	BM387763	5.34	5.47	5.25	5.25	4.02	5.25	1.43	down	2.85E-01	8.95E-01	-	-
1383815_at	Zfyve1	zinc finger, FYVE domain containing 1	299188	Rn.205587	BF543208	5.08	3.47	3.50	3.42	3.57	3.53	1.43	down	3.92E-01	8.95E-01	-	-
1386833_at	Bcl6b	B-cell CLL/lymphoma 6, member B (zinc finger protein)	360551	Rn.137148	BF554138	2.64	2.62	2.64	3.97	2.65	2.82	1.43	up	2.85E-01	8.95E-01	-	-
1373184_at	Csgalnact2	chondroitin sulfate N-acetylgalactosaminyltransferase 2	297554	Rn.3853	BF410842	2.46	2.56	4.53	2.76	2.67	2.58	1.43	down	4.92E-01	8.95E-01	-	-
1372605_at	Gatad1	GATA zinc finger domain containing 1	500005	Rn.203407	AA925258	4.76	5.28	5.66	5.97	5.56	5.70	1.43	up	1.53E-01	8.95E-01	-	-
1377713_at	Foxn3	forkhead box N3	314374	Rn.105640	AI639381	7.48	7.37	6.60	7.42	7.63	7.94	1.43	up	1.84E-01	8.95E-01	-	-
1373398_at	Trim37	Tripartite motif-containing 37	360592	Rn.9335	BI275184	6.22	6.98	6.81	5.46	7.29	5.74	1.43	down	4.52E-01	8.95E-01	-	-
1398491_at	Ildr1	immunoglobulin-like domain containing receptor 1	303914	Rn.155292	BM383434	2.53	2.51	2.54	3.03	3.43	2.65	1.43	up	8.63E-02	8.95E-01	-	-
1369095_at	Ppp1r9a	protein phosphatase 1, regulatory (inhibitor) subunit 9A	84685	Rn.10849	NM_053473	2.54	2.53	2.65	2.58	2.55	4.13	1.43	up	3.83E-01	8.95E-01	-	-
1372388_at	Wdr48	WD repeat domain 48	363164	Rn.8675	AI227930	3.82	4.24	3.29	3.99	5.00	3.89	1.43	up	3.18E-01	8.95E-01	-	-
1384788_at	Daglb	diacylglycerol lipase, beta	304289	Rn.44074	BF393298	6.08	4.94	4.59	4.55	4.36	5.17	1.43	down	3.73E-01	8.95E-01	-	-
1367979_s_at	Cyp51	cytochrome P450, subfamily 51	25427	Rn.107152	BG664123	6.54	7.25	6.08	6.82	5.34	6.18	1.43	down	4.04E-01	8.95E-01	-	-
1396093_at	---	---	---	Rn.210450	BF405335	2.29	2.28	3.82	2.29	2.29	2.28	1.42	down	3.74E-01	8.95E-01	-	-
1372537_at	---	---	---	---	BI289642	7.89	8.44	7.77	8.80	7.86	8.97	1.42	up	2.73E-01	8.95E-01	-	-
1372466_at	---	---	---	Rn.164421	AI408571	5.42	5.82	5.84	6.13	5.96	6.52	1.42	up	7.78E-02	8.95E-01	-	-
1395595_at	Mki67ip	Mki67 (FHA domain) interacting nucleolar phosphoprotein	246042	Rn.20901	BG667615	6.54	5.42	4.86	4.53	5.82	4.95	1.42	down	4.58E-01	8.95E-01	-	-
1381754_at	---	---	---	---	BE116951	6.44	5.66	4.14	6.09	5.81	5.87	1.42	up	4.94E-01	8.95E-01	-	-
1374984_at	Epb4.1l5	erythrocyte protein band 4.1-like 5	304733	Rn.2480	AA858925	8.38	7.93	8.56	7.91	7.15	8.29	1.42	down	2.56E-01	8.95E-01	-	-
1391972_a_at	Zswim4	zinc finger, SWIM-type containing 4	304655	Rn.128757	BE108410	2.39	2.46	3.86	2.39	2.40	2.39	1.42	down	3.46E-01	8.95E-01	-	-
1371964_at	Grsf1	G-rich RNA sequence binding factor 1	305256	Rn.66912	BM385050	8.27	7.90	8.17	7.32	7.66	7.84	1.42	down	5.45E-02	8.95E-01	-	-
1377243_at	---	---	---	---	AI172211	3.68	4.15	2.60	3.57	4.69	3.70	1.42	up	4.28E-01	8.95E-01	-	-
1373699_at	---	---	---	Rn.165462	BM391164	2.36	2.71	2.39	3.06	2.37	3.56	1.42	up	2.32E-01	8.95E-01	-	-
1376192_at	Nat8	N-acetyltransferase 9 (GCN5-related, putative)	303669	Rn.19920	AI070138	6.71	7.02	6.82	8.02	6.41	7.66	1.42	up	3.60E-01	8.95E-01	-	-
1395519_at	MGC95152	similar to B230212L03Rik protein	297109	Rn.92940	BG670960	5.66	6.70	7.66	6.04	6.11	6.34	1.42	down	4.32E-01	8.95E-01	-	-
1397627_at	Diaph1	diaphanous homolog 1 (Drosophila)	307483	Rn.3004	BE128082	3.07	4.26	3.75	3.38	2.69	3.47	1.42	down	2.94E-01	8.95E-01	-	-
1370364_at	Arfgap1	ADP-ribosylation factor GTPase activating protein 1	246310	Rn.11219	U35776	3.52	5.58	3.45	4.29	5.25	4.53	1.42	up	5.36E-01	8.95E-01	-	-
1375186_at	Dph3	DPH3, KTI11 homolog (S. cerevisiae)	680594	Rn.3539	AI169144	9.55	8.94	9.83	8.45	8.30	9.05	1.42	down	2.99E-01	8.95E-01	-	-
1372317_at	Ehd1	EH-domain containing 1	293692	Rn.8141	AI177867	8.25	8.52	8.86	8.08	7.95	8.06	1.42	down	4.95E-02	8.95E-01	-	-
1374183_at	Eapp	E2F-associated phosphoprotein	299043	Rn.55623	AI705068	6.98	6.98	6.41	7.50	7.05	7.35	1.42	up	9.44E-02	8.95E-01	-	-
1380485_at	Ccdc71	Coiled-coil domain containing 71	498678	Rn.140756	BE106894	4.03	2.84	2.65	2.75	2.76	2.47	1.42	down	3.12E-01	8.95E-01	-	-
1371471_at	Gfpt2	glutamine fructose-6-phosphate transaminase 2	292624	Rn.8075	BF281741	8.82	8.87	8.24	9.05	9.20	9.21	1.42	up	6.98E-02	8.95E-01	-	-
1377553_at	Leng9	glioma tumor suppressor candidate region gene 2	292596	Rn.92802	BF407226	3.55	3.04	2.96	2.68	2.67	2.67	1.42	down	5.13E-02	8.95E-01	-	-
1376572_a_at	Svil	Leukocyte receptor cluster (LRC) member 9	361256	Rn.36324	AI045448	2.74	4.82	4.43	3.19	3.05	4.22	1.42	down	5.27E-01	8.95E-01	-	-
1369633_at	Cxcl12	supervillin	24772	Rn.54439	AF189724	6.61	4.85	5.22	5.65	4.79	4.70	1.42	down	4.54E-01	8.95E-01	-	-
1398818_at	Gng5	chemokine (C-X-C motif) ligand 12 (stromal cell-derived factor 1)	79218	Rn.2695	NM_024377	2.53	2.42	2.52	2.67	2.50	3.82	1.42	up	2.88E-01	8.95E-01	-	-
1383346_at	Ercc4	guanine nucleotide binding protein (G protein), gamma 5	304719	Rn.195555	BF387821	3.89	4.04	2.73	3.91	3.77	4.51	1.42	up	3.40E-01	8.95E-01	-	-
1377130_at	---	excision repair cross-complementing rodent repair deficiency, complementatic	---	Rn.7919	AW526352	5.40	4.73	6.50	4.96	5.58	4.57	1.42	down	4.39E-01	8.95E-01	-	-
1378357_at	---	---	---	Rn.167864	AI556522	5.99	6.94	7.80	7.33	7.71	7.23	1.42	up	4.01E-01	8.95E-01	-	-
1371664_at	Pxn	paxillin	360820	Rn.75	BG673589	7.53	7.38	7.41	6.94	6.53	7.33	1.42	down	9.69E-02	8.95E-01	-	-
1378243_at	Tmem17	transmembrane protein 17	360985	Rn.8102	AA923937	5.29	4.34	4.98	3.39	4.68	5.01	1.42	down	4.21E-01	8.95E-01	-	-
1385011_at	Smarca4	SWI/SNF related, matrix associated, actin dependent regulator of chromatin,	171379	Rn.23417	BM385181	6.17	6.18	2.56	4.83	3.30	5.25	1.42	down	7.23E-01	9.12E-01	-	-
1389172_at	---	---	---	Rn.166715	AI179391	7.68	6.36	5.20	6.51	4.86	6.33	1.42	down	5.96E-01	8.95E-01	-	-
1383982_at	---	---	---	Rn.9102	BE112063	4.30	5.28	4.75	4.79	5.70	5.36	1.42	up	2.58E-01	8.95E-01	-	-
1398724_at	Glis2	GLIS family zinc finger 2	302946	Rn.166896	BE112211	4.11	4.07	4.90	3.16	4.06	4.33	1.42	down	3.15E-01	8.95E-01	-	-
1375928_at	Setd8 /// Setd8-ps	SET domain containing (lysine methyltransferase) 8 /// SET domain containin	498178	/// 689820	Rn.8879	BI285329	6.05	7.01	7.13	7.32	6.84	7.55	1.42	up	2.75E-01	8.95E-01	-	-
1383147_at	---	---	---	Rn.203277	AW526373	4.45	4.26	4.50	5.45	4.89	4.39	1.42	up	1.82E-01	8.95E-01	-	-
1370123_a_at	Cttn	cortactin	60465	Rn.107869	AF054618	5.30	4.24	4.28	3.93	3.55	4.81	1.42	down	3.73E-01	8.95E-01	-	-
1370100_at	Pik3r2	phosphoinositide-3-kinase, regulatory subunit 2 (beta)	29741	Rn.22497	NM_022185	2.56	2.64	2.65	4.09	2.65	2.64	1.42	up	3.51E-01	8.95E-01	-	-
1391091_at	Cyld	cylindromatosis (turban tumor syndrome)	312937	Rn.168938	AI406286	4.20	3.72	5.25	4.07	3.31	4.26	1.42	down	3.97E-01	8.95E-01	-	-
1372561_at	Smap2	small ArfGAP2	298500	Rn.203765	AI234095	6.78	5.78	5.23	7.19	5.88	6.25	1.42	up	4.43E-01	8.95E-01	-	-
1394476_at	Zfp709	Zinc finger protein 709	286773	Rn.123575	AW553213	3.51	4.40	6.04	5.61	5.76	4.10	1.42	up	6.06E-01	8.95E-01	-	-
1371176_at	Nfic	nuclear factor I/C	29228	Rn.86582	AB012233	4.18	4.16	3.44	5.00	4.15	4.14	1.42	up	2.47E-01	8.95E-01	-	-
1372923_at	Pex11b	peroxisomal biogenesis factor 11 beta	310682	Rn.24248	BG377340	5.66	6.32	6.64	6.86	6.30	6.98	1.42	up	2.25E-01	8.95E-01	-	-
1385708_at	MGC93861	hypothetical protein LOC682010	682010	Rn.212099	BG378707	4.01	4.02	3.29	3.27	3.28	3.24	1.42	down	1.04E-01	8.95E-01	-	-
1380504_at	Acaa2	Acetyl-Coenzyme A acyltransferase 2	170465	Rn.3786	BI282488	2.67	2.54	2.96	4.58	2.53	2.58	1.42	up	4.99E-01	8.95E-01	-	-
1370788_a_at	Prlr	prolactin receptor	24684	Rn.9757	L48060	8.94	10.14	9.48	8.67	8.64	9.72	1.42	down	3.64E-01	8.95E-01	-	-
1387170_at	Cenk2a1	cenA-kinase 2, alpha 1 polypeptide	116549	Rn.4231	NM_053824	4.64	5.38	4.72	4.65	3.36	5.21	1.42	down	4.41E-01	8.95E-01	-	-
1370446_at	Nme7	non-metastatic cells 7, protein expressed in (nucleoside-diphosphate kinase)	171566	Rn.82718	AF202049	9.25	9.42	10.26	9.16	8.98	9.27	1.42	down	1.92E-01	8.95E-01	-	-
1382105_at	Gnb5	guanine nucleotide binding protein (G protein), beta 5	83579	Rn.23042	AI603217	6.38	6.58	6.93	6.88	7.41	7.12	1.42	up	8.60E-02	8.95E-01	-	-
1385377_at	---	---	---	Rn.203048	AA858605	2.55	2.54	2.58	4.07	2.62	2.50	1.42	up	3.72E-01	8.95E-01	-	-
1387416_at	Rest	REST-silencing transcription factor	83618	Rn.10879	NM_031788	3.12	3.22	3.23	4.04	3.67	3.38	1.42	up	5.90E-02	8.95E-01	-	-
1374987_at	---	---	---	Rn.220617	AI232974	8.24	7.74	8.05	7.41	7.21	7.89	1.42	down	1.12E-01	8.95E-01	-	-
1376863_at	---	---	---	---	BE109118	6.87	6.69	5.66	5.35	6.15	6.19	1.42	down	3.35E-01	8.95E-01	-	-
1373986_at	---	---	---	Rn.165814	AI410107	9.02	7.04	7.83	7.59	7.08	7.69	1.42	down	4.49E-01	8.95E-01	-	-
1375973_at	Arih1	ariadne ubiquitin-conjugating enzyme E2 binding protein homolog 1 (Drosoph	300756	Rn.29865	AI600108	5.66	6.23	5.39	6.43	5.83	6.53	1.42	up	2.00E-01	8.

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1372631_at	Tk1	thymidine kinase 1, soluble	24834	Rn.217952	AI170596	3.61	3.66	2.17	4.21	3.50	3.24	1.42	up	4.25E-01	8.95E-01	-	-
1388691_at	Ubqln4	ubiquilin 4	310633	Rn.17785	AI177410	3.08	2.47	4.17	3.39	2.13	2.69	1.42	down	4.60E-01	8.95E-01	-	-
1384187_at	Ap1s2	adaptor-related protein complex 1, sigma 2 subunit	302671	Rn.17309	BF551686	2.53	2.61	2.63	2.56	2.71	4.01	1.42	up	3.36E-01	8.95E-01	-	-
1376024_at	Stim1	stromal interaction molecule 1	361618	Rn.106771	AW914992	2.38	2.35	2.36	2.35	3.70	2.55	1.42	up	2.97E-01	8.95E-01	-	-
1368414_at	Slc5a2	solute carrier family 5 (sodium/glucose cotransporter), member 2	64522	Rn.5887	NM_022590	6.32	5.37	7.17	6.07	6.09	5.19	1.42	down	4.46E-01	8.95E-01	-	-
1388720_at	---	---	---	Rn.1130	BM390713	4.89	4.82	4.41	4.76	5.60	5.27	1.42	up	1.55E-01	8.95E-01	-	-
1372465_at	Nol6	nucleolar protein family 6 (RNA-associated)	313167	Rn.220667	AI409184	6.37	6.39	5.65	6.88	6.62	6.41	1.42	up	1.47E-01	8.95E-01	-	-
1395324_at	---	---	---	Rn.205031	BM385905	2.46	2.44	3.82	2.42	2.47	2.32	1.42	down	3.35E-01	8.95E-01	-	-
1382923_at	Syncrip	synaptotagmin binding, cytoplasmic RNA interacting protein	363113	Rn.202606	AI072424	7.92	8.77	8.62	7.74	7.98	8.07	1.42	down	1.46E-01	8.95E-01	-	-
1368272_at	Got1	glutamic-oxaloacetic transaminase 1, soluble (aspartate aminotransferase 1)	24401	Rn.5819	D00252	6.96	7.46	7.36	7.03	5.83	7.41	1.42	down	3.70E-01	8.95E-01	-	-
1396441_at	---	---	---	---	BE108895	3.93	2.93	2.61	2.60	2.64	2.72	1.42	down	2.77E-01	8.95E-01	-	-
1377642_at	Cav2	caveolin 2	363425	Rn.81070	BE349669	4.27	2.75	2.94	2.92	2.79	2.75	1.42	down	3.56E-01	8.95E-01	-	-
1372436_at	Tpd52l2	tumor protein D52-like 2	296480	Rn.23937	BG668434	7.98	7.97	8.14	7.85	6.97	7.75	1.42	down	1.51E-01	8.95E-01	-	-
1382603_at	---	---	---	Rn.198553	AW521319	2.42	2.41	2.44	2.41	3.94	2.43	1.42	up	3.78E-01	8.95E-01	-	-
1374924_at	---	---	---	Rn.204955	BE098025	5.73	5.57	5.49	5.81	6.41	6.07	1.42	up	5.62E-02	8.95E-01	-	-
1389072_at	Mtmr4	myotubularin related protein 4	287607	Rn.2567	AI412323	5.94	5.35	5.39	6.41	5.73	6.04	1.42	up	1.42E-01	8.95E-01	-	-
1374768_at	Ccdc65	coiled-coil domain containing 65	362994	Rn.34654	BI279857	2.78	2.76	2.75	3.27	3.89	2.64	1.42	up	2.38E-01	8.95E-01	-	-
1376106_at	Tmem178	transmembrane protein 178	362691	Rn.17530	AI010157	4.66	3.54	5.63	4.21	3.76	4.36	1.42	down	4.71E-01	8.95E-01	-	-
1369049_at	Rere	arginine-glutamic acid dipeptide (RE) repeats	116665	Rn.10277	NM_053885	3.43	3.43	3.42	3.41	4.89	3.48	1.42	up	3.56E-01	8.95E-01	-	-
1388871_at	Ash2l	ash2 (absent, small, or homeotic)-like (Drosophila)	290829	Rn.219095	BG378089	6.00	6.62	5.31	6.45	6.58	6.40	1.42	up	2.59E-01	8.95E-01	-	-
1399125_at	Inpp1	inositol polyphosphate-1-phosphatase	316376	Rn.20288	BI275516	3.16	3.49	3.54	3.59	4.32	3.78	1.42	up	1.13E-01	8.95E-01	-	-
1374870_at	Col27a1	Collagen, type XXVII, alpha 1	298101	Rn.53800	BF286402	4.04	3.66	2.35	4.26	3.64	3.66	1.42	up	4.13E-01	8.95E-01	-	-
1398824_at	Tmed2	transmembrane emp24 domain trafficking protein 2	65165	Rn.1022	NM_031722	8.62	8.31	7.76	8.63	8.38	9.18	1.42	up	2.20E-01	8.95E-01	-	-
1398859_at	Sec16a	SEC16 homolog A (S. cerevisiae)	114089	Rn.199218	AA850070	5.15	7.05	6.95	6.40	6.65	7.59	1.42	up	5.22E-01	8.95E-01	-	-
1370379_at	Prss8	protease, serine, 8 (prostasin)	192107	Rn.107364	AF202076	7.75	9.48	8.41	8.23	8.12	7.78	1.42	down	3.93E-01	8.95E-01	-	-
1388722_at	Dnajb1	DnaJ (Hsp40) homolog, subfamily B, member 1	361384	Rn.128947	AA945704	8.26	7.76	7.88	7.16	7.33	7.90	1.42	down	1.38E-01	8.95E-01	-	-
1380119_at	---	---	---	Rn.151748	AA996432	2.87	2.89	2.88	3.45	3.73	2.96	1.41	up	8.93E-02	8.95E-01	-	-
1383239_at	Zcchc7	zinc finger, CCHC domain containing 7	298086	Rn.56971	BF406915	4.09	4.08	3.08	4.94	3.29	4.52	1.41	up	4.49E-01	8.95E-01	-	-
1390090_at	---	---	---	Rn.219251	AA944459	6.41	5.77	5.50	6.82	6.26	6.10	1.41	up	2.24E-01	8.95E-01	-	-
1385072_at	Galm	galactose mutarotase (aldose 1-epimerase)	313843	Rn.83639	AA997048	9.37	9.75	9.61	8.89	9.05	9.28	1.41	down	3.48E-02	8.95E-01	-	-
1376546_at	RGD1565432	similar to hypothetical protein	499157	Rn.77399	BE120498	6.66	7.05	7.72	7.70	7.22	8.01	1.41	up	2.64E-01	8.95E-01	-	-
1394643_at	---	---	---	Rn.174768	AA819409	3.14	3.55	3.01	3.56	3.71	3.94	1.41	up	6.34E-02	8.95E-01	-	-
1388721_at	Hspb8	heat shock protein 8	113906	Rn.102906	BG380282	2.40	3.89	2.41	2.40	2.42	2.38	1.41	down	3.72E-01	8.95E-01	-	-
1368212_at	Sfrs11	splicing factor, arginine/serine-rich 11	502603	Rn.11095	BF281311	6.15	6.07	6.14	5.58	5.55	5.74	1.41	down	1.48E-03	8.95E-01	-	-
1382189_at	Sdc2	syndecan 2	25615	Rn.11127	AI574779	8.64	9.25	9.06	8.25	8.43	8.77	1.41	down	1.03E-01	8.95E-01	-	-
1390127_at	Dixdc1	DIX domain containing 1	363062	Rn.8331	BI296216	3.03	2.97	2.53	3.81	3.23	3.00	1.41	up	1.57E-01	8.95E-01	-	-
1367686_at	Serp1	stress-associated endoplasmic reticulum protein 1	80881	Rn.2119	AI103695	8.49	8.41	8.33	8.84	8.25	9.65	1.41	up	2.88E-01	8.95E-01	-	-
1395552_s_at	Ankrd13c	ankyrin repeat domain 13C	885374	Rn.100818	BG671371	6.34	6.64	7.04	5.95	6.32	6.24	1.41	down	9.66E-02	8.95E-01	-	-
1388368_at	Cnksr3	Cnksr family member 3	308113	Rn.137681	AW253242	5.61	6.54	5.73	4.83	5.37	6.17	1.41	down	3.62E-01	8.95E-01	-	-
1395858_at	---	---	---	---	AI548127	2.45	2.45	2.50	2.46	4.00	2.44	1.41	up	3.87E-01	8.95E-01	-	-
1388354_at	Ascc3l1	activating signal cointegrator 1 complex subunit 3-like 1	296126	Rn.76239	BE349703	7.11	7.15	6.69	6.52	6.05	6.88	1.41	down	1.51E-01	8.95E-01	-	-
1375187_at	---	---	---	Rn.12112	BF281701	2.40	2.38	2.40	2.68	2.40	3.61	1.41	up	2.43E-01	8.95E-01	-	-
1382178_at	Fam83h	family with sequence similarity 83, member H	362937	Rn.16898	BI275934	2.34	3.97	2.33	2.37	2.33	2.44	1.41	down	4.10E-01	8.95E-01	-	-
1368558_s_at	Aif1	allograft inflammatory factor 1	29427	Rn.32080	NM_017196	3.44	3.73	2.69	4.63	3.68	3.06	1.41	up	4.16E-01	8.95E-01	-	-
1385094_at	---	---	---	Rn.199740	BE096277	2.65	2.62	2.64	2.55	4.22	2.64	1.41	up	4.09E-01	8.95E-01	-	-
1395790_at	Zbtb33	zinc finger and BTB domain containing 33	501506	Rn.169266	BF409032	3.48	5.42	3.92	4.75	4.78	4.80	1.41	up	4.43E-01	8.95E-01	-	-
1390905_at	Mast4	microtubule associated serine/threonine kinase family member 4	310040	Rn.43251	AW533482	2.82	3.48	3.33	3.31	4.13	3.69	1.41	up	1.82E-01	8.95E-01	-	-
1368703_at	Pdlim5	PDZ and LIM domain 5	64353	Rn.17933	NM_053326	5.06	6.53	5.69	5.47	4.41	5.90	1.41	down	4.63E-01	8.95E-01	-	-
1398220_at	---	---	---	Rn.171653	BE121176	2.29	2.29	2.30	3.80	2.30	2.28	1.41	up	3.77E-01	8.95E-01	-	-
1392909_at	---	---	---	Rn.17699	AI7005674	3.49	3.20	2.77	3.30	3.82	3.83	1.41	up	1.41E-01	8.95E-01	-	-
1389674_at	Znf282	zinc finger protein 282	297065	Rn.152208	BI286654	2.44	2.41	2.29	2.36	3.87	2.40	1.41	up	3.75E-01	8.95E-01	-	-
1388259_at	Snrpn	small nuclear ribonucleoprotein polypeptide N	81781	Rn.11169	M29294	3.90	2.36	2.36	2.35	2.42	2.35	1.41	down	3.87E-01	8.95E-01	-	-
1371404_at	Eif4b	eukaryotic translation initiation factor 4B	300253	Rn.95954	AI172206	8.20	9.05	9.18	9.18	9.17	9.58	1.41	up	2.10E-01	8.95E-01	-	-
1396460_at	---	---	---	Rn.155328	AW522969	3.85	2.35	2.36	2.35	2.36	2.35	1.41	down	3.72E-01	8.95E-01	-	-
1372898_at	---	---	---	Rn.22756	AA893807	7.89	7.79	7.34	8.15	7.92	8.45	1.41	up	8.48E-02	8.95E-01	-	-
1392717_at	---	---	---	Rn.204842	BE109171	3.07	3.06	4.08	3.07	2.59	3.06	1.41	down	2.53E-01	8.95E-01	-	-
1374836_at	Rrp9	ribosomal RNA processing 9, small subunit (SSU) processome component, ho	363134	Rn.11840	AA964554	4.55	4.61	3.69	4.93	4.71	4.70	1.41	up	1.79E-01	8.95E-01	-	-
1384435_at	Tmem68	transmembrane protein 68	312946	Rn.11754	AA964258	4.98	6.16	5.26	3.88	5.45	4.61	1.41	down	4.75E-01	8.95E-01	-	-
1373438_at	Ube2o	ubiquitin-conjugating enzyme E2O	303689	Rn.209068	BE329352	2.94	3.18	2.54	3.53	3.48	3.15	1.41	up	8.85E-02	8.95E-01	-	-
1390241_at	Gigyf1	GRB10 interacting GYF protein 1	304378	Rn.206405	BI296888	6.80	5.09	5.27	5.22	5.10	5.35	1.41	down	4.13E-01	8.95E-01	-	-
1398968_at	N-pac	cytokine-like nuclear factor n-pac	360477	Rn.2639	AI168979	7.26	6.46	6.02	6.39	5.47	6.39	1.41	down	3.52E-01	8.95E-01	-	-
1398501_at	Lrrc61	leucine rich repeat containing 61	500111	Rn.140918	BE102282	5.38	7.20	6.68	7.12	5.70	4.94	1.41	down	5.83E-01	8.95E-01	-	-
1376467_at	Mllt1	Myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila);	301119	Rn.33401	AI009054	2.37	2.37	3.83	2.37	2.37	2.33	1.41	down	3.65E-01	8.95E-01	-	-
1390255_at	Ablim3	actin binding LIM protein family, member 3	307395	Rn.39037	BG381583	7.26	7.74	7.65	8.02	7.84	8.29	1.41	up	6.46E-02	8.95E-01	-	-
1374665_at	Gemin4	gem (nuclear organelle) associated protein 4	497958	Rn.53	BG057541	4.02	2.40	2.42	2.40	2.41	2.54	1.41	down	4.08E-01	8.95E-01	-	-
1369402_at	Adnp	activity-dependent neuroprotector homeobox	64622	Rn.48777	NM_022681	5.95	6.45	6.51	6.58	6.98	6.85	1.41	up	7.78E-02	8.95E-01	-	-
1396059_at	Ubxn4	UBX domain protein 4	304766	Rn.2022	BF289251	4.81	4.89	5.68	5.97	5.06	5.85	1.41	up	2.78E-01	8.95E-01	-	-
1373940_at	Nck1	NCK adaptor protein 1	300955	Rn.222028	BM386507	4.50	4.18	4.38	3.69	3.92	3.95	1.41	down	1.56E-02	8.95E-01	-	-
1382506_at	---	---	---	Rn.114503	AI044841	2.52	2.68	4.03	2.50	2.52	2.70	1.41	down	3.60E-01	8.95E-01	-	-
1384486_at	---	---	---	Rn.169204	BI288961	5.84	6.31	6.71	5.66	5.85	5.86	1.41	down	1.28E-01	8.95E-01	-	-
1383179_at	---	---	---	Rn.15161	BI291413	5.55	4.80	5.31	4.10	5.33	4.73	1.41	down	2.97E-01	8.95E-01	-	-
1373906_at	Fam173b	family with sequence similarity 173, member B	499561	Rn.30929	AI104594	7.76	6.82	7.39	7.09	6.03	7.35	1.41	down	3.65E-01	8.95E-01	-	-
1369236_at	Prdm4	PR domain containing 4	170820	Rn.162921	NM_133312	2.63	3.28	3.15	3.34	3.79	3.43	1.41	up	1.06E-01	8.95E-01	-	-
1369996_at	Polr2f	polymerase (RNA) II (DNA directed) polypeptide F	83503	Rn.28212	NM_031335	7.24	7.84	7.17	7.57	8.02	8.15	1.41	up	1.45E-01	8.95E-01	-	-
1373769_at	Pgm2	phosphoglucomutase 2	289832	Rn.203347	AI776913	5.74	5.46	4.59	6.18	5.04	6.06	1.41	up	3.77E-01	8.95E-01	-	-
1370057_at	Carp1	cysteine and glycine-rich protein 1	29276	Rn.108075	NM_017148	8.03	5.34	4.89	5.44	6.05	5.27	1.41	down	6.47E-01	8.95E-01	-	-
1368083_at	Ccnh	cyclin H	84389	Rn.23255	NM_052981	4.62	5.12	5.58	6.04	4.44	6.34	1.41	up	4.87E-01	8.95E-01	-	-
1373500_at	Lrpprc	leucine-rich PPR-motif containing	313867	Rn.92051	BI294727	6.93	8.00	7.55	7.68	7.98	8.31	1.41	up	2.40E-01	8.95E-01	-	-
1377331_at	---	---	---	Rn.147450	AW532489	5.12	4.57	3.78	4.92	5.11	4.94	1.41	up	2.74E-01	8.95E-01	-	-
1367746_a_at	Flot2	flotillin 2	83764	Rn.2105	NM_031830	5.68	7.39	6.18	6.90	6.81	7.02	1.41	up	3.84E-01	8.95E-01	-	-
1391944_at	184a /// RGD1566	family with sequence similarity 184, member A /// similar to minichromosome c	361853 /// 499437	Rn.201992	BI296237	3.42	3.12	3.38	4.58	3.42	3.42	1.41	up	2.79E-01	8.95E-01	-	-
1389111_at	---	---	---	Rn.17462	BF396316	5.34	5.17	6.44	4.82	4.72	5.92	1.41	down	4.21E-01	8.95E-01	-	-
1389383_at	Sec24a	SEC24 family, member A (S. cerevisiae)	287275	Rn.7981	BI289855	7.00	6.73	7.13	7.33	7.39	7.64	1.41	up	2.97E-02	8.95E-01	-	-
1396229_at	---	---	---	Rn.147179	BG378004	7.25	8.76	8.14	8.02	8.84	8.79	1.41	up	3.87E-01	8.95E-01	-	-
1382171_at	Tsc22d2	TSC22 domain family, member 2	499624	Rn.167784	AI454310	4.87	4.08	5.06	5.23	5.17	5.09	1.41	up	1.78E-01	8.95E-01	-	-
1392861_at	---	---	---	Rn.8802	BG373422	2.40	2.60	2.41	2.43	3.78	2.69	1.41	up	3.02E-01	8.95E-01	-	-
1391370_at	---	---	---	Rn.156016	AW532474	3.04	3.16	5.89	2.96	2.98	4.66	1.41	down	6.71E-01	9.01E-01	-	-
1379085_at	RGD1561878	similar to mKIAA0978 protein	311553	Rn.199307	BF396507	6.45	7.79	6.44	6.40	8.25	7.52	1.41	up	5.18E-01	8.95E-01	-	-
1394509_at	---	---	---	Rn.169833	BE114001	2.61	4.79	5.22	3.73	3.73	3.67	1.41	down	5.72E-01	8.95E-01	-	-
1369433_at	Cep78	centrosomal protein 78kDa	60347	Rn.42936	NM_021741	3.02	3.58	3.03	2.37	3.02	2.74	1.41	down	1.32E-01	8.95E-01	-	-
1376912_at	RGD1310324	hypothetical LOC287388	287388	Rn.82639	BI290097	2.65	2.80	2.78	2.60	3.93	3.19	1.41	up	2.70E-01	8.95E-01	-	-
1398809_at	Nde1	nudE nuclear distribution gene E homolog 1 (A. nidulans)	83836	Rn.20222	NM_053347	5.89	3.87	3.91	5.48	4.05	5.63	1.41	up	5.84E-01	8.95E-01	-	-
1381843_at	---	---	---	Rn.135076	AI548139	3.58	2.94	2.50	2.53	4.48	2.52	1.41	down	1.88E-01	8.95E-01	-	-
1369310_at	Basp1	brain abundant, membrane attached signal protein 1	64160	Rn.37779	NM_022300	5.41	4.22	4.48	4.53	4.09	4.00	1.41	down	2.79E-01	8.95E-01	-	-
1399123_at	Ints6	integrator complex subunit 6	361057	Rn.202377	BI302415	6.31	5.52	6.41	6.00	5.05	5.71	1.41	down	2.81E-01	8.95E-01	-	-
1383194_a_at	---	---	---	Rn.6374	AI030349	4.88	4.87	4.02	5.04	4.88	5.34	1.41	up	1.92E-01	8.95E-01	-	-
1371623_at	LOC685888	hypothetical protein LOC685888	685888	Rn.145356	AI411896	5.86	5.74	7.21	5.72	5.47	6.13	1.41	down	3.84E-01	8.95E-01	-	-
1387875_at	Ptk2	PTK2 protein tyrosine kinase 2	25614	Rn.2809	BI294798	6.22	6.10	5.80	5.44	5.13	6.06	1.41	down	1.74E-01	8.95E-01	-	-
1388555_at	Txndc17	thioredoxin domain containing 17	287474	Rn.18447	AI104292	11.43	11.18	11.57	11.16	10.55	10.97	1.41	down	8.04E-02	8.95E-01	-	-
1383566_at	---	---	---	Rn.35484	AW527690	2.53	2.62	2.46	2.49	4.18	2.43	1.41	up	4.37E-01	8.95E-01	-	-
1388335_at	Rbm17	RNA binding motif protein 17	291295	Rn.20694	BF396644	8.52	9.50	9.00	9.19	9.55	9.77	1.41	up	2.05E-01	8.95E-01	-	-
1382139_at	Rfx7	regulatory factor X, 7	315804	Rn.58758	BE108950	6.30	5.95	6.26	6.16	7.43	6.42	1.41	up	2.85E-01	8.95E-01	-	-
1392470_at	NIPBL	Nipped-B homolog (Drosophila)	294787	Rn.11589	AI180223	2.74	3.00	2.41	3.00	3.28	3.37	1.41	up	7.06E-02	8.95E-01	-	-
1373402_at	Dnajc14	DnaJ (Hsp40) homolog, subfamily C, member 14	114481	Rn.114340	AA848980	3.15	3.60	5.25	4.10	2.65	3.76	1.41	down	5.57E-01	8.95E-01	-	-
1367732_at	Gnb1	guanine nucleotide binding protein (G protein), beta polypeptide 1	24400	Rn.126047	U34958	7.72	8.04	7.92	7.67	7.24	7.27	1.41	down	4.17E-02	8.95E-01	-	-
1384895_at	---	---	---	---	AI044507	3.80	4.97	4.56	5.95	3.46	5.41	1.41	up	5.83E-01	8.95E-01	-	-
1397618_at	Spag9	sperm associated antigen 9	360600	Rn.24583	BF559398	4.27	5.76	4.08	3.99	4.03	4.62	1.41	down	4.34E-01	8.95E-01	-	-
1367833_at	Psmc5	proteasome (prosome, macropain) 26S subunit, ATPase, 5	81827	Rn.10972	NM_031149	9.15	9.27	9.55	8.79	8.27	9.43	1.41	down	2.36E-01	8.95E-01	-	-
1371520_at	Znf291	zinc finger protein 291	117521	Rn.163002	BI296732	3.48	3.47	4.77	3.44	3.29	3.51	1.41	down	3.19E-01	8.95E-01	-	-
1375843_at	Aig1	androgen-induced 1	292486	Rn.14443	BI290029	6.83	6.83	7.31	8.44	6.91	7.10	1.41	up	3.85E-01	8.95E-01	-	-
1389292_at	Rab18	RAB18, member RAS oncogene family	307039	Rn.53248	AI411439	6.68	6.66	6.19	6.75	6.47	7.79	1.41	up	3.16E-01	8.95E-01	-	-
1393758_at	Tlc1d	tetratricopeptide repeat domain 14	310314	Rn.144252	AI535253	3.04	4.01	3.33	2.97	2.97	2.95	1.41	down	1.61E-01	8.95E-01	-	-
1389071_at	Fusip1	FUS interacting protein (serine-arginine rich) 1	362630	Rn.162118	AI070564	4.43	4.44	3.52	4.25	4.73	4.89	1.41	up	2.41E-01	8.95E-01	-	-
1370947_at	Setd4	SET domain containing 4	245975	Rn.24842	AI228197	3.16	4.08	3.74	4.15	4.35	3.97	1.41	up	1.62E-01	8.95E-01	-	-
1398383_at	Cyb561	cytochrome b-561	303601	Rn.14673	BI282184	6.27	7.36	7.44	7.27	7.45	7.84	1.41	up	2.96E-01	8.95E-01	-	-
1373210_at	Lamb1	laminin, beta 1	298941	Rn.48387	BI296460	7.38	7.02	6.37	7.24	7.17	7.85	1.41	up	2.45E-01	8.95E-01	-	-
1389416_at	RGD1560398	RGD1560398	498192	Rn.204292	BI296051	3.64	4.09	3.26	3.60	2.65	3.25	1.41	down	2.47E-01	8.95E-01	-	-
1390267_at	Fars2	phenylalanyl-tRNA synthetase 2, mitochondrial	306879	Rn.8968	AW915175	7.40	6.80	7.79	7.01	6.22	7.28	1.41	down	3.12E-01	8.95E-01	-	-
1388966_at	---	---	---	Rn.164782	BM388250	5.12	3.30	2.82	3.03	3.42	3.30	1.41	down	5.24E-01	8.95E-01	-	-
1389009_at	Rarc1	arginine/serine-rich coiled-coil 1	361956	Rn.7317	BF418778	5.83	5.41	4.15	4.59	3.88	5.54	1.41	down	5.28E-01	8.95E-01	-	-
1389627_at	Znf746	zinc finger protein 746	312303	Rn.48855	BF550270	3.39	3.84	2.80	4.43	3.31	3.78	1.41	up	3.28E-01	8.95E-01	-	-
1372003_at	---	---	---	Rn.17235	BI296755	2.77	3.63	3.66	3.95	3.05	4.54	1.41	up	3.99E-01	8.95E-01	-	-
1396216_at	Lrrc8a	leucine rich repeat containing 8 family, member A	311846	Rn.33512	BF551351	6.32	7.15	6.70	7.17	7.05	7.44	1.41	up	1.39E-01	8.95E-01	-	-
1383487_at	---	---	---	Rn.91059	AW530484	3.72	4.25	5.94	5.99	4.48	4.91	1.41	up	5.73E-01	8.95E-01	-	-
1382156_at	---	---	---	---	BF409417	2.38	2.39	2.31	3.34	2.83	2.39	1.41	up	1.49E-01	8.95E-01	-	-
1395432_at	---	---	---	Rn.205643	AI716103	3.74	2.99	3.72	2.99	3.00	2.98	1.41	down	1.15E-01	8.95E-01	-	-
1380445_at	---	---	---	Rn.216575	BI294409	3.02	3.00	2.68	4.26	2.97	2.95	1.41	up	3.32E-01	8.95E-01	-	-
1367880_at	Lamb2	laminin, beta 2	25473	Rn.774	NM_012974	6.03	5.68	4.86	4.87	6.28	3.93	1.41	down	5.55E-01	8.95E-01	-	-
1397795_at	Avil	Advillin	79253	Rn.20161	AW533928	2.57	2.52	2.59	2.54	3.90	2.71	1.41	up	3.14E-01	8.95E-01	-	-
1380349_at	---	---	---	Rn.168578	BI395595	4.36	4.97	3.81	5.02	4.97	4.64	1.41	up	2.37E-01	8.95E-01	-	-
1371987_at	Pols	polymerase (DNA directed) sigma	306672	Rn.22554	BI274697	4.70	4.47	3.03	3.76	4.49	5.44	1.41	up	5.27E-01	8.95E-01	-	-
1388700_at	Foxn3	Forkhead box N3	314374	Rn.105640	AW253004	8.13	7.93	8.19	7.86	9.32	8.55	1.41	up	3.13E-01	8.95E-01	-	-
1382972_at	Utp15	UTP15, U3 small nucleolar ribonucleoprotein, homolog (S. cerevisiae)	310019	Rn.7959	BE103344	5.36	4.31	4.07	4.82	4.43	5.96	1.41	up	4.62E-01	8.95E-01	-	-
1372905_at	Vcl	vinculin	305679	Rn.164613	AW433888	5.23	5.37	5.11	4.62	4.92	4.99	1.41	down	2.73E-02	8.95E-01	-	-
1371026_at	Ppfia4	protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interactin	140592	Rn.105913	AY057064	2.44	2.49	3.84	2.44	2.44	2.41	1.41	down	3.44E-01	8.95E-01	-	-
1399083_at	hd11 /// LOC6861	abhydrolase domain containing 11 /// similar to abhydrolase domain containin	360831 /// 686139	Rn.195940	BF283000	5.40	6.98	5.73	5.97	6.66	6.96	1.41	up	4.33E-01	8.95E-01	-	-
1369705_at	Slc6a20	solute carrier family 6 (neurotransmitter transporter), member 20	311911	Rn.161982	AI166634	7.52	8.47	7.56	8.32	7.94	7.80	1.41	down	4.59E-01	8.95E-01	-	-
1398766_at	Rpn1	ribophorin I	25596	Rn.4224	NM_013067	9.51	9.82	9.55	9.83	10.22	10.30	1.41	up	4.72E-02	8.95E-01	-	-
1395880_at	---	---	---	Rn.13277	BE110888	4.32	4.45	5.43	3.82	4.46	4.44	1.41	down	2.94E-01	8.95E-01	-	-
1367477_at	Mrpl53	mitochondrial ribosomal protein L53	362388	Rn.6046	BM386162	8.57	9.02	8.85	8.44	8.02	8.49	1.

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)				REG	MTC
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval		
1383058_at	---	---	---	Rn.4287	AI410438	9.76	10.91	10.83	9.76	10.08	10.20	1.40	down	2.79E-01	8.95E-01	-	-
1377126_at	Commd7	COMM domain containing 7	296285	Rn.92689	BM386954	8.42	7.97	7.60	7.30	7.69	7.54	1.40	down	1.37E-01	8.95E-01	-	-
1386410_at	---	---	---	Rn.169898	AW531135	4.15	2.33	2.35	3.45	2.92	3.93	1.40	up	5.05E-01	8.95E-01	-	-
1379334_at	Gldc	Glycine dehydrogenase (decarboxylating)	309312	Rn.17101	BF547086	7.75	4.90	6.13	7.41	6.65	6.18	1.40	up	6.15E-01	8.95E-01	-	-
1382782_at	Mrps2	mitochondrial ribosomal protein S2	362094	Rn.48907	AI102331	4.02	5.18	4.95	5.27	4.58	5.77	1.40	up	3.78E-01	8.95E-01	-	-
1373675_at	Glrx2	glutaredoxin 2	114022	Rn.203029	AW525635	8.68	8.17	9.15	8.50	7.65	8.38	1.40	down	2.75E-01	8.95E-01	-	-
1392117_at	---	---	---	Rn.210852	BF401109	2.73	2.72	2.62	4.41	2.42	2.71	1.40	up	4.76E-01	8.95E-01	-	-
1381564_at	Glmn	glomulin, FKBP associated protein	289437	Rn.44333	AI763657	2.43	4.84	3.06	3.31	3.90	4.59	1.40	up	5.78E-01	8.95E-01	-	-
1386837_x_at	Znf574	zinc finger protein 574	308434	Rn.15466	BF556285	2.78	4.21	2.75	2.78	2.77	2.72	1.40	down	3.68E-01	8.95E-01	-	-
1368573_at	Kpnb1	karyopherin (importin) beta 1	24917	Rn.11061	NM_017063	8.72	8.93	8.67	9.46	9.35	8.98	1.40	up	4.18E-02	8.95E-01	-	-
1377770_at	Fbxo28	F-box protein 28	305105	Rn.12792	AI168965	4.92	4.09	4.18	4.24	3.74	3.74	1.40	down	1.91E-01	8.95E-01	-	-
1372096_at	Oxsr1	oxidative-stress responsive 1	316064	Rn.203085	BI296082	5.12	5.40	6.65	4.73	4.95	6.03	1.40	down	4.74E-01	8.95E-01	-	-
1378977_at	---	---	---	Rn.203401	AI178197	5.92	6.64	6.52	6.41	7.01	7.12	1.40	up	1.95E-01	8.95E-01	-	-
1369453_at	Epn1	Epsin 1	117277	Rn.30007	NM_057136	4.74	4.84	5.56	4.54	4.58	4.55	1.40	down	1.30E-01	8.95E-01	-	-
1371555_at	Snx12	sorting nexin 12	363478	Rn.2280	AI599411	8.91	9.39	9.27	8.72	8.78	8.61	1.40	down	3.25E-02	8.95E-01	-	-
1391663_at	---	---	---	Rn.165811	AI511259	8.38	8.01	8.55	7.43	8.00	8.04	1.40	down	1.26E-01	8.95E-01	-	-
1388165_at	Porf-2	preoptic regulatory factor-2	500901	Rn.6996	X53232	3.74	5.59	4.92	4.40	4.03	4.36	1.40	down	4.28E-01	8.95E-01	-	-
1388425_at	Oaf	OAF homolog (Drosophila)	315594	Rn.1638	BG671569	5.01	4.16	5.53	4.77	3.44	5.01	1.40	down	4.83E-01	8.95E-01	-	-
1378674_at	En2	engrailed homeobox 2	499964	Rn.156472	BI293056	2.40	2.38	2.41	2.39	3.84	2.43	1.40	up	3.63E-01	8.95E-01	-	-
1375764_at	Chmp2b	Chromatin modifying protein 2B	363720	Rn.105547	BE111346	3.33	4.48	4.95	5.51	2.94	5.77	1.40	up	6.58E-01	8.98E-01	-	-
1373268_at	Map4	microtubule-associated protein 4	367171	Rn.203122	BM383953	6.62	6.76	6.45	7.17	7.28	6.85	1.40	up	3.57E-02	8.95E-01	-	-
1372777_at	---	---	---	Rn.164997	BM385774	7.46	6.81	7.56	6.85	6.66	6.86	1.40	down	1.18E-01	8.95E-01	-	-
1387799_at	Fxyd2	FXYD domain-containing ion transport regulator 2	29639	Rn.6700	AF129400	10.38	10.24	10.70	10.06	10.01	9.78	1.40	down	3.87E-02	8.95E-01	-	-
1381012_at	Serpinf1	serine (or cysteine) peptidase inhibitor, clade F, member 1	287526	Rn.16902	BI303349	3.47	4.32	3.73	4.36	3.71	4.91	1.40	up	3.18E-01	8.95E-01	-	-
1370334_at	Plekhb1	pleckstrin homology domain containing, family B (evectins) member 1	64471	Rn.8415	AF081582	3.97	4.03	4.09	3.96	3.12	3.54	1.40	down	1.17E-01	8.95E-01	-	-
1390203_at	---	---	---	Rn.16431	AI411149	3.82	3.22	4.02	3.14	3.17	3.27	1.40	down	1.17E-01	8.95E-01	-	-
1387866_at	Myo9b	myosin IXb	25486	Rn.33792	AI178160	4.45	4.43	5.90	4.44	4.45	4.43	1.40	down	3.72E-01	8.95E-01	-	-
1370173_at	Sod2	superoxide dismutase 2, mitochondrial	24787	Rn.10488	BG671549	8.07	7.73	9.18	7.33	8.11	8.08	1.40	down	3.90E-01	8.95E-01	-	-
1372505_at	Ykt6	YKT6 v-SNARE homolog (S. cerevisiae)	64351	Rn.6525	BM391393	6.11	5.43	6.08	5.73	4.78	5.66	1.40	down	2.66E-01	8.95E-01	-	-
1388341_at	Rangap1	RAN GTPase activating protein 1	362965	Rn.107099	BI285671	7.12	6.93	7.48	6.87	6.53	6.67	1.40	down	6.11E-02	8.95E-01	-	-
1373658_at	Racgap1	Rac GTPase-activating protein 1	315298	Rn.101301	AI409259	3.58	2.52	2.33	2.32	2.33	2.32	1.40	down	2.80E-01	8.95E-01	-	-
1396574_at	LOC685233	Hypothetical protein LOC685233	685233	Rn.20927	AW523624	2.42	2.36	3.93	2.41	2.43	2.41	1.40	down	3.96E-01	8.95E-01	-	-
1387196_at	Khdrbs3	KH domain containing, RNA binding, signal transduction associated 3	64015	Rn.54682	NM_022249	5.94	3.94	3.94	4.03	4.29	4.03	1.40	down	5.08E-01	8.95E-01	-	-
1378177_at	LOC686816	similar to gem (nuclear organelle) associated protein 5	686816	---	BM385007	3.27	4.05	3.62	3.27	2.97	3.24	1.40	down	1.17E-01	8.95E-01	-	-
1374523_at	Pgls	6-phosphogluconolactonase	290636	Rn.19855	AI231339	5.52	5.38	6.12	5.28	5.29	4.99	1.40	down	1.21E-01	8.95E-01	-	-
1367614_at	Anxa1	annexin A1	25380	Rn.1792	NM_012904	4.83	3.73	2.37	4.33	4.63	3.44	1.40	up	5.74E-01	8.95E-01	-	-
1373776_at	---	---	---	---	AI406341	5.18	7.38	5.30	6.60	6.11	6.61	1.40	up	5.43E-01	8.95E-01	-	-
1383382_at	LOC681740	similar to jumonji protein	681740	---	BI294931	5.51	4.62	4.68	5.69	5.56	5.01	1.40	up	2.41E-01	8.95E-01	-	-
1395837_at	---	---	---	Rn.202770	BE119517	3.88	2.43	2.50	2.46	2.48	2.41	1.40	down	3.62E-01	8.95E-01	-	-
1372635_at	---	---	---	Rn.129499	BF282163	3.58	5.18	3.74	3.21	2.96	4.85	1.40	down	5.66E-01	8.95E-01	-	-
1394280_at	Nusap1	nucleolar and spindle associated protein 1	311336	Rn.10693	AA964152	3.85	2.39	2.39	2.39	2.40	2.38	1.40	down	3.73E-01	8.95E-01	-	-
1376082_at	Evi1	ecotropic viral integration site 1	294924	Rn.20198	BE107033	4.86	5.41	4.54	4.76	4.78	3.80	1.40	down	3.01E-01	8.95E-01	-	-
1398888_at	H3f3b	H3 histone, family 3B	117056	Rn.198918	AI408819	8.26	8.12	8.38	8.75	8.59	8.89	1.40	up	1.32E-02	8.95E-01	-	-
1378242_at	---	---	---	Rn.171018	BE106915	2.45	2.44	2.30	2.89	3.37	2.39	1.40	up	1.64E-01	8.95E-01	-	-
1379457_at	Crispld2	cysteine-rich secretory protein LCCL domain containing 2	171547	Rn.4346	AI175861	2.59	2.53	2.45	2.51	3.74	2.79	1.40	up	2.65E-01	8.95E-01	-	-
1385296_at	Trmt12	tRNA methyltransferase 12 homolog (S. cerevisiae)	314999	Rn.105294	AA963783	2.47	2.52	2.51	2.82	3.35	2.78	1.40	up	5.73E-02	8.95E-01	-	-
1393015_at	RGD1310587	similar to hypothetical protein FLJ14146	360894	Rn.39189	BG375354	9.32	9.12	8.89	8.30	8.68	8.88	1.40	down	8.36E-02	8.95E-01	-	-
1389539_at	Nfkbia	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, al	25493	Rn.12550	AW672589	3.01	3.25	2.54	3.88	3.04	3.35	1.40	up	2.04E-01	8.95E-01	-	-
1368428_at	Xpnpep2	X-prolyl aminopeptidase (aminopeptidase P) 2, membrane-bound	117522	Rn.56142	NM_057155	9.73	10.29	10.35	9.78	9.14	9.99	1.40	down	2.05E-01	8.95E-01	-	-
1371574_at	Ghitm	growth hormone inducible transmembrane protein	290596	Rn.98375	BF284759	9.94	10.17	9.89	10.22	10.49	10.75	1.40	up	4.98E-02	8.95E-01	-	-
1369666_at	Gpd2	glycerol-3-phosphate dehydrogenase 2, mitochondrial	25062	Rn.89705	U08027	3.92	3.40	3.22	2.75	3.17	3.16	1.40	down	1.28E-01	8.95E-01	-	-
1378951_at	---	---	---	Rn.37248	AI233142	2.98	4.16	2.79	2.89	2.78	2.80	1.40	down	3.20E-01	8.95E-01	-	-
1373574_at	Cnpy4	canopy 4 homolog (zebrafish)	363886	Rn.6578	BI285607	4.82	4.89	4.64	5.61	5.31	4.89	1.40	up	9.46E-02	8.95E-01	-	-
1368548_at	Slc12a1	solute carrier family 12 (sodium/potassium/chloride transporters), member 1	25065	Rn.14799	NM_019134	7.09	6.43	6.46	6.44	6.71	5.37	1.40	down	3.52E-01	8.95E-01	-	-
1377402_at	Cdk10	Cdc2-dependent kinase 10	361434	Rn.20472	BI296989	4.46	4.27	4.02	4.25	5.52	4.43	1.40	up	3.06E-01	8.95E-01	-	-
1391819_at	RGD1307394	similar to hypothetical protein ET	360667	Rn.16739	BM390584	2.52	2.50	4.73	2.64	2.54	3.11	1.40	down	5.57E-01	8.95E-01	-	-
1374263_at	---	---	---	Rn.209134	BF396108	2.94	2.76	2.86	3.75	2.92	3.34	1.40	up	1.21E-01	8.95E-01	-	-
1396127_at	---	---	---	---	BF288545	5.76	5.52	4.78	4.69	4.57	5.34	1.40	down	2.70E-01	8.95E-01	-	-
1388574_at	Wars	tryptophanyl-tRNA synthetase	314442	Rn.14939	BG670966	4.41	4.84	4.05	4.49	4.38	5.89	1.40	up	4.16E-01	8.95E-01	-	-
1380513_at	Rpap2	RNA polymerase II associated protein 2	305120	Rn.49042	BE095638	5.13	5.04	4.87	5.67	5.12	5.71	1.40	up	7.63E-02	8.95E-01	-	-
1396725_at	---	---	---	Rn.110279	BF410556	3.84	2.40	2.43	2.41	2.42	2.39	1.40	down	3.63E-01	8.95E-01	-	-
1393814_at	Zan	zonadhesin	304379	Rn.217227	BF405433	2.55	2.50	2.66	2.81	3.83	2.53	1.40	up	2.89E-01	8.95E-01	-	-
1388755_at	Sec23a	Sec23 homolog A (S. cerevisiae)	58817	Rn.203115	AI179139	3.43	3.79	3.81	4.10	3.49	4.89	1.40	up	3.15E-01	8.95E-01	-	-
1387354_at	Stat1	signal transducer and activator of transcription 1	25124	Rn.33229	NM_032612	4.56	4.85	4.20	4.64	2.89	4.63	1.40	down	4.72E-01	8.95E-01	-	-
1385804_x_at	Wdr36	WD repeat domain 36	361305	---	AA956841	5.39	4.74	5.02	4.31	4.41	4.98	1.40	down	1.60E-01	8.95E-01	-	-
1386750_at	Pkd2l2	polycystic kidney disease 2-like 2	291683	Rn.207191	BF290862	5.37	7.14	5.93	5.49	5.21	6.28	1.40	down	4.73E-01	8.95E-01	-	-
1383165_at	RGD1310209	similar to KIAA1324 protein	362019	Rn.22751	BM390462	4.05	4.17	4.65	5.60	3.82	4.90	1.40	up	4.27E-01	8.95E-01	-	-
1371763_at	RGD1309534	similar to RIKEN cDNA 4931406C07	363016	Rn.3085	BI274533	11.38	11.78	11.70	11.27	10.84	11.20	1.40	down	3.62E-02	8.95E-01	-	-
1377472_at	Ext1	exostoses (multiple)-like 1	313610	Rn.50146	BE110173	2.67	2.44	2.49	3.03	2.87	3.15	1.40	up	1.05E-02	8.95E-01	-	-
1393346_at	Ccdc125	coiled-coil domain containing 125	499518	Rn.21916	BI279863	5.43	7.68	6.68	6.54	6.61	8.10	1.40	up	5.89E-01	8.95E-01	-	-
1393922_at	Efcab7	EF-hand calcium binding domain 7	362549	Rn.162071	BF567535	4.39	4.08	3.62	3.92	2.70	4.01	1.40	down	3.65E-01	8.95E-01	-	-
1391649_a_at	---	---	---	Rn.128940	AW915522	3.20	4.28	5.28	4.30	4.37	5.55	1.40	up	5.41E-01	8.95E-01	-	-
1376029_at	Rgl2	ral guanine nucleotide dissociation stimulator-like 2	294283	Rn.216644	BI295991	7.01	5.78	6.56	5.91	6.42	5.57	1.40	down	3.29E-01	8.95E-01	-	-
1392673_at	Cdc37l1	cell division cycle 37 homolog (S. cerevisiae)-like 1	293886	Rn.60570	BF552510	3.89	4.19	2.74	4.75	3.27	4.26	1.40	up	4.79E-01	8.95E-01	-	-
1393800_at	---	---	---	---	AW526472	2.47	2.49	2.56	2.80	3.47	2.68	1.40	up	1.21E-01	8.95E-01	-	-
1388525_at	Rnf149	ring finger protein 149	363222	Rn.28251	AI171788	5.87	6.37	6.92	6.59	7.28	6.73	1.40	up	2.57E-01	8.95E-01	-	-
1371884_at	Ttc3	tetratricopeptide repeat domain 3	360702	Rn.214632	AI009909	6.54	6.49	4.63	5.78	7.10	6.23	1.40	up	5.46E-01	8.95E-01	-	-
1389981_at	Rbm27	RNA binding motif protein 27	361317	Rn.218050	BE116889	3.05	3.21	3.23	3.04	3.43	4.47	1.40	up	3.22E-01	8.95E-01	-	-
1399159_a_at	Vamp3	vesicle-associated membrane protein 3	29528	Rn.219999	NM_057097	8.74	8.52	9.26	8.63	7.69	8.74	1.40	down	2.91E-01	8.95E-01	-	-
1378439_at	---	---	---	Rn.28907	AI175531	2.50	2.50	3.95	2.48	2.51	2.51	1.40	down	3.73E-01	8.95E-01	-	-
1384048_at	RGD1310712	similar to EMSY protein	361607	---	BI297740	4.11	2.73	2.74	2.57	2.91	2.64	1.40	down	3.61E-01	8.95E-01	-	-
1368905_at	Ces2	carboxylesterase 2 (intestine, liver)	171118	Rn.14535	NM_133586	6.04	7.09	6.54	6.58	7.24	7.30	1.40	up	2.72E-01	8.95E-01	-	-
1374764_at	Nol14	nucleolar protein 14	289724	Rn.12567	BG378053	5.03	5.05	3.56	4.44	5.55	5.10	1.40	up	4.56E-01	8.95E-01	-	-
1371527_at	Emp1	epithelial membrane protein 1	25314	Rn.19723	BI275741	3.82	2.56	2.67	2.54	2.56	2.49	1.40	down	2.97E-01	8.95E-01	-	-
1377359_at	Slc10a3	solute carrier family 10 (sodium/bile acid cotransporter family), member 3	501665	Rn.140462	BM384440	2.62	4.04	2.63	2.95	2.28	2.61	1.40	down	3.97E-01	8.95E-01	-	-
1385349_at	Cetn4	centrin 4	688611	Rn.57022	BF389818	2.88	3.64	3.02	3.25	3.32	4.42	1.40	up	3.39E-01	8.95E-01	-	-
1383467_at	Epc2	enhancer of polycomb homolog 2 (Drosophila)	362132	Rn.23462	AW918173	5.35	5.32	7.24	5.79	5.59	5.07	1.40	down	5.11E-01	8.95E-01	-	-
1398897_at	Ube2v1	ubiquitin-conjugating enzyme E2 variant 1	296390	Rn.220168	AI411988	6.41	6.97	7.34	6.30	5.94	7.03	1.40	down	3.14E-01	8.95E-01	-	-
1392269_at	Sin3a	SIN3 homolog A, transcription regulator (yeast)	363067	Rn.63749	BE116983	5.73	4.02	2.85	3.01	4.87	3.26	1.40	down	6.60E-01	8.98E-01	-	-
1374559_at	Rnf26	ring finger protein 26	300659	Rn.15010	AI171211	5.84	5.40	4.11	6.33	5.05	5.43	1.40	up	4.94E-01	8.95E-01	-	-
1389022_at	---	---	---	---	AI102760	3.45	4.15	3.18	2.82	2.51	4.00	1.40	down	4.22E-01	8.95E-01	-	-
1380060_at	Top1mt	topoisomerase (DNA) I, mitochondrial	300229	Rn.31307	AI175848	2.46	2.44	4.29	2.45	2.48	2.81	1.40	down	4.80E-01	8.95E-01	-	-
1374135_at	Ipo4	importin 4	290228	Rn.107154	AI233262	4.11	4.21	4.06	4.82	4.09	4.91	1.40	up	1.42E-01	8.95E-01	-	-
1394371_at	Nufip1	nuclear fragile X mental retardation protein interacting protein 1	364430	Rn.154742	BF556765	3.27	3.37	5.51	4.11	3.13	3.47	1.40	down	5.72E-01	8.95E-01	-	-
1382477_at	BI564247 /// Ser	similar to SUMO/sentrin specific protease 5 /// SUMO/sentrin specific proteas	303874 /// 499574	Rn.161817	AW532560	4.47	5.49	5.11	4.59	4.38	4.66	1.40	down	1.95E-01	8.95E-01	-	-
1372647_at	---	---	---	---	BM386957	3.89	2.47	2.47	2.45	2.42	2.51	1.40	down	3.66E-01	8.95E-01	-	-
1387232_at	Bmp4	bone morphogenetic protein 4	25296	Rn.10318	NM_012827	6.82	7.57	6.44	7.38	7.67	7.22	1.40	up	2.47E-01	8.95E-01	-	-
1376576_at	Dusp11	dual specificity phosphatase 11 (RNA/RNP complex 1-interacting)	297412	Rn.24649	BM387750	7.21	7.48	7.52	7.22	5.97	7.59	1.40	down	3.89E-01	8.95E-01	-	-
1383831_at	Qrsl1	glutaminyl-tRNA synthase (glutamine-hydrolyzing)-like 1	309911	Rn.116771	BI280298	3.45	3.32	2.87	3.31	3.15	4.62	1.40	up	3.86E-01	8.95E-01	-	-
1375756_at	Aif1l	allograft inflammatory factor 1-like	362107	Rn.17100	BF408518	8.01	6.88	7.20	6.84	7.27	6.54	1.40	down	2.94E-01	8.95E-01	-	-
1389428_at	---	---	---	Rn.163818	AI104431	8.17	8.53	8.21	8.12	7.13	8.21	1.40	down	2.55E-01	8.95E-01	-	-
1393507_at	---	---	---	Rn.16294	AI045715	3.91	2.36	2.39	2.47	2.39	2.35	1.40	down	3.99E-01	8.95E-01	-	-
1397706_at	---	---	---	Rn.48640	BF388794	5.00	4.98	4.16	4.77	5.13	5.68	1.40	up	2.75E-01	8.95E-01	-	-
1383859_at	---	---	---	Rn.175343	AA963376	2.40	3.10	2.46	3.88	2.82	2.70	1.40	up	3.29E-01	8.95E-01	-	-
1383307_at	Tmem186	transmembrane protein 186	497863	Rn.34474	AI717533	5.84	5.29	5.35	4.83	4.83	5.37	1.40	down	1.29E-01	8.95E-01	-	-
1397740_at	Sfxn1	sideroflexin 1	364678	Rn.115752	AA964229	7.64	7.29	7.18	7.34	5.73	7.59	1.40	down	4.66E-01	8.95E-01	-	-
1379299_at	Ercc8	excision repair cross-complementing rodent repair deficiency, complementatic	310071	Rn.107979	BE106364	2.79	2.37	2.63	4.04	2.47	2.72	1.40	up	3.92E-01	8.95E-01	-	-
1398853_at	Psmb3	proteasome (prosome, macropain) subunit, beta type 3	29676	Rn.94551	AI169273	6.30	7.84	7.04	7.35	7.50	7.77	1.40	up	3.54E-01	8.95E-01	-	-
1377838_at	RGD1562218	similar to RIKEN cDNA 0610039J04	292100	Rn.25199	BI287018	6.60	6.35	7.09	6.22	6.03	6.34	1.40	down	1.12E-01	8.95E-01	-	-
1380064_at	---	---	---	Rn.169991	BE113961	3.77	3.77	4.68	3.77	3.77	3.23	1.40	down	2.44E-01	8.95E-01	-	-
1396058_at	---	---	---	Rn.167131	BG669136	3.56	2.78	3.14	2.79	2.48	2.78	1.40	down	1.23E-01	8.95E-01	-	-
1399053_at	---	---	---	Rn.1096	BM391257	5.99	5.32	5.98	5.92	4.32	5.61	1.40	down	4.19E-01	8.95E-01	-	-
1373068_at	Ifrd2	interferon-related developmental regulator 2	300994	Rn.8306	AI236977	5.63	6.27	5.98	6.65	6.31	6.36	1.40	up	8.76E-02	8.95E-01	-	-
1383305_at	---	---	---	---	AW530081	3.03	4.19	4.14	3.57	4.75	4.49	1.40	up	4.08E-01	8.95E-01	-	-
1373146_at	Ssx2ip	synovial sarcoma, X breakpoint 2 interacting protein	308023	Rn.70527	AI176240	3.32	3.13	3.33	3.11	3.79	4.32	1.40	up	2.50E-01	8.95E-01	-	-
1373464_at	Tbc1d22a	TBC1 domain family, member 22a	366968	---	BF418962	3.24	4.19	4.16	4.69	4.10	4.24	1.40	up	2.50E-01	8.95E-01	-	-
1376161_at	Tmed4	transmembrane emp24 protein transport domain containing 4	305502	Rn.21479	AI235294	4.27	4.64	4.93	4.73	4.70	5.86	1.40	up	3.24E-01	8.95E-01	-	-
1389315_at	Git2	G protein-coupled receptor kinase interacting ArfGAP 2	304546	Rn.77521	AI408598	4.52	4.97	5.80	5.63	3.81	4.41	1.40	down	5.03E-01	8.95E-01	-	-
1367915_at	Dgat1	diacylglycerol O-acyltransferase homolog 1 (mouse)	84497	Rn.252	NM_053437	3.96	4.44	7.06	3.91	4.87	5.24	1.40	down	6.69E-01	9.00E-01	-	-
1370655_a_at	Snip	SNAP25-interacting protein	56029	Rn.207205	AF156981	3.17	2.98	3.04	4.71	3.03	2.90	1.40	up	4.57E-01	8.95E-01	-	-
1374703_at	---	---	---	Rn.164711	BI304209	5.88	6.37	5.40	6.69	6.35	6.06	1.40	up	2.25E-01	8.95E-01	-	-
1367907_a_at	Cltb	clathrin, light chain (Lcb)	116561	Rn.3440	M19262	7.51	7.55	7.41	7.12	6.59	7.32	1.40	down	9.84E-02	8.95E-01	-	-
1373218_at	---	---	---	Rn.23904	BG381061	5.22	6.25	5.39	6.42	5.82	6.06	1.40	up	2.56E-01	8.95E-01	-	-
1398699_at	Man2b1	mannosidase, alpha, class 2B, member 1	361378	Rn.102840	BE114558	7.00	7.64	7.25	7.75	7.72	7.86	1.40	up	6.75E-02	8.95E-01	-	-
1393419_at	Rcbtb2	regulator of chromosome condensation (RCC1) and BTB (POZ) domain conta	290363	Rn.125257	BF522089	2.52	2.79	2.62	3.60	2.82	2.96	1.40	up	1.30E-01	8.95E-01	-	-
1379469_at	Tbl1x	transducin (beta)-like 1 X-linked	302711	Rn.107002	AA955760	7.86	8.27	7.15	8.63	7.92	8.18	1.40	up	2.83E-01	8.95E-01	-	-
1387112_at	Plp1	proteolipid protein 1	24943	Rn.4550	NM_030990	2.72	2.72	4.17	2.72	2.74	2.71	1.40	down	3.75E-01	8.95E-01	-	-
1370049_at	Smpd2	sphingomyelin phosphodiesterase 2, neutral	83537	Rn.18572	NM_031360	3.46	4.03	4.24	4.11	4.45	4.61	1.40	up	1.55E-01	8.95E-01	-	-
1389215_at	Sephs1	selenophosphate synthetase 1	291314	Rn.100803	AI407424	5.44	6.88	6.84	7.07	6.47	7.07	1.39	up	4.02E-01	8.95E-01	-	-
1392874_at	---	---	---	Rn.124369	AI019937	7.52	8.01	7.80	7.91	7.98	8.88	1.39	up	2.34E-01	8.95E-01	-	-
1387641_at	Rab5a	RAB5A, member RAS oncogene family	64633	Rn.44477	NM_022692	6.55	6.46	5.64	6.26	7.02	6.81	1.39	up	2.64E-01	8.95E-01	-	-
1385284_at	---	---	---	Rn.168278	AI577488	6.00	3.84	3.84	3.84	3.90	4.51	1.39	down	5.58E-01	8.95E-01	-	-
1385050_at	Znf292	zinc finger protein 292	50552	Rn.106753	BF397804	2.83	4.09	2.77	3.78	2.77	4.58	1.39	up	5.19E-01	8.95E-01	-	-
1375164_at	Atp2a2	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2	29693	Rn.2305	AA800212	3.21	3.37	3.44	4.28	2.86	4.33	1.39	up	3.81E-01	8.95E-01	-	-
1382962_at	Lpar2	lysophosphatidic acid receptor 2	498609	Rn.14855	AA894167	4.98	4.75	4.02	5.17	4.79	5.22	1.39	up	2.09E-01	8.95E-01	-	-
1396411_at	90 /// LOC685826	similar to Phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic subunit alpl11 /// 685590 /// 68	Rn.190480	BE117439	2.74	4.10	5.33	4.18	2.82	3.73	1.39	down	6.02E-01	8.95E-01	-	-
1394548_at	Cpm	carboxypeptidase M	314855	Rn.23887	BF282781	3.82	2.38	2.41	2.38	2.39	2.39	1.39	down	3.70E-01	8.95E-01	-	-
1393647_at	Hat1	histone acetyltransferase 1	296501	Rn.139751	BI285581	7.98	7.92	7.54	6.86	7.36	7.78	1.39	up	1.87E-01	8.95E-01	-	-
1367485_at	Tcea1	transcription elongation factor A (SII) 1	362479	Rn.6738	BM

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1379173_at	---	---	---	Rn.171021	BF394515	2.80	2.60	2.72	4.03	2.78	2.74	1.39	up	3.27E-01	8.95E-01	-	-
1388931_at	Mrpl13	mitochondrial ribosomal protein L13	299938	Rn.107776	AA799440	6.09	6.75	5.20	5.95	6.45	7.07	1.39	up	4.39E-01	8.95E-01	-	-
1374372_at	---	---	---	Rn.63512	BF392147	6.18	5.65	4.58	6.35	5.20	6.29	1.39	up	4.72E-01	8.95E-01	-	-
1368552_at	Grpel1	GrpE-like 1, mitochondrial	79563	Rn.10630	NM_024487	8.35	8.15	8.13	9.14	8.43	8.49	1.39	up	1.16E-01	8.95E-01	-	-
1367993_at	Clip1	CAP-GLY domain containing linker protein 1	65201	Rn.22069	NM_031745	2.42	2.47	2.43	2.44	2.46	3.85	1.39	up	3.65E-01	8.95E-01	-	-
1375906_at	LOC683034	hypothetical protein LOC683034	683034	---	BM389920	6.95	7.10	7.47	7.35	7.57	8.03	1.39	up	1.34E-01	8.95E-01	-	-
1379703_at	Dennd3	DENN/MADD domain containing 3	315055	Rn.43070	BF288207	6.55	5.73	5.83	5.47	5.70	5.52	1.39	down	1.47E-01	8.95E-01	-	-
1381601_at	---	---	---	Rn.199274	BI293235	5.60	6.17	6.37	5.61	5.72	5.38	1.39	down	1.31E-01	8.95E-01	-	-
1371774_at	Sat1	spermidine/spermine N1-acetyl transferase 1	302642	Rn.107986	AA893220	7.84	7.39	7.82	8.10	8.40	7.98	1.39	up	6.81E-02	8.95E-01	-	-
1393377_at	---	---	---	---	BE100936	3.03	4.01	5.94	4.79	4.86	4.75	1.39	up	6.08E-01	8.95E-01	-	-
1376173_at	---	---	---	---	BI292125	6.27	7.36	7.06	7.43	7.47	7.21	1.39	up	2.26E-01	8.95E-01	-	-
1374253_at	RGD1307235	similar to RIKEN cDNA 2310035C23	309053	Rn.38292	BI291355	9.06	8.90	8.25	8.67	7.89	8.22	1.39	down	2.29E-01	8.95E-01	-	-
1388269_at	Hbg1	hemoglobin, gamma A	94164	Rn.203045	BE108901	2.31	2.31	3.73	2.31	2.31	2.30	1.39	down	3.73E-01	8.95E-01	-	-
1374654_at	Btrc	beta-transducin repeat containing	361765	Rn.21800	BE109603	2.90	5.00	5.69	4.46	5.26	5.29	1.39	up	6.19E-01	8.95E-01	-	-
1383380_at	Rpp38	ribonuclease P/MRP 38 subunit (human)	291317	Rn.2690	AA859346	4.52	2.51	2.81	2.71	2.81	2.90	1.39	down	4.93E-01	8.95E-01	-	-
1398268_at	Nfyc	nuclear transcription factor-Y gamma	25337	Rn.1457	BI296061	4.65	4.30	3.94	4.28	4.86	5.19	1.39	up	2.31E-01	8.95E-01	-	-
1367874_at	Rhoq	ras homolog gene family, member Q	85428	Rn.4169	NM_053522	3.79	3.76	3.45	3.88	4.80	3.74	1.39	up	2.44E-01	8.95E-01	-	-
1373816_at	Ap1g1	adaptor-related protein complex 1, gamma 1 subunit	171494	Rn.9446	BM383443	8.79	8.30	8.48	8.10	8.09	7.96	1.39	down	3.55E-02	8.95E-01	-	-
1384333_at	ctr2 /// LOC301686	ARP2 actin-related protein 2 homolog (yeast) /// similar to ARP2 actin-related	289820 /// 301861	Rn.102249	AW920881	3.81	2.44	2.46	2.44	2.45	2.39	1.39	down	3.55E-01	8.95E-01	-	-
1383291_at	C7 /// Tubb2c	complement component 7 /// tubulin, beta 2c	117517 /// 296554	Rn.33787	BF282631	8.02	7.05	5.90	8.09	8.48	5.83	1.39	up	6.68E-01	9.00E-01	-	-
1396420_at	---	---	---	Rn.209424	BF395914	2.41	2.39	2.41	3.83	2.41	2.39	1.39	up	3.76E-01	8.95E-01	-	-
1379143_at	---	---	---	Rn.147738	BF409564	3.80	2.38	2.40	2.39	2.39	2.37	1.39	down	3.69E-01	8.95E-01	-	-
1384265_at	Pold3	polymerase (DNA-directed), delta 3, accessory subunit	293144	Rn.162469	BI278347	5.94	5.27	5.03	4.62	5.34	4.86	1.39	down	2.42E-01	8.95E-01	-	-
1368018_at	Mkln1	muskelin 1, intracellular mediator containing kelch motifs	83536	Rn.6383	NM_031359	6.37	6.17	6.11	6.22	5.13	5.87	1.39	down	2.27E-01	8.95E-01	-	-
1388282_s_at	Klra5 /// Ly49s7	killer cell lectin-like receptor, subfamily A, member 5 /// Ly49 stimulatory recep	297666 /// 494203	Rn.37467	U56824	3.04	3.08	3.12	3.12	4.06	3.49	1.39	up	1.59E-01	8.95E-01	-	-
1376294_at	---	---	---	---	Rn.15191	BG375533	4.98	5.16	5.74	4.49	4.51	5.47	1.39	down	2.99E-01	8.95E-01	-	-
1377456_at	---	---	---	---	---	BE116775	4.46	4.50	3.30	4.42	4.57	4.69	1.39	up	3.05E-01	8.95E-01	-	-
1376337_at	Smarca2	SWI/SNF related, matrix associated, actin dependent regulator of chromatin,	361745	Rn.94939	AI170385	11.00	10.99	10.93	10.66	10.44	10.40	1.39	down	5.02E-03	8.95E-01	-	-
1391635_at	Ctdspl	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phos	301056	Rn.37030	AI044500	4.75	5.27	5.18	5.21	5.85	5.57	1.39	up	1.26E-01	8.95E-01	-	-
1389466_at	Ccdc6	Coiled-coil domain containing 6	691155	Rn.164708	BG374280	10.69	10.33	10.57	10.42	9.65	10.09	1.39	down	1.29E-01	8.95E-01	-	-
1377844_at	Ptgr2	prostaglandin reductase 2	299194	Rn.203285	AI411520	7.48	7.39	8.18	7.18	6.84	7.61	1.39	down	2.30E-01	8.95E-01	-	-
1396207_at	Rdx	radixin	315655	Rn.203261	BF565167	6.47	6.58	6.67	6.39	5.98	5.93	1.39	down	3.78E-02	8.95E-01	-	-
1370638_at	Ank3	ankyrin 3, epithelial	361833	Rn.220009	AF069525	7.93	8.04	7.96	8.06	8.49	8.81	1.39	up	9.70E-02	8.95E-01	-	-
1394884_s_at	Sabp1	single-stranded DNA binding protein 1	54304	Rn.10922	AI171809	7.17	8.14	8.29	8.36	8.45	8.20	1.39	up	2.58E-01	8.95E-01	-	-
1386096_at	Mtf2	metal response element binding transcription factor 2	360905	Rn.20300	BG666758	2.48	2.48	2.90	4.17	2.50	2.61	1.39	up	4.44E-01	8.95E-01	-	-
1398928_at	Cuta	cutA divalent cation tolerance homolog (E. coli)	294288	Rn.2595	BG378296	8.30	9.03	8.25	8.74	9.21	9.05	1.39	up	1.76E-01	8.95E-01	-	-
1383482_at	---	---	---	Rn.164773	AI578183	4.14	4.90	4.78	4.07	4.08	4.25	1.39	down	1.25E-01	8.95E-01	-	-
1373643_at	---	---	---	Rn.122118	AI170928	4.11	3.04	4.72	3.53	3.36	3.55	1.39	down	3.93E-01	8.95E-01	-	-
1384208_at	Igj	immunoglobulin joining chain	360922	Rn.17804	BM385222	2.32	2.31	2.33	3.49	2.32	2.57	1.39	up	2.53E-01	8.95E-01	-	-
1395182_at	Klhl20	kelch-like 20 (Drosophila)	304920	Rn.44191	AI411008	2.53	3.85	2.61	2.51	2.54	2.53	1.39	down	3.32E-01	8.95E-01	-	-
1368937_at	Ncoa2	nuclear receptor coactivator 2	83724	Rn.49152	NM_031822	3.66	4.56	4.37	3.90	2.97	4.29	1.39	down	3.79E-01	8.95E-01	-	-
1385128_at	---	---	---	Rn.163252	BE108716	2.46	2.47	2.47	2.50	3.76	2.57	1.39	up	3.13E-01	8.95E-01	-	-
1383190_at	Elmod2	ELMO/CED-12 domain containing 2	688581	Rn.94192	BE113297	4.48	4.91	4.24	4.39	5.43	5.22	1.39	up	2.72E-01	8.95E-01	-	-
1372790_at	Mdh1	Malate dehydrogenase 1, NAD (soluble)	24551	Rn.13492	BG671530	7.57	7.72	7.91	6.87	7.35	7.56	1.39	down	1.04E-01	8.95E-01	-	-
1394184_at	---	---	---	Rn.29194	AI177746	3.94	2.52	2.52	2.54	2.55	2.48	1.39	down	3.74E-01	8.95E-01	-	-
1381310_at	LOC691574	similar to ubiquitin-associated protein 1	691574	Rn.107376	BI296611	3.96	3.97	3.44	4.75	3.97	4.07	1.39	up	1.92E-01	8.95E-01	-	-
1373660_at	Afg3l1	AFG3(ATPase family gene 3)-like 1 (S. cerevisiae)	361436	Rn.41391	BI280384	6.07	6.99	6.59	7.46	6.54	7.06	1.39	up	2.78E-01	8.95E-01	-	-
1378139_at	---	---	---	Rn.22289	AI412468	5.87	5.76	3.65	4.32	5.96	6.42	1.39	up	6.51E-01	8.96E-01	-	-
1382247_a_at	---	---	---	---	BE111497	4.57	6.01	5.34	4.97	4.15	5.38	1.39	down	4.40E-01	8.95E-01	-	-
1380902_at	---	---	---	Rn.170988	BE106303	3.08	3.21	2.91	2.87	3.18	4.56	1.39	up	4.22E-01	8.95E-01	-	-
1388206_a_at	Eif5	eukaryotic translation initiation factor 5	56783	Rn.40123	K01677	7.72	8.39	8.55	8.59	8.51	8.98	1.39	up	1.81E-01	8.95E-01	-	-
1399163_a_at	Homer1	homer homolog 1 (Drosophila)	29546	Rn.37500	BM388880	8.81	8.66	7.95	8.84	8.93	9.07	1.39	up	1.60E-01	8.95E-01	-	-
1371356_at	Tenc1	tensin like C1 domain containing phosphatase (tensin 2)	315326	Rn.105953	BI294836	2.72	5.35	2.86	2.94	5.21	4.19	1.39	up	6.84E-01	9.03E-01	-	-
1390197_at	RGD1565146	similar to hypothetical gene supported by AF226663	498150	---	BG375560	2.92	3.49	2.56	3.89	3.04	3.45	1.39	up	2.66E-01	8.95E-01	-	-
1389299_at	Pcyt1a	phosphate cytidylyltransferase 1, choline, alpha	140544	Rn.81192	BG673255	8.58	8.06	8.34	7.66	7.94	7.96	1.39	down	5.89E-02	8.95E-01	-	-
1377436_at	Gpatch1	G patch domain containing 1	292810	Rn.64293	BE108338	6.51	6.48	6.49	6.29	5.91	5.86	1.39	down	2.56E-02	8.95E-01	-	-
1376182_at	Falz	Fetal Alzheimer antigen	303617	Rn.49972	BM383074	4.50	4.85	6.16	4.46	4.60	5.03	1.39	down	4.28E-01	8.95E-01	-	-
1391683_at	---	---	---	Rn.7783	BF563946	4.62	4.81	3.54	4.01	3.38	4.16	1.39	down	3.65E-01	8.95E-01	-	-
1371336_at	Hn1	hematological and neurological expressed 1	287828	Rn.198910	AA942716	4.57	5.39	4.69	4.73	5.31	6.02	1.39	up	3.57E-01	8.95E-01	-	-
1373854_at	---	---	---	Rn.3583	AI175795	7.22	6.95	7.66	6.82	6.45	7.14	1.39	down	1.75E-01	8.95E-01	-	-
1368947_at	Gadd45a	growth arrest and DNA-damage-inducible, alpha	25112	Rn.10250	NM_024127	6.04	5.95	5.99	6.70	5.92	6.78	1.39	up	1.61E-01	8.95E-01	-	-
1373140_at	---	---	---	Rn.203119	AA851740	5.84	5.35	6.35	6.44	6.44	6.08	1.39	up	2.06E-01	8.95E-01	-	-
1393824_at	RGD1559505	Similar to RIKEN cDNA 9030409E16	498953	Rn.137003	BG377414	5.80	5.16	6.30	5.08	5.23	5.54	1.39	down	2.58E-01	8.95E-01	-	-
1368526_at	Pex3	peroxisomal biogenesis factor 3	83519	Rn.11773	NM_031350	3.72	4.37	2.76	2.72	2.76	3.96	1.39	down	4.91E-01	8.95E-01	-	-
1374658_at	---	---	---	---	BF420262	6.62	7.25	8.67	6.70	7.41	7.01	1.39	down	5.02E-01	8.95E-01	-	-
1373212_at	Atp5s	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit s (factor B	362749	Rn.106766	BI296531	3.66	3.73	2.65	3.23	4.19	4.03	1.39	up	3.62E-01	8.95E-01	-	-
1380235_at	Hs2st1	heparan sulfate 2-O-sulfotransferase 1	292155	Rn.98872	AW530083	2.79	2.78	2.18	3.59	2.79	2.78	1.39	up	2.35E-01	8.95E-01	-	-
1381993_at	Clic2	chloride intracellular channel 2	294141	Rn.103254	BI293548	4.68	4.73	5.38	4.67	4.10	4.61	1.39	down	1.77E-01	8.95E-01	-	-
1389710_at	Sos1	Son of sevenless homolog 1 (Drosophila)	313845	Rn.91864	BF558393	4.94	5.36	6.09	5.15	4.82	5.02	1.39	down	2.49E-01	8.95E-01	-	-
1374296_at	---	---	---	Rn.203816	BM387574	7.37	8.50	7.65	8.33	8.46	8.14	1.39	up	2.52E-01	8.95E-01	-	-
1379957_at	Slfn8	schlafen 8	303378	Rn.137139	BE107457	5.00	3.52	3.38	3.52	3.46	3.51	1.39	down	4.16E-01	8.95E-01	-	-
1388345_at	---	---	---	---	AI599882	6.90	7.56	6.98	7.53	7.91	7.43	1.39	up	1.38E-01	8.95E-01	-	-
1388336_at	Harbi1l	harbinger transposase derived 1-like	362164	Rn.98797	AI411514	3.77	4.16	4.31	4.11	4.12	5.43	1.39	up	3.71E-01	8.95E-01	-	-
1392636_at	---	---	---	Rn.12098	AA964319	3.24	2.73	2.95	2.71	4.24	3.39	1.39	up	3.72E-01	8.95E-01	-	-
1378070_at	---	---	---	Rn.18121	BE099891	3.74	3.74	2.93	3.78	4.31	3.73	1.39	up	2.23E-01	8.95E-01	-	-
1368319_a_at	Homer1	homer homolog 1 (Drosophila)	29546	Rn.37500	AB007688	4.21	4.39	5.37	4.20	4.20	4.17	1.39	down	2.61E-01	8.95E-01	-	-
1369726_at	Tapbp	TAP binding protein	25217	Rn.51023	NM_033098	3.05	3.03	4.27	2.68	3.03	3.23	1.39	down	3.44E-01	8.95E-01	-	-
1368716_at	Ppp1r14c	protein phosphatase 1, regulatory (inhibitor) subunit 14c	171010	Rn.87667	NM_133425	4.12	4.57	3.17	3.58	5.41	4.29	1.39	up	5.24E-01	8.95E-01	-	-
1398068_at	RGD1306119	similar to transcriptional regulating protein 132	314306	Rn.63117	BE107742	2.95	2.82	2.76	4.19	2.81	2.93	1.39	up	3.50E-01	8.95E-01	-	-
1395574_at	---	---	---	Rn.171029	BE118358	5.28	4.87	6.41	5.76	6.09	6.12	1.39	up	3.78E-01	8.95E-01	-	-
1380065_at	Ankrd57	ankyrin repeat domain 57	503306	Rn.55986	AI169118	4.19	2.89	2.98	2.88	2.93	2.84	1.39	down	3.23E-01	8.95E-01	-	-
1382538_at	---	---	---	Rn.54997	AI559902	5.22	4.32	4.45	5.03	5.65	4.72	1.39	up	2.98E-01	8.95E-01	-	-
1368774_a_at	Espn	espin	56227	Rn.91373	NM_019622	9.53	9.40	9.42	8.80	8.77	9.36	1.39	down	7.20E-02	8.95E-01	-	-
1372404_at	Rac2	ras-related C3 botulinum toxin substrate 2 (rho family, small GTP binding prot	366957	Rn.2863	AI010476	2.65	2.65	2.65	3.47	3.24	2.64	1.39	up	1.30E-01	8.95E-01	-	-
1395388_at	---	---	---	Rn.55992	BI282029	10.16	9.94	10.16	10.56	10.15	10.97	1.39	up	1.31E-01	8.95E-01	-	-
1370176_at	Trak2	trafficking protein, kinesin binding 2	171086	Rn.26957	BG378620	6.93	7.76	7.06	7.23	7.79	8.14	1.39	up	2.71E-01	8.95E-01	-	-
1368614_at	Mtxlpl	MLX interacting protein-like	171078	Rn.144656	NM_133552	3.82	3.90	4.50	4.14	3.83	2.84	1.39	down	3.52E-01	8.95E-01	-	-
1371309_at	Tmbim6	transmembrane BAX inhibitor motif containing 6	24822	Rn.107678	BI276999	10.81	11.13	10.78	10.85	12.04	11.23	1.38	up	2.72E-01	8.95E-01	-	-
1393494_at	---	---	---	Rn.163654	AA866419	3.06	3.11	3.06	3.46	3.08	4.09	1.38	up	1.86E-01	8.95E-01	-	-
1387009_at	Capn1	calpain 1	29153	Rn.6037	NM_019152	3.66	2.29	2.30	2.29	2.23	2.32	1.38	down	3.60E-01	8.95E-01	-	-
1381898_at	---	---	---	Rn.168270	AI576907	4.17	4.54	4.49	4.67	5.20	4.75	1.38	up	7.99E-02	8.95E-01	-	-
1386274_at	Slc17a2	solute carrier family 17 (sodium phosphate), member 2	306950	Rn.28363	AI169925	4.58	4.97	4.43	5.32	5.15	4.92	1.38	up	7.73E-02	8.95E-01	-	-
1374536_at	---	---	---	Rn.96136	BG671506	8.19	8.29	7.12	8.32	7.99	8.71	1.38	up	3.34E-01	8.95E-01	-	-
1384553_at	RGD1305685	similar to hypothetical protein FLJ13089	360811	Rn.202650	BE118056	3.39	3.39	2.62	3.39	3.40	4.03	1.38	up	2.32E-01	8.95E-01	-	-
1389742_at	---	---	---	Rn.65227	AW520758	6.52	5.71	6.68	5.74	5.52	6.24	1.38	down	2.73E-01	8.95E-01	-	-
1377705_at	---	---	---	---	BF549971	4.39	3.14	2.59	5.11	3.19	3.22	1.38	up	6.01E-01	8.95E-01	-	-
1377185_at	RGD1562622	similar to RIKEN cDNA 6330442E10 gene	503035	Rn.43946	BG667451	2.37	2.39	2.39	3.57	2.39	2.60	1.38	up	2.66E-01	8.95E-01	-	-
1382213_at	Dpp8	dipeptidylpeptidase 8	315758	Rn.17532	AI535527	7.37	8.08	7.74	8.44	8.01	8.15	1.38	up	1.23E-01	8.95E-01	-	-
1379647_at	---	---	---	Rn.15307	BI295140	2.55	2.73	3.54	2.41	2.41	2.58	1.38	down	2.08E-01	8.95E-01	-	-
1383357_a_at	Reln1	RELT-like 1	289635	Rn.165637	BF403558	7.73	8.46	7.40	7.88	8.02	9.10	1.38	up	3.97E-01	8.95E-01	-	-
1392635_at	---	---	---	Rn.207125	BM387415	2.39	3.31	2.72	4.73	2.72	2.37	1.38	up	5.81E-01	8.95E-01	-	-
1367763_at	Acat1	acetyl-coenzyme A acetyltransferase 1	25014	Rn.4054	D13921	9.05	9.17	10.80	9.29	9.07	9.26	1.38	down	4.56E-01	8.95E-01	-	-
1382379_at	Rnf138	ring finger protein 138	84196	Rn.6814	AW530177	5.28	3.69	4.07	3.57	4.28	3.79	1.38	down	4.21E-01	8.95E-01	-	-
1392175_at	Ncor1	Nuclear receptor co-repressor 1	54299	Rn.24948	AA956966	4.22	2.51	2.67	2.64	2.52	2.83	1.38	down	4.44E-01	8.95E-01	-	-
1372704_at	Ostc	oligosaccharyltransferase complex subunit	362040	Rn.1889	BE098941	8.37	9.44	9.00	9.53	8.50	10.19	1.38	up	4.65E-01	8.95E-01	-	-
1376833_at	Tmem222	transmembrane protein 222	313021	Rn.102748	AW525740	5.40	5.92	6.79	5.59	5.42	5.69	1.38	down	3.17E-01	8.95E-01	-	-
1382148_at	---	---	---	Rn.24639	AA923980	4.44	5.42	3.91	3.91	4.14	4.31	1.38	down	3.62E-01	8.95E-01	-	-
1374591_at	Ptprd	protein tyrosine phosphatase, receptor type, D	313278	Rn.99077	AI409042	7.67	6.73	7.15	7.53	7.78	7.65	1.38	up	1.72E-01	8.95E-01	-	-
1383593_at	Tmem56	Transmembrane protein 56	365924	Rn.65373	BE113211	7.01	7.74	8.48	6.74	6.59	8.51	1.38	down	5.65E-01	8.95E-01	-	-
1374620_at	Ceacam1	carcinoembryonic antigen-related cell adhesion molecule 1 (biliary glycoprote	81613	Rn.91235	BM392373	4.91	5.39	5.64	5.33	5.67	6.35	1.38	up	2.73E-01	8.95E-01	-	-
1386999_at	Ywhab	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, t	56011	Rn.8653	NM_019377	9.39	9.60	9.46	10.02	10.07	9.76	1.38	up	1.52E-02	8.95E-01	-	-
1379665_at	Ppwd1	peptidylprolyl isomerase domain and WD repeat containing 1	294711	Rn.144258	AI177835	3.97	3.86	3.97	3.95	5.29	3.96	1.38	up	3.51E-01	8.95E-01	-	-
1370191_at	Azin1	antizyme inhibitor 1	58961	Rn.6290	AI411263	4.11	4.10	3.55	4.04	4.95	4.17	1.38	up	2.38E-01	8.95E-01	-	-
1377292_at	---	---	---	Rn.160418	BF403668	3.90	2.52	2.64	2.55	2.56	2.55	1.38	down	3.48E-01	8.95E-01	-	-
1386817_at	---	---	---	---	H32518	3.52	3.40	2.56	2.57	2.57	2.93	1.38	down	2.24E-01	8.95E-01	-	-
1382045_at	Tbc1d15	TBC1 domain family, member 15	366896	Rn.15910	BI304056	5.08	5.54	6.12	5.39	6.48	6.27	1.38	up	3.55E-01	8.95E-01	-	-
1392201_at	---	---	---	Rn.50083	BI288953	3.45	2.53	4.39	3.31	2.55	3.10	1.38	down	4.66E-01	8.95E-01	-	-
1373621_at	Gmpr2	guanosine monophosphate reductase 2	192357	Rn.155406	BI285949	5.01	5.22	5.39	4.99	4.10	5.13	1.38	down	2.44E-01	8.95E-01	-	-
1381503_at	---	---	---	Rn.105992	AI073168	7.37	7.70	8.17	8.31	8.20	8.14	1.38	up	1.19E-01	8.95E-01	-	-
1393804_at	RGD1307055	similar to hypothetical protein FLJ22490	362472	Rn.34473	BF386537	6.58	6.68	6.11	6.30	7.66	6.81	1.38	up	3.41E-01	8.95E-01	-	-
1375068_at	Med22	mediator complex subunit 22	499762	Rn.202721	AI410604	3.81	4.58	4.05	4.66	4.60	4.58	1.38	up	1.12E-01	8.95E-01	-	-
1377601_at	RGD1311257	similar to C21orf70 protein	294333	Rn.22122	BM386514	3.09	3.14	4.81	3.27	3.25	3.13	1.38	down	4.56E-01	8.95E-01	-	-
1374297_at	Dync1i1	Dynein cytoplasmic 1 light intermediate chain 1	252902	Rn.2064	BE100843	7.42	7.00	6.57	7.85	7.21	7.33	1.38	up	2.10E-01	8.95E-01	-	-
1391472_at	Dzip1	DAZ interacting protein 1	364475	Rn.24061	AI502851	2.46	2.45	2.46	2.46	3.87	2.45	1.38	up	3.79E-01	8.95E-01	-	-
1396162_at	---	---	---	Rn.165584	AI008298	2.55	2.59	3.91	2.55	2.55	2.55	1.38	down	3.54E-01	8.95E-01	-	-
1374585_at	Ecdh2	enoyl Coenzyme A hydratase domain containing 1	361465	Rn.4220	AW915152	5.35	6.31	7.28	5.62	5.71	6.21	1.38	down	4.89E-01	8.95E-01	-	-
1393833_at	Angel1	angel homolog 1 (Drosophila)	362765	Rn.135058	AI576461	4.20	4.68	4.66	5.26	4.65	5.02	1.38	up	1.19E-01	8.95E-01	-	-
1375269_at	Dera	2-deoxyribose-5-phosphate aldolase homolog (C. elegans)	690945	---	BM391516	7.89	7.77	7.40	7.05	6.72	7.90	1.38	down	2.87E-01	8.95E-01	-	-
1369729_at	Arl5a	ADP-ribosylation factor-like 5A	117050	Rn.2803	NM_053979	10.82	9.95	10.65	10.23	9.79	10.01	1.38	down	1.87E-01	8.95E-01	-	-
1384464_at	Scap	SREBF chaperone	301024	Rn.99548	AI145323	4.12	4.91	5.71	4.25	4.17	4.92	1.38	down	4.18E-01	8.95E-01	-	-
1373482_at	Traf3	Tnf receptor-associated factor 3	362788	Rn.12033	BI303106	5.35	6.58	6.21	5.49	5.84	5.41	1.38	down	2.94E-01	8.95E-01	-	-
1369426_at	Chd8	chromodomain helicase DNA binding protein 8	65027	Rn.98337	NM_022933	5.21	4.21	3.98	4.00	4.01	3.99	1.38	down	2.85E-01	8.95E-01	-	-
1391573_at	Tnfrsf21	tumor necrosis factor receptor superfamily, member 21	316256	Rn.98293	AA891842	9.29	9.65	9.58	10.01	9.85	10.06	1.38	up	2.10E-02	8.95E-01	-	-
1378876_at	---	---	---	Rn.46671	BE114024	2.43	2.41	4.44	2.57	2.43	2.88	1.38	down	5.33E-01	8.95E-01	-	-
1384621_at	---	---	---	Rn.164850	AA924327	2.74	2.69	2.74	2.66	3.23	3.68	1.38	up	1.91E-01	8.95E-01	-	-
1374503_at	Pbx3	pre-B-cell leukemia homeobox 3	311876	Rn.162662	AI709810	3.43	3.41	2.66	3.85	3.63	3.42	1.38	up	1.70E-01	8.95E-01	-	-
1367935_at	Smu1	smu-1 suppressor of mec-8 and unc-52 homolog (C. elegans)	117541	Rn.54953	NM_057195	7.12	7.36	8.24	8.12	7.92	8.08	1.38	up	2.49E-01	8.95E-01	-	-
1386164_at	Cdc25	Cell division cycle 2-like 5 (cholinesterase-related cell division controller)	306998	Rn.23420	AI170800	4.14	3.88	4.25	4.64	4.72	4.31	1.38	up	4.81E-02	8.95E-01	-	-
1383864_at	---	---	---	Rn.165828	BF412512	2.66	4.37	3.38	4.55	2.82	4.45	1.38	up	5.67E-01	8.95E-01	-	-
1377571_at	Nat14	N-acetyltransferase 14	361500	Rn.140257	BI276514	4.80

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1371999_at	---	---	---	Rn.164410	BI303641	5.62	5.83	6.09	5.87	6.68	6.37	1.38	up	1.65E-01	8.95E-01	-	-
1375353_at	Cables1	Cdk5 and Abl enzyme substrate 1	307585	Rn.43941	BI296696	2.62	3.07	2.62	2.76	4.37	2.58	1.38	up	4.73E-01	8.95E-01	-	-
1374922_at	Gpn2	GPN-loop GTPase 2	362614	Rn.32671	AI013096	3.90	5.51	4.68	5.38	5.09	5.02	1.38	up	3.88E-01	8.95E-01	-	-
1393704_at	LOC500584	similar to casein kinase 1, gamma 3 isoform 2	500584	Rn.107738	AI136988	3.01	3.64	3.70	3.73	3.96	4.06	1.38	up	1.26E-01	8.95E-01	-	-
1386836_at	Znf574	zinc finger protein 574	308434	Rn.15466	BF556285	2.48	3.71	2.42	2.42	2.41	2.39	1.38	down	3.32E-01	8.95E-01	-	-
1388919_at	Znf541	zinc finger protein 541	308108	Rn.215336	AW144669	8.52	7.81	7.78	7.52	7.48	7.72	1.38	down	1.42E-01	8.95E-01	-	-
1368154_at	Gucy1a3	guanylate cyclase 1, soluble, alpha 3	497757	Rn.1974	M57405	3.04	2.64	2.68	3.54	2.95	3.27	1.38	up	9.36E-02	8.95E-01	-	-
1373953_at	Slc4a1ap	solute carrier family 4 (anion exchanger), member 1, adaptor protein	298805	Rn.36032	BI290779	4.12	3.67	3.86	4.82	3.85	4.37	1.38	up	2.08E-01	8.95E-01	-	-
1389902_at	H13	histocompatibility 13	311545	Rn.12102	BI285090	7.68	8.46	8.72	8.28	8.57	9.39	1.38	up	3.68E-01	8.95E-01	-	-
1369091_at	Chrnb1	cholinergic receptor, nicotinic, beta 1 (muscle)	24261	Rn.44611	NM_012528	3.34	3.33	3.83	3.30	2.57	3.24	1.38	down	1.62E-01	8.95E-01	-	-
1389327_at	Mrpl32	mitochondrial ribosomal protein L32	291206	Rn.13489	BF282675	6.79	6.84	6.26	7.08	7.08	7.13	1.38	up	6.91E-02	8.95E-01	-	-
1399025_at	Mier1	mesoderm induction early response 1 homolog (Xenopus laevis)	313418	Rn.36542	AW916140	7.23	6.93	5.77	6.66	7.68	6.98	1.38	up	4.36E-01	8.95E-01	-	-
1387665_at	Bhmt	betaine-homocysteine methyltransferase	81508	Rn.11406	U96133	4.69	5.40	4.67	5.02	3.70	4.65	1.38	down	3.70E-01	8.95E-01	-	-
1370260_at	Add3	adducin 3 (gamma)	25230	Rn.76589	AI407835	7.85	7.09	6.48	7.13	6.21	6.69	1.38	down	3.87E-01	8.95E-01	-	-
1373046_at	Dazap1	DAZ associated protein 1	362836	Rn.16769	AW918273	5.94	6.66	5.84	6.84	6.58	6.41	1.38	up	1.78E-01	8.95E-01	-	-
1393083_at	Tox	Thymocyte selection-associated high mobility group box	362481	Rn.161967	AI102529	2.73	2.93	4.38	2.73	2.74	3.19	1.38	down	4.39E-01	8.95E-01	-	-
1389867_at	---	---	---	Rn.30004	BI281086	4.47	4.82	7.01	5.19	4.88	4.84	1.38	down	5.94E-01	8.95E-01	-	-
1387117_at	Zranb2	zinc finger, RAN-binding domain containing 2	58821	Rn.11361	AF013965	6.99	6.76	5.93	6.52	6.00	5.77	1.38	down	3.02E-01	8.95E-01	-	-
1398372_at	Rmnd5b	required for meiotic nuclear division 5 homolog B (S. cerevisiae)	497900	Rn.8249	BG380297	2.59	2.60	2.72	3.38	2.70	3.21	1.38	up	8.93E-02	8.95E-01	-	-
1373461_at	Rai12	retinoic acid induced 12	287446	Rn.9041	AI412649	4.81	5.09	3.44	4.77	4.55	5.40	1.38	up	4.62E-01	8.95E-01	-	-
1397960_at	Armcx3	armadillo repeat containing, X-linked 3	367902	Rn.44741	AI030168	2.47	2.46	2.50	3.97	2.48	2.38	1.38	up	4.19E-01	8.95E-01	-	-
1377789_at	---	---	---	Rn.13199	AI145035	7.78	8.48	6.68	7.92	7.59	8.81	1.38	up	5.08E-01	8.95E-01	-	-
1374502_at	Rab3gap2	RAB3 GTPase activating protein subunit 2	289350	Rn.101730	AI180286	3.63	4.32	5.36	4.48	3.65	3.79	1.38	down	4.58E-01	8.95E-01	-	-
1370337_at	Ctcf	CCCTC-binding factor (zinc finger protein)	83726	Rn.18612	AF133725	5.78	5.77	6.49	4.96	6.06	5.64	1.38	down	3.11E-01	8.95E-01	-	-
1371611_at	Ext2	exostoses (multiple) 2	311215	Rn.2878	BM387363	5.50	5.67	4.96	5.47	6.34	5.70	1.38	up	2.41E-01	8.95E-01	-	-
1383642_at	---	---	---	---	BG374114	6.60	6.17	6.65	6.66	5.26	6.10	1.38	down	3.48E-01	8.95E-01	-	-
1383422_at	Bend5	BEN domain containing 5	362564	Rn.87596	AW229401	9.25	9.34	9.63	8.95	9.09	8.80	1.38	down	3.18E-02	8.95E-01	-	-
1372977_at	Map4k5	mitogen-activated protein kinase kinase kinase kinase 5	503027	Rn.212028	BI291366	2.73	2.72	2.74	2.49	3.05	4.04	1.38	up	3.63E-01	8.95E-01	-	-
1379461_at	Zfp445	zinc finger protein 445	301076	Rn.100996	BE120147	6.15	6.93	6.66	6.47	5.28	6.59	1.38	down	3.85E-01	8.95E-01	-	-
1391348_at	Pank3	pantothenate kinase 3	360511	Rn.13643	BI296886	3.85	3.79	4.51	3.33	3.97	3.47	1.38	down	1.98E-01	8.95E-01	-	-
1378778_a_at	---	---	---	Rn.59729	BF394727	6.58	6.66	6.81	6.12	6.94	7.38	1.38	up	4.37E-01	8.95E-01	-	-
1369491_at	Dao	D-amino-acid oxidase	114027	Rn.81058	NM_053626	10.12	9.97	10.37	9.56	9.91	9.59	1.38	down	4.63E-02	8.95E-01	-	-
1381981_at	---	---	---	Rn.17233	BE101088	7.75	6.81	7.27	6.82	6.46	7.17	1.38	down	2.44E-01	8.95E-01	-	-
1370036_at	Suox	sulfite oxidase	81805	Rn.25720	NM_031127	9.49	9.36	9.45	8.94	9.01	8.96	1.38	down	4.80E-04	8.95E-01	-	-
1372504_at	Dpm3 /// Dpm3-ps	dolichyl-phosphate mannosyltransferase polypeptide 3 /// dolichyl-phosphate	502017 /// 692000	Rn.20619	AI179780	7.75	7.81	7.96	8.67	7.98	8.26	1.38	up	9.08E-02	8.95E-01	-	-
1380131_at	Wdr37	WD repeat domain 37	307075	Rn.163358	BE116354	6.90	6.42	6.42	5.64	6.40	6.31	1.38	down	1.83E-01	8.95E-01	-	-
1370525_at	Ube2d2	ubiquitin-conjugating enzyme E2D 2	641452	Rn.7390	U13176	3.51	4.05	4.91	2.95	3.51	4.63	1.38	down	5.11E-01	8.95E-01	-	-
1371819_at	Hdac5	histone deacetylase 5	84580	Rn.79883	BF403027	3.79	4.16	3.68	3.68	5.03	4.31	1.38	up	3.30E-01	8.95E-01	-	-
1382176_at	Klhl11	Kelch-like 11 (Drosophila)	287706	Rn.25079	AI454666	3.23	2.82	3.79	3.04	2.53	2.89	1.38	down	2.23E-01	8.95E-01	-	-
1374312_at	Uck1	uridine-cytidine kinase 1	311864	Rn.20148	BI297050	5.44	6.15	4.93	6.03	5.62	6.26	1.38	up	3.11E-01	8.95E-01	-	-
1371797_at	Cad	carbamoyl-phosphate synthetase 2, aspartate transcarbamylase, and dihydro	24240	Rn.19416	BM391890	3.59	4.57	3.32	4.38	4.54	3.95	1.38	up	3.32E-01	8.95E-01	-	-
1394944_at	---	---	---	Rn.43625	AI410195	4.01	3.19	3.24	3.20	3.10	2.76	1.38	down	1.95E-01	8.95E-01	-	-
1385699_at	Ythdf1	YTH domain family, member 1	296467	Rn.16949	BI283897	4.22	4.99	4.45	4.91	4.56	5.57	1.38	up	2.84E-01	8.95E-01	-	-
1371113_a_at	Tfrc	transferrin receptor	64678	Rn.98672	M58040	3.51	4.00	4.30	2.86	3.88	3.69	1.38	down	2.97E-01	8.95E-01	-	-
1387653_at	Tanax	tanaxin-associated factor X	60428	Rn.2315	AF262357	7.72	7.68	7.45	8.00	7.98	8.28	1.38	up	2.54E-02	8.95E-01	-	-
1376810_at	Aphosphl /// Parp4	M-phase phosphoprotein 8 /// poly (ADP-ribose) polymerase family, member 4	290270 /// 361046	Rn.42579	AI103325	3.41	4.01	3.89	4.47	4.02	4.21	1.38	up	1.09E-01	8.95E-01	-	-
1373916_at	Ep300	E1A binding protein p300	170915	Rn.12447	AI237356	5.88	5.29	7.34	5.90	5.58	5.64	1.38	down	4.95E-01	8.95E-01	-	-
1398217_at	Zbtb41	zinc finger and BTB domain containing 41	289052	Rn.51461	BE108367	4.06	2.90	2.85	2.83	2.75	2.84	1.38	down	3.07E-01	8.95E-01	-	-
1392686_at	Nkd2	naked cuticle homolog 2 (Drosophila)	308068	Rn.198099	AI072336	4.33	2.55	3.02	2.70	2.92	2.90	1.38	down	4.38E-01	8.95E-01	-	-
1371643_at	Ccnd1	cyclin D1	58919	Rn.22279	AW143798	8.42	9.58	7.95	8.99	8.80	9.53	1.38	up	4.34E-01	8.95E-01	-	-
1372947_at	Plsb3	plastin 3 (T-isoform)	81748	Rn.32103	BG672591	4.79	3.88	5.23	4.55	4.53	3.43	1.38	down	4.43E-01	8.95E-01	-	-
1373122_at	Jub	jub, ajuba homolog (Xenopus laevis)	85265	Rn.144617	BI284400	4.93	6.13	5.96	4.87	5.97	4.79	1.38	down	4.36E-01	8.95E-01	-	-
1375185_at	Ipo7	importin 7	308939	Rn.203234	BM390183	5.91	6.29	5.77	6.25	6.28	6.83	1.38	up	1.32E-01	8.95E-01	-	-
1369919_at	Tef	thyrotrophic embryonic factor	29362	Rn.59871	NM_019194	3.54	5.40	3.30	3.30	3.57	3.98	1.38	down	5.42E-01	8.95E-01	-	-
1376062_at	Sdc1	syndecan 1	25216	Rn.11176	BG375315	2.38	2.37	2.39	2.43	2.72	2.37	1.38	up	3.54E-01	8.95E-01	-	-
1374384_at	Cryga	crystallin, gamma A	684028	---	BF543345	4.15	4.78	3.08	4.09	4.45	4.85	1.38	up	4.43E-01	8.95E-01	-	-
1382877_at	Dhx35	DEAH (Asp-Glu-Ala-His) box polypeptide 35	362260	Rn.118078	AW525179	5.06	5.86	5.61	6.23	4.13	4.79	1.38	down	5.26E-01	8.95E-01	-	-
1376949_at	Rce1	RCE1 homolog, prenyl protein peptidase (S. cerevisiae)	309153	Rn.105170	BE099848	3.31	3.35	3.68	3.95	3.98	3.79	1.38	up	2.39E-02	8.95E-01	-	-
1389846_at	Tpm3	Tropomyosin 3, gamma	117557	Rn.37575	BE104273	6.71	7.29	7.38	7.80	7.26	7.69	1.38	up	1.58E-01	8.95E-01	-	-
1382455_at	---	---	---	Rn.49234	BG379564	6.85	6.42	5.57	6.19	5.00	6.26	1.38	down	4.56E-01	8.95E-01	-	-
1388564_at	RGD1303127	similar to hypothetical protein FLJ20436	360206	Rn.884	BF283612	3.22	3.93	3.22	4.05	3.31	4.39	1.38	up	3.11E-01	8.95E-01	-	-
1368915_at	Kmo	kynurenine 3-monooxygenase (kynurenine 3-hydroxylase)	59113	Rn.35029	NM_021593	9.31	9.67	9.85	9.31	9.02	9.12	1.38	down	6.37E-02	8.95E-01	-	-
1375508_at	---	---	---	Rn.154745	BE095963	6.13	4.37	4.13	4.17	4.67	4.41	1.38	down	5.17E-01	8.95E-01	-	-
1389494_at	Ccdc88b	coiled-coil domain containing 88B	361715	Rn.22455	BM388595	3.90	3.30	3.47	2.83	3.06	3.40	1.38	down	1.33E-01	8.95E-01	-	-
1373086_at	Pcif1	PDX1 C-terminal inhibiting factor 1	362269	Rn.4193	AI102818	5.92	4.82	4.79	5.41	3.62	5.12	1.38	down	5.30E-01	8.95E-01	-	-
1371872_at	Nap1l1	Nucleosome assembly protein 1-like 1	89825	Rn.162938	BE108905	7.62	7.77	8.15	8.01	8.34	8.57	1.38	up	1.13E-01	8.95E-01	-	-
1369078_at	Mapk1	mitogen activated protein kinase 1	116590	Rn.34914	NM_053842	4.87	6.07	5.13	4.78	4.43	5.48	1.38	down	3.89E-01	8.95E-01	-	-
1373269_at	---	---	---	Rn.161389	AI407751	5.04	6.42	6.34	6.00	6.69	6.49	1.38	up	4.05E-01	8.95E-01	-	-
1389857_at	Wbp5	WW domain binding protein 5	680354	Rn.6930	BG378874	6.49	5.96	5.44	6.92	5.83	6.52	1.38	up	3.56E-01	8.95E-01	-	-
1392684_at	Dci	dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoyl-Coenzyme A isome	29740	Rn.80835	BE098511	2.65	2.59	3.61	2.60	2.31	2.56	1.38	down	2.51E-01	8.95E-01	-	-
1369973_at	Xdh	xanthine dehydrogenase	497811	Rn.202951	NM_017154	8.20	7.91	8.50	7.70	7.84	7.69	1.38	down	5.96E-02	8.95E-01	-	-
1383055_at	---	---	---	Rn.203252	AW143805	5.85	6.33	6.95	7.08	6.80	6.63	1.38	up	2.55E-01	8.95E-01	-	-
1388549_at	Ncoa4	nuclear receptor coactivator 4	619385	Rn.198999	AI228248	7.21	7.22	7.02	7.71	7.46	7.66	1.38	up	1.03E-02	8.95E-01	-	-
1388117_at	Snrpb	small nuclear ribonucleoprotein polypeptides B and B1	171365	Rn.3437	AI411893	4.27	5.19	4.55	4.20	4.31	4.14	1.37	down	1.73E-01	8.95E-01	-	-
1387206_at	B4galt6	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 6	65196	Rn.21126	NM_031740	3.32	3.91	3.07	3.89	3.52	4.28	1.37	up	2.40E-01	8.95E-01	-	-
1382173_at	---	---	---	---	BF283569	2.52	2.59	3.74	2.50	2.51	2.46	1.37	down	3.13E-01	8.95E-01	-	-
1372460_at	130 /// RGD15627	similar to SET protein (Phosphatase 2A inhibitor I2PP2A) (I-2PP2A) (Templat	47 /// 313310 /// 50	Rn.76937	BG381708	8.84	8.03	9.77	8.23	8.32	8.72	1.37	down	4.31E-01	8.95E-01	-	-
1389754_at	---	---	---	---	AI555295	2.46	2.37	3.67	2.37	2.38	2.36	1.37	down	3.33E-01	8.95E-01	-	-
1379002_at	---	---	---	Rn.31067	AI169333	2.38	2.53	2.37	2.36	3.67	2.62	1.37	up	3.16E-01	8.95E-01	-	-
1390798_at	Ptprc	protein tyrosine phosphatase, receptor type, C	24699	Rn.90166	BF288130	4.23	2.87	2.87	2.84	2.90	2.86	1.37	down	3.67E-01	8.95E-01	-	-
1385525_at	Clec1b	C-type lectin domain family 1, member b	500336	Rn.162772	AI029991	2.89	2.87	2.90	2.88	2.91	4.26	1.37	up	3.68E-01	8.95E-01	-	-
1373867_at	Jarid1a	Jumonji, AT rich interactive domain 1A (Rbp2 like)	312678	Rn.134218	BI289360	5.74	5.79	5.77	6.19	6.60	5.88	1.37	up	9.37E-02	8.95E-01	-	-
1369268_at	Atf3	activating transcription factor 3	25389	Rn.9664	NM_012912	2.41	2.47	2.42	2.48	2.42	3.78	1.37	up	3.60E-01	8.95E-01	-	-
1393453_at	Sav1	salvador homolog 1 (Drosophila)	299116	Rn.14087	BI290287	5.96	5.29	5.41	4.82	4.94	5.52	1.37	down	1.97E-01	8.95E-01	-	-
1384469_at	Abca5	ATP-binding cassette, sub-family A (ABC1), member 5	286970	Rn.35782	AI502224	2.53	2.49	2.55	2.54	2.86	3.55	1.37	up	2.02E-01	8.95E-01	-	-
1385534_at	Ngfrap1	nerve growth factor receptor (TNFRSF16) associated protein 1	117089	Rn.3126	BG381021	3.07	2.94	3.24	3.03	4.30	3.30	1.37	up	3.11E-01	8.95E-01	-	-
1382898_at	---	---	---	Rn.66436	BG376849	3.56	4.73	4.19	4.56	4.18	5.11	1.37	up	3.49E-01	8.95E-01	-	-
1388988_at	Abhd14b	abhydrolase domain containing 14b	300983	Rn.2080	AI175070	8.55	9.30	8.66	8.20	8.46	8.47	1.37	down	1.41E-01	8.95E-01	-	-
1372837_at	Wdfy2	WD repeat and FYVE domain containing 2	305956	Rn.40475	BI277033	4.87	3.75	5.25	4.16	3.83	4.50	1.37	down	4.01E-01	8.95E-01	-	-
1371437_at	Sec13	SEC13 homolog (S. cerevisiae)	297522	Rn.1553	BM986228	9.88	9.73	9.80	9.44	8.77	9.84	1.37	down	2.19E-01	8.95E-01	-	-
1378392_at	Dnaja3	DnaJ (Hsp40) homolog, subfamily A, member 3	360481	Rn.198254	BG377107	8.64	9.19	8.48	8.98	9.17	9.53	1.37	up	1.63E-01	8.95E-01	-	-
1397176_at	Mettl6	methyltransferase like 6	290564	Rn.29892	AI104417	4.63	5.05	4.47	6.01	4.66	4.86	1.37	up	3.69E-01	8.95E-01	-	-
1373656_at	Ppp1r3d	protein phosphatase 1, regulatory subunit 3D	689995	Rn.93537	AI713313	2.87	2.34	2.88	3.77	3.03	2.68	1.37	up	2.79E-01	8.95E-01	-	-
1394430_at	---	---	---	Rn.168003	AI511275	3.86	3.85	3.71	3.98	3.69	5.13	1.37	up	3.59E-01	8.95E-01	-	-
1387306_a_at	Egr2	early growth response 2	114090	Rn.89235	D83508	2.47	2.46	2.49	3.12	3.22	2.46	1.37	up	1.26E-01	8.95E-01	-	-
1374917_at	Sec63	SEC63 homolog (S. cerevisiae)	300858	Rn.24233	AI548571	2.26	3.35	3.90	3.43	3.26	4.20	1.37	up	4.59E-01	8.95E-01	-	-
1385244_at	Adam4	a disintegrin and metalloprotease domain 4	57022	Rn.209651	BF390070	3.80	3.51	2.58	2.84	2.70	2.98	1.37	down	2.89E-01	8.95E-01	-	-
1378368_at	L3mbtl3	l(3)mbt-like 3 (Drosophila)	309550	Rn.204097	BF402723	2.36	2.86	2.37	2.36	4.25	2.36	1.37	up	5.22E-01	8.95E-01	-	-
1370925_at	Atp9b	ATPase, class II, type 9B	291411	Rn.40336	BG380816	4.52	4.50	4.51	4.68	5.34	4.89	1.37	up	7.86E-02	8.95E-01	-	-
1379294_at	---	---	---	Rn.13051	AA957424	3.85	2.77	2.41	2.61	2.64	2.64	1.37	down	3.55E-01	8.95E-01	-	-
1370799_at	Slc9a1	Solute carrier family 9 (sodium/hydrogen exchanger), member 1	24782	Rn.5025	AF462063	5.64	5.63	7.01	5.40	5.99	5.51	1.37	down	4.04E-01	8.95E-01	-	-
1388473_at	---	---	---	Rn.105661	BF418041	3.73	4.29	4.24	4.28	4.23	5.12	1.37	up	2.50E-01	8.95E-01	-	-
1391136_at	Klk1b21	kallikrein 1-related peptidase b21	292866	Rn.79284	BI291725	3.81	2.42	2.45	2.41	2.50	2.41	1.37	down	3.77E-01	8.95E-01	-	-
1394033_at	Rbbp9	retinoblastoma binding protein 9	29459	Rn.162693	AA956258	4.37	5.88	6.43	4.60	4.80	5.91	1.37	down	5.69E-01	8.95E-01	-	-
1397898_at	---	---	---	---	BI293701	2.53	2.48	2.54	2.51	3.77	2.65	1.37	up	3.17E-01	8.95E-01	-	-
1393363_at	Zmym2	zinc finger, MYM-type 2	306913	Rn.22885	AI116670	6.93	7.18	6.75	7.09	7.89	7.24	1.37	up	1.70E-01	8.95E-01	-	-
1376763_at	---	---	---	Rn.6906	AW915423	5.37	5.37	5.34	5.88	4.58	6.99	1.37	up	5.46E-01	8.95E-01	-	-
1376664_at	Slc7a6os	solute carrier family 7, member 6 opposite strand	246187	Rn.18683	BM386170	3.64	3.36	3.21	3.62	4.15	3.81	1.37	up	8.23E-02	8.95E-01	-	-
1373196_at	Efha2	EF hand domain family, member A2	364601	Rn.23547	BF404514	6.37	4.94	5.21	5.61	6.27	6.02	1.37	up	3.95E-01	8.95E-01	-	-
1392598_at	---	---	---	Rn.164582	AA893326	10.86	10.26	10.10	9.65	10.13	10.07	1.37	down	1.73E-01	8.95E-01	-	-
1385494_at	Tbc1d23	TBC1 domain family, member 23	304019	Rn.203120	BM390350	3.40	5.34	5.13	3.73	3.49	5.27	1.37	down	6.10E-01	8.95E-01	-	-
1383274_at	Pcbp3	poly(rC) binding protein 3	294336	Rn.107537	AA956005	2.42	2.41	2.42	3.75	2.42	2.45	1.37	up	3.57E-01	8.95E-01	-	-
1372255_at	Rars	arginyl-tRNA synthetase	297191	Rn.18711	BF283284	7.19	8.25	7.76	7.85	8.41	8.30	1.37	up	2.62E-01	8.95E-01	-	-
1387932_at	Slc1a1	solute carrier family 1 (neuronal/epithelial high affinity glutamate transporter, s	25550	Rn.6384	U39555	9.49	9.27	9.13	9.14	8.57	8.81	1.37	down	8.08E-02	8.95E-01	-	-
1371358_at	Gpsn2	glycoprotein, synaptic 2	191576	Rn.107358	BI282960	5.73	7.01	6.15	6.34	6.93	7.01	1.37	up	3.50E-01	8.95E-01	-	-
1392564_at	Mll5	myeloid/lymphoid or mixed-lineage leukemia 5 (trithorax homolog, Drosophila	311968	Rn.106040	BI299176	2.59	2.58	3.87	2.57	2.51	2.58	1.37	down	3.45E-01	8.95E-01	-	-
1385783_at	Wwc2	WW and C2 domain containing 2	498830	Rn.114737	BF413697	7.40	6.31	8.00	6.67	7.30	6.37	1.37	down	4.66E-01	8.95E-01	-	-
1367701_at	Ramp2	receptor (G protein-coupled) activity modifying protein 2	58966	Rn.107168	NM_031646	4.22	2.50	2.40	2.76	2.51	2.49	1.37	down	4.87E-01	8.95E-01	-	-
1388642_at	Ei24	etoposide induced 2.4 mRNA	300514	Rn.6593	AI412114	7.99	8.41	8.09	8.24	8.69	8.93	1.37	up	1.27E-01	8.95E-01	-	-
1375856_at	---	---	---	Rn.7450	AI102258	7.53	7.11	5.92	7.23	7.26	7.45	1.37	up	4.02E-01	8.95E-01	-	-
1382270_at	---	---	---	Rn.164820	BM384387	5.33	2.56	2.57	2.92	2.97	3.20	1.37	down	6.48E-01	8.96E-01	-	-
1373126_at	---	---	---	Rn.1563	AW918188	6.78	6.59	5.85	6.78	6.39	7.42	1.37	up	3.30E-01	8.95E-01	-	-
1388247_at	---	---	---	---	U48828	2.75	2.68	3.07	3.35	3.45	3.08	1.37	up	4.96E-02	8.95E-01	-	-
1387229_at	Slc2a2	solute carrier family 2 (facilitated glucose transporter), member 2	25351	Rn.89295	NM_012879	6.81	6.23	6.07	5.68	5.33	6.73	1.37	down	3.94E-01	8.95E-01	-	-
1368957_at	Gng7	guanine nucleotide binding protein (G protein), gamma 7	58979	Rn.11335	NM_024138	4.32	4.64	3.20	4.10	3.65	5.78	1.37	up	5.91E-01	8.95E-01	-	-
1378972_at	Wwc1	WW and C2 domain containing 1	303039	Rn.101912	AI071547	7.85	7.76	7.21	8.18	7.70	8.31	1.37	up	1.88E-01	8.95E-01	-	-
1368138_at	Mapt	microtubule-associated protein tau	29477	Rn.2455	BE107978	9.64	10.00	9.83	9.66	9.23	9.21	1.37	down	6.34E-02	8.95E-01	-	-
1390794_at	LOC690214	similar to peptide deformylase-like protein	690214	Rn.165329	BI289098	7.58	6.99	6.13	7.55	7.13	7.39	1.37	up	3.57E-01	8.95E-01	-	-
1375878_at	Gapvd1	GTPase activating protein and VPS9 domains 1	311880	Rn.22293	BE102596	5.55	4.63	4.80	4.61	3.85	5.16	1.37	down	3.92E-01	8.95E-01	-	-
1398929_at	Eif3s6ip	eukaryotic translation initiation factor 3, subunit 6 interacting protein	300069	Rn.22102	AW525691	8.32	9.00	7.90	8.78	8.68	9.13	1.37	up	2.61E-01	8.95E-01	-	-
1382754_at	---	---	---	Rn.14621	H33080	2.50	2.52	2.50	2.99	2.52	3.38	1.37	up	1.39E-01	8.95E-01	-	-
1371827_at	Syvn1	synovial apoptosis inhibitor 1, synovioli	361712	Rn.162486	AA946430	7.73	8.19	8.14	8.69	8.24	8.50	1.37	up	8.01E-02	8.95E-01	-	-
1396250_at	Coro1c	coronin, actin binding protein 1C	501841	Rn.45957	BF558291	5.55	5.24	5.05	6.04	6.04	5.13	1.37	up	2.48E-01	8.95E-01	-	-
1390021_at	Hist1h2bh	histone cluster 1, H2bh	306945	Rn.199024	BM391206	8.24	8.62	7.69	7.61	7.54	8.02	1.37	down	2.16E-01	8.95E-01	-	-
1383067_a_at	Dtymk	deoxythymidylate kinase (thymidylate kinase)	301622	Rn.95	AW141143	2.75	3.20	4.32	2.78	2.92	3.20	1.37	down	4.00E-01	8.95E-01	-	-
1397277_at	---	---	---	---	AW920386	3.34	3.34	3.06	3.49	4.29	3.34	1.37	up	2.17E-01	8.95E-01	-	-
1399122_at	---	---	---	Rn.8410	BI278603	4.32	3.94	5.67	3.91	3.61

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1378932_at	Srprb	Signal recognition particle receptor, B subunit	300965	Rn.138078	AI103196	5.85	6.23	5.37	6.03	5.80	6.98	1.37	up	3.57E-01	8.95E-01	-	-
1388778_at	---	---	---	Rn.17629	BF284876	11.86	12.61	12.64	12.64	12.79	13.03	1.37	up	1.79E-01	8.95E-01	-	-
1383331_at	---	---	---	Rn.8380	BF548234	3.21	3.71	3.70	4.48	3.57	3.93	1.37	up	2.19E-01	8.95E-01	-	-
1384601_at	Lrba	LPS-responsive vesicle trafficking, beach and anchor containing	361975	Rn.2120	AI112177	6.06	5.21	6.30	4.13	6.89	5.19	1.37	down	6.31E-01	8.95E-01	-	-
1388621_at	Med11	mediator complex subunit 11	287456	Rn.19345	BG378803	5.82	6.11	5.24	5.59	6.53	6.41	1.37	up	3.12E-01	8.95E-01	-	-
1368660_at	Rapgef3	Rap guanine nucleotide exchange factor (GEF) 3	59326	Rn.42899	NM_021690	2.50	2.67	3.67	2.49	2.46	2.52	1.37	down	2.84E-01	8.95E-01	-	-
1377699_at	Bach1	BTB and CNC homology 1, basic leucine zipper transcription factor 1	304127	Rn.29793	BF395437	4.06	3.82	4.20	3.88	3.96	3.88	1.37	down	2.39E-01	8.95E-01	-	-
1367865_at	Lkap	limkain b1	170946	Rn.27366	NM_133421	6.84	6.79	6.88	6.77	5.50	6.88	1.37	down	3.65E-01	8.95E-01	-	-
1383005_at	---	---	---	Rn.165051	BM383579	3.63	4.35	5.70	5.05	4.48	5.51	1.37	up	5.39E-01	8.95E-01	-	-
1380722_at	---	---	---	---	AA859912	4.19	5.58	5.67	6.80	4.44	5.55	1.37	up	6.16E-01	8.95E-01	-	-
1368014_at	Ptges	prostaglandin E synthase	59103	Rn.7730	AF280967	2.46	2.45	3.74	2.43	2.46	2.39	1.37	down	3.49E-01	8.95E-01	-	-
1395571_at	Pcgf3	polycomb group ring finger 3	305624	Rn.8211	BF557189	3.92	5.47	6.35	5.08	6.44	5.58	1.37	up	6.09E-01	8.95E-01	-	-
1390153_at	---	---	---	Rn.166896	BG378721	2.60	3.08	5.06	3.13	3.08	3.18	1.37	down	5.81E-01	8.95E-01	-	-
1373247_at	---	---	---	Rn.48895	AW435407	3.11	2.88	4.91	3.33	3.11	3.10	1.37	down	5.23E-01	8.95E-01	-	-
1390808_at	ap1a /// RGD15641	microfibrillar-associated protein 1A /// similar to microfibrillar-associated protei	287415 /// 499878	Rn.93042	AW534721	6.98	5.95	6.58	6.42	5.37	6.36	1.37	down	3.75E-01	8.95E-01	-	-
1376189_at	Zmym1	zinc finger, MYM-type 1	313604	Rn.19963	AA849377	2.63	3.55	2.58	2.81	4.51	2.80	1.37	up	5.25E-01	8.95E-01	-	-
1382592_at	Ccdc99	coiled-coil domain containing 99	303037	Rn.54949	AI059054	2.43	2.88	2.70	3.50	2.95	2.91	1.37	up	1.20E-01	8.95E-01	-	-
1387882_at	Klf9	Kruppel-like factor 9	117560	Rn.19481	AI071565	3.62	2.38	2.30	2.35	2.35	2.23	1.37	down	3.51E-01	8.95E-01	-	-
1395533_at	Hars	histidyl-tRNA synthetase	307492	Rn.35537	BF552813	5.96	6.30	5.01	5.31	7.03	6.29	1.37	up	5.14E-01	8.95E-01	-	-
1381428_a_at	---	---	---	Rn.203229	AI177364	11.11	11.22	10.86	10.62	10.38	10.84	1.37	down	5.52E-02	8.95E-01	-	-
1372944_at	Drg2	developmentally regulated GTP binding protein 2	497915	Rn.3095	BI275710	4.16	4.54	4.45	4.14	3.87	3.77	1.37	down	5.16E-02	8.95E-01	-	-
1367501_at	Srp72	signal recognition particle 72	498351	Rn.2930	BM383845	5.35	4.73	5.11	5.26	5.40	5.88	1.37	up	1.58E-01	8.95E-01	-	-
1395060_at	---	---	---	Rn.205718	AI764218	2.61	2.50	2.53	4.03	2.51	2.45	1.37	up	4.34E-01	8.95E-01	-	-
1390207_at	Lats2	large tumor suppressor 2	305922	Rn.48618	BM390283	6.79	6.84	6.53	6.56	5.99	6.26	1.37	down	7.60E-02	8.95E-01	-	-
1395375_at	Ttc9c	tetratricopeptide repeat domain 9C	309196	Rn.162477	BG672758	6.00	6.16	6.46	5.53	6.18	6.54	1.37	down	3.54E-01	8.95E-01	-	-
1392729_at	---	---	---	Rn.23746	AI502692	2.94	2.85	3.49	2.96	4.18	3.50	1.37	up	3.30E-01	8.95E-01	-	-
1373423_at	Vps36	Vacuolar protein sorting 36 homolog (S. cerevisiae)	290851	Rn.12707	AI170766	3.57	3.46	5.17	3.78	3.50	3.57	1.37	down	4.65E-01	8.95E-01	-	-
1376518_at	---	---	---	---	BF396739	2.64	4.32	2.70	2.39	3.21	2.71	1.37	down	4.94E-01	8.95E-01	-	-
1374412_at	Fbxw11	F-box and WD repeat domain containing 11	303024	Rn.159760	BF557666	7.68	7.94	7.11	6.15	7.45	7.77	1.37	down	4.60E-01	8.95E-01	-	-
1398869_at	Psmc4	proteasome (prosome, macropain) 26S subunit, ATPase, 4	117262	Rn.11341	BG378826	8.00	8.44	9.03	7.88	8.00	8.23	1.37	down	2.28E-01	8.95E-01	-	-
1380205_at	Enth	Enthoprotin	360515	Rn.222041	AI712549	8.34	8.29	7.84	9.04	8.03	8.75	1.37	up	2.56E-01	8.95E-01	-	-
1377006_at	Cct6a	Chaperonin containing Tcp1, subunit 6A (zeta 1)	288620	Rn.33807	AA875047	6.79	7.58	8.44	7.50	6.54	7.42	1.37	down	4.70E-01	8.95E-01	-	-
1377710_at	---	---	---	Rn.16831	AI385197	2.67	2.65	2.70	2.66	4.08	2.64	1.37	up	3.96E-01	8.95E-01	-	-
1398815_at	Gani4	antigen peptide transporter 1-like	303298	Rn.20245	BG379594	2.84	3.25	3.05	3.01	4.12	3.37	1.37	up	2.66E-01	8.95E-01	-	-
1369152_at	Ppp3r1	protein phosphatase 3, regulatory subunit B, alpha isoform (calcineurin B, typ	29748	Rn.42903	NM_017309	8.50	7.94	8.01	7.35	7.89	7.85	1.37	down	1.43E-01	8.95E-01	-	-
1387544_at	Mk1	Mk1 protein	171436	Rn.201717	NM_134399	6.18	5.96	6.53	5.96	5.77	5.60	1.37	down	8.31E-02	8.95E-01	-	-
1389162_at	Nfu1	NFU1 iron-sulfur cluster scaffold homolog (S. cerevisiae)	297416	Rn.161843	BI277328	8.08	8.79	8.64	8.88	8.64	9.34	1.37	up	2.03E-01	8.95E-01	-	-
1367516_at	Dhrsp1	dishrobrevin binding protein 1	641528	Rn.187290	BG375549	7.81	8.08	8.90	7.76	8.23	8.15	1.37	up	3.06E-01	8.95E-01	-	-
1381826_at	---	---	---	Rn.41403	AI070839	5.77	5.72	5.82	5.90	6.42	6.35	1.37	up	5.19E-02	8.95E-01	-	-
1388233_at	Cish	cytokine inducible SH2-containing protein	83681	Rn.14523	AF065161	2.42	2.40	2.42	2.38	3.72	2.49	1.37	up	3.54E-01	8.95E-01	-	-
1396227_at	Mrrf	mitochondrial ribosome recycling factor	311903	Rn.105234	BG374845	4.97	5.61	6.01	4.97	5.36	4.91	1.37	down	2.48E-01	8.95E-01	-	-
1397137_at	---	---	---	---	BE114426	2.39	2.57	2.41	2.40	3.94	2.38	1.37	up	4.34E-01	8.95E-01	-	-
1389282_at	Itga3	Integrin alpha 3	360606	Rn.154664	BI292586	2.69	4.10	2.65	2.67	2.76	2.66	1.37	down	3.98E-01	8.95E-01	-	-
1378868_at	RGD1310810	similar to RIKEN cDNA 4930444A02	306549	Rn.39247	BE096173	2.54	2.83	2.53	2.97	3.42	2.86	1.37	up	8.63E-02	8.95E-01	-	-
1391016_at	Wars2	tryptophanyl tRNA synthetase 2 (mitochondrial)	690854	Rn.204847	AI235914	8.02	7.45	8.04	7.40	7.48	7.28	1.37	down	8.93E-02	8.95E-01	-	-
1391083_at	Arhgap22	Rho GTPase activating protein 22	306279	Rn.27999	BM384457	3.87	5.04	5.45	4.13	4.01	4.87	1.37	down	4.54E-01	8.95E-01	-	-
1376858_at	LOC686809	similar to protein 7 transactivated by hepatitis B virus X antigen	686809	---	BI281836	3.75	3.28	3.23	2.94	3.28	2.70	1.37	down	1.29E-01	8.95E-01	-	-
1375560_at	Npl2	N-acetylneuraminate pyruvate lyase 2 (putative)	293949	Rn.13905	AA945579	6.20	7.01	7.39	6.68	5.74	6.83	1.37	down	4.09E-01	8.95E-01	-	-
1398746_at	Nanp	N-acetylneuraminic acid phosphatase	311530	Rn.210573	BF399464	2.37	2.37	2.38	3.05	2.38	3.05	1.37	up	1.14E-01	8.95E-01	-	-
1394992_at	---	---	---	Rn.209141	BF389891	6.13	6.39	6.84	5.61	5.83	6.58	1.37	down	2.80E-01	8.95E-01	-	-
1390770_at	---	---	---	---	BF396139	4.57	3.91	3.36	4.58	3.69	4.92	1.37	up	4.26E-01	8.95E-01	-	-
1372986_at	Jdp2	Jun dimerization protein 2	116674	Rn.10721	BF394170	3.74	3.94	3.71	3.54	5.03	4.17	1.37	up	3.65E-01	8.95E-01	-	-
1377768_at	Kctd1	potassium channel tetramerisation domain containing 1	291772	Rn.27416	BE107485	4.23	3.16	3.96	3.09	6.43	3.18	1.37	up	7.15E-01	9.10E-01	-	-
1398612_at	Akr1c12	aldo-keto reductase family 1, member C12	361266	---	BM383010	11.42	11.97	11.73	11.25	11.36	11.17	1.37	down	5.55E-02	8.95E-01	-	-
1368395_at	Gpc3	glypican 3	25236	Rn.9717	NM_012774	3.74	3.79	3.96	3.87	4.39	4.58	1.37	up	1.13E-01	8.95E-01	-	-
1392391_at	Dag1	dystroglycan 1 (dystrophin-associated glycoprotein 1)	114489	Rn.36260	BE112061	3.22	3.21	3.46	4.79	3.19	3.26	1.36	up	4.43E-01	8.95E-01	-	-
1374249_at	RGD1304580	similar to Hypothetical protein MGC38513	292781	Rn.2550	AI168982	5.91	5.11	3.63	5.00	5.89	5.10	1.36	up	5.70E-01	8.95E-01	-	-
1393508_at	---	---	---	Rn.18728	AI044805	7.37	7.02	6.95	7.43	7.74	7.52	1.36	up	4.78E-02	8.95E-01	-	-
1375571_at	Zzef1	Zinc finger, ZZ-type with EF hand domain 1	287476	Rn.24218	AW251798	5.80	3.74	2.97	3.89	5.17	4.80	1.36	up	6.53E-01	8.97E-01	-	-
1392181_at	---	---	---	Rn.50702	BE120481	2.37	2.36	3.98	2.45	2.36	2.55	1.36	down	4.54E-01	8.95E-01	-	-
1377848_at	Fam175a	family with sequence similarity 175, member A	289468	Rn.106875	AW535219	3.11	3.24	3.29	4.07	3.23	3.68	1.36	up	1.45E-01	8.95E-01	-	-
1376315_at	Edem2	ER degradation enhancer, mannosidase alpha-like 2	296304	Rn.18635	BI282297	6.20	3.40	2.79	3.41	5.24	5.10	1.36	up	7.28E-01	9.13E-01	-	-
1398776_at	Rpn2	ribophorin II	64701	Rn.2879	NM_031698	7.22	8.54	8.62	8.55	8.31	8.86	1.36	up	4.05E-01	8.95E-01	-	-
1382684_at	---	---	---	Rn.148790	BI293639	2.26	3.17	2.53	4.52	2.27	2.52	1.36	up	5.88E-01	8.95E-01	-	-
1395157_at	Nedd4	neural precursor cell expressed, developmentally down-regulated gene 4	25489	Rn.99540	BI286685	5.72	5.99	6.11	6.55	6.10	6.51	1.36	up	7.31E-02	8.95E-01	-	-
1371854_at	---	---	---	Rn.8506	BG374451	4.23	4.53	4.20	4.81	4.20	5.30	1.36	up	2.53E-01	8.95E-01	-	-
1378697_at	Rbms2	RNA binding motif, single stranded interacting protein 2	288771	Rn.162925	BI300550	4.77	2.86	2.62	2.87	2.74	3.30	1.36	down	5.58E-01	8.95E-01	-	-
1387059_at	Stk39	serine/threonine kinase 39, STE20/SPS1 homolog (yeast)	54348	Rn.34414	NM_019362	2.70	2.45	3.61	2.50	2.48	2.44	1.36	down	2.74E-01	8.95E-01	-	-
1395190_at	Akr1b10	aldo-keto reductase family 1, member B10 (aldose reductase)	299972	Rn.8473	AI408099	3.95	2.60	2.66	2.63	2.64	2.59	1.36	down	3.66E-01	8.95E-01	-	-
1378268_at	---	---	---	Rn.147740	AI554986	2.43	2.47	2.47	3.64	2.46	2.61	1.36	up	2.95E-01	8.95E-01	-	-
1368055_a_at	Lmna	lamin A	60374	Rn.44161	BI282866	5.83	4.99	3.96	4.60	3.84	5.01	1.36	down	5.22E-01	8.95E-01	-	-
1387120_at	Psmc3	proteasome (prosome, macropain) 26S subunit, ATPase 3	29677	Rn.11173	NM_031595	8.06	8.96	9.01	8.35	7.77	8.57	1.36	down	3.15E-01	8.95E-01	-	-
1384725_at	Rnf145	Ring finger protein 145	287212	Rn.102005	AI407241	5.64	4.94	4.41	6.10	5.29	4.94	1.36	up	4.15E-01	8.95E-01	-	-
1398879_at	Tmem66	transmembrane protein 66	290796	Rn.101865	BE329031	6.47	6.62	7.54	7.41	7.52	7.05	1.36	up	2.85E-01	8.95E-01	-	-
1389260_at	Ubxn6	UBX domain protein 6	363329	Rn.7230	AI008393	5.45	5.54	4.63	5.50	5.69	5.78	1.36	up	2.11E-01	8.95E-01	-	-
1394495_at	Qk	quaking	499022	Rn.85462	AW522740	2.54	2.52	2.54	2.46	3.19	3.29	1.36	up	1.61E-01	8.95E-01	-	-
1383551_at	Bpgm	2,3-bisphosphoglycerate mutase	296973	Rn.204528	AW144812	4.72	4.99	4.34	4.74	4.79	5.86	1.36	up	3.39E-01	8.95E-01	-	-
1367970_at	Pfn2	profilin 2	81531	Rn.203100	NM_030873	2.51	3.05	3.59	2.63	2.54	2.64	1.36	down	2.26E-01	8.95E-01	-	-
1392024_at	---	---	---	Rn.202792	BF419641	3.46	2.61	2.33	2.32	2.33	2.41	1.36	down	2.58E-01	8.95E-01	-	-
1380521_at	Hcls1	hematopoietic cell specific Lyn substrate 1	288077	Rn.15578	BF556183	2.16	2.15	2.16	2.16	3.51	2.16	1.36	up	3.75E-01	8.95E-01	-	-
1382433_at	---	---	---	Rn.144522	AW526548	2.79	2.96	4.74	2.96	3.18	3.00	1.36	down	5.16E-01	8.95E-01	-	-
1377068_at	Tpst1	Tyrosylprotein sulfotransferase 1	288617	Rn.144004	AI011182	2.40	2.39	2.40	2.29	3.88	2.37	1.36	up	4.35E-01	8.95E-01	-	-
1376187_at	Slc35d1	Solute carrier family 35 (UDP-glucuronic acid/UDP-N-acetylgalactosamine du	298280	Rn.19332	AI177887	6.45	6.24	6.54	6.16	5.72	6.02	1.36	down	4.60E-02	8.95E-01	-	-
1392797_at	RGD1311265	similar to CGI-41 protein	361976	Rn.100135	AI045916	4.62	4.84	4.62	5.06	5.08	5.27	1.36	up	1.14E-02	8.95E-01	-	-
1371896_at	Gadd45gip1	growth arrest and DNA-damage-inducible, gamma interacting protein 1	288916	Rn.161715	AI411436	9.21	9.17	8.70	9.42	9.46	9.54	1.36	up	5.76E-02	8.95E-01	-	-
1384509_a_at	Pcdh17	protocadherin 17	306055	Rn.198988	BF558681	8.64	8.62	8.58	8.33	7.46	8.72	1.36	down	2.97E-01	8.95E-01	-	-
1371046_at	Sptbn1	spectrin, beta, non-erythrocytic 1	305614	Rn.93208	AW920849	4.09	4.55	3.77	4.43	5.27	4.06	1.36	up	3.49E-01	8.95E-01	-	-
1389500_at	---	---	---	Rn.216504	BM383122	3.00	2.64	2.94	3.69	2.93	3.30	1.36	up	1.44E-01	8.95E-01	-	-
1383636_at	---	---	---	Rn.12729	AA897509	7.08	6.92	6.02	6.65	7.38	7.34	1.36	up	3.32E-01	8.95E-01	-	-
1391460_at	---	---	---	Rn.29012	BF408186	5.97	6.28	5.45	6.04	6.44	6.57	1.36	up	1.97E-01	8.95E-01	-	-
1367858_at	Mmp11	matrix metallopeptidase 11	25481	Rn.11123	NM_012980	2.99	3.55	4.49	4.20	3.53	4.64	1.36	up	4.58E-01	8.95E-01	-	-
1384728_at	Foxn3	forkhead box N3	314374	Rn.105640	BE112826	4.15	5.32	6.23	5.96	4.71	6.37	1.36	up	5.97E-01	8.95E-01	-	-
1378372_at	---	---	---	Rn.203112	AI574994	3.24	4.44	3.07	2.92	3.32	3.17	1.36	down	3.76E-01	8.95E-01	-	-
1382166_at	Srprb	signal recognition particle receptor, B subunit	300965	Rn.138078	BF407425	6.68	6.46	6.60	7.70	6.09	7.30	1.36	up	4.10E-01	8.95E-01	-	-
1396191_at	Eif5b	Eukaryotic translation initiation factor 5B	308306	Rn.203410	BF395978	3.32	3.59	4.04	3.49	2.62	3.49	1.36	down	2.82E-01	8.95E-01	-	-
1367783_at	Gabarapl2	GABA(A) receptor-associated protein like 2	64670	Rn.64537	NM_022706	9.11	9.24	9.71	8.98	8.88	8.86	1.36	down	7.55E-02	8.95E-01	-	-
1396908_at	---	---	---	Rn.205474	AI716549	4.78	2.66	2.59	3.05	2.58	3.06	1.36	down	5.77E-01	8.95E-01	-	-
1393173_at	Rasa1	RAS p21 protein activator (GTPase activating protein) 1	25676	Rn.12223	BG668164	2.62	3.85	2.60	2.59	2.60	2.54	1.36	down	3.39E-01	8.95E-01	-	-
1398389_at	---	---	---	Rn.164862	AI236196	9.09	8.75	8.31	8.86	9.50	9.14	1.36	up	2.02E-01	8.95E-01	-	-
1398764_at	Rpl21	ribosomal protein L21	79449	Rn.83200	NM_053330	11.27	11.68	11.49	11.78	11.89	12.11	1.36	up	4.30E-02	8.95E-01	-	-
1373293_at	Lsg1	large subunit GTPase 1 homolog (S. cerevisiae)	288029	Rn.41256	BM392010	3.85	6.05	4.41	5.30	5.17	5.19	1.36	up	5.36E-01	8.95E-01	-	-
1371784_at	Dnajc7	DnaJ (Hsp40) homolog, subfamily C, member 7	303536	Rn.92155	BI285682	5.77	6.27	4.97	6.21	6.13	5.99	1.36	up	3.08E-01	8.95E-01	-	-
1378170_at	Aff4	AF4/FMR2 family, member 4	303132	Rn.17594	AI566957	5.05	5.27	5.28	6.03	5.24	5.68	1.36	up	1.39E-01	8.95E-01	-	-
1392629_a_at	Zcrb1	zinc finger CCHC-type and RNA binding motif 1	362990	Rn.136969	BF386158	8.25	8.58	8.09	8.74	8.41	9.11	1.36	up	1.48E-01	8.95E-01	-	-
1378448_at	Itgb1bp1	integrin beta 1 binding protein 1	298914	Rn.29469	BI295914	2.48	2.37	2.37	2.37	3.83	2.36	1.36	up	4.12E-01	8.95E-01	-	-
1382086_at	---	---	---	Rn.19680	AI235883	2.61	2.45	3.62	2.45	2.46	2.43	1.36	down	2.93E-01	8.95E-01	-	-
1375721_at	---	---	---	Rn.8959	BF408438	6.26	6.36	7.35	6.40	6.14	6.09	1.36	down	2.85E-01	8.95E-01	-	-
1398431_at	Car8	carbonic anhydrase 8	297814	Rn.22066	BI294910	3.05	2.52	3.16	2.44	2.56	2.38	1.36	down	9.38E-02	8.95E-01	-	-
1390058_at	LOC361990	similar to DKFZP547E1010 protein	361990	Rn.15859	BI291197	8.49	9.13	8.17	9.48	8.44	9.22	1.36	up	3.49E-01	8.95E-01	-	-
1382416_at	---	---	---	---	AI112428	3.58	4.46	3.96	4.74	3.27	4.65	1.36	down	6.25E-01	8.95E-01	-	-
1384380_at	---	---	---	Rn.205033	AI535316	2.62	3.23	2.63	3.70	2.60	3.52	1.36	up	3.23E-01	8.95E-01	-	-
1393373_at	Opn3	opsin 3	498289	Rn.204549	BI289640	3.61	4.55	5.04	3.90	3.73	4.24	1.36	down	3.71E-01	8.95E-01	-	-
1383821_at	---	---	---	Rn.120615	AA899489	6.15	5.54	5.58	5.57	4.99	5.37	1.36	down	1.62E-01	8.95E-01	-	-
1384858_a_at	Utp23	UTP23, small subunit (SSU) processome component, homolog (yeast)	299900	Rn.24551	AA964590	2.72	3.95	2.93	3.37	4.27	3.30	1.36	up	4.16E-01	8.95E-01	-	-
1375376_at	LOC688579	Hypothetical protein LOC688579	688579	Rn.155460	AA997231	2.25	2.92	2.21	3.67	2.32	2.73	1.36	up	3.89E-01	8.95E-01	-	-
1397972_at	---	---	---	Rn.209482	BF390528	2.52	3.73	2.53	2.48	2.52	2.45	1.36	down	3.31E-01	8.95E-01	-	-
1396376_at	---	---	---	---	BF393935	4.16	2.61	2.61	2.67	2.64	2.74	1.36	down	4.37E-01	8.95E-01	-	-
1374090_at	LOC361990	similar to DKFZP547E1010 protein	361990	Rn.15859	BI296363	3.88	4.65	5.17	4.64	5.94	4.47	1.36	up	4.98E-01	8.95E-01	-	-
1389655_at	Ptrh2	peptidyl-tRNA hydrolase 2	287593	Rn.13456	AA892330	6.22	7.01	5.05	5.41	6.71	7.50	1.36	up	6.22E-01	8.95E-01	-	-
1389595_at	Dus2	dihydrouridine synthase 2-like, SMM1 homolog (S. cerevisiae)	291978	Rn.18304	BM386615	6.49	5.86	8.45	6.25	6.77	6.44	1.36	down	6.05E-01	8.95E-01	-	-
1370223_at	Arfrp1	ADP-ribosylation factor related protein 1	117051	Rn.10973	AI170798	6.58	6.00	6.09	6.65	6.73	6.62	1.36	up	7.18E-02	8.95E-01	-	-
1392032_at	Grap	GRB2-related adaptor protein	363616	Rn.63315	BF418025	2.50	2.95	3.98	3.09	2.50	2.50	1.36	down	4.07E-01	8.95E-01	-	-
1380393_at	Cryz	crystallin, zeta	362061	Rn.6746	AI409083	10.60	10.38	10.79	9.94	10.38	10.12	1.36	down	6.36E-02	8.95E-01	-	-
1391274_at	---	---	---	Rn.91765	BI292056	9.21	8.95	9.87	9.25	8.46	8.99	1.36	down	2.82E-01	8.95E-01	-	-
1371909_at	Med23	mediator complex subunit 23	309565	Rn.6604	AA850406	6.36	4.04	3.73	3.47	4.51	4.81	1.36	down	6.56E-01	8.98E-01	-	-
1375300_at	Wnk1	WNK lysine deficient protein kinase 1	116477	Rn.27409	AI235878	4.63	4.05	3.99	3.76	3.76	3.80	1.36	down	9.38E-02	8.95E-01	-	-
1370460_at	Usp15	ubiquitin specific peptidase 15	171329	Rn.161933	AF106857	5.39	5.54	5.22	5.30	4.16	5.35	1.36	down	3.90E-01	8.95E-01	-	-
1368289_at	Gc	group specific component	24384	Rn.1437	AA944965	4.11	3.18	2.74	2.74	3.21	2.76	1.36	down	3.62E-01	8.95E-01	-	-
1386132_at	RGD1565480	similar to hypothetical protein MGC35130	500511	Rn.162072	AI227648	2.53	2.53	2.61	2.58	3.90	2.53	1.36	up	3.78E-01	8.95E-01	-	-
1398398_at	RGD1562218	similar to RIKEN cDNA 0610039J04	292100	Rn.25199	BG372451	5.76	5.05	5.06	5.71	5.75	5.74	1.36	up	1.33E-01	8.95E-01	-	-
1395268_at	Wwp1	WW domain containing E3 ubiquitin protein ligase 1	297930	Rn.144867	BM383223	8.77	9.53	9.38	8.47	8.63	9.25	1.36	down	2.50E-01	8.95E-01	-	-
1367793_at	Ddt	D-dopachrome tautomerase	29318	Rn.3464	NM_024131	8.69	9.78	9.36	9.73	9.70	9.73	1.36	up	2.33E-01	8.95E-01	-	-
1387774_at	Ywhaz	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, z	25578	Rn.1292	D17615	11.43	11.38	11.50	11.07	10.91	10.99	1.36	down	1.65E-03	8.95E-01	-	-
1369941_at	Dap	death-associated protein	64322	Rn.1531	NM_022526	5.13	5.83	4.79	5.73	5.14	6.22	1.36	up	3.68E-01	8.95E-01	-	-
1379347_at	---	---	---	Rn.203284	BM389290	4.63	3.75	2.91	3.36	3.53	3.07	1.36	down	4.36E-01	8.95E-01	-	-
1399129_at	RGD1309765	similar to hypothetical protein	290746	Rn.99891	AA924317	7.58	7.25	7.02	6.58	6.75	7.18	1.36	down	1.41E-01	8.95E-01	-	-
1379465_at	LOC311134	hypothetical LOC311134	311134	Rn.44069	AW520896	2.45	2.44	2.47	2.45	3.83	2.42	1.36	up	3.93E-01	8.95E-01	-	-
1376703_at	Nup37	nucleoporin 37	299706	Rn.135562	AI501977	4.65	3.94	5.02	3.35	3.70	5.23	1.36	down	5.38E-01	8.95E-01	-	-
1398319_at	---	---	---	Rn.32307	AI071000	6.34	6.23	7.82	6.53	6.25	6.28	1.36	down	4.43E-01	8.95E-01	-	-
1380627_at	---	---	---	---	BF404531	2.46	2.45	2.47	2.45	3.81	2.44	1.

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicats)				
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG MTC
1391027_at	---	---	---	Rn.29932	AI236184	5.02	4.24	3.99	4.04	3.95	3.94	1.36	down	2.28E-01	8.95E-01	- -
1379514_at	---	---	---	Rn.15638	AA926014	4.41	2.89	2.93	3.18	2.87	2.86	1.36	down	4.38E-01	8.95E-01	- -
1381100_at	---	---	---	Rn.199629	BE108751	6.36	6.90	6.71	6.60	7.33	7.36	1.36	up	2.13E-01	8.95E-01	- -
1386477_at	---	---	---	Rn.199394	AI170046	2.47	2.52	2.49	2.47	2.45	3.89	1.36	up	4.09E-01	8.95E-01	- -
1380094_a_at	Zfp212	Zinc finger protein 212	297066	Rn.204902	AI178375	4.45	4.76	4.94	4.93	4.86	5.69	1.36	up	2.20E-01	8.95E-01	- -
1383682_at	---	---	---	Rn.147429	BG378133	4.76	5.96	4.86	6.20	5.83	4.87	1.36	up	4.72E-01	8.95E-01	- -
1389006_at	---	---	---	Rn.4301	AI170394	2.41	2.45	2.46	2.61	3.58	2.45	1.36	up	2.82E-01	8.95E-01	- -
1397826_at	Epb4.9	erythrocyte protein band 4.9	361069	Rn.9618	AI677633	6.53	5.37	5.59	6.58	6.40	5.82	1.36	up	3.57E-01	8.95E-01	- -
1396928_at	---	---	---	Rn.205279	AI548614	4.26	4.99	3.48	3.17	4.41	3.82	1.36	down	4.79E-01	8.95E-01	- -
1382188_at	Gpatch4	g-patch domain containing 4	298228	Rn.20196	BF397703	3.99	3.97	5.12	3.97	4.48	3.31	1.36	down	4.38E-01	8.95E-01	- -
1382633_at	---	---	---	Rn.146928	BE120748	6.43	5.49	5.73	5.17	5.18	5.99	1.36	down	3.24E-01	8.95E-01	- -
1388164_at	H2-T23	histocompatibility 2, T region locus 23	294228	---	AF029241	7.11	5.72	5.06	5.32	5.95	7.93	1.36	up	6.81E-01	9.03E-01	- -
1373978_at	Ncbp1	nuclear cap binding protein subunit 1, 80kDa	298075	Rn.1348	AI410277	9.48	8.87	9.16	8.97	8.33	8.90	1.36	down	1.74E-01	8.95E-01	- -
1371387_at	Cox7b	cytochrome c oxidase subunit VIIb	303393	Rn.2026	AA866477	11.19	11.04	11.25	11.33	12.00	11.46	1.36	up	1.12E-01	8.95E-01	- -
1390217_at	Garnl1	GTPase activating Rap/RanGAP domain-like 1	56785	Rn.86984	BF283227	6.15	6.69	5.96	6.53	6.75	6.84	1.36	up	1.37E-01	8.95E-01	- -
1394019_at	---	---	---	---	BI283971	5.41	6.91	5.85	6.66	6.43	6.40	1.36	up	3.89E-01	8.95E-01	- -
1377111_at	---	---	---	Rn.39254	BI295188	3.04	3.58	2.48	3.82	2.78	3.82	1.36	up	4.03E-01	8.95E-01	- -
1383285_at	---	---	---	---	BG671375	4.07	4.67	3.87	5.03	4.17	4.72	1.36	up	2.73E-01	8.95E-01	- -
1381850_at	Ppp1r12a	protein phosphatase 1, regulatory (inhibitor) subunit 12A	116670	Rn.162937	BF398081	5.91	4.61	2.64	4.71	3.45	3.69	1.36	down	6.90E-01	9.05E-01	- -
1389592_at	---	---	---	Rn.23816	AI317817	4.78	5.35	4.26	4.62	5.19	5.89	1.36	up	4.15E-01	8.95E-01	- -
1387687_at	Igsf6	immunoglobulin superfamily, member 6	171064	Rn.204094	NM_133542	2.61	2.56	2.64	4.19	2.37	2.57	1.36	up	4.89E-01	8.95E-01	- -
1374006_at	Kat3	kynurenine aminotransferase III	541589	Rn.28263	BI295878	8.70	8.45	7.68	7.63	7.55	8.33	1.36	down	3.26E-01	8.95E-01	- -
1372092_at	Trak2	trafficking protein, kinesin binding 2	171086	Rn.26957	BI278968	6.17	5.94	6.79	6.49	7.08	6.64	1.36	up	2.29E-01	8.95E-01	- -
1388942_at	LOC679880	hypothetical protein LOC679880	679880	---	BM390129	8.46	8.92	8.70	8.66	9.28	9.45	1.36	up	1.85E-01	8.95E-01	- -
1377137_at	Acox2	acyl-Coenzyme A oxidase 2, branched chain	252898	Rn.10622	X95189	2.72	3.65	2.73	2.71	2.40	2.66	1.36	down	2.44E-01	8.95E-01	- -
1373034_at	Wrb	tryptophan rich basic protein	288233	Rn.103351	AI177128	7.55	6.42	5.90	5.51	5.89	7.16	1.36	down	5.64E-01	8.95E-01	- -
1394625_at	Tmem144	transmembrane protein 144	361998	Rn.72480	AI234811	7.93	7.53	8.09	7.42	7.35	7.46	1.36	down	6.21E-02	8.95E-01	- -
1370384_a_at	Prlr	prolactin receptor	24684	Rn.9757	M57668	7.45	8.40	7.19	7.23	6.87	7.63	1.36	down	3.63E-01	8.95E-01	- -
1387011_at	Lcn2	lipocalin 2	170496	Rn.11303	NM_130741	2.33	2.34	2.36	3.65	2.35	2.33	1.36	up	3.73E-01	8.95E-01	- -
1385722_at	Sim2	single-minded homolog 2 (Drosophila)	304071	Rn.113883	AW534696	3.88	2.59	2.57	2.55	2.65	2.53	1.36	down	3.70E-01	8.95E-01	- -
1374482_at	Ctps2	CTP synthase II	619580	Rn.13683	AW142993	2.63	3.02	2.68	2.83	3.47	3.35	1.36	up	1.29E-01	8.95E-01	- -
1393845_a_at	Trnc4	transmembrane channel-like 4	308310	Rn.138375	AI556940	2.22	3.52	2.23	2.22	2.21	1.36	down	3.66E-01	8.95E-01	- -
1383246_at	Armc7	armadillo repeat containing 7	287827	Rn.198899	AI146111	3.72	2.41	2.44	2.41	2.43	2.40	1.36	down	3.67E-01	8.95E-01	- -
1383064_at	---	---	---	Rn.164799	AI137878	7.07	6.00	6.42	5.46	6.86	5.86	1.36	down	4.47E-01	8.95E-01	- -
1368750_a_at	Pde4d	phosphodiesterase 4D, cAMP-specific (phosphodiesterase E3 dunce homolo	24627	Rn.163460	NM_017032	3.02	3.10	4.05	3.01	2.90	2.95	1.36	down	2.59E-01	8.95E-01	- -
1398411_at	---	---	---	---	BI278952	7.22	7.19	5.84	7.78	7.48	6.32	1.36	up	5.29E-01	8.95E-01	- -
1375029_at	Usp1	ubiquitin specific peptidase like 1	288447	Rn.86346	AI235912	6.51	5.58	5.21	4.71	5.38	5.89	1.36	down	4.43E-01	8.95E-01	- -
1374790_at	Gnpg	n-acetylglucosamine-1-phosphate transferase, gamma subunit	287134	Rn.2814	AW433892	6.10	6.39	5.84	6.78	6.46	6.40	1.36	up	9.21E-02	8.95E-01	- -
1373547_at	RGD1308147	similar to expressed sequence AW209491	307008	Rn.6513	AA849782	4.23	4.38	5.35	4.99	4.93	5.35	1.35	up	3.06E-01	8.95E-01	- -
1376947_at	Rbbp6	retinoblastoma binding protein 6	308968	Rn.95305	AI178158	6.02	6.58	7.35	6.96	7.12	7.17	1.35	up	3.25E-01	8.95E-01	- -
1397666_at	---	---	---	Rn.48609	BG668889	2.34	2.63	3.37	2.34	2.35	2.34	1.35	down	2.25E-01	8.95E-01	- -
1382364_at	RGD1310427	similar to KIAA0090 protein	362643	Rn.42115	BI293914	6.15	6.03	5.53	6.13	6.42	6.48	1.35	up	1.16E-01	8.95E-01	- -
1389267_at	---	---	---	Rn.16311	BF394196	2.32	2.31	3.76	2.48	4.22	3.00	1.35	up	5.68E-01	8.95E-01	- -
1369795_at	Kcnj12	potassium inwardly-rectifying channel, subfamily J, member 12	117052	Rn.10406	NM_053981	4.66	5.33	5.34	5.37	5.72	5.55	1.35	up	1.49E-01	8.95E-01	- -
1368748_at	Tesk2	testis-specific kinase 2	170908	Rn.144652	NM_133396	2.33	3.72	2.34	2.35	2.34	2.39	1.35	down	3.96E-01	8.95E-01	- -
1373510_at	Vamp1	vesicle-associated membrane protein 1	25624	Rn.31977	BF281373	3.78	2.74	2.74	2.63	2.55	2.75	1.35	down	2.81E-01	8.95E-01	- -
1377149_at	---	---	---	---	BM386122	5.68	5.27	5.89	5.69	4.00	5.83	1.35	down	5.15E-01	8.95E-01	- -
1369560_at	Gpd1	glycerol-3-phosphate dehydrogenase 1 (soluble)	60666	Rn.44452	NM_022215	5.31	5.33	5.68	5.31	4.40	5.29	1.35	down	2.46E-01	8.95E-01	- -
1398813_at	Uba3	ubiquitin-like modifier activating enzyme 3	117553	Rn.162761	NM_057205	6.39	6.31	6.70	6.19	5.49	6.41	1.35	down	2.21E-01	8.95E-01	- -
1391393_at	Ube3a	ubiquitin protein ligase E3A	361585	Rn.198497	BE117623	8.73	8.91	8.31	8.79	9.23	9.24	1.35	up	1.34E-01	8.95E-01	- -
1395764_at	---	---	---	Rn.210453	BF398145	2.57	3.01	2.62	4.38	2.59	2.55	1.35	up	5.18E-01	8.95E-01	- -
1385428_at	Xpo4	exportin 4	290280	Rn.204363	AI072630	5.30	5.63	5.39	5.81	5.74	6.08	1.35	up	3.58E-02	8.95E-01	- -
1377187_at	Rbm12b	RNA binding motif protein 12B	313069	Rn.18198	BI291427	3.47	3.36	4.13	3.08	3.39	3.18	1.35	down	1.62E-01	8.95E-01	- -
1393933_at	Sorl1	sortilin-related receptor, LDLR class A repeats-containing	300652	Rn.92871	AW144823	5.32	5.70	5.38	5.34	6.56	5.81	1.35	up	3.10E-01	8.95E-01	- -
1396239_at	RGD1566036	similar to RIKEN cDNA 2310008H04	498119	Rn.162069	AI502035	2.60	2.57	2.53	3.03	3.44	2.55	1.35	up	1.67E-01	8.95E-01	- -
1378751_at	Mapk4	mitogen-activated protein kinase 4	54268	Rn.146899	BF395788	2.46	2.39	3.72	2.46	2.41	2.39	1.35	down	3.71E-01	8.95E-01	- -
1393811_at	RGD1561537	similar to putative repair and recombination helicase RAD26L	361197	Rn.12539	BF397269	7.26	8.33	7.80	7.72	6.29	8.08	1.35	down	5.24E-01	8.95E-01	- -
1377597_at	Arid2	AT rich interactive domain 2 (Arid-rfx like)	366980	Rn.42849	BI300888	3.46	3.89	4.62	4.59	3.73	4.96	1.35	up	4.27E-01	8.95E-01	- -
1373481_at	R3hdm1	R3H domain containing 1	304763	Rn.60443	AI227908	5.75	5.71	5.63	5.87	6.54	6.00	1.35	up	1.01E-01	8.95E-01	- -
1374573_at	Dync2li1	dynein cytoplasmic 2 light intermediate chain 1	298767	Rn.12074	BE113181	4.40	5.59	5.32	5.30	5.28	6.04	1.35	up	3.75E-01	8.95E-01	- -
1395919_at	Eapp	E2F-associated phosphoprotein	299043	Rn.56623	AI556163	6.59	6.87	6.49	6.88	7.11	7.27	1.35	up	5.17E-02	8.95E-01	- -
1392499_at	Pfas	phosphoribosylformylglycinamidine synthase	287420	Rn.17467	H32997	5.24	4.08	5.25	4.40	4.24	4.62	1.35	down	3.40E-01	8.95E-01	- -
1376941_at	Wbscr16	Williams-Beuren syndrome chromosome region 16 homolog (human)	360796	Rn.40552	BI274409	4.56	4.83	4.56	4.66	3.38	4.60	1.35	down	3.63E-01	8.95E-01	- -
1384537_at	---	---	---	Rn.135266	BE116395	6.72	6.53	5.71	6.15	8.35	5.78	1.35	up	6.38E-01	8.95E-01	- -
1370872_at	Hnrnpa3	heterogeneous nuclear ribonucleoprotein A3	362152	Rn.107690	BM392140	9.13	8.67	8.82	9.22	9.14	9.57	1.35	up	8.30E-02	8.95E-01	- -
1394181_at	Ndnl2	Necdin-like 2	309259	Rn.9406	AI176506	6.64	6.95	6.87	7.30	7.22	7.24	1.35	up	1.05E-02	8.95E-01	- -
1372597_at	Mrpl14	mitochondrial ribosomal protein L14	301250	Rn.35669	BE113348	5.30	5.66	5.35	5.71	4.37	4.91	1.35	down	3.42E-01	8.95E-01	- -
1377182_at	Itgb3bp	integrin beta 3 binding protein (beta3-endonexin)	362548	Rn.91426	BM387863	5.12	3.45	2.70	3.22	3.29	3.46	1.35	down	5.76E-01	8.95E-01	- -
1368063_a_at	Y1521	splicing factor Y1521-B	170956	Rn.48752	NM_133423	6.42	7.24	6.85	7.45	7.31	7.07	1.35	up	1.70E-01	8.95E-01	- -
1377575_s_at	Znf213	zinc finger protein 213	287094	Rn.98676	BF414677	3.91	3.07	3.04	2.97	2.76	2.96	1.35	down	2.11E-01	8.95E-01	- -
1379691_at	Prpf38b	PRP38 pre-mRNA processing factor 38 (yeast) domain containing B	499691	Rn.7210	BM389372	9.39	9.17	8.99	9.18	8.65	8.41	1.35	down	1.62E-01	8.95E-01	- -
1374022_at	---	---	---	Rn.18035	AI406707	6.59	7.50	6.72	6.50	6.04	6.96	1.35	down	3.25E-01	8.95E-01	- -
1373040_at	Eif3f	eukaryotic translation initiation factor 3, subunit F	293427	Rn.41724	BI281752	9.79	9.21	8.70	9.61	9.41	10.00	1.35	up	2.92E-01	8.95E-01	- -
1389064_at	Fem1c	fem-1 homolog c (C.elegans)	302288	Rn.22697	BE111732	5.15	5.05	4.89	4.98	5.14	6.27	1.35	up	3.51E-01	8.95E-01	- -
1387280_a_at	Slc7a5	solute carrier family 7 (cationic amino acid transporter, y+ system), member 5	50719	Rn.32261	NM_017353	2.39	2.37	2.38	2.38	3.53	2.54	1.35	up	2.93E-01	8.95E-01	- -
1377836_at	RGD1560796	similar to suppressor of hairy wing homolog 4 isoform 1	315798	Rn.219406	AI638997	3.62	2.98	3.15	2.62	2.73	3.09	1.35	down	1.41E-01	8.95E-01	- -
1373400_at	---	---	---	---	AW918535	8.72	8.66	8.62	7.91	8.30	8.48	1.35	down	6.23E-02	8.95E-01	- -
1376650_at	Golga5	golgi autoantigen, golgin subfamily a, 5	299258	Rn.205745	BF399323	4.82	5.16	5.15	5.46	5.47	5.50	1.35	up	1.87E-02	8.95E-01	- -
1385246_at	---	---	---	Rn.74356	AI717564	2.61	2.52	2.54	2.53	3.77	2.68	1.35	up	3.30E-01	8.95E-01	- -
1398382_at	Nat13	N-acetyltransferase 13	288108	Rn.65040	AI175556	7.90	8.49	8.51	8.47	8.45	9.29	1.35	up	2.71E-01	8.95E-01	- -
1373520_at	---	---	---	Rn.94887	BI285960	5.46	5.69	6.65	5.51	5.83	5.14	1.35	down	3.54E-01	8.95E-01	- -
1393265_at	Syncrip	Synaptotagmin binding, cytoplasmic RNA interacting protein	363113	Rn.202606	BF546659	4.66	5.01	4.67	4.65	5.82	5.18	1.35	up	2.92E-01	8.95E-01	- -
1395353_at	RGD1306148	similar to KIAA0368	313196	Rn.154631	AW144304	5.08	4.77	3.39	5.15	4.54	4.86	1.35	up	4.72E-01	8.95E-01	- -
1385638_at	---	---	---	Rn.146200	AI029927	5.33	5.56	5.34	5.75	6.43	5.35	1.35	up	2.49E-01	8.95E-01	- -
1376710_at	---	---	---	Rn.121641	BE113252	7.55	7.12	8.04	7.22	7.59	6.61	1.35	down	3.27E-01	8.95E-01	- -
1388731_at	Zadh2	zinc binding alcohol dehydrogenase, domain containing 2	291403	Rn.12321	AA850919	6.08	6.71	6.04	6.76	6.72	6.66	1.35	up	1.16E-01	8.95E-01	- -
1369642_at	Pafah1b2	platelet-activating factor acetylhydrolase, isoform 1b, subunit 2	64189	Rn.24751	BM392366	6.68	6.73	7.00	6.30	5.89	6.91	1.35	down	2.36E-01	8.95E-01	- -
1373946_at	Armc10	armadillo repeat containing 10	296758	Rn.2408	AI409943	4.90	6.82	5.59	5.83	6.24	6.55	1.35	up	5.07E-01	8.95E-01	- -
1388523_at	Txndc12	thioredoxin domain containing 12 (endoplasmic reticulum)	298370	Rn.5953	BM392352	6.81	7.13	6.93	7.38	7.32	7.48	1.35	up	1.38E-02	8.95E-01	- -
1373469_at	RGD1565496	similar to Butyrate-induced transcript 1	300783	Rn.767	BF408841	6.71	5.84	5.55	6.23	6.37	6.82	1.35	up	3.26E-01	8.95E-01	- -
1391848_at	Rbm27	RNA binding motif protein 27	361317	Rn.218050	BG376780	5.97	6.59	7.17	6.60	6.00	5.82	1.35	down	3.58E-01	8.95E-01	- -
1388131_at	Tubb2b	tubulin, beta 2b	291081	Rn.37849	X03369	9.67	10.58	10.06	9.45	9.64	9.90	1.35	down	2.14E-01	8.95E-01	- -
1373732_at	Acp6	acid phosphatase 6, lysophosphatidic	290305	Rn.103296	BM386224	4.37	4.50	4.03	5.08	4.02	5.10	1.35	up	3.19E-01	8.95E-01	- -
1375927_at	---	---	---	Rn.203708	BE100774	2.69	2.86	3.24	2.58	2.41	2.50	1.35	down	6.24E-02	8.95E-01	- -
1376642_at	Smpdl3b /// Xkr8	sphingomyelin phosphodiesterase, acid-like 3B /// XK, Kell blood group comp	313033 /// 362619	Rn.13596	BF548463	2.36	2.84	2.85	3.49	2.85	3.02	1.35	up	1.57E-01	8.95E-01	- -
1393020_at	---	---	---	---	BE115368	7.50	7.73	7.40	6.36	7.26	7.71	1.35	down	3.46E-01	8.95E-01	- -
1370509_at	Pdp2	pyruvate dehydrogenase phosphatase isoenzyme 2	246311	Rn.220381	AF062741	8.48	8.22	7.49	7.60	7.58	7.70	1.35	down	2.22E-01	8.95E-01	- -
1389835_at	---	---	---	---	AI598405	3.56	4.66	3.61	4.37	4.49	4.28	1.35	up	2.98E-01	8.95E-01	- -
1373228_at	RGD1560755	similar to D8Ertd354e protein	361165	Rn.17086	BI288760	9.13	7.78	6.12	6.24	7.37	7.71	1.35	up	5.72E-01	8.95E-01	- -
1396305_at	---	---	---	Rn.146563	BI274350	3.53	2.54	2.39	2.38	2.40	2.37	1.35	down	2.91E-01	8.95E-01	- -
1369617_at	Ube2n	ubiquitin-conjugating enzyme E2N	116725	Rn.165094	NM_053928	6.78	6.88	6.35	5.95	6.36	6.41	1.35	down	1.17E-01	8.95E-01	- -
1380971_at	---	---	---	Rn.204732	BE120747	2.39	2.39	2.42	3.76	2.40	2.34	1.35	up	4.01E-01	8.95E-01	- -
1379310_at	---	---	---	Rn.4150	AI101880	4.84	5.21	5.37	5.35	5.98	5.40	1.35	up	1.64E-01	8.95E-01	- -
1376164_at	Sf4	splicing factor 4	290666	Rn.67035	BM383641	7.16	6.98	6.61	7.60	7.57	6.88	1.35	up	2.02E-01	8.95E-01	- -
1393309_at	LOC503192	zinc finger protein ZFP	503192	Rn.216519	AI145786	4.42	3.85	4.51	4.03	4.79	5.25	1.35	up	3.51E-01	8.95E-01	- -
1396124_at	---	---	---	---	AW916396	6.36	6.34	6.94	5.92	6.55	5.88	1.35	down	2.12E-01	8.95E-01	- -
1378300_at	Dpf3	D4, zinc and double PHD fingers, family 3	299186	Rn.38975	AI711102	6.27	2.99	2.99	4.91	2.98	3.06	1.35	down	7.49E-01	9.19E-01	- -
1388423_at	RGD1302996	hypothetical protein MGC:15854	294231	Rn.106287	BM385163	6.01	5.57	4.91	5.14	4.66	5.39	1.35	down	3.24E-01	8.95E-01	- -
1379376_at	---	---	---	Rn.16467	BG372891	2.52	2.44	3.74	2.48	2.50	2.41	1.35	down	3.64E-01	8.95E-01	- -
1377524_at	RGD1307155	similar to CG18661-PA	302998	Rn.202598	AI044320	7.84	7.70	7.68	7.81	7.00	7.11	1.35	down	1.68E-01	8.95E-01	- -
1394729_at	---	---	---	Rn.208595	AI714037	5.29	4.06	2.74	5.34	4.61	3.43	1.35	up	6.63E-01	8.99E-01	- -
1379211_at	Pdgfrb	platelet derived growth factor receptor, beta polypeptide	24629	Rn.98311	AI071374	3.60	2.36	2.44	2.36	2.38	2.36	1.35	down	3.39E-01	8.95E-01	- -
1371848_at	Phgdh1	phosphoglycerate dehydrogenase like 1	361094	Rn.2539	BM391894	6.12	6.95	6.26	6.23	5.39	6.41	1.35	down	3.45E-01	8.95E-01	- -
1378508_at	Ssh1	slingshot homolog 1 (Drosophila)	304580	Rn.131309	BE108221	2.48	2.65	3.63	2.47	2.48	2.51	1.35	down	2.92E-01	8.95E-01	- -
1381832_at	Pycrl	pyrroline-5-carboxylate reductase-like	300035	Rn.40859	BE098813	7.59	6.76	5.46	6.67	7.36	7.08	1.35	up	5.41E-01	8.95E-01	- -
1376601_at	---	---	---	Rn.24818	BF397526	5.99	5.83	4.57	5.82	4.97	6.90	1.35	up	5.78E-01	8.95E-01	- -
1385124_at	Trib2	tribbles homolog 2 (Drosophila)	313974	Rn.162852	BE114077	8.05	8.59	8.50	7.67	7.80	8.37	1.35	down	1.88E-01	8.95E-01	- -
1372224_at	Chmp7	CHMP family, member 7	364419	Rn.136789	BE119694	5.76	6.79	5.98	6.57	6.65	6.61	1.35	up	2.40E-01	8.95E-01	- -
1382552_at	RGD1560155	similar to mKIAA0934 protein	307067	Rn.219346	AW522677	2.83	4.60	2.91	3.23	2.90	2.91	1.35	down	5.00E-01	8.95E-01	- -
1394849_at	Zbtb20	zinc finger and BTB domain containing 20	288105	Rn.168502	BF402012	6.94	6.18	5.83	5.74	6.35	5.56	1.35	down	3.46E-01	8.95E-01	- -
1377683_at	RGD1307615	similar to hypothetical protein FLJ13045	362084	Rn.17709	AI407061	5.78	5.72	6.36	5.12	5.58	5.86	1.35	down	2.19E-01	8.95E-01	- -
1375813_at	Akap8l	A kinase (PRKA) anchor protein 8-like	299569	Rn.107308	BE102687	3.25	3.83	2.98	5.10	3.03	3.24	1.35	up	5.72E-01	8.95E-01	- -
1396776_at	---	---	---	---	BF392898	2.38	2.36	2.37	2.37	3.68	2.37	1.35	up	3.78E-01	8.95E-01	- -
1388907_at	Necap1	NECAP endocytosis associated 1	312694	Rn.58356	BF400873	7.57	7.95	8.15	7.41	7.50	7.46	1.35	down	6.68E-02	8.95E-01	- -
1380533_at	App	amyloid beta (A4) precursor protein	54226	Rn.2104	AI408064	7.71	7.58	8.33	7.80	7.19	7.33	1.35	down	2.15E-01	8.95E-01	- -
1370002_at	Arhgef1	Rho guanine nucleotide exchange factor (GEF) 1	60323	Rn.64481	NM_021694	4.77	3.86	4.28	3.81	3.90	3.89	1.35	down	1.77E-01	8.95E-01	- -
1391062_at	LOC887694	similar to elongation protein 4 homolog	887694	Rn.199104	AA875129	2.92	3.02	4.42	4.26	3.67	3.72	1.35	up	4.52E-01	8.95E-01	- -
1381859_at	Fam91a1	family with sequence similarity 91, member A1	689997	Rn.8212	BE097018	2.34	2.35	3.55	4.31	2.84	2.40	1.35	up	5.72E-01	8.95E-01	- -
1378973_at	Otud7b	OTU domain containing 7B	310677	Rn.199225	BF396260	4.71	6.04	5.97	6.01	6.01	6.00	1.35	up	3.75E-01	8.95E-01	- -
1377657_at	Ibtk	inhibitor of Bruton agammaglobulinemia tyrosine kinase	315858	Rn.35504	AW525218	4.51	5.98	4.02	5.04	4.87	5.90	1.35	up	5.52E-01	8.95E-01	- -
1384498_at	---	---	---	Rn.203495	BI274185	4.29	3.50	3.92	3.78	3.05	3.58	1.35	down	2.41E-01	8.95E-01	- -
1391206_at	RGD1311892	similar to hypothetical protein FLJ10901	289399	Rn.48092	AW533313	4.12	4.65	3.92	4.91	4.79	4.59	1.35	up	1.38E-01	8.95E-01	- -
1386982_at	Mgat2	mannosyl (alpha-1,6-)-glycoprotein beta-1,2-N-acetylglucosaminyltransferase	94273	Rn.2342	NM_053604	4.57	4.62	4.58	5.18	5.00	4.89	1.35	up	7.00E-03	8.95E-01	- -
1373775_at	Dennd5a	DENN/MADD domain containing 5A	308942	Rn.107101	BI276835	3.69	3.37	3.74	4.10	4.24	3.76	1.35	up	7.69E-02	8.95E-01	- -
1383358_at	Akap1	A kinase (PRKA) anchor protein 1	114124	Rn.163146	AI072577	7.75	6.86	5.55	6.96	7.26	7.25	1.35	up	5.41E-01	8.95E-01	- -
1391928_at	Gopc	golgi associated PDZ and coiled-coil motif containing	309774	Rn.27865	BF418827	6.85	6.59	6.90	5.81	6.42	6.82	1.35	down	2.37E-01	8.95E-01	- -
1398751_at	Rps7	ribosomal protein S7	29258	Rn.107039	NM_017570	9.50	9.95	10.14	10.14	10.20	10.55	1.35	up	1.33E-01	8.95E-01	- -
1373056_at	Tmed4	transmembrane emp24 protein transport domain containing 4	305502	Rn.21479	AI409861	8.36	8.50	8.23	8.91	8.49	8.97	1.35	up	6.49E-02	8.95E-01	- -
1385711_at	Dimt1l	DIM1 dimethyladenosine transferase 1-like (S. cerevisiae)	294718	Rn.25178	AW507178	4.31	4.66	4.42	4.85	3.20	4.04	1.35	down	4.26E-01	8.95E-01	- -
1389152_at	Zfyve27	zinc finger, FYVE domain containing 27	309376	Rn.99939	AI412984	3.76	5.46	6.35	4.99	5.98	5.90	1.35	up	6.28E-01	8.95E-01	- -

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1387039_at	Gpc1	glypican 1	58920	Rn.7044	NM_030828	3.63	2.66	2.65	2.40	2.64	2.61	1.35	down	2.69E-01	8.95E-01	-	-
1385393_at	---	---	---	Rn.131829	BE099283	6.26	5.04	5.05	5.11	4.99	4.96	1.35	down	3.51E-01	8.95E-01	-	-
1399131_at	LOC683519	similar to ribosomal protein, mitochondrial, S22	683519	Rn.201796	AI703580	6.71	7.76	6.71	7.41	7.27	7.79	1.35	up	3.27E-01	8.95E-01	-	-
1377868_at	Gprasp2	G protein-coupled receptor associated sorting protein 2	317405	Rn.101194	AW530090	3.10	3.84	4.50	3.88	3.15	3.13	1.35	down	4.18E-01	8.95E-01	-	-
1388706_at	RGD1308923	LOC362678	362678	Rn.7678	BF524995	3.60	3.64	2.92	4.07	3.65	3.74	1.35	up	1.82E-01	8.95E-01	-	-
1390944_at	Chmp4c	chromatin modifying protein 4C	361916	Rn.162567	BM384937	6.90	6.67	7.30	6.08	6.86	6.64	1.35	down	2.23E-01	8.95E-01	-	-
1384106_at	Sgms1	sphingomyelin synthase 1	353229	Rn.204495	AW141276	7.84	8.28	7.43	7.96	8.17	8.71	1.35	up	2.68E-01	8.95E-01	-	-
1372827_at	Ppid	peptidylprolyl isomerase D (cyclophilin D)	361967	Rn.136915	AA957342	7.57	7.78	7.98	6.92	7.67	7.47	1.35	down	1.67E-01	8.95E-01	-	-
1381857_at	Rasa1	RAS p21 protein activator (GTPase activating protein) 1	25676	Rn.12223	AA963157	4.78	3.57	3.12	3.81	4.47	4.47	1.35	up	4.74E-01	8.95E-01	-	-
1383705_at	---	---	---	Rn.21473	BG670702	7.31	7.65	7.46	7.52	8.05	8.15	1.35	up	1.23E-01	8.95E-01	-	-
1383071_at	Mtpn	myotrophin	79215	Rn.3239	BG667380	4.68	4.58	5.78	4.21	4.50	5.05	1.35	down	4.02E-01	8.95E-01	-	-
1370972_x_at	RT1-CE5	RT1 class I, CE5	309607	---	BI300597	5.84	5.20	5.21	5.26	4.66	5.05	1.35	down	1.96E-01	8.95E-01	-	-
1390475_at	Rngtt	RNA guanylyltransferase and 5'-phosphatase	313131	Rn.8497	AI412632	6.51	5.25	6.61	5.13	5.94	6.02	1.35	down	4.58E-01	8.95E-01	-	-
1383222_at	---	---	---	Rn.1708	AA892299	2.96	2.95	3.71	2.95	2.44	2.94	1.35	down	2.33E-01	8.95E-01	-	-
1390985_at	---	---	---	Rn.165041	AA956519	6.23	7.13	7.68	6.33	6.12	7.31	1.35	down	4.87E-01	8.95E-01	-	-
1380875_at	---	---	---	Rn.206678	BE106717	3.75	5.02	4.87	4.96	5.27	4.68	1.35	up	3.82E-01	8.95E-01	-	-
1379513_at	Tmem30b	transmembrane protein 30B	314224	Rn.37794	BE108949	4.63	3.06	2.57	3.06	3.00	2.93	1.35	down	5.30E-01	8.95E-01	-	-
1388335_at	Tagln2	transgelin 2	304983	Rn.104497	BI285865	5.02	4.31	4.10	5.16	5.22	4.34	1.35	up	3.41E-01	8.95E-01	-	-
1377287_at	Mars2	methionyl-tRNA synthetase 2, mitochondrial	316403	Rn.9355	AA957673	5.05	5.01	6.16	5.06	5.07	4.81	1.35	down	3.29E-01	8.95E-01	-	-
1388638_at	Sirt6	sirtuin 6 (silent mating type information regulation 2, homolog) 6 (S. cerevisiae	299638	Rn.8108	AW525725	3.01	3.10	2.91	4.49	2.81	3.00	1.35	up	4.69E-01	8.95E-01	-	-
1382572_at	---	---	---	Rn.37924	AI577469	2.48	3.13	2.62	2.56	3.26	3.69	1.35	up	3.28E-01	8.95E-01	-	-
1399102_at	Slc38a10	solute carrier family 38, member 10	303740	Rn.18664	BG377901	5.99	5.85	4.45	5.01	6.03	6.54	1.34	up	5.56E-01	8.95E-01	-	-
1376683_at	---	---	---	Rn.17857	AI175363	5.90	4.75	4.97	4.82	4.17	5.34	1.34	down	4.31E-01	8.95E-01	-	-
1372262_at	---	---	---	Rn.1750	BI285626	7.86	8.01	7.54	7.91	7.99	8.79	1.34	up	2.47E-01	8.95E-01	-	-
1368907_at	Scamp5	secretory carrier membrane protein 5	65171	Rn.24420	NM_031726	2.91	3.48	4.11	3.05	3.10	3.07	1.34	down	2.86E-01	8.95E-01	-	-
1390047_at	---	---	---	Rn.4181	BG378174	3.80	3.59	3.54	3.80	2.38	3.47	1.34	down	3.84E-01	8.95E-01	-	-
1389979_at	Tnpo3	transportin 3	296954	Rn.164462	BI274235	4.55	4.64	5.62	4.61	4.53	4.40	1.34	down	2.86E-01	8.95E-01	-	-
1385853_at	Baz1a	bromodomain adjacent to zinc finger domain, 1A	314126	Rn.1864	BF560180	2.87	3.21	2.66	3.05	3.10	3.88	1.34	up	2.42E-01	8.95E-01	-	-
1391512_at	Mtmr1	Myotubularin related protein 1	317296	Rn.18311	AI029734	4.74	5.54	5.17	5.73	5.52	5.50	1.34	up	1.53E-01	8.95E-01	-	-
1389021_at	Asnsd1	asparagine synthetase domain containing 1	299507	Rn.43900	BF284746	5.87	7.21	6.00	6.82	6.38	7.16	1.34	up	4.27E-01	8.95E-01	-	-
1378038_at	---	---	---	Rn.205472	BF393884	3.70	3.16	2.67	3.99	4.12	2.69	1.34	up	4.77E-01	8.95E-01	-	-
1384791_at	B3gnt2	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 2	305571	Rn.1970	AI112158	5.12	4.24	3.34	2.92	4.41	4.09	1.34	down	5.66E-01	8.95E-01	-	-
1395618_at	Copa4	COP9 constitutive photomorphogenic homolog subunit 4 (Arabidopsis)	360915	Rn.7506	BG673431	4.37	5.68	5.17	6.44	4.58	5.47	1.34	up	5.53E-01	8.95E-01	-	-
1380157_at	Ube2g2	ubiquitin-conjugating enzyme E2G 2	294331	Rn.139603	BG379007	2.37	2.53	3.45	2.54	3.61	2.93	1.34	down	7.05E-01	9.08E-01	-	-
1388388_at	Mea1	male-enhanced antigen 1	685131	Rn.95299	AI179127	10.10	9.90	9.68	10.28	10.55	10.13	1.34	up	6.96E-02	8.95E-01	-	-
1379796_at	Comtd1	catechol-O-methyltransferase domain containing 1	305685	Rn.38717	AI717605	2.38	2.37	2.40	2.38	3.68	2.37	1.34	up	3.84E-01	8.95E-01	-	-
1380193_at	---	---	---	Rn.20596	BM387449	4.33	5.09	4.74	4.53	4.77	6.15	1.34	up	4.83E-01	8.95E-01	-	-
1388196_at	Nckap1	NCK-associated protein 1	58823	Rn.2611	BM383722	7.95	8.30	8.43	8.34	8.78	8.85	1.34	up	1.18E-01	8.95E-01	-	-
1382070_at	Atf7ip	activating transcription factor 7 interacting protein	312800	Rn.98469	AA819758	2.74	3.21	3.64	2.63	2.84	2.83	1.34	down	1.86E-01	8.95E-01	-	-
1395776_at	---	---	---	Rn.202789	BF396580	2.50	2.49	2.54	3.82	2.51	2.48	1.34	up	3.90E-01	8.95E-01	-	-
1383019_at	---	---	---	Rn.166309	BF558478	4.64	5.21	3.94	3.66	4.72	4.13	1.34	down	4.23E-01	8.95E-01	-	-
1370884_at	Spr	sepiapterin reductase (7,8-dihydrobiopterin:NADP+ oxidoreductase)	29270	Rn.6658	M36410	6.31	5.87	5.95	7.08	6.42	5.90	1.34	up	3.09E-01	8.95E-01	-	-
1399057_at	Morf4l1	mortality factor 4 like 1	300891	Rn.156201	BE109080	9.06	9.45	9.08	9.52	9.12	10.23	1.34	up	2.87E-01	8.95E-01	-	-
1384340_a_at	Ard1a	ARD1 homolog A, N-acetyltransferase (S. cerevisiae)	363518	Rn.12061	AA997134	5.01	5.35	5.42	4.93	6.36	5.77	1.34	up	3.80E-01	8.95E-01	-	-
1378543_at	---	---	---	Rn.219342	BE108222	6.79	7.50	7.07	7.91	7.17	7.56	1.34	up	2.26E-01	8.95E-01	-	-
1385113_at	Hoxc10	homeo box C10	315338	Rn.58550	BF396205	3.08	2.44	4.13	2.59	2.46	3.32	1.34	down	4.89E-01	8.95E-01	-	-
1378003_at	Lrrc8b	leucine rich repeat containing 8 family, member B	305135	Rn.170566	BM391860	5.36	4.98	5.12	4.12	4.98	5.09	1.34	down	2.57E-01	8.95E-01	-	-
1373343_at	---	---	---	Rn.28934	AI175820	2.49	3.39	2.50	3.14	3.95	2.58	1.34	up	4.40E-01	8.95E-01	-	-
1375406_s_at	Fnbp1	formin binding protein 1	192348	Rn.20445	BF419792	6.85	7.25	7.67	7.24	6.08	7.17	1.34	down	3.90E-01	8.95E-01	-	-
1380933_at	---	---	---	Rn.149123	AI639190	3.96	2.96	2.97	2.56	2.96	3.09	1.34	down	3.15E-01	8.95E-01	-	-
1397888_at	---	---	---	Rn.175632	BM389787	4.41	5.47	5.38	4.69	5.80	6.04	1.34	up	4.71E-01	8.95E-01	-	-
1389139_at	Ttc15	tetratricopeptide repeat domain 15	314013	Rn.104175	BG665007	7.51	6.29	7.03	6.91	6.75	5.91	1.34	down	4.16E-01	8.95E-01	-	-
1379669_at	---	---	---	---	BI275651	8.08	8.47	8.26	8.25	9.06	8.79	1.34	up	1.83E-01	8.95E-01	-	-
1376266_at	---	---	---	Rn.16604	AA819086	4.32	3.48	3.41	3.50	2.94	3.49	1.34	down	2.85E-01	8.95E-01	-	-
1392387_at	---	---	---	Rn.205989	AI549050	3.84	5.57	4.02	3.45	4.39	4.32	1.34	down	5.34E-01	8.95E-01	-	-
1387730_at	Pax8	paired box 8	81819	Rn.10392	NM_031141	5.79	5.87	5.94	5.07	5.96	5.29	1.34	down	1.93E-01	8.95E-01	-	-
1394460_at	---	---	---	Rn.40664	BF564428	3.80	4.31	3.87	3.62	3.60	3.49	1.34	down	6.09E-02	8.95E-01	-	-
1379112_at	Arid4a	AT rich interactive domain 4A (Rbp1 like)	314205	Rn.108963	AW552585	2.35	3.36	3.69	3.83	3.65	3.18	1.34	up	3.95E-01	8.95E-01	-	-
1396719_at	---	---	---	Rn.131671	BF399856	4.54	3.02	2.83	3.60	2.79	2.72	1.34	down	5.23E-01	8.95E-01	-	-
1388727_at	Cdc26	cell division cycle 26	366381	Rn.203072	BM387151	3.16	3.51	3.39	3.79	3.49	4.06	1.34	up	9.51E-02	8.95E-01	-	-
1388683_at	Lsmd1	LSM domain containing 1	287429	Rn.2677	AI411174	8.50	8.43	7.45	8.18	8.64	8.82	1.34	up	3.36E-01	8.95E-01	-	-
1371673_at	Vps72	vacuolar protein sorting 72 homolog (S. cerevisiae)	310661	Rn.1986	AI413005	2.67	4.25	2.68	3.14	4.55	3.19	1.34	up	5.76E-01	8.95E-01	-	-
1393308_at	---	---	---	Rn.25047	BE110640	2.90	4.45	3.60	3.60	5.01	3.62	1.34	up	5.48E-01	8.95E-01	-	-
1379525_at	Crls1	cardiolipin synthase 1	366196	Rn.35982	BF559514	7.85	8.61	8.37	8.81	8.29	9.02	1.34	up	2.46E-01	8.95E-01	-	-
1392286_at	---	---	---	Rn.125958	BF420742	4.96	5.16	4.64	5.35	5.20	5.48	1.34	up	7.06E-02	8.95E-01	-	-
1384326_at	---	---	---	Rn.220120	BF560443	7.77	8.10	7.88	7.05	7.35	8.06	1.34	down	2.51E-01	8.95E-01	-	-
1370951_at	Ppap2b	phosphatidic acid phosphatase type 2B	192270	Rn.12038	Y07783	2.47	2.46	2.48	2.46	3.76	2.46	1.34	up	3.80E-01	8.95E-01	-	-
1384295_at	Hspa14	heat shock protein 14	307133	Rn.137392	AI111363	5.50	6.59	6.86	6.54	6.37	7.32	1.34	up	4.52E-01	8.95E-01	-	-
1372906_at	RGD1309540	similar to hypothetical protein MGC40841; similar to hypothetical protein MGC	299530	Rn.154938	AI009796	3.39	4.04	3.69	3.37	4.46	4.57	1.34	up	3.76E-01	8.95E-01	-	-
1390789_at	Acad11	acyl-Coenzyme A dehydrogenase family, member 11	315973	Rn.8651	BI296347	7.51	7.78	7.40	8.35	7.82	7.79	1.34	up	1.17E-01	8.95E-01	-	-
1391656_at	Cpm	carboxypeptidase M	314855	Rn.23887	AI101416	3.72	2.44	2.45	2.47	2.44	2.42	1.34	down	3.75E-01	8.95E-01	-	-
1383216_at	---	---	---	Rn.168651	BM390667	3.22	3.30	3.01	3.33	3.25	4.23	1.34	up	2.61E-01	8.95E-01	-	-
1368165_at	Prps1	phosphoribosyl pyrophosphate synthetase 1	29562	Rn.9761	M29392	5.70	4.79	4.07	4.35	4.43	4.51	1.34	down	4.21E-01	8.95E-01	-	-
1380952_at	Tada1	transcriptional adaptor 1 (HFI1 homolog, yeast) like	360874	Rn.23978	BF395639	2.58	2.45	2.45	3.90	2.41	2.44	1.34	up	4.39E-01	8.95E-01	-	-
1392994_at	LOC499330	similar to Nicotinamide riboside kinase 1	499330	Rn.19716	AW522671	5.67	6.75	7.00	6.19	6.08	5.87	1.34	down	3.68E-01	8.95E-01	-	-
1391602_at	Drg1	developmentally regulated GTP binding protein 1	305470	Rn.102143	AW527113	5.47	5.27	4.07	3.84	4.50	5.19	1.34	down	5.08E-01	8.95E-01	-	-
1384889_at	---	---	---	Rn.168067	AI535467	3.90	2.73	2.45	3.02	3.72	3.61	1.34	up	4.37E-01	8.95E-01	-	-
1372728_at	Sort1	sortilin 1	83576	Rn.11286	BE103745	3.87	2.56	2.41	2.54	2.36	2.67	1.34	down	4.20E-01	8.95E-01	-	-
1371596_at	Rnps1	ribonucleic acid binding protein S1	287113	Rn.7235	AI008971	7.10	7.79	7.49	8.09	7.92	7.64	1.34	up	1.49E-01	8.95E-01	-	-
1389974_at	---	---	---	Rn.163729	BF555171	3.91	4.73	4.36	4.85	4.79	4.62	1.34	up	1.62E-01	8.95E-01	-	-
1378175_at	---	---	---	Rn.164816	AW921557	3.44	3.91	5.81	3.12	4.53	4.23	1.34	down	6.41E-01	8.95E-01	-	-
1372248_at	Sesn1	sestrin 1	294518	Rn.22395	AI411742	4.36	4.32	3.66	3.77	3.72	3.58	1.34	down	1.43E-01	8.95E-01	-	-
1369473_at	Pgm1	phosphoglucomutase 1	24645	Rn.9970	NM_017033	4.41	4.73	5.42	4.49	3.93	4.87	1.34	down	3.52E-01	8.95E-01	-	-
1396925_at	---	---	---	Rn.147321	BF542680	5.59	6.74	7.44	6.71	7.58	6.75	1.34	up	5.26E-01	8.95E-01	-	-
1390501_at	---	---	---	Rn.97119	BE101157	2.53	4.55	4.19	4.28	3.19	5.07	1.34	up	6.35E-01	8.95E-01	-	-
1384011_a_at	Fastkd3	FAST kinase domains 3	290946	Rn.105763	BF287623	7.27	7.73	8.51	7.59	7.29	7.90	1.34	up	3.44E-01	8.95E-01	-	-
1377082_at	---	---	---	Rn.45449	BF567763	2.31	3.18	3.19	3.30	3.18	3.47	1.34	up	2.32E-01	8.95E-01	-	-
1388141_at	Cetn3	centrin 3	170895	Rn.3974	BI293883	6.51	7.11	7.10	7.17	7.25	7.58	1.34	up	1.44E-01	8.95E-01	-	-
1384169_a_at	Vav2	vav 2 guanine nucleotide exchange factor	296903	Rn.98555	AA900477	7.09	6.63	7.42	7.71	6.39	8.30	1.34	up	5.25E-01	8.95E-01	-	-
1394818_at	---	---	---	Rn.163606	AI176867	7.35	8.28	7.94	8.22	7.94	8.68	1.34	up	2.89E-01	8.95E-01	-	-
1383744_at	---	---	---	Rn.106882	AI146250	4.63	4.15	4.01	4.21	5.05	4.79	1.34	up	2.43E-01	8.95E-01	-	-
1380226_at	Samd10	Sterile alpha motif domain containing 10	499957	Rn.139640	BG376544	3.23	3.01	4.54	3.04	3.23	3.24	1.34	down	4.29E-01	8.95E-01	-	-
1395410_at	Ppp2r3a	protein phosphatase 2 (formerly 2A), regulatory subunit B", alpha	363122	Rn.93024	AI717707	3.12	3.11	3.16	3.77	3.80	3.10	1.34	up	1.37E-01	8.95E-01	-	-
1383437_at	Rab17	RAB17, member RAS oncogene family	503269	Rn.24214	AI547691	7.82	8.33	6.78	6.55	7.56	7.55	1.34	down	4.96E-01	8.95E-01	-	-
1375047_at	Spata5	spermatogenesis associated 5	361935	Rn.116828	BI295760	3.95	3.70	3.86	4.00	3.83	4.96	1.34	up	3.04E-01	8.95E-01	-	-
1373139_at	---	---	---	Rn.203512	AI012608	3.42	4.65	3.89	4.13	4.96	4.13	1.34	up	4.02E-01	8.95E-01	-	-
1398917_at	Rpl7	ribosomal protein L7	297755	Rn.129121	BF281221	10.04	10.37	10.26	10.51	10.56	10.87	1.34	up	4.77E-02	8.95E-01	-	-
1386507_at	---	---	---	---	AA799858	5.24	4.62	5.42	4.60	4.76	4.65	1.34	down	1.63E-01	8.95E-01	-	-
1389084_at	---	---	---	Rn.19811	AI177159	4.95	6.15	6.27	5.34	5.04	5.72	1.34	down	4.16E-01	8.95E-01	-	-
1392192_at	---	---	---	Rn.153421	BF413231	4.21	3.77	3.35	3.53	3.01	3.52	1.34	down	2.32E-01	8.95E-01	-	-
1385814_at	Map3k3	mitogen activated protein kinase kinase kinase 3	303604	Rn.72680	H32486	2.48	2.86	2.49	3.13	2.76	3.21	1.34	up	8.62E-02	8.95E-01	-	-
1395808_at	---	---	---	---	AI137122	2.55	2.55	2.40	2.64	2.80	3.33	1.34	up	1.20E-01	8.95E-01	-	-
1377609_at	Hipk1	homeodomain interacting protein kinase 1	365895	Rn.4151	BE112251	7.63	8.02	7.75	8.34	8.34	7.99	1.34	up	6.05E-02	8.95E-01	-	-
1374709_at	---	---	---	Rn.19878	AI406795	7.48	6.87	6.76	7.23	5.32	7.31	1.34	down	5.73E-01	8.95E-01	-	-
1373825_at	Scyl2	SCY1-like 2 (S. cerevisiae)	314717	Rn.103930	BG373078	8.31	8.12	8.57	7.74	8.08	7.92	1.34	down	5.94E-02	8.95E-01	-	-
1378413_at	---	---	---	Rn.146196	BG379394	3.46	3.31	3.57	3.52	4.22	3.86	1.34	up	1.23E-01	8.95E-01	-	-
1378990_at	---	---	---	---	BI274964	3.89	2.63	2.68	2.62	2.65	2.66	1.34	down	3.62E-01	8.95E-01	-	-
1390132_at	---	---	---	Rn.48189	BF282059	6.11	6.43	6.71	5.71	6.06	6.21	1.34	down	1.38E-01	8.95E-01	-	-
1368075_at	Lipa	lipase A, lysosomal acid, cholesterol esterase	25055	Rn.48656	NM_012732	7.13	7.31	6.52	7.23	7.13	7.87	1.34	up	2.73E-01	8.95E-01	-	-
1373416_at	Fndc3b	fibronectin type III domain containing 3B	294925	Rn.757	AI176320	4.29	4.59	3.83	4.28	4.58	5.12	1.34	up	2.71E-01	8.95E-01	-	-
1375502_at	Ccdc112	Coiled-coil domain containing 112	498858	Rn.23933	BE113152	2.36	2.37	2.36	3.61	2.37	2.37	1.34	up	3.65E-01	8.95E-01	-	-
1373831_at	LOC619574	hypothetical protein LOC619574	619574	Rn.162222	AW920524	2.45	2.35	2.37	3.05	2.42	2.96	1.34	up	9.97E-02	8.95E-01	-	-
1382117_at	Setd6	SET domain containing 6	291844	Rn.18307	BF417345	6.11	7.67	8.25	7.93	7.41	7.95	1.34	up	5.59E-01	8.95E-01	-	-
1369291_at	Agtr1a	angiotensin II receptor, type 1a	24180	Rn.214849	NM_030985	4.92	4.42	4.51	5.16	5.03	4.92	1.34	up	6.79E-02	8.95E-01	-	-
1375889_at	Sms	spermine synthase	363469	Rn.103619	AI228536	6.49	7.59	7.00	6.90	7.62	7.81	1.34	up	3.72E-01	8.95E-01	-	-
1399148_s_at	Glt25d1	glycosyltransferase 25 domain containing 1	290637	Rn.105830	AI013567	3.13	4.04	4.93	4.09	3.80	5.47	1.34	up	5.95E-01	8.95E-01	-	-
1391719_at	---	---	---	---	BE098936	4.89	4.06	3.86	3.92	3.79	3.84	1.34	down	2.56E-01	8.95E-01	-	-
1372399_at	Cobra1	cofactor of BRCA1	311796	Rn.8119	BM392127	8.63	7.79	7.59	8.13	8.78	8.37	1.34	up	3.18E-01	8.95E-01	-	-
1395148_at	RGD1561090	Similar to protein tyrosine phosphatase, receptor type, D	313278	Rn.99077	BF388173	2.32	2.30	3.59	2.30	2.33	2.31	1.34	down	3.79E-01	8.95E-01	-	-
1398392_at	---	---	---	Rn.45202	BF405932	2.96	2.83	2.93	3.31	3.13	3.54	1.34	up	2.80E-02	8.95E-01	-	-
1389254_at	Qser1	Glutamine and serine rich 1	311266	Rn.123081	AA800519	7.54	6.70	5.96	7.10	7.48	6.88	1.34	up	4.36E-01	8.95E-01	-	-
1371704_at	Ddx23	DEAD (Asp-Glu-Ala-Asp) box polypeptide 23	300208	Rn.2319	BI274402	4.90	5.10	4.56	5.75	4.95	5.13	1.34	up	2.21E-01	8.95E-01	-	-
1392906_at	Ubl4	ubiquitin-like 4	293864	Rn.1138	AW528860	6.70	7.19	6.06	6.82	6.84	7.56	1.34	up	3.61E-01	8.95E-01	-	-
1391676_at	---	---	---	Rn.167988	AI51097	5.72	6.42	5.97	5.55	5.73	5.57	1.34	down	1.19E-01	8.95E-01	-	-
1367767_at	Hmgcl	3-hydroxymethyl-3-methylglutaryl-Coenzyme A lyase	79238	Rn.12297	NM_024386	7.73	8.52	8.31	7.93	7.70	7.67	1.34	down	1.70E-01	8.95E-01	-	-
1380683_at	Ptprd	protein tyrosine phosphatase, receptor type, D	313278	Rn.99077	BE107433	4.06	2.53	2.23	2.52	2.52	2.52	1.34	down	4.99E-01	8.95E-01	-	-
1393894_at	Cyp4a8	cytochrome P450, family 4, subfamily a, polypeptide 8	266674	Rn.10034	AW142784	10.44	10.37	10.06	10.92	10.45	10.76	1.34	up	8.02E-02	8.95E-01	-	-
1387393_at	Dlg3	discs, large homolog 3 (Drosophila)	58948	Rn.10238	NM_031639	2.44	2.42	2.45	2.61	3.56	2.41	1.34	up	3.01E-01	8.95E-01	-	-
1383674_at	Tmem219	transmembrane protein 219	308986	Rn.106269	BF419619	6.27	7.66	7.41	6.52	7.99	8.09	1.34	up	5.59E-01	8.95E-01	-	-
1368303_at	Per2	period homolog 2 (Drosophila)	63840	Rn.25935	NM_031678	7.52	6.06	4.93	6.63	6.60	6.54	1.34	up	6.04E-01	8.95E-01	-	-
1373316_at	---	---	---	---	BF409329	3.18	3.65	3.45	3.55	3.58	4.42	1.34	up	2.56E-01	8.95E-01	-	-
1395958_at	---	---	---	---	BF396619	7.58	6.77	8.08	7.18	6.96	7.02	1.34	down	3.39E-01	8.95E-01	-	-
1384098_at	Rnf125	ring finger protein 125	361296	Rn.163367	AA925710	4.76	5.44	6.72	4.64	4.99	6.01	1.34	down	5.83E-01	8.95E-01	-	-
1384680_at	---	---	---	Rn.164851	AA924336	2.89	4.09	3.05	3.01	2.93	2.84	1.34	down	3.31E-01	8.95E-01	-	-
1397445_at	---	---	---	Rn.207131	AW535703	3.58	2.37	2.36	4.45	2.39	2.73	1.34	up	6.07E-01	8.95E-01	-	-
1379834_at	---	---	---	Rn.176356	BG374488	2.44	3.58	2.77	3.05	3.16	3.85	1.34	up	3.74E-01	8.95E-01	-	-
1389712_at	---	---	---	Rn.28809	BF405936	3.65	2.32	2.37	2.36	2.37	2.35	1.34	down	3.90E-01	8.95E-01	-	-
1396292_at	---	---	---	Rn.210852	BG379069	3.93	2.71	2.69	2.82	2.76	2.48	1.34	down	3.76E-01	8.95E-01	-	-
1389403_at	Bmp7	bone morphogenetic protein 7	85272	Rn.18030	AI013715	5.24	6.40	6.50	6.24	5.13	5.52	1.34	down	4.63E-01	8.95E-01	-	-
1391866_at	Npat	nuclear protein, ataxia-telangiectasia locus	315666	Rn.18968	AI014116	2.74	2.52	3.15	3.11	3.45	3.11	1.34	up	1.23E-01	8.95E-01	-	-
1382245_at	---	---	---	Rn.117671	BF397984	8.62	8.74	8.57	9.62	8.83	8.73	1.34	up	2.18E-01	8.95E-01	-	-
1397508_at	Ddx18	DEAD (Asp-Glu-Ala-Asp) box polypeptide 18	308490	Rn.26598	BE106682	6.78	6.00	4.55	7.08	5.75	5.77	1.34	up	6.22E-01	8.95E-01	-	-
1371188_a_at	Ubtf	upstream binding transcription factor, RNA polymerase I	25574	Rn.22469	AI407688	4.67	5.86	6.

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1393652_at	Ztrb1	zinc finger and BTB domain containing 1	314246	Rn.210488	BF398438	5.44	5.35	5.76	4.64	4.86	5.80	1.34	down	3.28E-01	8.95E-01	-	-
1398854_at	Rpl24	ribosomal protein L24	64307	Rn.92808	BI297634	8.90	9.49	9.07	9.29	9.59	9.84	1.34	up	1.51E-01	8.95E-01	-	-
1379803_at	Cbl	Cas-Br-M (murine) ecotropic retroviral transforming sequence	500985	Rn.35589	BE116890	3.52	3.46	2.91	3.52	3.43	4.20	1.34	up	2.49E-01	8.95E-01	-	-
1394719_at	---	---	---	Rn.169068	AI071992	2.46	2.42	3.72	2.45	2.47	2.44	1.34	down	3.81E-01	8.95E-01	-	-
1393990_at	Znf503	zinc finger protein 503	305687	Rn.37928	AA956230	4.29	3.77	5.46	4.85	5.98	3.95	1.34	up	6.16E-01	8.95E-01	-	-
1379418_at	---	---	---	Rn.145699	AW916753	6.91	6.24	5.71	5.85	5.94	5.81	1.34	down	3.00E-01	8.95E-01	-	-
1391618_at	Kifap3	kinesin-associated protein 3	289168	Rn.163223	AI227800	5.79	6.15	5.66	5.71	6.51	6.64	1.34	up	2.68E-01	8.95E-01	-	-
1398962_at	Fam108a1	family with sequence similarity 108, member A1	299617	Rn.15712	BM388453	5.54	6.57	5.92	6.20	6.46	6.62	1.34	up	2.66E-01	8.95E-01	-	-
1384154_at	Wbp4	WW domain binding protein 4 (formin binding protein 21)	114765	Rn.163280	BF554739	7.14	7.74	7.15	6.38	6.78	7.61	1.34	down	3.71E-01	8.95E-01	-	-
1376704_a_at	Ndn|2	necdin-like 2	309259	Rn.9408	BM390112	6.92	7.52	7.59	7.86	7.92	7.50	1.34	up	1.73E-01	8.95E-01	-	-
1382284_at	Nek3	NIMA (never in mitosis gene a)-related kinase 3	306576	Rn.45730	AW525175	2.55	3.74	5.96	3.70	2.44	4.85	1.34	down	7.49E-01	9.19E-01	-	-
1383548_at	Ankrd49	ankyrin repeat domain 49	315434	Rn.15268	BI290887	5.00	4.67	4.17	4.66	5.89	4.54	1.34	up	4.47E-01	8.95E-01	-	-
1389301_at	Mbnl2	muscleblind-like 2	680445	Rn.1940	AI176665	7.80	7.89	8.34	8.43	7.98	8.87	1.34	up	2.43E-01	8.95E-01	-	-
1367875_at	Gak	cyclin G associated kinase	81659	Rn.11012	NM_031030	8.36	7.79	8.26	7.90	7.28	7.99	1.34	down	2.17E-01	8.95E-01	-	-
1381205_at	Snapc5	Small nuclear RNA activating complex, polypeptide 5	691501	Rn.47597	AW531791	8.22	8.61	8.62	8.89	8.70	9.11	1.34	up	7.54E-02	8.95E-01	-	-
1378925_at	Crem	cAMP responsive element modulator	25620	Rn.10251	AW529408	4.29	3.13	3.05	2.89	2.94	3.40	1.34	down	3.88E-01	8.95E-01	-	-
1378642_at	RGD1307071	similar to uncharacterized hypothalamus protein HT013	311502	Rn.23999	AI112858	4.38	4.59	4.18	4.02	3.35	4.54	1.34	down	3.16E-01	8.95E-01	-	-
1383749_at	Phospho1	phosphatase, orphan 1	287644	Rn.162166	AI112954	2.69	2.40	2.69	2.83	2.69	3.52	1.34	up	2.01E-01	8.95E-01	-	-
1388344_at	Samp	SAP domain containing ribonucleoprotein	362819	Rn.1506	BI283112	8.58	8.72	8.88	8.14	8.77	8.02	1.34	down	1.67E-01	8.95E-01	-	-
1367597_at	Rps8	ribosomal protein S8	65136	Rn.3198	NM_031706	11.14	11.49	11.32	11.69	11.52	11.98	1.34	up	6.93E-02	8.95E-01	-	-
1376790_at	---	---	---	Rn.30808	AI010439	4.66	5.47	5.44	5.09	5.90	5.83	1.34	up	3.24E-01	8.95E-01	-	-
1372490_at	---	---	---	Rn.19992	BF283759	5.32	5.26	4.06	5.13	5.59	5.17	1.34	up	3.92E-01	8.95E-01	-	-
1392766_at	---	---	---	Rn.166285	AI059752	2.46	2.45	2.47	3.72	2.46	2.44	1.34	up	3.79E-01	8.95E-01	-	-
1381096_at	---	---	---	Rn.156433	BM385837	3.24	3.21	3.26	3.21	4.55	3.19	1.34	up	4.08E-01	8.95E-01	-	-
1382964_at	---	---	---	---	BI282553	7.96	6.36	7.90	7.27	6.91	6.78	1.34	down	4.87E-01	8.95E-01	-	-
1386945_a_at	Prkab1	protein kinase, AMP-activated, beta 1 non-catalytic subunit	83803	Rn.3619	NM_031976	6.12	6.09	5.26	6.36	6.29	6.06	1.34	up	2.34E-01	8.95E-01	-	-
1392979_at	Cacybp	calcyclin binding protein	289144	Rn.11540	AW916443	7.67	8.32	8.29	7.13	7.90	8.00	1.34	down	2.93E-01	8.95E-01	-	-
1396091_at	LOC687516	similar to zinc finger protein 146	687516	---	BI296193	5.44	6.24	6.36	6.15	6.33	6.81	1.33	up	2.99E-01	8.95E-01	-	-
1389621_at	Fip1l1	FIP1 like 1 (S. cerevisiae)	289582	Rn.138993	BE113454	7.40	8.30	8.18	8.11	8.66	8.36	1.33	up	2.67E-01	8.95E-01	-	-
1376299_at	Jarid1a	jumonji, AT rich interactive domain 1A (Rbp2 like)	312678	Rn.134218	BI288889	4.31	4.76	5.94	6.19	5.25	4.85	1.33	up	5.43E-01	8.95E-01	-	-
1382897_at	LOC311026	similar to mKIAA1461 protein	311026	Rn.91553	BF393872	3.80	2.55	2.60	2.52	2.64	2.53	1.33	down	3.67E-01	8.95E-01	-	-
1378380_at	Pak4	p21 protein (Cdc42/Rac)-activated kinase 4	292756	Rn.18543	BE098920	4.81	6.73	5.11	6.10	5.71	6.09	1.33	up	5.33E-01	8.95E-01	-	-
1386718_at	Akr1c19	aldo-keto reductase family 1, member C19	307096	Rn.206655	BF566188	4.59	5.35	4.84	4.45	4.84	4.26	1.33	down	2.15E-01	8.95E-01	-	-
1388882_at	Slc30a9	Solute carrier family 30 (zinc transporter), member 9	498358	Rn.159709	BM389066	7.36	7.79	7.50	7.97	7.80	8.12	1.33	up	5.84E-02	8.95E-01	-	-
1370186_at	Psmb9	proteasome (prosome, macropain) subunit, beta type 9 (large multifunctional	24967	Rn.13686	AI599350	2.62	3.09	3.10	2.94	3.20	3.92	1.33	up	2.79E-01	8.95E-01	-	-
1369263_at	Wnt5a	wingless-type MMTV integration site family, member 5A	64566	Rn.48749	NM_022631	6.27	6.83	6.41	6.51	6.83	7.41	1.33	up	2.53E-01	8.95E-01	-	-
1385395_at	Stx17	syntaxin 17	252853	Rn.204688	AI549268	3.62	5.32	5.00	5.33	5.06	4.79	1.33	up	4.87E-01	8.95E-01	-	-
1381000_at	---	---	---	Rn.13309	BM386311	2.43	2.41	2.44	3.69	2.43	2.41	1.33	up	3.79E-01	8.95E-01	-	-
1392912_at	Cacybp	calcyclin binding protein	289144	Rn.11540	BG664561	6.58	6.82	7.24	6.24	6.24	6.91	1.33	down	2.30E-01	8.95E-01	-	-
1369971_a_at	Hnrpd	heterogeneous nuclear ribonucleoprotein D	79256	Rn.94022	AB046616	8.13	8.84	9.36	8.93	9.09	9.55	1.33	up	3.60E-01	8.95E-01	-	-
1387074_at	Rgs2	regulator of G-protein signaling 2	84583	Rn.1892	AY043246	4.37	4.35	3.67	4.74	4.61	4.29	1.33	up	1.94E-01	8.95E-01	-	-
1393352_at	RGD1310552	similar to hypothetical protein MGC38960	300836	Rn.23973	BI293882	6.45	6.86	6.25	7.15	7.08	6.57	1.33	up	1.80E-01	8.95E-01	-	-
1375788_at	Rpl7	Ribosomal protein L7	297755	Rn.129121	BM388719	8.02	8.25	8.29	8.50	8.35	8.95	1.33	up	1.05E-01	8.95E-01	-	-
1397233_at	Dclk3	doublecortin-like kinase 3	316023	Rn.93158	AW529479	4.42	4.63	5.26	4.67	5.82	5.09	1.33	up	3.81E-01	8.95E-01	-	-
1388761_at	Hdac1	histone deacetylase 1	297893	Rn.1863	AI180339	4.82	5.15	3.88	4.90	5.13	5.06	1.33	up	3.39E-01	8.95E-01	-	-
1376592_at	Mcee	methylmalonyl CoA epimerase	293829	Rn.3420	BG379780	8.27	7.42	6.88	6.89	7.37	7.06	1.33	down	3.87E-01	8.95E-01	-	-
1370948_a_at	45 /// LOC681252	similar to Myristoylated alanine-rich C-kinase substrate (MARCKS) (ACAMP-43 /// 294446 /// 68		Rn.9560	BE111706	4.71	3.21	3.63	3.61	3.82	2.87	1.33	down	4.77E-01	8.95E-01	-	-
1384799_at	RGD1561931	similar to KIAA2022 protein	302396	Rn.62924	BF416137	2.70	2.65	4.18	3.06	2.72	2.50	1.33	down	4.74E-01	8.95E-01	-	-
1397698_at	---	---	---	Rn.171495	AW917627	5.31	5.40	4.60	5.44	5.32	5.81	1.33	up	2.31E-01	8.95E-01	-	-
1379859_at	---	---	---	Rn.144137	AA964506	2.78	2.93	2.90	3.56	3.41	2.89	1.33	up	1.19E-01	8.95E-01	-	-
1377665_at	Atg2a	ATG2 autophagy related 2 homolog A (S. cerevisiae)	688488	Rn.162488	AA998979	3.35	3.65	4.39	3.31	3.80	3.04	1.33	down	3.38E-01	8.95E-01	-	-
1394120_a_at	---	---	---	Rn.227	AI176775	2.75	2.70	2.82	2.84	3.65	3.03	1.33	up	1.68E-01	8.95E-01	-	-
1399117_at	RGD1311745	similar to RIKEN cDNA 1110059G10	301079	Rn.161980	BF546356	4.74	5.37	4.60	5.24	5.01	5.71	1.33	up	2.56E-01	8.95E-01	-	-
1383198_at	RGD1310651	similar to hypothetical protein MGC20460	362297	Rn.198102	AI598511	6.33	5.47	5.06	5.22	5.17	5.22	1.33	down	3.31E-01	8.95E-01	-	-
1372740_at	303259 /// LOC68	similar to Map4k5-pending protein /// similar to misshapen-like kinase 1 isofor	303259 /// 687705	Rn.32511	AA925557	7.18	8.64	7.54	6.88	7.33	6.89	1.33	down	4.71E-01	8.95E-01	-	-
1371328_at	---	---	---	---	BM986552	9.22	9.99	9.51	10.10	9.83	10.05	1.33	up	1.58E-01	8.95E-01	-	-
1369061_at	Gsr	glutathione reductase	116686	Rn.19721	NM_053906	5.41	5.05	5.44	5.42	4.02	5.22	1.33	down	4.10E-01	8.95E-01	-	-
1372565_at	Htra3	HtrA serine peptidase 3	360959	Rn.15228	BI274192	3.63	2.40	2.43	2.41	2.40	2.40	1.33	down	3.64E-01	8.95E-01	-	-
1392809_at	---	---	---	Rn.147170	AI072437	4.19	3.86	3.87	3.74	3.76	3.18	1.33	up	1.31E-01	8.95E-01	-	-
1398927_at	RGD1307161	similar to 0610010K06Rik protein	305031	Rn.3660	BF406225	5.46	6.55	6.36	6.34	6.70	6.57	1.33	up	3.04E-01	8.95E-01	-	-
1379943_at	---	---	---	Rn.169315	AA943822	2.97	2.97	2.72	3.07	2.94	3.88	1.33	up	2.47E-01	8.95E-01	-	-
1384181_at	---	---	---	Rn.169113	AI547486	6.53	6.63	6.52	6.05	5.81	6.57	1.33	down	1.44E-01	8.95E-01	-	-
1374592_at	Btbd6	BTB (POZ) domain containing 6	690367	Rn.6057	BI282671	6.56	6.56	6.35	7.18	6.55	6.98	1.33	up	1.05E-01	8.95E-01	-	-
1386883_at	Gsk3a	glycogen synthase kinase 3 alpha	50686	Rn.36807	NM_017344	3.61	3.37	3.28	3.52	2.37	3.13	1.33	down	3.02E-01	8.95E-01	-	-
1368267_at	Pomt1	protein-O-mannosyltransferase 1	84430	Rn.162659	NM_053406	3.22	3.35	2.71	3.26	4.04	3.22	1.33	up	2.80E-01	8.95E-01	-	-
1374144_at	---	---	---	Rn.7993	BF402375	7.20	7.53	6.58	7.33	7.18	8.05	1.33	up	3.44E-01	8.95E-01	-	-
1380698_at	---	---	---	Rn.136195	BE108305	2.38	2.43	2.38	2.38	3.68	2.37	1.33	up	3.96E-01	8.95E-01	-	-
1390012_at	Man2b1	Mannosidase, alpha, class 2B, member 1	361378	Rn.102840	BI288861	3.07	3.46	3.13	4.49	3.25	3.17	1.33	up	4.02E-01	8.95E-01	-	-
1384518_at	Phf14	PHD finger protein 14	500030	Rn.11764	BE107536	6.12	7.23	6.80	7.45	6.75	7.19	1.33	up	3.39E-01	8.95E-01	-	-
1385810_at	Lrrc51	leucine rich repeat containing 51	293156	Rn.162471	BF546013	2.74	2.57	2.75	3.23	2.74	3.33	1.33	up	9.41E-02	8.95E-01	-	-
1394886_at	Idh1	isocitrate dehydrogenase 1 (NADP+), soluble	24479	Rn.3561	AI235545	7.15	5.03	4.56	5.43	6.08	3.99	1.33	down	7.02E-01	9.07E-01	-	-
1371937_at	RGD1562618	similar to RIKEN cDNA 6030419C18 gene	501007	Rn.45705	BG381652	3.81	3.79	2.99	3.87	3.81	4.14	1.33	up	2.26E-01	8.95E-01	-	-
1370501_at	Ube2g1	ubiquitin-conjugating enzyme E2G 1 (UBC7 homolog, C. elegans)	64631	Rn.163149	BM389287	5.86	6.05	6.91	6.51	7.06	6.50	1.33	up	3.27E-01	8.95E-01	-	-
1395483_at	---	---	---	Rn.176530	BI296524	2.53	2.85	2.54	2.53	4.10	2.53	1.33	up	4.82E-01	8.95E-01	-	-
1383024_at	---	---	---	Rn.169312	AW521625	2.52	2.47	2.53	2.72	2.53	3.52	1.33	up	2.43E-01	8.95E-01	-	-
1381282_at	---	---	---	Rn.63148	BF416808	4.98	5.68	6.07	5.06	4.96	5.46	1.33	down	3.08E-01	8.95E-01	-	-
1390481_a_at	Ube2t	ubiquitin-conjugating enzyme E2T (putative)	360847	Rn.18835	AW531714	3.60	2.38	2.40	2.38	2.39	2.37	1.33	down	3.63E-01	8.95E-01	-	-
1392958_at	Cyld	cylindromatosis (turban tumor syndrome)	312937	Rn.168938	AI547426	7.00	7.48	7.22	7.38	6.97	8.59	1.33	up	4.58E-01	8.95E-01	-	-
1393847_at	Nkiras1	NFKB inhibitor interacting Ras-like 1	305751	Rn.98363	AI502379	3.06	3.15	2.92	4.09	3.20	3.09	1.33	up	2.70E-01	8.95E-01	-	-
1371313_at	Rpl23a	ribosomal protein L23a	360572	Rn.114743	AI172199	10.22	10.55	10.51	10.87	10.56	11.09	1.33	up	8.95E-02	8.95E-01	-	-
1376487_at	Rhcg	Rh family, C glycoprotein	293048	Rn.18789	AI044046	5.08	3.62	3.67	3.82	4.30	3.02	1.33	down	5.32E-01	8.95E-01	-	-
1389529_at	Fam168a	Family with sequence similarity 168, member A	361614	Rn.137163	AI409595	2.51	2.33	3.09	3.37	2.41	3.39	1.33	up	3.57E-01	8.95E-01	-	-
1381053_at	---	---	---	Rn.173068	BF404772	2.55	2.82	2.56	3.86	2.85	2.45	1.33	up	3.89E-01	8.95E-01	-	-
1383166_at	Ncoa1	nuclear receptor coactivator 1	313929	Rn.165307	BE100595	3.26	4.76	5.00	4.69	2.93	4.16	1.33	down	6.13E-01	8.95E-01	-	-
1377270_a_at	Dcp1b	DCP1 decapping enzyme homolog b (S. cerevisiae)	500305	Rn.98474	BF396493	3.16	3.51	3.92	4.79	3.25	3.79	1.33	up	4.56E-01	8.95E-01	-	-
1395855_at	Arih2	ariadne homolog 2 (Drosophila)	316905	Rn.9570	AW918630	3.42	3.74	3.93	4.20	3.55	4.57	1.33	up	2.81E-01	8.95E-01	-	-
1371930_at	ars /// RGD156231	glutaminyl-tRNA synthetase /// similar to glutaminyl-tRNA synthetase	290868 /// 501055	Rn.98697	BG380882	9.08	9.42	8.89	9.47	9.26	9.90	1.33	up	1.64E-01	8.95E-01	-	-
1385240_at	Wdr33	WD repeat domain 33	307524	Rn.22892	AW523099	5.22	5.68	5.61	5.24	3.61	6.43	1.33	down	6.45E-01	8.95E-01	-	-
1368859_at	Pym1a	pym homolog/hydrolase 1A, magnesium dependent, alpha isoform	24666	Rn.37403	NM_017038	6.10	7.09	6.43	6.68	6.73	7.45	1.33	up	3.42E-01	8.95E-01	-	-
1376779_at	Foxo1	forkhead box O1	84482	Rn.116108	BI295511	5.53	5.73	5.45	5.98	6.26	5.70	1.33	up	8.66E-02	8.95E-01	-	-
1374172_at	---	---	---	Rn.12548	AI010883	2.75	2.75	3.49	2.82	2.44	2.49	1.33	down	2.08E-01	8.95E-01	-	-
1374796_at	Sgcb	sarcoglycan, beta (dystrophin-associated glycoprotein)	680229	Rn.98258	AI413058	2.54	2.71	2.53	3.45	2.70	2.88	1.33	up	1.51E-01	8.95E-01	-	-
1398869_at	Arhgap17	Rho GTPase activating protein 17	63994	Rn.64581	BF411165	2.29	3.67	2.30	2.29	2.44	2.28	1.33	down	4.21E-01	8.95E-01	-	-
1376021_at	---	---	---	Rn.23110	BM384049	7.47	7.16	7.66	6.87	6.79	7.39	1.33	down	1.59E-01	8.95E-01	-	-
1388500_at	---	---	---	Rn.15902	AI180252	3.46	2.53	2.49	2.44	2.49	2.32	1.33	down	2.66E-01	8.95E-01	-	-
1394784_at	Esf1	ESF1, nucleolar pre-rRNA processing protein, homolog (S. cerevisiae)	366203	Rn.22208	BF522436	6.75	6.58	6.81	5.26	6.69	6.94	1.33	down	4.80E-01	8.95E-01	-	-
1371211_a_at	Nrg1	neuregulin 1	112400	Rn.37438	U02315	7.17	8.22	6.68	6.80	7.77	6.26	1.33	down	5.51E-01	8.95E-01	-	-
1390398_at	---	---	---	Rn.4018	AI179372	5.32	5.32	7.37	5.32	5.96	5.49	1.33	down	5.92E-01	8.95E-01	-	-
1397929_at	---	---	---	Rn.171873	AW443692	2.65	3.43	3.05	2.64	2.67	2.60	1.33	down	1.44E-01	8.95E-01	-	-
1398858_at	Rpl13	ribosomal protein L13	81765	Rn.908	NM_031101	8.17	9.22	8.71	8.98	8.93	9.42	1.33	up	2.91E-01	8.95E-01	-	-
1395565_at	Copa4	COP9 constitutive photomorphogenic homolog subunit 4 (Arabidopsis)	360915	Rn.7506	BG669198	6.46	7.47	6.26	7.24	6.81	7.37	1.33	up	3.73E-01	8.95E-01	-	-
1392349_at	Slc5a3	solute carrier family 5 (inositol transporters), member 3	114507	Rn.208396	BE116021	2.66	4.16	2.89	2.34	3.22	2.91	1.33	down	4.82E-01	8.95E-01	-	-
1388618_at	Ndi2	nidogen 2	302448	Rn.98892	BM389302	7.35	7.01	6.99	7.60	7.01	7.97	1.33	up	2.43E-01	8.95E-01	-	-
1399121_at	---	---	---	Rn.13353	BE111600	5.23	5.77	5.66	5.62	6.36	5.91	1.33	up	2.06E-01	8.95E-01	-	-
1367804_at	Apcs	amyloid P component, serum	29339	Rn.109007	NM_017170	4.71	4.25	4.92	4.70	6.18	4.24	1.33	up	5.41E-01	8.95E-01	-	-
1378487_at	---	---	---	Rn.206279	BF403191	3.71	2.44	2.47	2.47	2.44	2.44	1.33	down	3.86E-01	8.95E-01	-	-
1371072_at	Ncoa6	nuclear receptor coactivator 6	116464	Rn.9077	AF228043	4.79	4.15	2.97	3.47	3.45	3.76	1.33	down	4.90E-01	8.95E-01	-	-
1371689_at	---	---	---	Rn.163742	BE107334	8.33	8.66	8.97	8.84	9.07	9.28	1.33	up	1.37E-01	8.95E-01	-	-
1399140_at	---	---	---	---	AA965202	9.32	8.22	8.66	8.28	8.32	8.37	1.33	down	2.70E-01	8.95E-01	-	-
1373346_at	RGD1306508	similar to hypothetical protein CL25084	289874	Rn.102123	AI009492	9.20	9.26	8.94	9.45	9.37	9.82	1.33	up	7.13E-02	8.95E-01	-	-
1369747_at	Nat1 /// Nat2	N-acetyltransferase 1 (arylamine N-acetyltransferase) /// N-Acetyltransferase-1	116631 /// 116632	Rn.198370	U17261	4.44	5.07	4.08	5.80	4.32	4.72	1.33	up	4.81E-01	8.95E-01	-	-
1373294_at	Commd8	COMM domain containing 8	289603	Rn.24797	AI234292	8.84	9.35	8.64	9.28	9.36	9.43	1.33	up	1.29E-01	8.95E-01	-	-
1379021_s_at	---	---	---	Rn.81481	AI170497	6.85	3.46	3.77	3.71	4.07	5.08	1.33	down	7.40E-01	9.16E-01	-	-
1373024_at	Ap3s1	adaptor-related protein complex 3, sigma 1 subunit	302290	Rn.3070	BI296511	5.62	6.19	5.65	5.79	6.43	6.48	1.33	up	2.28E-01	8.95E-01	-	-
1378118_at	---	---	---	Rn.199357	BI285675	2.54	2.52	3.82	2.54	2.54	2.56	1.33	down	3.93E-01	8.95E-01	-	-
1387753_s_at	Magi3	membrane associated guanylate kinase, WW and PDZ domain containing 3	245903	Rn.162823	NM_139084	4.01	4.42	4.79	3.41	4.98	3.59	1.33	down	4.93E-01	8.95E-01	-	-
1392535_at	Pycrl	pyrroline-5-carboxylate reductase-like	300035	Rn.40859	AI199002	4.75	4.89	4.86	5.10	5.35	5.29	1.33	up	9.32E-03	8.95E-01	-	-
1368152_at	Zdhhc7	zinc finger, DHHC-type containing 7	170906	Rn.7790	NM_133394	4.50	6.10	3.23	4.90	4.79	5.36	1.33	up	6.53E-01	8.97E-01	-	-
1370440_at	Slc15a4	solute carrier family 15, member 4	246280	Rn.10770	AB000280	3.88	4.40	4.37	3.93	3.25	4.25	1.33	down	2.92E-01	8.95E-01	-	-
1374489_at	Gpbp2	GC-rich promoter binding protein 2	363195	Rn.3595	BF282573	2.39	2.34	3.64	2.38	2.38	2.37	1.33	down	3.89E-01	8.95E-01	-	-
1374086_at	Arhgap21	Rho GTPase activating protein 21	307178	Rn.162259	BF282296	4.66	5.24	4.71	5.32	5.26	5.27	1.33	up	9.41E-02	8.95E-01	-	-
1380303_at	LOC687827	similar to Serine/threonine-protein kinase Haspin (Haploid germ cell-specific r	687827	---	BF398611	2.31	2.30	3.55	2.31	2.31	2.31	1.33	down	3.79E-01	8.95E-01	-	-
1391995_at	Trim37	tripartite motif-containing 37	360592	Rn.9335	BG377975	5.05	5.78	6.09	4.83	5.06	5.80	1.33	down	3.89E-01	8.95E-01	-	-
1373923_at	Rdh10	Retinol dehydrogenase 10 (all-trans)	353252	Rn.16968	BF283756	4.70	7.01	5.94	5.27	4.79	6.37	1.33	down	6.41E-01	8.95E-01	-	-
1392593_a_at	Prr12	proline rich 12	361569	Rn.17182	AI555789	3.46	4.17	2.45	3.57	2.45	2.84	1.33	down	5.29E-01	8.95E-01	-	-
1384892_at	---	---	---	Rn.146636	AI029798	4.50	2.67	3.06	2.72	3.28	2.99	1.33	down	5.17E-01	8.95E-01	-	-
1372233_at	Ergic3	ERGIC and golgi 3	296306	Rn.22956	AI228649	9.08	9.08	8.96	9.28	9.73	9.34	1.33	up	4.84E-02	8.95E-01	-	-
1371888_at	mrpl24	mitochondrial ribosomal protein L24	295224	Rn.162593	AA892843	8.55	8.51	8.79	8.11	8.08	8.43	1.33	down	4.53E-02	8.95E-01	-	-
1383623_at	Thyn1	thymocyte nuclear protein 1	300470	Rn.87291	BM383909	5.28	5.88	5.03	5.29	6.10	6.05	1.33	up	3.23E-01	8.95E-01	-	-
1396113_at	---	---	---	Rn.199261	AI111683	6.12	5.56	4.91	4.92	5.49	4.94	1.33	down	3.58E-01	8.95E-01	-	-
1374914_at	Ppard	peroxisome proliferator-activated receptor delta	25682	Rn.96181	AI230294	2.42	2.46	2.43	2.40	3.04	3.10	1.33	up	1.41E-01	8.95E-01	-	-
1388735_at	---	---	---	Rn.50158	BF405161	3.80	5.94	4.28	3.39	4.27	5.13	1.33	down	6.42E-01	8.95E-01	-	-
1383723_at	Specc1l	SPECC1-like	361828	Rn.63017	BF418837	3.24	3.84	3.53	4.65	3.96	3.23	1.33	up	4.07E-01	8.95E-01	-	-
1390460_at	---	---	---	Rn.20348	AI407307	2.76	2.83	2.39	2.86	2.83	3.52	1.33	up	1.96E-01	8.95E-01	-	-
1371814_at	Ube2g2	ubiquitin-conjugating enzyme E2G 2	294331	Rn.139603	BI282191	6.84	7.12	6.79	7.59	7.16	7.23	1.33	up	7.13E-02	8.95E-01	-	-
1372479_at	---	---	---	Rn.8739	AI175666	8.04	6.83	6.76	8.61	7.51	6.73	1.33	up	5.83E-01	8.95E-01	-	-
1372890_at	---	---	---	Rn.165322	BM388696	5.22	4.97	5.24	5.38	5.45	5.82	1.33	up	6.49E-02	8.95E-01	-	-
1371966_at	Pomt1	protein-L-isoaspartate (D-aspartate) O-methyltransferase 1	25604	Rn.86985	BM392375	6.76	7.33	6.67	7.16	7.28	7.55	1.33	up	1.57E-01	8.95E-01	-	-
1384548_at	Rpl32	ribosomal protein L32	28298	Rn.110966	BM388159

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1389019_at	---	---	---	Rn.222040	AI178561	5.29	5.60	6.34	4.70	5.60	5.72	1.33	down	4.15E-01	8.95E-01	-	-
1373790_at	Car14	carbonic anhydrase 14	791259	Rn.201792	AI045400	4.14	3.89	3.61	3.37	4.47	5.02	1.33	up	4.68E-01	8.95E-01	-	-
1396280_at	Gpkow	G patch domain and KOW motifs	679890	Rn.147981	BI277872	5.66	5.85	4.40	6.43	4.74	4.96	1.33	up	5.81E-01	8.95E-01	-	-
1381711_at	---	---	---	---	BE100967	5.87	3.29	6.06	6.08	6.25	6.06	1.33	up	7.32E-01	9.14E-01	-	-
1373803_a_at	Ghr	growth hormone receptor	25235	Rn.2178	AI170771	8.90	9.26	10.45	9.16	8.82	9.42	1.33	down	4.62E-01	8.95E-01	-	-
1391295_at	---	---	---	Rn.204522	AI136393	2.44	2.39	3.64	2.41	2.49	2.36	1.33	down	3.77E-01	8.95E-01	-	-
1383181_at	Dnajc9	DnaJ (Hsp40) homolog, subfamily C, member 9	364240	Rn.16186	AI704947	8.89	8.42	8.23	8.11	7.94	8.27	1.33	down	1.33E-01	8.95E-01	-	-
1398783_at	Gps1	G protein pathway suppressor 1	117039	Rn.16873	NM_053969	6.31	6.44	5.66	6.22	6.44	6.98	1.33	up	2.86E-01	8.95E-01	-	-
1382991_at	Tia1	TIA1 cytotoxic granule-associated RNA binding protein	312510	Rn.198158	AA963798	3.36	3.09	2.62	2.61	2.62	2.61	1.33	down	1.36E-01	8.95E-01	-	-
1382797_at	RGD1560433	similar to 1500019C08Rik protein	296750	---	AW526331	4.68	4.11	3.35	5.21	4.02	4.12	1.33	up	4.95E-01	8.95E-01	-	-
1371136_at	Ppm1b	protein phosphatase 1B, magnesium dependent, beta isoform	24667	Rn.4143	AJ271834	5.21	5.14	4.89	4.65	4.33	5.04	1.33	down	1.48E-01	8.95E-01	-	-
1382711_at	Zkscan1	zinc finger with KRAB and SCAN domains 1	498160	Rn.113295	AI030337	4.48	4.47	3.60	4.33	4.57	4.88	1.33	up	2.86E-01	8.95E-01	-	-
1380765_at	---	---	---	Rn.14919	BE117715	3.56	2.33	2.34	2.34	2.35	2.33	1.33	down	3.76E-01	8.95E-01	-	-
1374071_at	Fam118a	family with sequence similarity 118, member A	300120	Rn.36745	BG670800	5.43	5.56	5.22	4.71	4.65	5.63	1.33	down	2.90E-01	8.95E-01	-	-
1377924_at	---	---	---	Rn.101829	BE113414	6.52	6.19	7.48	6.25	6.29	6.43	1.33	down	3.57E-01	8.95E-01	-	-
1383656_at	---	---	---	Rn.18634	BM387554	7.17	6.68	8.15	7.24	6.65	6.89	1.33	down	4.30E-01	8.95E-01	-	-
1376554_at	---	---	---	Rn.79171	BE121079	6.92	7.16	7.56	7.81	7.56	7.49	1.33	up	1.25E-01	8.95E-01	-	-
1371603_at	Prr3	proline rich 3	361788	Rn.94992	BI291379	6.18	4.74	4.25	5.62	5.38	5.39	1.33	up	5.25E-01	8.95E-01	-	-
1380164_at	Tk2	thymidine kinase 2, mitochondrial	291824	Rn.160594	AI411787	4.44	4.31	4.49	5.50	4.48	4.48	1.33	up	3.03E-01	8.95E-01	-	-
1390467_at	---	---	---	Rn.204739	AB026259	4.37	3.23	2.51	2.99	2.54	3.36	1.33	down	5.31E-01	8.95E-01	-	-
1391475_at	Hnrpl	heterogeneous nuclear ribonucleoprotein L-like	313842	Rn.161893	AI235376	6.30	5.71	5.85	5.62	4.76	6.27	1.33	down	4.39E-01	8.95E-01	-	-
1383001_at	RGD1560812	RGD1560812	500640	Rn.16708	AI178157	2.79	2.69	3.32	3.18	3.16	3.68	1.33	up	1.90E-01	8.95E-01	-	-
1385964_at	---	---	---	Rn.3315	AI237569	5.98	6.18	6.22	6.54	6.58	6.47	1.33	up	7.62E-03	8.95E-01	-	-
1370529_a_at	Pld1	phospholipase D1	25096	Rn.11132	U89550	2.90	3.04	3.09	2.60	2.70	4.51	1.32	down	6.84E-01	9.03E-01	-	-
1375036_at	---	---	---	Rn.203269	AI172146	6.40	5.36	5.75	5.37	5.54	5.38	1.32	down	2.56E-01	8.95E-01	-	-
1376994_at	---	---	---	Rn.166414	BE098799	6.11	5.23	5.14	6.08	5.68	5.92	1.32	up	2.86E-01	8.95E-01	-	-
1375093_at	Rbks	ribokinase	362706	Rn.145214	AI236089	5.46	6.27	8.86	6.14	6.54	6.68	1.32	down	7.16E-01	9.10E-01	-	-
1375533_at	Vgll4	vestigial like 4 (Drosophila)	297523	Rn.23131	BI289645	4.35	5.06	5.07	5.02	5.07	5.60	1.32	up	2.50E-01	8.95E-01	-	-
1380974_at	---	---	---	Rn.206764	BG381707	2.46	2.61	3.52	2.45	2.46	2.45	1.32	down	2.88E-01	8.95E-01	-	-
1374265_at	---	---	---	Rn.166593	BF395101	3.46	3.30	3.53	3.36	3.43	4.72	1.32	up	4.16E-01	8.95E-01	-	-
1382152_at	Kdm5b	lysine (K)-specific demethylase 5B	304809	Rn.22866	AI234336	5.87	5.79	4.66	4.84	4.82	5.44	1.32	down	4.08E-01	8.95E-01	-	-
1385093_at	RGD1565033	similar to hypothetical protein LOC284018 isoform b	498014	Rn.143962	BG379949	4.03	3.54	3.32	3.95	3.27	4.89	1.32	up	4.73E-01	8.95E-01	-	-
1372684_at	Smtn	smoothelin	289734	Rn.40766	AW435036	3.57	3.39	3.90	2.94	3.89	2.81	1.32	down	3.35E-01	8.95E-01	-	-
1385601_at	Frg1l	FSHD region gene 1-like	361156	---	BE115019	5.86	5.79	6.94	5.79	4.93	6.66	1.32	down	5.52E-01	8.95E-01	-	-
1380263_at	RGD1309634	hypothetical LOC305452	305452	Rn.7798	BI290769	3.01	4.20	2.65	5.44	2.64	3.00	1.32	up	7.05E-01	9.08E-01	-	-
1380106_at	Sf1	splicing factor 1	117855	Rn.1074	BF283079	5.08	6.73	4.99	4.85	5.68	5.05	1.32	down	5.48E-01	8.95E-01	-	-
1383225_at	---	---	---	Rn.2894	BF396682	2.35	2.34	2.35	3.57	2.35	2.33	1.32	up	3.80E-01	8.95E-01	-	-
1393224_at	---	---	---	Rn.161296	AW529774	6.38	6.99	6.64	7.24	6.91	7.08	1.32	up	1.12E-01	8.95E-01	-	-
1368921_a_at	Cd44	Cd44 molecule	25406	Rn.1120	NM_012924	2.48	2.74	2.57	2.66	2.65	3.71	1.32	up	3.23E-01	8.95E-01	-	-
1386943_at	Pllp	plasma membrane proteolipid (plasmolipin)	64364	Rn.1721	NM_022533	10.19	10.46	9.16	10.42	10.60	10.01	1.32	up	4.04E-01	8.95E-01	-	-
1377273_at	---	---	---	Rn.206138	BF389637	4.24	4.13	4.71	4.15	3.97	3.74	1.32	down	1.31E-01	8.95E-01	-	-
1383844_at	Arhgef15	Rho guanine nucleotide exchange factor (GEF) 15	287418	Rn.26985	BI296898	6.53	6.12	6.03	5.14	6.40	5.93	1.32	down	3.67E-01	8.95E-01	-	-
1382191_at	Pias1	protein inhibitor of activated STAT, 1	300772	Rn.24369	AI228848	4.79	4.15	4.09	4.24	3.67	3.91	1.32	down	2.20E-01	8.95E-01	-	-
1368133_at	Mpdz	multiple PDZ domain protein	29365	Rn.6684	NM_019196	4.21	4.62	5.87	5.15	4.61	3.73	1.32	down	5.67E-01	8.95E-01	-	-
1370728_at	Il13ra1	interleukin 13 receptor, alpha 1	252963	Rn.81270	AY044251	4.13	3.57	2.89	3.54	3.13	5.13	1.32	up	5.97E-01	8.95E-01	-	-
1370885_at	Ctsz	cathepsin Z	252929	Rn.1475	AA849399	3.70	3.11	3.73	3.11	3.12	3.08	1.32	down	1.16E-01	8.95E-01	-	-
1389339_at	Arsa	Arylsulfatase A	315222	Rn.23323	BF284062	7.08	6.29	5.58	6.67	6.43	7.06	1.32	up	4.38E-01	8.95E-01	-	-
1382998_at	Shisa3	shisa homolog 3 (Xenopus laevis)	498356	Rn.198968	BF291169	3.57	3.18	3.46	3.19	3.23	2.57	1.32	down	1.71E-01	8.95E-01	-	-
1389926_at	lik /// RGD156144	nemo like kinase /// similar to nemo like kinase	363942 /// 497961	Rn.113514	AI764477	9.37	9.43	9.37	9.37	8.23	9.36	1.32	down	3.47E-01	8.95E-01	-	-
1390586_at	RGD1560601	similar to Jumonji/ARID domain-containing protein 1C (SmcX protein)	317432	Rn.147997	AA924192	6.15	5.53	5.93	4.08	5.99	6.33	1.32	down	6.07E-01	8.95E-01	-	-
1389708_at	Atpbd4	ATP binding domain 4	362191	Rn.107116	AW142960	5.45	4.12	3.19	4.26	5.43	4.29	1.32	up	6.23E-01	8.95E-01	-	-
1387790_at	Paics	phosphoribosylaminoimidazole carboxylase, phosphoribosylaminoimidazole s	140946	Rn.3015	NM_080910	9.29	9.65	10.05	10.06	10.08	10.06	1.32	up	1.38E-01	8.95E-01	-	-
1389308_at	Dnajb11	DnaJ (Hsp40) homolog, subfamily B, member 11	360734	Rn.14603	BI295873	8.41	8.39	9.12	8.92	8.66	9.55	1.32	up	3.21E-01	8.95E-01	-	-
1390049_at	Fhl1	four and a half LIM domains 1	25177	Rn.54261	BI298356	5.44	4.16	4.19	4.55	3.40	4.62	1.32	down	5.23E-01	8.95E-01	-	-
1392918_at	Cct8	chaperonin containing Tcp1, subunit 8 (theta)	288305	Rn.98524	BE115650	7.61	7.74	8.42	7.37	7.35	7.83	1.32	down	2.43E-01	8.95E-01	-	-
1376992_a_at	Ccdc84	coiled-coil domain containing 84	689046	Rn.154647	AI058900	4.69	5.42	4.39	4.79	4.26	4.24	1.32	down	3.20E-01	8.95E-01	-	-
1391523_at	---	---	---	Rn.8868	AA955605	2.80	2.37	2.40	2.37	3.56	2.84	1.32	up	3.42E-01	8.95E-01	-	-
1383808_at	Ttll1	tubulin tyrosine ligase-like family, member 1	362669	Rn.99535	AA818423	2.83	2.80	3.84	2.84	2.45	2.97	1.32	down	3.45E-01	8.95E-01	-	-
1375027_at	---	---	---	Rn.218427	AI407365	7.57	7.49	7.04	6.91	6.79	7.19	1.32	down	1.17E-01	8.95E-01	-	-
1386229_at	Cir	CBF1 interacting corepressor	362149	Rn.99641	AI101392	6.23	5.63	6.34	5.55	5.46	5.99	1.32	down	2.16E-01	8.95E-01	-	-
1378995_at	RGD1310552	Similar to hypothetical protein MGC38960	300836	Rn.23973	BF420814	3.65	3.04	3.93	3.31	3.06	3.04	1.32	down	2.21E-01	8.95E-01	-	-
1374547_at	Serf2	small EDRK-rich factor 2	502663	Rn.109370	BI285509	6.31	5.95	5.87	5.61	6.47	6.25	1.32	up	2.86E-01	8.95E-01	-	-
1373383_at	Mterfd1	MTERF domain containing 1	299514	Rn.103375	AA848807	7.05	7.51	7.99	7.20	6.72	7.41	1.32	down	3.00E-01	8.95E-01	-	-
1398729_s_at	LOC682058	similar to nucleolar protein with MIF4G domain 1	682058	---	AW525946	9.93	9.39	8.97	9.55	8.74	8.79	1.32	down	3.51E-01	8.95E-01	-	-
1386123_at	---	---	---	Rn.175011	BF553538	2.36	2.67	3.26	2.36	2.37	2.35	1.32	down	2.02E-01	8.95E-01	-	-
1372625_at	Ppp1r12c	protein phosphatase 1, regulatory (inhibitor) subunit 12C	499076	Rn.41379	AA851663	5.72	5.79	4.69	5.18	4.76	5.04	1.32	down	3.45E-01	8.95E-01	-	-
1368529_at	Cd99l2	CD99 molecule-like 2	171485	Rn.20204	AF481858	3.03	5.12	3.03	3.76	4.92	3.72	1.32	up	6.41E-01	8.95E-01	-	-
1395072_at	---	---	---	Rn.207073	AW534686	2.53	2.36	2.48	2.49	3.33	2.75	1.32	up	1.87E-01	8.95E-01	-	-
1380747_at	---	---	---	Rn.204621	BE098757	5.25	4.92	2.90	5.79	4.67	3.82	1.32	up	6.87E-01	9.04E-01	-	-
1368330_at	Aatf	apoptosis antagonizing transcription factor	114512	Rn.15500	NM_053720	5.92	6.30	4.91	5.33	6.44	6.57	1.32	up	5.19E-01	8.95E-01	-	-
1372179_at	Hpcal1	hippocalcin-like 1	50871	Rn.102820	BM389406	7.28	6.33	6.07	5.83	6.45	6.19	1.32	down	3.80E-01	8.95E-01	-	-
1377196_at	LOC683733	similar to Transcription factor 7-like 2 (HMG box transcription factor 4) (T-cell-	683733	---	BI279936	5.14	3.90	3.78	3.44	3.85	4.33	1.32	down	4.70E-01	8.95E-01	-	-
1374283_at	Falz	fetal Alzheimer antigen	303617	Rn.49972	BF419505	4.47	4.48	4.81	4.67	3.36	4.52	1.32	down	4.00E-01	8.95E-01	-	-
1374707_at	RGD1309922	similar to 2610301G19Rik protein	306007	Rn.31320	BM384854	6.61	5.69	4.18	5.59	4.59	5.08	1.32	down	6.26E-01	8.95E-01	-	-
1371880_at	Sp1	Sp1 transcription factor	24790	Rn.44609	AI179662	6.81	6.14	5.82	6.62	6.76	6.59	1.32	up	2.44E-01	8.95E-01	-	-
1371671_at	Gprc5b	G protein-coupled receptor, family C, group 5, member B	293546	Rn.47330	AI228513	5.64	3.23	2.52	2.75	5.04	2.40	1.32	down	7.64E-01	9.23E-01	-	-
1372502_at	Nf2	neurofibromin 2 (merlin)	25744	Rn.46695	AI579645	4.51	5.15	4.54	5.08	5.24	5.09	1.32	up	1.32E-01	8.95E-01	-	-
1385571_at	LOC679623	similar to Nuclear autoantigen Sp-100 (Speckled 100 kDa) (Nuclear dot-assoc	679623	Rn.198848	AA923865	2.78	2.45	5.33	2.37	4.59	2.37	1.32	down	7.48E-01	9.19E-01	-	-
1389134_at	---	---	---	Rn.3805	BF551369	6.02	4.97	5.86	4.95	5.41	5.27	1.32	down	3.16E-01	8.95E-01	-	-
1367878_at	Stx5	syntaxin 5	65134	Rn.5782	NM_031704	6.29	6.26	6.74	7.29	6.37	6.83	1.32	up	2.60E-01	8.95E-01	-	-
1388516_at	LOC499235	LRRGT00141	499235	Rn.122632	AI104258	8.88	8.46	8.34	9.08	9.09	8.72	1.32	up	1.22E-01	8.95E-01	-	-
1380078_at	---	---	---	Rn.25351	AW144384	2.43	2.42	3.67	2.43	2.44	2.44	1.32	down	3.85E-01	8.95E-01	-	-
1393431_at	LOC687575	similar to Splicing factor U2AF 35 kDa subunit (U2 auxiliary factor 35 kDa sub	687575	Rn.216659	AI500737	7.49	7.48	7.37	7.61	7.65	8.28	1.32	up	1.38E-01	8.95E-01	-	-
1374553_at	Fam32a	family with sequence similarity 32, member A	498600	Rn.7484	AW535229	7.18	7.10	7.80	6.98	6.96	6.94	1.32	down	1.40E-01	8.95E-01	-	-
1392432_at	Fgf10	Fibroblast growth factor 10	25443	Rn.44439	AA998022	3.88	2.55	2.58	2.66	2.67	2.48	1.32	down	4.16E-01	8.95E-01	-	-
1388932_at	Gls	glutaminase	24398	Rn.5762	AI577681	2.81	2.59	2.61	2.72	3.42	3.08	1.32	up	1.32E-01	8.95E-01	-	-
1385987_at	---	---	---	Rn.207366	BE098157	6.35	3.97	5.19	4.35	5.11	4.84	1.32	down	6.07E-01	8.95E-01	-	-
1382000_at	Mxd4	Max dimerization protein 4	360961	Rn.3279	AW520897	2.36	3.13	3.76	2.62	2.88	2.55	1.32	down	3.89E-01	8.95E-01	-	-
1389146_at	Fam107b	family with sequence similarity 107, member B	499796	Rn.105966	BF283267	8.98	8.93	8.63	8.39	8.39	8.57	1.32	down	3.24E-02	8.95E-01	-	-
1378385_at	---	---	---	---	AI548474	6.04	2.56	2.66	2.47	5.06	2.52	1.32	down	7.92E-01	9.33E-01	-	-
1395707_at	---	---	---	Rn.17648	BG670971	2.84	3.48	3.48	3.48	3.51	4.01	1.32	up	2.17E-01	8.95E-01	-	-
1391434_at	Rab3a	RAB3A, member RAS oncogene family	25531	Rn.44409	BF389910	3.62	4.52	3.59	4.54	4.15	4.24	1.32	up	2.85E-01	8.95E-01	-	-
1388643_at	Fut8	fucosyltransferase 8 (alpha (1,6) fucosyltransferase)	432392	Rn.1717	AI177839	4.49	3.92	3.99	5.41	4.14	4.07	1.32	up	4.41E-01	8.95E-01	-	-
1388443_at	K2ap1 /// LOC6875	cyclin-dependent kinase 2-associated protein 1 /// similar to CDK2 (cyclin-dep	360804 /// 687549	Rn.40447	AI177871	8.49	8.37	8.78	8.59	8.73	9.54	1.32	up	2.79E-01	8.95E-01	-	-
1383266_at	Sfrp1	secreted frizzled-related protein 1	84402	Rn.163333	AW144660	6.54	7.29	6.13	7.70	6.19	7.28	1.32	up	5.14E-01	8.95E-01	-	-
1377105_at	Zfp91	zinc finger protein 91	246282	Rn.1772	BM385715	10.52	9.74	9.91	10.56	10.38	10.43	1.32	up	1.72E-01	8.95E-01	-	-
1388494_at	Col4a2	collagen, type IV, alpha 2	306628	Rn.2237	BI281705	6.77	6.41	6.11	5.37	6.27	6.45	1.32	down	3.55E-01	8.95E-01	-	-
1368059_at	Crym	crystallin, mu	117024	Rn.24561	NM_053955	11.90	12.06	11.85	11.71	11.23	11.67	1.32	down	7.28E-02	8.95E-01	-	-
1386959_a_at	Map2k5	mitogen activated protein kinase kinase 5	29568	Rn.11054	NM_017246	9.20	8.68	8.84	8.68	8.71	8.91	1.32	down	4.80E-01	8.95E-01	-	-
1382060_at	---	---	---	Rn.30208	BE115085	2.83	3.37	2.83	2.81	3.57	3.86	1.32	up	3.29E-01	8.95E-01	-	-
1374508_at	Nphp1	nephronophthisis 1 (juvenile) homolog (human)	296136	Rn.32745	BG663343	8.17	8.33	8.48	8.71	8.60	8.89	1.32	up	3.10E-02	8.95E-01	-	-
1373251_at	Lysmd1	LysM, putative peptidoglycan-binding, domain containing 1	499671	Rn.160047	BI289957	2.59	2.61	3.76	2.59	2.60	2.57	1.32	down	3.59E-01	8.95E-01	-	-
1395437_at	---	---	---	Rn.171508	BF287018	2.50	2.52	3.72	2.50	2.49	3.12	1.32	up	3.81E-01	8.95E-01	-	-
1374043_at	Gramd3	GRAM domain containing 3	307288	Rn.53932	AI317841	6.35	7.17	7.47	7.08	7.78	7.34	1.32	up	3.64E-01	8.95E-01	-	-
1384173_at	Skap1	src kinase associated phosphoprotein 1	286975	Rn.35285	BI290909	2.40	2.39	2.40	3.50	2.40	2.50	1.32	up	3.16E-01	8.95E-01	-	-
1368619_at	Ddx25	DEAD (Asp-Glu-Ala-Asp) box polypeptide 25	58856	Rn.205263	NM_031630	3.20	2.66	2.56	3.73	2.51	3.38	1.32	up	3.88E-01	8.95E-01	-	-
1391485_at	---	---	---	---	BF290955	5.33	5.89	5.03	6.87	6.38	4.21	1.32	up	6.64E-01	8.99E-01	-	-
1371644_at	Twf1	twinfilin, actin-binding protein, homolog 1 (Drosophila)	315265	Rn.162971	BF283086	9.92	10.30	10.20	9.39	9.91	9.92	1.32	down	1.30E-01	8.95E-01	-	-
1379807_at	---	---	---	Rn.165487	BE109195	4.73	5.00	5.47	4.16	4.78	5.05	1.32	down	3.05E-01	8.95E-01	-	-
1387877_at	Ftcd	formiminotransferase cyclodeaminase	89833	Rn.20140	BE096729	7.55	9.08	8.83	7.96	8.40	7.89	1.32	down	4.69E-01	8.95E-01	-	-
1370253_at	Rpl22	ribosomal protein L22	81768	Rn.21738	AI228150	11.74	11.49	11.36	11.81	11.90	12.09	1.32	up	4.45E-02	8.95E-01	-	-
1376877_at	Cdcp1	CUB domain containing protein 1	301082	Rn.7729	AA893164	2.33	2.32	3.62	2.32	2.33	2.42	1.32	down	4.05E-01	8.95E-01	-	-
1388713_at	Thtpa	thiamine triphosphatase	305889	Rn.163276	AW919094	5.96	6.26	6.10	6.49	5.92	7.12	1.32	up	3.28E-01	8.95E-01	-	-
1379901_at	Tbc1d17	TBC1 domain family, member 17	292886	Rn.203954	BG375857	4.62	4.73	3.80	4.96	4.88	4.50	1.32	up	2.84E-01	8.95E-01	-	-
1388136_at	Timm9	translocase of inner mitochondrial membrane 9 homolog (yeast)	171139	Rn.8459	BF282660	6.10	5.99	6.05	6.37	6.72	6.26	1.32	up	4.81E-02	8.95E-01	-	-
1376668_at	Ttc39a	tetratricopeptide repeat domain 39A	298366	Rn.24241	BM388328	4.82	3.69	5.02	4.84	3.66	3.82	1.32	down	5.10E-01	8.95E-01	-	-
1379354_at	Ext2	exostosin (multiple) 2	310803	Rn.6718	AA851239	2.28	2.79	2.30	2.28	3.98	2.31	1.32	up	5.30E-01	8.95E-01	-	-
1380185_at	RGD1564541	similar to hypothetical protein FLJ22965	313433	Rn.198467	BI303290	4.91	4.64	5.03	5.00	5.30	5.49	1.32	up	9.27E-02	8.95E-01	-	-
1397652_at	---	---	---	Rn.50044	BE108399	5.62	5.68	4.64	5.00	6.29	5.85	1.32	up	4.73E-01	8.95E-01	-	-
1371606_at	Wdtc1	WD and tetratricopeptide repeats 1	313020	Rn.16646	AA819633	5.87	6.85	6.34	6.83	6.59	6.83	1.32	up	2.45E-01	8.95E-01	-	-
1375779_at	---	---	---	Rn.201436	BI296535	4.37	4.17	3.37	4.68	2.74	3.28	1.32	down	5.73E-01	8.95E-01	-	-
1367966_at	pp3 /// LOC67876	dipeptidylpeptidase 3 /// similar to Dipeptidyl-peptidase 3 (Dipeptidyl-peptidas	114591 /// 678760	Rn.10902	NM_053748	7.78	7.60	8.24	7.37	7.57	7.47	1.32	down	1.13E-01	8.95E-01	-	-
1398960_at	LOC316484 /// LO	chaperonin containing Tcp1, subunit 6A (zeta 1) /// similar to chaperonin subu	20 /// 316484 /// 68	Rn.33807	AI172328	8.39	8.41	8.98	7.97	8.55	8.06	1.32	down	2.04E-01	8.95E-01	-	-
1387636_a_at	Tmem14c	transmembrane protein 14C	171432	Rn.145406	NM_134395	5.44	6.65	6.25	6.75	6.31	6.48	1.32	up	3.49E-01	8.95E-01	-	-
1393237_at	Eif2s3x	eukaryotic translation initiation factor 2, subunit 3, structural gene X-linked	299027	Rn.220237	AI577833	7.04	6.84	7.93	6.57	6.95	7.10	1.32	down	3.38E-01	8.95E-01	-	-
1373256_at	Chd3	Chromodomain helicase DNA binding protein 3	303241	Rn.204523	BM391119	3.99	5.12	4.79	5.01	5.13	4.96	1.32	up	3.01E-01	8.95E-01	-	-
1374392_at	---	---	---	Rn.219089	BE113385	5.96	6.95	7.18	6.41	7.56	7.33	1.32	up	4.78E-01	8.95E-01	-	-
1372228_at	Asmtl	acetylserotonin O-methyltransferase-like	288527	Rn.8135	BF420745	4.56	4.75	4.56	4.81	5.11	5.16	1.32	up	3.32E-02	8.95E-01	-	-
1383778_at	---	---	---	Rn.24348	AW917920	4.39	3.49	3.84	3.34	3.30	3.88	1.32	down	2.81E-01	8.95E-01	-	-
1374415_at	Polr3e	polymerase (RNA) III (DNA directed) polypeptide E (80kD)	361640	Rn.11830	BF416982	3.33	3.18	2.29	2.90	3.18	3.92	1.32	up	4.19E-01	8.95E-01	-	-
1373201_at	Dbt	dihydrolipoamide branched chain transacylase E2	29611	Rn.198610	AI412898	5.45	6.07	6.08	5.81	6.14	6.85	1.32	up	3.44E-01	8.95E-01	-	-
1367801_at	Ece1	endothelin converting enzyme 1	94204	Rn.7000	NM_053596	3.31	3.95	3.73	3.73	4.21	4.26	1.32	up	1.88E-01	8.95E-01	-	-
1383303_at	Acsm3	acyl-CoA synthetase medium-chain family member 3	24763	Rn.88644	BI282211	9.98	9.14	10.83	9.89	9.71	9.15	1.32	down	4.97E-01	8.95E-01	-	-
1380766_a_at	RGD1563510	similar to RIKEN cDNA 8430427H17 gene	362240	Rn.162697	BF386689	2.75	2.75	2.57	4.00	2.77	2.51	1.32	up	4.35E-01	8.95E-01	-	-
1393832_at	Rbm43	RNA binding motif protein 43	311020	Rn.117592	AI136337	2.54	3.11	5.40	3.27	3.33	3.24	1.32	down	6.71E-01	9.01E-01	-	-
1372521_at	Rnd2	Rho family GTPase 2	303553	Rn.22162	AI136709	3.90	3.90	2.71	3.46	3.28	4.97	1.32	up	5.81E-01	8.95E-01	-	-
1371662_at	Kars	lysyl-tRNA synthetase	292028	Rn.46593	AA892250	6.28	7.25	6.39	7.06	6.83	7.23	1.32	up	2.89E-01	8.95E-01	-	-
1381969_at	Rbpj	recombination signal binding protein for immunoglobulin kappa J region	679028	Rn.58803	AA998296	5.06	4.41	6.46	4.24	5.04	5.46	1.32	down	5.99E-01	8.95E-01	-	-
1372393_at	Fbxo18	F-box only protein 18

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicats)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1373885_at	Cbx5	chromobox homolog 5 (HP1 alpha homolog, Drosophila)	300266	Rn.101856	BF398015	7.18	6.76	7.75	6.62	6.88	6.99	1.32	down	2.66E-01	8.95E-01	-	-
1394737_at	RGD1311345	similar to CG9752-PA	361201	Rn.53930	BE108874	8.81	9.06	8.65	8.58	8.33	8.42	1.32	down	4.64E-02	8.95E-01	-	-
1389803_at	---	---	---	Rn.47082	BF415514	6.42	5.68	5.26	5.72	6.60	6.23	1.32	up	4.02E-01	8.95E-01	-	-
1382151_at	Trub1	TruB pseudouridine (psi) synthase homolog 1 (E. coli)	361775	Rn.24324	AI145625	4.17	2.69	2.66	2.67	2.66	3.01	1.32	down	4.81E-01	8.95E-01	-	-
1387921_at	Zc3h14	zinc finger CCCH type containing 14	192359	Rn.98359	AB032932	6.59	7.21	7.40	6.92	5.99	7.10	1.32	down	4.01E-01	8.95E-01	-	-
1376470_at	Fnbp4	formin binding protein 4	311183	Rn.66946	BG372703	3.74	2.48	2.53	2.49	2.51	2.57	1.32	down	3.91E-01	8.95E-01	-	-
1388446_at	---	---	---	Rn.98368	BF397834	6.39	5.97	6.25	6.00	6.92	6.88	1.32	up	2.90E-01	8.95E-01	-	-
1396663_at	---	---	---	Rn.212286	BI300284	2.52	2.50	2.59	2.83	3.47	2.49	1.32	up	2.38E-01	8.95E-01	-	-
1376718_at	Mblac1	metallo-beta-lactamase domain containing 1	304346	Rn.38936	AI575121	5.09	4.70	4.09	4.76	4.59	5.72	1.32	up	4.35E-01	8.95E-01	-	-
1389209_at	Lmf2	lipase maturation factor 2	315218	Rn.38271	BG666095	5.59	4.02	3.93	4.39	3.53	4.42	1.32	down	5.53E-01	8.95E-01	-	-
1373373_at	---	---	---	Rn.118522	BI295011	7.66	7.71	7.93	8.02	7.90	8.58	1.32	up	1.52E-01	8.95E-01	-	-
1371330_at	Rpl11	ribosomal protein L11	362631	Rn.14687	BI284252	10.11	10.40	10.38	10.56	10.55	10.98	1.32	up	8.20E-02	8.95E-01	-	-
1374157_at	Pde4b	Phosphodiesterase 4B, cAMP specific	24626	Rn.37733	AA858930	2.84	2.93	2.94	2.94	3.74	3.21	1.32	up	1.67E-01	8.95E-01	-	-
1392891_at	Pds5b	PDS5, regulator of cohesion maintenance, homolog B (S. cerevisiae)	304218	Rn.105768	AW553812	3.25	2.85	3.07	2.85	3.30	4.20	1.32	up	3.94E-01	8.95E-01	-	-
1395614_at	OC690372 /// U2af	similar to U2 (RNU2) small nuclear RNA auxiliary factor 2 isoform b /// U2 sm	308335 /// 690372	Rn.15383	AI407215	3.13	3.24	4.48	3.52	3.24	2.92	1.32	down	4.43E-01	8.95E-01	-	-
1374448_at	Reck	reversion-inducing-cysteine-rich protein with kazal motifs	313488	Rn.7365	AW523759	4.25	2.69	2.70	3.42	2.57	2.47	1.32	down	5.45E-01	8.95E-01	-	-
1368916_at	Asl	argininosuccinate lyase	59085	Rn.64591	NM_021577	6.18	6.65	8.02	7.15	7.77	7.12	1.32	up	5.39E-01	8.95E-01	-	-
1383271_at	Ccdc59	coiled-coil domain containing 59	314799	Rn.30179	BM391624	5.23	6.10	6.07	5.83	6.48	6.28	1.32	up	3.16E-01	8.95E-01	-	-
1388957_at	---	---	---	Rn.7479	AA891790	7.06	6.58	6.26	6.00	6.03	6.68	1.32	down	2.87E-01	8.95E-01	-	-
1384760_a_at	LOC683516	similar to Zinc finger X-linked protein ZXDB	683516	---	AI136549	5.30	5.08	4.85	4.40	4.29	5.35	1.32	down	3.37E-01	8.95E-01	-	-
1379303_at	Arih2	ariadne homolog 2 (Drosophila)	316005	Rn.9570	AA864841	2.81	2.80	2.81	2.80	2.81	3.99	1.32	up	3.72E-01	8.95E-01	-	-
1378446_at	---	---	---	Rn.165685	BI283723	4.59	5.49	4.60	4.58	4.37	4.54	1.32	down	2.61E-01	8.95E-01	-	-
1389482_at	Krcc1	lysine-rich coiled-coil 1	312437	Rn.7008	BI279701	6.68	6.95	6.77	7.05	6.98	7.55	1.32	up	1.17E-01	8.95E-01	-	-
1386979_at	Tpo1	developmentally regulated protein TPO1	170907	Rn.4099	NM_133395	6.52	4.89	5.15	5.59	6.40	5.76	1.32	up	5.21E-01	8.95E-01	-	-
1388664_at	Scrib	scribbled homolog (Drosophila)	362938	Rn.138068	BI282719	3.73	3.72	3.72	3.33	3.50	3.16	1.32	down	1.53E-02	8.95E-01	-	-
1376205_at	---	---	---	Rn.147025	BI286851	3.33	3.44	2.47	3.78	3.33	3.32	1.32	up	3.12E-01	8.95E-01	-	-
1385517_at	Gtf2i	general transcription factor II i	353256	Rn.27575	AI716835	6.43	5.30	6.08	5.94	5.14	6.55	1.32	down	3.83E-01	8.95E-01	-	-
1378322_at	Atg4d	ATG4 autophagy related 4 homolog D (S. cerevisiae)	686505	Rn.202643	BM385592	7.63	7.55	8.09	8.23	8.38	7.86	1.32	up	1.60E-01	8.95E-01	-	-
1380725_at	Tapan5	tetraspanin 5	362048	Rn.98240	AW251317	5.79	6.52	5.81	6.18	6.56	6.58	1.32	up	2.22E-01	8.95E-01	-	-
1375368_at	Pgp	phosphoglycolate phosphatase	287115	Rn.4311	BF420654	4.43	4.84	5.80	4.88	4.37	4.64	1.32	down	4.13E-01	8.95E-01	-	-
1376416_at	Trappc9	trafficking protein particle complex 9	315959	Rn.155796	BI296287	4.18	3.24	3.24	2.98	3.26	3.23	1.31	down	2.91E-01	8.95E-01	-	-
1368898_at	Smad7	SMAD family member 7	81516	Rn.29980	AW521447	4.79	4.26	4.58	4.26	4.26	3.92	1.31	down	1.09E-01	8.95E-01	-	-
1374632_at	Jmjd6	jumonji domain containing 6	360665	Rn.202659	AI232697	4.70	5.13	5.10	4.88	3.97	4.91	1.31	down	3.06E-01	8.95E-01	-	-
1388143_at	Col18a1	collagen, type XVIII, alpha 1	85251	Rn.12030	BI288582	2.34	3.68	2.36	2.32	2.35	2.53	1.31	down	4.29E-01	8.95E-01	-	-
1393600_at	---	---	---	Rn.16421	AA817969	2.91	3.76	3.77	3.76	3.76	4.10	1.31	up	2.67E-01	8.95E-01	-	-
1373963_at	Hdhd3	haloacid dehalogenase-like hydrolase domain containing 3	688746	Rn.17659	BF284337	6.55	5.77	5.79	5.81	5.43	5.67	1.31	down	2.32E-01	8.95E-01	-	-
1373445_at	Nol8	nucleolar protein 8	361221	Rn.20702	BI298198	4.39	5.88	7.86	5.97	6.41	6.93	1.31	up	7.24E-01	9.13E-01	-	-
1376075_at	Psen1	presenilin 1	29192	Rn.44440	BM385544	4.78	6.87	5.84	5.11	5.78	5.42	1.31	down	5.67E-01	8.95E-01	-	-
1384293_at	Ncor1	nuclear receptor co-repressor 1	54299	Rn.24948	BE100543	6.87	7.41	6.71	8.29	6.46	7.43	1.31	up	5.27E-01	8.95E-01	-	-
1371655_at	Mpdu1	mannose-P-dolichol utilization defect 1	303244	Rn.17468	BI281806	6.98	6.62	6.77	7.53	6.78	7.25	1.31	up	1.78E-01	8.95E-01	-	-
1393330_at	---	---	---	---	AI137898	7.39	7.27	6.54	7.40	7.23	7.75	1.31	up	2.67E-01	8.95E-01	-	-
1372642_at	---	---	---	Rn.13357	BE113397	6.69	6.38	6.17	6.39	7.34	6.69	1.31	up	2.85E-01	8.95E-01	-	-
1388383_at	---	---	---	Rn.84364	AI412740	7.00	6.06	5.87	5.93	5.83	6.00	1.31	down	3.27E-01	8.95E-01	-	-
1371212_at	Nrg1	neuregulin 1	112400	Rn.37438	U02315	4.13	4.80	4.09	4.94	4.84	4.42	1.31	up	2.31E-01	8.95E-01	-	-
1388526_at	Gstz1	glutathione transferase zeta 1	683857	Rn.216913	AI199075	8.34	8.35	8.25	8.66	8.47	8.99	1.31	up	6.34E-02	8.95E-01	-	-
1372208_at	Ppp1r1b	protein phosphatase 1, regulatory (inhibitor) subunit 1B	360616	Rn.70366	AA942959	6.34	6.35	5.90	6.25	6.37	7.16	1.31	up	2.91E-01	8.95E-01	-	-
1392942_at	RGD1563325	similar to hypothetical protein MGC17943	362857	Rn.19351	BM383823	5.69	4.11	5.00	4.82	3.65	5.14	1.31	down	5.73E-01	8.95E-01	-	-
1368437_at	Car4	carbonic anhydrase 4	29242	Rn.51389	NM_019174	5.42	5.30	7.35	7.86	7.24	6.16	1.31	up	6.68E-01	9.00E-01	-	-
1390850_at	Adfp	Adipose differentiation related protein	298199	Rn.101967	AA874941	10.03	9.44	8.69	8.98	8.76	9.24	1.31	down	3.93E-01	8.95E-01	-	-
1371470_at	Adh4 /// Adh5	alcohol dehydrogenase 4 (class II), pi polypeptide /// alcohol dehydrogenase	100145871 /// 29642	Rn.98159	AI411895	8.70	9.17	8.14	9.04	8.67	9.48	1.31	up	3.58E-01	8.95E-01	-	-
1377644_at	RGD1308706	similar to RIKEN cDNA 4921524J17	291925	Rn.12969	BF284809	6.81	6.51	7.93	6.62	6.38	7.09	1.31	down	4.57E-01	8.95E-01	-	-
1395427_at	---	---	---	Rn.2860	AW918981	6.34	6.02	5.58	6.79	6.25	6.07	1.31	up	2.68E-01	8.95E-01	-	-
1383170_at	---	---	---	Rn.7599	AW143788	5.64	6.32	3.86	6.39	5.34	5.27	1.31	up	6.56E-01	8.98E-01	-	-
1374191_at	Rhbdf1	rhomboid 5 homolog 1 (Drosophila)	303008	Rn.6381	AA956764	2.78	2.63	2.64	3.30	3.15	2.79	1.31	up	7.03E-02	8.95E-01	-	-
1372213_at	LOC500300	similar to hypothetical protein MGC6835	500300	Rn.22047	BM390487	2.50	3.78	2.45	2.54	2.50	2.50	1.31	down	4.17E-01	8.95E-01	-	-
1387265_at	Dgkg	diacylglycerol kinase, gamma	25666	Rn.10544	NM_013126	3.45	2.47	2.51	2.47	2.46	2.31	1.31	down	2.92E-01	8.95E-01	-	-
1397545_at	---	---	---	Rn.92948	BM386640	2.46	2.87	2.80	3.10	2.77	3.44	1.31	up	1.65E-01	8.95E-01	-	-
1387126_at	Atp2c1	ATPase, Ca++ transporting, type 2C, member 1	170699	Rn.5805	NM_131907	3.75	3.97	3.75	4.42	4.42	3.81	1.31	up	1.40E-01	8.95E-01	-	-
1386877_at	Ap2s1	adaptor-related protein complex 2, sigma 1 subunit	65046	Rn.37866	NM_022952	6.65	7.49	6.75	6.51	6.66	6.54	1.31	down	2.16E-01	8.95E-01	-	-
1392951_at	---	---	---	Rn.164642	AW521231	7.34	7.19	8.56	7.08	7.24	7.59	1.31	down	4.40E-01	8.95E-01	-	-
1384116_at	rCG_21373	similar to vacuolar protein sorting 37D	687208	Rn.217242	AA924216	5.60	4.49	4.43	4.57	4.50	4.27	1.31	down	3.74E-01	8.95E-01	-	-
1372888_at	Ube4a	ubiquitination factor E4A	315908	Rn.102204	BI294856	6.88	6.80	7.43	6.34	6.78	6.81	1.31	down	1.92E-01	8.95E-01	-	-
1371487_at	Sh3bgrl3	SH3 domain binding glutamic acid-rich protein-like 3	298544	Rn.18564	BG666075	6.76	5.37	4.20	6.16	4.85	4.14	1.31	down	6.99E-01	9.07E-01	-	-
1393848_at	Rrm2	ribonucleotide reductase M2	362720	Rn.144946	AA957260	2.50	3.57	2.58	2.50	2.51	2.47	1.31	down	3.14E-01	8.95E-01	-	-
1386571_at	RGD1562626	Similar to adaptor molecule SRCASM	287622	Rn.200155	AF567145	4.25	4.80	5.22	4.48	4.23	4.38	1.31	down	2.46E-01	8.95E-01	-	-
1397685_at	---	---	---	Rn.52800	BF553180	2.56	2.63	2.64	2.63	3.80	2.57	1.31	up	3.83E-01	8.95E-01	-	-
1373709_at	Fam149b1	family with sequence similarity 149, member B1	289900	Rn.28239	BI281706	5.20	6.03	5.21	5.51	6.20	5.91	1.31	up	3.11E-01	8.95E-01	-	-
1388625_at	Ints10	integrator complex subunit 10	290679	Rn.23365	BM390149	3.68	4.56	4.57	4.65	4.55	4.79	1.31	up	2.66E-01	8.95E-01	-	-
1393407_at	Fbxw2	F-box and WD repeat domain containing 2	311881	Rn.103250	AW915859	3.54	4.00	2.83	2.83	3.53	3.53	1.31	down	3.95E-01	8.95E-01	-	-
1384538_at	Msto1	misato homolog 1 (Drosophila)	295237	Rn.26620	BE115544	3.69	4.50	3.71	4.53	4.38	4.16	1.31	up	2.43E-01	8.95E-01	-	-
1394708_at	Gabpb1l	GA binding protein transcription factor, beta subunit 1-like	364738	Rn.61149	BF288532	3.81	2.86	2.84	3.10	2.39	2.83	1.31	down	3.60E-01	8.95E-01	-	-
1383845_at	---	---	---	---	AI059929	5.60	5.73	6.26	6.08	6.64	6.05	1.31	up	2.32E-01	8.95E-01	-	-
1389657_at	Znf524	zinc finger protein 524	365179	Rn.24795	AI175762	3.52	4.58	4.98	3.87	4.62	3.42	1.31	down	5.21E-01	8.95E-01	-	-
1383150_at	---	---	---	---	BE114751	4.37	4.54	7.34	4.39	5.73	4.95	1.31	down	7.24E-01	9.13E-01	-	-
1390829_at	---	---	---	Rn.170003	BG374590	5.89	5.54	4.66	4.62	4.99	5.31	1.31	down	3.99E-01	8.95E-01	-	-
1387704_at	Esr1	estrogen receptor 1	24890	Rn.10595	NM_012689	7.02	7.21	6.95	7.08	5.89	7.03	1.31	down	3.78E-01	8.95E-01	-	-
1397788_at	---	---	---	---	AW521711	6.71	6.67	5.34	7.20	6.63	6.07	1.31	up	5.17E-01	8.95E-01	-	-
1368173_at	Nol5	nucleolar protein 5	60373	Rn.43930	NM_021754	5.91	5.96	6.77	6.85	5.76	7.21	1.31	up	4.90E-01	8.95E-01	-	-
1380460_at	RGD1311267	similar to RIKEN cDNA 4931426K16 gene	311429	Rn.19612	AI602203	2.30	3.46	2.30	2.29	2.30	2.30	1.31	down	3.69E-01	8.95E-01	-	-
1375884_at	MGC105560	similar to Hypothetical protein BC014729	500941	Rn.120559	AW520742	6.50	6.34	6.17	5.86	5.76	6.21	1.31	down	7.89E-02	8.95E-01	-	-
1395875_at	Tkt37	tetratricopeptide repeat domain 37	294595	Rn.49948	BG379050	5.95	5.80	4.56	6.26	5.64	5.59	1.31	up	4.70E-01	8.95E-01	-	-
1389600_at	/// LOC685563 ///	hypothetical protein LOC363306 /// similar to Discs large homolog 5 (Placenta	75 /// 685563 /// 68	Rn.220859	AW524433	3.66	3.03	2.96	2.74	2.84	2.89	1.31	down	1.61E-01	8.95E-01	-	-
1399166_a_at	Bcl7b	B-cell CLL/lymphoma 7B	368001	Rn.37635	BF420294	5.97	5.51	5.37	5.73	6.24	6.05	1.31	up	1.71E-01	8.95E-01	-	-
1392504_at	RGD1306613	similar to RIKEN cDNA 1600012F09	306994	Rn.8045	BI297184	4.64	5.51	4.60	4.35	5.90	5.67	1.31	up	5.27E-01	8.95E-01	-	-
1394904_at	Necap1	NECAP endocytosis associated 1	312694	Rn.58356	BF392629	3.24	3.13	2.96	3.36	3.43	3.73	1.31	up	4.76E-02	8.95E-01	-	-
1393134_at	Sephs1	selenophosphate synthetase 1	291314	Rn.100803	BG375377	4.28	4.38	3.14	4.30	4.37	4.32	1.31	up	3.82E-01	8.95E-01	-	-
1368070_at	Stx8	syntaxin 8	59074	Rn.20291	NM_031656	6.96	5.71	6.41	6.84	6.60	6.83	1.31	up	3.50E-01	8.95E-01	-	-
1377310_at	---	---	---	Rn.22341	BG374304	2.84	3.71	3.46	3.34	3.82	4.02	1.31	up	2.99E-01	8.95E-01	-	-
1381402_at	---	---	---	Rn.33502	BE108294	3.21	3.56	3.21	4.26	3.49	3.40	1.31	up	2.58E-01	8.95E-01	-	-
1368936_at	Txnl1	thioredoxin-like 1	140922	Rn.40430	NM_080887	7.68	8.14	8.26	8.22	8.77	8.26	1.31	up	1.95E-01	8.95E-01	-	-
1386958_at	Txnrd1	thioredoxin reductase 1	58819	Rn.67581	NM_031614	3.46	4.03	2.94	3.39	3.54	4.67	1.31	up	4.86E-01	8.95E-01	-	-
1392692_at	---	---	---	Rn.170398	BE107050	6.89	6.88	7.10	6.30	6.21	7.18	1.31	down	2.84E-01	8.95E-01	-	-
1388994_at	Fzd6	frizzled homolog 6 (Drosophila)	282581	Rn.2740	AW917849	3.50	3.49	3.18	3.50	4.16	3.69	1.31	up	1.55E-01	8.95E-01	-	-
1383384_at	LOC682988	similar to mediator of RNA polymerase II transcription, subunit 18 homolog	682988	Rn.217365	BG381725	4.06	3.25	4.47	3.26	3.73	3.61	1.31	down	3.68E-01	8.95E-01	-	-
1393558_at	Itga6	integrin, alpha 6	114517	Rn.161799	AI137931	3.94	5.30	4.82	4.23	3.88	4.76	1.31	down	4.56E-01	8.95E-01	-	-
1377079_a_at	Ppox	protoporphyrinogen oxidase	289219	Rn.24738	BF386283	6.94	6.83	6.24	6.33	6.39	6.11	1.31	down	1.70E-01	8.95E-01	-	-
1382037_at	Crim1	cysteine rich transmembrane BMP regulator 1 (chordin like)	298744	Rn.54364	AI600057	6.40	6.55	4.93	6.83	5.81	6.42	1.31	up	5.47E-01	8.95E-01	-	-
1383669_at	---	---	---	---	AI556424	2.41	3.57	2.45	3.68	3.10	2.81	1.31	up	4.41E-01	8.95E-01	-	-
1380632_at	Tmem55a	transmembrane protein 55A	362490	Rn.16907	BF547901	3.78	3.77	3.59	4.05	3.55	4.72	1.31	up	3.19E-01	8.95E-01	-	-
1384250_a_at	---	---	---	Rn.23945	AA818098	3.96	3.87	3.41	4.83	3.71	3.88	1.31	up	3.66E-01	8.95E-01	-	-
1383753_at	---	---	---	Rn.204988	BF401106	4.23	4.97	4.74	3.85	4.29	4.62	1.31	down	2.80E-01	8.95E-01	-	-
1376724_at	---	---	---	Rn.15423	AI170671	7.03	6.33	6.20	5.72	6.38	6.30	1.31	down	3.04E-01	8.95E-01	-	-
1370175_a_at	Zfp384	zinc finger protein 384	171018	Rn.9637	AI177799	3.97	4.25	4.11	4.01	3.23	3.92	1.31	down	2.04E-01	8.95E-01	-	-
1375957_at	---	---	---	Rn.16340	AW434654	3.45	2.68	2.92	3.47	3.93	2.84	1.31	up	3.72E-01	8.95E-01	-	-
1378936_at	Cstf2	cleavage stimulation factor, 3' pre-RNA subunit 2	683927	Rn.170541	AW533986	3.99	4.21	4.34	3.99	3.07	4.32	1.31	down	3.70E-01	8.95E-01	-	-
1391599_at	---	---	---	Rn.163701	AA875010	6.04	6.08	5.04	6.08	6.84	5.61	1.31	up	4.35E-01	8.95E-01	-	-
1396885_at	Smtn	smoothelin	289734	Rn.40766	BF543321	2.61	2.68	3.66	2.59	2.60	2.59	1.31	down	3.12E-01	8.95E-01	-	-
1371297_at	Rpl7a	ribosomal protein L7a	296596	Rn.144857	BI281697	10.57	10.83	10.31	10.86	10.85	11.16	1.31	up	9.89E-02	8.95E-01	-	-
1380713_at	---	---	---	Rn.161163	BG376879	2.64	3.17	3.12	3.10	3.12	3.87	1.31	up	2.69E-01	8.95E-01	-	-
1390631_at	---	---	---	Rn.66300	BE107619	3.03	3.03	2.33	3.35	3.46	2.75	1.31	up	2.92E-01	8.95E-01	-	-
1382300_at	Tnpo3	transportin 3	296954	Rn.164462	BF284236	2.87	3.52	3.11	4.72	2.82	3.13	1.31	up	5.62E-01	8.95E-01	-	-
1392490_at	---	---	---	Rn.14832	BM390676	6.65	7.55	7.54	7.71	7.42	7.79	1.31	up	2.86E-01	8.95E-01	-	-
1377914_at	Srrm1	serine/arginine repetitive matrix 1	313820	Rn.39266	AI059437	7.21	7.36	6.79	7.41	7.03	7.08	1.31	up	4.89E-01	8.95E-01	-	-
1373590_at	Stom	stomatin	296655	Rn.16958	BI295949	8.53	8.87	8.96	8.18	8.17	8.84	1.31	down	2.06E-01	8.95E-01	-	-
1391811_at	---	---	---	Rn.203417	AI556437	3.67	5.36	3.31	4.08	4.51	4.93	1.31	up	5.96E-01	8.95E-01	-	-
1390700_s_at	Hdac10	histone deacetylase 10	362981	Rn.107028	BG378690	2.31	2.34	2.54	2.32	3.73	2.31	1.31	up	4.58E-01	8.95E-01	-	-
1379797_at	---	---	---	Rn.203912	AI229704	3.21	3.64	2.59	2.74	2.94	2.60	1.31	down	2.91E-01	8.95E-01	-	-
1372614_at	RGD1311849	similar to mKIAA1797 protein	313346	Rn.17957	BF390044	4.19	4.16	2.44	2.94	3.08	3.59	1.31	down	5.58E-01	8.95E-01	-	-
1379335_at	Paip1	poly(A) binding protein interacting protein 1	365684	Rn.222035	AI639045	6.40	6.51	5.49	7.14	6.18	6.26	1.31	up	4.31E-01	8.95E-01	-	-
1394039_at	Klf5	Kruppel-like factor 5	84410	Rn.8952	BM382886	3.17	3.23	3.22	2.59	4.94	3.26	1.31	up	6.07E-01	8.95E-01	-	-
1396286_at	Ppm1f	Protein phosphatase 1F (PP2C domain containing)	287931	Rn.91922	AI237137	2.44	2.43	3.59	2.44	2.45	2.41	1.31	down	3.70E-01	8.95E-01	-	-
1392409_at	---	---	---	Rn.23173	AA957756	2.97	2.95	2.99	3.97	2.99	3.12	1.31	up	2.73E-01	8.95E-01	-	-
1370178_at	Cacnb2	calcium channel, voltage-dependent, beta 2 subunit	116600	Rn.10739	BG373973	3.49	3.48	2.26	3.22	3.51	3.68	1.31	up	4.16E-01	8.95E-01	-	-
1390356_at	---	---	---	Rn.15945	AW535401	8.60	8.42	8.33	7.47	8.16	8.54	1.31	down	2.94E-01	8.95E-01	-	-
1384307_at	---	---	---	Rn.145261	AI073243	2.42	2.41	2.46	2.89	2.46	3.10	1.31	up	1.11E-01	8.95E-01	-	-
1373027_at	Mll4	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila);	26955	Rn.58	AA944375	6.30	6.85	5.83	6.57	6.76	6.82	1.31	up	2.67E-01	8.95E-01	-	-
1369656_at	Pcyt1a	phosphate cytidylyltransferase 1, choline, alpha	140544	Rn.81192	M36071	5.26	5.68	5.53	5.92	4.64	4.74	1.31	down	4.14E-01	8.95E-01	-	-
1391057_at	Dnajc30	DnaJ (Hsp40) homolog, subfamily C, member 30	368190	Rn.29127	BE100195	2.49	4.45	2.40	2.49	2.43	3.26	1.31	down	6.17E-01	8.95E-01	-	-
1380515_at	Bbs7	Bardet-Biedl syndrome 7	361930	Rn.28442	AI170730	6.03	5.27	5.59	5.11	4.71	5.90	1.31	down	4.00E-01	8.95E-01	-	-
1383209_at	Fam116a	family with sequence similarity 116, member A	306229	Rn.4177	AW916721	3.73	3.87	4.15	3.87	4.83	4.21	1.31	up	2.72E-01	8.95E-01	-	-
1367688_at	Scamp4	secretory carrier membrane protein 4	65170	Rn.7309	NM_031725	2.37	2.68	2.41	2.96	2.42	3.24	1.31	up	2.12E-01	8.95E-01	-	-
1373038_at	Mllt10	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila);	361285	Rn.3620	AI145989	4.31	5.43	4.42	4.87	4.89	5.56	1.31	up	4.08E-01	8.95E-01	-	-
1390776_at	Irx3	iroquois homeobox 3	307721	Rn.22133	AI030203	8.16	8.33	7.77	8.81	8.30	8.32	1.31	up	1.71E-01	8.95E-01	-	-
1368672_at	Arg2	arginase type II	29215	Rn.11055	NM_019168	6.01	6.98	6.38	5.98	5.77	6.45	1.31	down	3.24E-01	8.95E-01	-	-
1385568_at	---	---	---	Rn.206418	AW526991	2.34	2.33	3.50	2.33	2.34	2.32	1.31	down	3.72E-01	8.95E-01	-	-
1367541_at	Mettl5	methyltransferase like 5	502632	Rn.117034	BE113965	7.01	7.16	7.15	7.26	7.36	7.86	1.31	up	1.12E-01	8.95E-01	-	-
1382215_at	---	---	---	---	AA875331	3.80	4.51	5.08	3.69	4.45	4.08	1.31	down	4.17E-01	8.95E-01	-	-
1371952_at	Rbm18	RNA binding motif protein 18	311902	Rn.2745	AI010954	4.93	5.08	5.49	4.71	4.78	4.85	1.31	down	8.74E-02	8.95E-01	-	-
1380158_at	---	---	---	Rn.1207	BF284973	5.45	6.45	6.58	6.32	6.69	6.64	1.31	up	3.58E-01	8.95E-01	-	-
1397516_at	Alg2	asparagine-linked glycosylation 2, alpha-1,3-mannosyltransferase homolog (S	313231	Rn.98222	AI412698	2.71	2.33	2.34	2.31	2.55	3.69	1.

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1375251_at	Ctdspl	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small pho	301056	Rn.37030	AI179323	3.55	2.62	2.94	2.60	5.01	2.67	1.31	up	6.69E-01	9.00E-01	-	-
1398920_at	LOC100294508	dyslexia susceptibility 2-like	100294508	---	AI228651	6.97	6.94	5.45	6.96	6.72	6.84	1.31	up	4.89E-01	8.95E-01	-	-
1382423_at	---	---	---	Rn.20338	AW920944	3.73	3.93	5.16	3.67	3.82	4.16	1.31	down	4.56E-01	8.95E-01	-	-
1387876_at	Stat5b	signal transducer and activator of transcription 5B	25126	Rn.54486	AI177626	3.96	2.84	2.79	2.78	2.62	3.03	1.31	down	3.89E-01	8.95E-01	-	-
1388326_at	Ndufs8	NADH dehydrogenase (ubiquinone) Fe-S protein 8	293652	Rn.3373	AA799479	7.71	8.93	8.59	8.47	9.15	8.77	1.31	up	4.06E-01	8.95E-01	-	-
1374229_at	Sppl2b	signal peptide peptidase-like 2B	362828	Rn.18529	BF411135	4.27	3.47	3.82	3.27	3.64	3.50	1.31	down	2.06E-01	8.95E-01	-	-
1399162_a_at	Ddb1	damage-specific DNA binding protein 1	64470	---	AJ277077	9.16	8.10	8.48	8.29	7.93	8.35	1.31	down	3.15E-01	8.95E-01	-	-
1383789_at	---	---	---	Rn.18412	BE118099	2.36	2.36	2.36	3.03	2.49	2.72	1.31	up	6.64E-02	8.95E-01	-	-
1387996_a_at	Hps1	Hermansky-Pudlak syndrome 1 homolog (human)	114638	Rn.17691	AF333326	2.94	3.51	3.14	2.93	2.58	2.92	1.31	down	1.31E-01	8.95E-01	-	-
1382681_at	---	---	---	Rn.164611	AA893948	3.71	2.58	2.67	2.59	2.66	2.55	1.31	down	3.48E-01	8.95E-01	-	-
1387008_at	Sfxn3	sideroflexin 3	65042	Rn.37545	NM_022948	4.51	2.61	2.63	3.25	3.85	3.80	1.31	up	5.91E-01	8.95E-01	-	-
1374798_at	---	---	---	Rn.203321	AA924151	4.69	4.65	5.26	5.30	5.20	5.24	1.31	up	1.25E-01	8.95E-01	-	-
1388151_at	Coro7	coronin 7	192276	Rn.13808	AI008369	4.62	4.56	4.43	4.23	3.83	4.39	1.31	down	9.46E-02	8.95E-01	-	-
1388816_at	Dlg1	Discs, large homolog 1 (Drosophila)	25252	Rn.89331	AI413080	7.25	6.68	7.02	6.67	6.39	6.73	1.31	down	1.21E-01	8.95E-01	-	-
1377363_at	Rab25	RAB25, member RAS oncogene family	310632	Rn.7929	AA945861	3.64	2.53	2.48	2.55	2.44	2.52	1.31	down	3.69E-01	8.95E-01	-	-
1398912_at	mrpl9	mitochondrial ribosomal protein L9	310653	Rn.763	BM389259	5.89	5.68	5.45	6.32	5.55	6.30	1.31	up	2.44E-01	8.95E-01	-	-
1379349_a_at	Rab5	RAB, member RAS oncogene family-like 5	288585	Rn.36074	AI406710	5.42	5.12	4.83	5.74	5.20	5.59	1.31	up	1.76E-01	8.95E-01	-	-
1368190_at	Ren	renin	24715	Rn.9831	J02941	2.35	2.51	2.42	3.63	2.42	2.39	1.31	up	4.03E-01	8.95E-01	-	-
1382892_a_at	Cyhr1	cysteine and histidine rich 1	315097	Rn.141005	AI171375	3.65	4.03	3.94	3.82	4.52	4.44	1.31	up	1.94E-01	8.95E-01	-	-
1379677_at	Tnfsf13	tumor necrosis factor (ligand) superfamily, member 13	287437	Rn.19955	BF286267	4.38	4.32	3.70	3.72	3.82	3.70	1.31	down	1.58E-01	8.95E-01	-	-
1388875_at	Cxxc1	CXXC finger 1 (PHD domain)	291440	Rn.86349	AI410353	3.97	4.18	3.62	3.02	4.22	3.38	1.31	down	3.83E-01	8.95E-01	-	-
1375552_at	Srp72	signal recognition particle 72	498351	Rn.2930	BG372976	6.15	7.42	7.30	7.27	7.48	7.27	1.31	up	4.04E-01	8.95E-01	-	-
1389586_at	---	---	---	Rn.220240	BE107169	5.17	4.54	5.42	4.73	4.67	4.57	1.31	down	2.25E-01	8.95E-01	-	-
1398877_at	Stip1	stress-induced phosphoprotein 1	192277	Rn.22614	BI283691	8.50	7.79	8.45	7.93	10.84	7.12	1.31	up	7.55E-01	9.20E-01	-	-
1394591_at	Zfp207	zinc finger protein 207	303763	Rn.163156	AI411280	7.67	7.94	8.00	7.34	7.63	7.48	1.31	down	4.24E-02	8.95E-01	-	-
1379405_at	---	---	---	---	AI235642	2.83	2.94	3.08	3.35	3.07	3.58	1.31	up	7.72E-02	8.95E-01	-	-
1373235_at	Syap1	Synapse associated protein 1	302678	Rn.63210	AA892370	5.35	5.60	5.11	5.32	6.09	5.81	1.31	up	2.18E-01	8.95E-01	-	-
1377089_a_at	Tspan5	tetraspanin 5	362048	Rn.98240	BG381571	4.77	4.60	4.81	5.70	4.72	4.92	1.31	up	2.75E-01	8.95E-01	-	-
1376150_at	---	---	---	Rn.23918	BI282755	2.73	3.28	3.65	2.86	2.93	2.73	1.31	down	2.34E-01	8.95E-01	-	-
1391470_at	Ipo5	Importin 5	306182	Rn.79893	AI407085	4.91	5.10	3.28	3.57	5.06	5.81	1.31	up	6.83E-01	9.03E-01	-	-
1383293_at	---	---	---	Rn.19057	BG669441	7.86	7.41	8.08	8.54	7.85	8.11	1.31	up	2.46E-01	8.95E-01	-	-
1389456_at	---	---	---	---	BI296591	3.69	3.98	3.95	3.93	4.92	3.93	1.31	up	3.25E-01	8.95E-01	-	-
1367710_at	Psme2	proteasome (prosome, macropain) activator subunit 2	29614	Rn.127779	NM_017257	7.72	8.33	7.37	8.10	7.77	8.01	1.31	up	3.85E-01	8.95E-01	-	-
1378248_at	Apbb2	amyloid beta (A4) precursor protein-binding, family B, member 2	305338	Rn.24283	BE110453	5.90	5.70	4.51	5.60	5.41	6.25	1.31	up	4.87E-01	8.95E-01	-	-
1390436_at	---	---	---	Rn.165241	BI300794	5.86	6.17	7.54	5.61	6.43	6.37	1.31	down	5.42E-01	8.95E-01	-	-
1391500_at	---	---	---	Rn.19393	BF282889	8.97	9.05	8.94	8.66	8.25	8.89	1.31	down	1.10E-01	8.95E-01	-	-
1384268_at	Ccnyl1	cyclin Y-like 1	316452	Rn.11723	AW435305	2.79	5.21	3.60	3.97	4.01	4.77	1.31	up	6.38E-01	8.95E-01	-	-
1393183_at	Stard5	StAR-related lipid transfer (START) domain containing 5	502348	Rn.62294	H33503	3.75	3.05	4.13	3.75	3.76	4.58	1.31	up	4.10E-01	8.95E-01	-	-
1383869_at	---	---	---	Rn.20510	AI071350	2.46	2.98	2.49	2.99	3.03	3.07	1.31	up	8.68E-02	8.95E-01	-	-
1367836_at	Cpt1a	carnitine palmitoyltransferase 1a, liver	25757	Rn.2856	NM_031559	6.58	7.06	6.44	7.20	6.77	7.26	1.31	up	1.92E-01	8.95E-01	-	-
1387669_a_at	Ephx1	epoxide hydrolase 1, microsomal	25315	Rn.3602	NM_012844	6.67	7.13	6.72	7.63	6.63	7.11	1.30	down	6.04E-01	8.95E-01	-	-
1378679_at	Usp25	ubiquitin specific peptidase 25	304150	Rn.23509	BG372484	6.17	6.28	5.69	6.22	6.18	6.89	1.30	up	2.61E-01	8.95E-01	-	-
1367775_at	Amacr	alpha-methylacyl-CoA racemase	25284	Rn.2590	NM_012816	10.49	10.64	10.68	10.15	10.44	10.07	1.30	down	3.65E-02	8.95E-01	-	-
1379301_at	---	---	---	Rn.28015	BM384812	5.73	5.78	4.27	5.75	5.59	5.59	1.30	up	4.83E-01	8.95E-01	-	-
1383883_at	Klhl30	kelch-like 30 (Drosophila)	316624	Rn.21220	BG380058	2.40	2.40	2.40	3.52	2.44	1.30	up	3.54E-01	8.95E-01	-	-
1387229_at	Ppig	peptidylprolyl isomerase G	83624	Rn.10898	NM_031793	5.94	3.89	4.93	5.03	5.42	5.46	1.30	up	5.61E-01	8.95E-01	-	-
1375858_at	Tusc4	tumor suppressor candidate 4	363138	Rn.3371	BI285715	6.77	6.54	5.55	6.22	6.89	6.90	1.30	up	4.28E-01	8.95E-01	-	-
1377194_a_at	Ccdc90b	coiled-coil domain containing 90B	308620	Rn.160643	BE107471	5.62	6.08	5.81	6.30	6.29	6.06	1.30	up	6.92E-02	8.95E-01	-	-
1370216_at	Ddr1	discoidin domain receptor tyrosine kinase 1	25678	Rn.7807	L26525	2.73	2.92	2.85	3.09	2.83	3.73	1.30	up	2.34E-01	8.95E-01	-	-
1382065_at	---	---	---	Rn.40572	BM388726	6.97	7.03	6.82	7.11	7.62	7.24	1.30	up	8.06E-02	8.95E-01	-	-
1385276_a_at	Dhx58	DEXH (Asp-Glu-X-His) box polypeptide 58	303538	Rn.105654	AA818849	5.43	5.72	3.16	4.59	4.34	4.24	1.30	down	6.63E-01	8.99E-01	-	-
1392536_at	---	---	---	Rn.3287	AI136839	4.63	5.21	4.81	5.66	4.78	5.36	1.30	up	2.84E-01	8.95E-01	-	-
1375210_at	RGD1307394	Similar to hypothetical protein ET	360667	Rn.16739	AW252841	3.97	5.83	5.87	7.22	3.58	6.03	1.30	up	7.73E-01	9.26E-01	-	-
1383090_at	Mrps14	mitochondrial ribosomal protein S14	289143	Rn.67	BF548676	7.82	8.60	8.45	8.60	8.69	8.73	1.30	up	1.88E-01	8.95E-01	-	-
1386866_a_at	Rbck1	RanBP-type and C3HC4-type zinc finger containing 1	60383	Rn.37161	NM_021764	2.87	3.02	2.89	3.02	3.60	3.32	1.30	up	9.04E-02	8.95E-01	-	-
1383447_at	Etv5	ets variant 5	303828	Rn.18397	AI101323	3.47	4.61	5.49	3.68	3.82	4.92	1.30	down	6.15E-01	8.95E-01	-	-
1383278_at	Centg2	centaurin, gamma 2	316611	Rn.25493	BF558819	7.83	7.93	8.07	8.15	8.27	8.56	1.30	up	5.11E-02	8.95E-01	-	-
1397457_at	---	---	---	Rn.152500	BE106796	3.41	4.16	5.98	4.56	3.85	3.98	1.30	down	6.55E-01	8.97E-01	-	-
1385862_at	Armc9	armadillo repeat containing 9	301579	Rn.27285	BF552350	2.59	2.55	2.58	2.55	2.71	3.61	1.30	up	3.09E-01	8.95E-01	-	-
1369135_at	Syt11	synaptotagmin XI	60568	Rn.9805	NM_031667	3.74	2.43	2.35	2.58	2.45	2.34	1.30	down	4.50E-01	8.95E-01	-	-
1372501_at	Sf3b3	splicing factor 3b, subunit 3	292019	Rn.7554	BI285007	3.70	2.83	2.85	2.76	2.62	2.85	1.30	down	2.62E-01	8.95E-01	-	-
1375063_at	RGD1565166	similar to MGC45438 protein	287059	Rn.23822	BI274344	2.82	3.51	6.15	3.92	3.98	3.45	1.30	down	7.28E-01	9.13E-01	-	-
1368842_at	Tcf4	transcription factor 4	84382	Rn.23354	BG377130	6.62	7.49	6.63	6.88	7.34	7.66	1.30	up	3.55E-01	8.95E-01	-	-
1376184_at	Lynx1	Ly6/neurotoxin 1	300018	Rn.32045	BG381127	2.52	2.70	2.56	2.78	2.70	3.45	1.30	up	1.89E-01	8.95E-01	-	-
1372129_at	Tbc1d9b	TBC1 domain family, member 9B	360520	Rn.137185	BG378054	5.26	4.95	4.76	5.40	5.35	5.36	1.30	up	6.28E-02	8.95E-01	-	-
1374743_at	Inadl	InaD-like (Drosophila)	313382	Rn.129128	BE115056	4.67	4.28	3.51	4.93	3.53	5.15	1.30	up	5.65E-01	8.95E-01	-	-
1379228_at	---	---	---	Rn.199414	BF418531	4.30	4.47	4.67	3.71	4.68	3.91	1.30	down	2.93E-01	8.95E-01	-	-
1372023_at	---	---	---	Rn.7314	BI279581	8.45	7.42	7.49	7.29	7.55	7.36	1.30	down	3.28E-01	8.95E-01	-	-
1373048_at	Actr10	actin-related protein 10 homolog (S. cerevisiae)	299121	Rn.36338	AI177051	6.77	6.89	5.94	6.58	6.94	7.23	1.30	up	3.37E-01	8.95E-01	-	-
1396639_at	---	---	---	Rn.208884	BE120718	3.51	2.35	2.36	2.37	2.36	2.35	1.30	down	3.78E-01	8.95E-01	-	-
1369353_at	Erbb4	v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian)	59323	Rn.163078	NM_021687	3.96	4.89	3.07	3.99	4.15	4.93	1.30	up	5.57E-01	8.95E-01	-	-
1392484_at	rCG_20739	hypothetical protein LOC100233176	100233176	Rn.98234	AA892339	7.99	7.70	7.68	6.72	7.35	8.15	1.30	down	4.19E-01	8.95E-01	-	-
1386266_at	---	---	---	Rn.204930	AI227948	3.82	3.10	3.93	3.23	2.76	3.72	1.30	down	3.70E-01	8.95E-01	-	-
1381410_a_at	Fgd5	FYVE, RhoGEF and PH domain containing 5	362402	Rn.16775	AI555744	2.71	2.70	2.39	2.77	3.50	2.67	1.30	up	2.47E-01	8.95E-01	-	-
1367667_at	Fdps	farnesyl diphosphate synthase (farnesyl pyrophosphate synthetase, dimethyl	83791	Rn.2848	NM_031840	8.59	9.05	7.09	8.78	8.13	8.97	1.30	up	5.85E-01	8.95E-01	-	-
1380102_at	FAM50A	family with sequence similarity 50, member A	293862	Rn.106134	BM386836	7.35	7.14	7.05	7.12	7.80	7.76	1.30	up	1.87E-01	8.95E-01	-	-
1374209_at	Erlin2	ER lipid raft associated 2	290823	Rn.12619	AI010575	9.05	8.71	9.36	8.62	8.80	8.56	1.30	down	1.32E-01	8.95E-01	-	-
1388331_at	Tra1	tumor rejection antigen gp96	362662	Rn.101146	BG057543	11.49	11.73	11.62	11.98	11.66	12.36	1.30	up	1.49E-01	8.95E-01	-	-
1395869_at	---	---	---	---	BI296231	4.24	2.86	2.85	2.66	3.29	2.85	1.30	down	4.87E-01	8.95E-01	-	-
1372246_at	Ostf1	osteoclast stimulating factor 1	259275	Rn.108470	BI294750	8.30	8.69	8.85	8.02	8.45	8.23	1.30	down	1.38E-01	8.95E-01	-	-
1376599_at	Atad2	ATPase family, AAA domain containing 2	314993	Rn.6690	AW915567	5.03	5.78	6.24	5.52	5.54	4.84	1.30	down	4.17E-01	8.95E-01	-	-
1372056_at	Cmtm6	CKLF-like MARVEL transmembrane domain containing 6	314035	Rn.98431	AI406887	6.53	6.66	6.85	6.64	6.89	7.36	1.30	down	6.51E-01	8.97E-01	-	-
1395214_at	RGD1562012	RGD1562012	497962	Rn.203215	BM391078	5.21	5.01	5.05	5.27	5.58	5.57	1.30	up	3.18E-02	8.95E-01	-	-
1384073_at	Adhfe1	alcohol dehydrogenase, iron containing, 1	362474	Rn.17173	BF543577	6.38	5.99	5.19	5.34	5.74	5.74	1.30	down	3.66E-01	8.95E-01	-	-
1386855_at	---	---	---	Rn.24116	AA944136	9.84	7.68	6.21	8.46	7.84	8.57	1.30	up	7.41E-01	9.17E-01	-	-
1384500_at	BI1305604 /// Shes	similar to CG2919-PA /// sushi, nidogen and EGF-like domains 1	316638 /// 362580	Rn.23447	BI286565	6.31	2.98	2.70	3.39	4.24	3.21	1.30	down	7.67E-01	9.24E-01	-	-
1380947_at	---	---	---	Rn.154035	BE108752	2.96	2.80	3.93	2.80	2.81	2.94	1.30	down	3.46E-01	8.95E-01	-	-
1391389_at	---	---	---	---	BF412451	3.50	2.36	2.40	2.37	2.38	2.36	1.30	down	3.64E-01	8.95E-01	-	-
1389723_at	Pik3ap1	phosphoinositide-3-kinase, regulatory subunit 4, p150	363131	Rn.8917	AI172265	5.86	6.76	6.17	7.02	6.02	6.90	1.30	up	4.06E-01	8.95E-01	-	-
1393356_at	---	---	---	Rn.23945	AA818098	7.12	6.55	4.66	6.28	6.50	6.69	1.30	up	6.39E-01	8.95E-01	-	-
1383675_at	---	---	---	Rn.216740	BG371620	3.41	5.06	3.12	4.17	3.83	4.73	1.30	up	5.94E-01	8.95E-01	-	-
1382039_at	Rab2b	RAB, member of RAS oncogene family-like 2B	362987	Rn.11822	AA944201	3.85	4.17	3.37	4.13	2.32	3.79	1.30	down	5.62E-01	8.95E-01	-	-
1388909_at	Oxnad1	oxidoreductase NAD-binding domain containing 1	306270	Rn.3785	AA891742	8.36	8.07	8.47	8.10	8.10	7.56	1.30	down	1.54E-01	8.95E-01	-	-
1381899_at	---	---	---	---	AW534794	2.83	2.73	4.29	2.68	3.28	2.75	1.30	down	5.18E-01	8.95E-01	-	-
1373982_at	RGD1306595	similar to hypothetical protein	287554	Rn.16586	BM385377	6.28	6.21	6.14	5.89	5.32	6.28	1.30	down	2.48E-01	8.95E-01	-	-
1379538_at	Cenpj	centromere protein J	305909	Rn.19524	BE104961	3.96	2.70	2.55	2.49	2.60	2.99	1.30	down	4.65E-01	8.95E-01	-	-
1375801_at	Ipmk	Inositol polyphosphate multikinase	171458	Rn.15187	BE113834	6.35	5.46	4.93	5.09	5.41	5.09	1.30	down	4.23E-01	8.95E-01	-	-
1373607_at	St3gal3	ST3 beta-galactoside alpha-2,3-sialyltransferase 3	64445	Rn.44390	BF418530	6.32	5.63	6.17	6.79	6.13	6.35	1.30	up	2.53E-01	8.95E-01	-	-
1397134_at	---	---	---	Rn.62549	BF414458	4.40	5.37	4.48	4.36	4.02	4.73	1.30	down	3.62E-01	8.95E-01	-	-
1393837_at	---	---	---	Rn.162778	AI145227	3.59	2.45	2.48	2.46	2.47	2.44	1.30	down	3.67E-01	8.95E-01	-	-
1392865_at	Fgf9	fibroblast growth factor 9	25444	Rn.25174	BG371594	9.19	9.03	9.07	8.97	7.94	9.24	1.30	down	3.95E-01	8.95E-01	-	-
1383348_at	---	---	---	Rn.18381	BF545309	7.86	8.44	8.20	7.83	7.59	7.95	1.30	down	1.28E-01	8.95E-01	-	-
1378143_at	Pdcd	phosducin-like	64013	Rn.51153	AI170625	3.30	4.02	3.73	3.78	4.02	4.40	1.30	up	2.37E-01	8.95E-01	-	-
1377578_at	---	---	---	Rn.203570	AI072161	5.00	5.08	3.93	5.19	5.37	4.58	1.30	up	4.36E-01	8.95E-01	-	-
1391994_at	---	---	---	Rn.30602	AI408264	5.76	6.22	5.86	6.06	6.13	6.80	1.30	up	2.37E-01	8.95E-01	-	-
1388855_at	Cul1	cullin 1	362356	Rn.68070	BI284428	7.93	7.94	8.09	8.52	8.18	8.41	1.30	up	2.85E-02	8.95E-01	-	-
1371807_at	RGD1311605	similar to apoptosis related protein APR-3; p18 protein	298841	Rn.3206	BE110607	7.67	7.83	7.31	7.08	6.80	7.80	1.30	down	3.20E-01	8.95E-01	-	-
1377311_at	Emx2	empty spiracles homeobox 2	499380	Rn.16276	AI045616	7.81	7.94	9.02	7.43	8.16	8.05	1.30	down	4.43E-01	8.95E-01	-	-
1378309_at	Usp20	ubiquitin specific peptidase 20	311856	Rn.27074	AW434880	6.45	6.85	6.13	6.10	5.98	6.21	1.30	down	1.56E-01	8.95E-01	-	-
1390701_at	---	---	---	Rn.15581	BG372551	4.85	4.89	5.26	4.70	4.09	4.70	1.30	down	2.77E-01	8.95E-01	-	-
1379729_at	Cpsf6	cleavage and polyadenylation specific factor 6	299811	Rn.164480	AI071906	2.91	3.34	3.23	4.37	3.13	3.12	1.30	up	4.30E-01	8.95E-01	-	-
1375608_at	---	---	---	---	AI137837	2.83	2.34	2.95	2.29	2.35	2.34	1.30	down	1.11E-01	8.95E-01	-	-
1393076_at	Vps13d	vacuolar protein sorting 13D (yeast)	313825	Rn.2644	AW918759	2.74	2.64	2.64	2.70	3.55	2.90	1.30	up	2.15E-01	8.95E-01	-	-
1389635_at	---	---	---	Rn.16982	BE120878	4.30	5.68	4.57	3.85	4.76	4.80	1.30	down	5.09E-01	8.95E-01	-	-
1374465_at	Uxt	ubiquitously expressed transcript	299313	Rn.203381	AI237098	8.31	8.78	8.79	8.51	8.08	8.15	1.30	down	1.44E-01	8.95E-01	-	-
1368030_at	Gnai3	guanine nucleotide binding protein (G protein), alpha inhibiting 3	25643	Rn.4368	J03219	6.63	6.80	6.83	6.03	6.64	6.44	1.30	down	1.15E-01	8.95E-01	-	-
1368427_at	---	---	---	---	NM_012773	6.99	7.27	6.35	7.12	7.16	7.46	1.30	up	2.64E-01	8.95E-01	-	-
1373928_at	Il17re	interleukin 17 receptor E	362417	Rn.129068	BM383766	2.39	3.49	2.39	2.38	2.39	2.36	1.30	down	3.60E-01	8.95E-01	-	-
1382868_at	Sema6a	sema domain, transmembrane domain (TM), and cytoplasmic domain, (sema	361324	Rn.203621	BM387083	7.94	8.41	8.84	7.93	8.09	8.02	1.30	down	2.23E-01	8.95E-01	-	-
1379477_at	---	---	---	Rn.205204	AI555261	3.49	4.11	6.19	4.70	4.25	5.98	1.30	up	7.14E-01	9.10E-01	-	-
1374196_at	Lancl1	LanC lantibiotic synthetase component C-like 1 (bacterial)	114515	Rn.38972	AI710389	5.24	5.66	6.21	5.20	6.45	6.60	1.30	up	5.10E-01	8.95E-01	-	-
1378169_at	Acot3 /// Acot4	acyl-CoA thioesterase 3 /// acyl-CoA thioesterase 4	314304 /// 681337	Rn.203185	BI295569	4.41	3.02	3.56	3.49	2.96	3.40	1.30	down	4.31E-01	8.95E-01	-	-
1392936_at	m25 /// RGD1565	RNA binding motif protein 25 /// similar to RNA binding motif protein 25	366693 /// 497865	Rn.220196	AW434972	9.21	9.22	9.53	9.14	9.26	8.42	1.30	down	2.50E-01	8.95E-01	-	-
1390042_at	Tmem140	transmembrane protein 140	362334	Rn.203463	AI071166	6.76	7.09	5.74	6.76	5.73	5.95	1.30	down	4.96E-01	8.95E-01	-	-
1382503_at	Irf2	interferon regulatory factor 2	290749	Rn.107887	BE109551	3.50	3.55	2.31	2.31	2.30	3.61	1.30	down	5.59E-01	8.95E-01	-	-
1393750_at	G2e3	G2/M-phase specific E3 ubiquitin ligase	299002	Rn.126080	BI303408	2.53	2.52	2.54	3.49	2.71	2.52	1.30	up	2.71E-01	8.95E-01	-	-
1396309_at	Tbc1d19	TBC1 domain family, member 19	289857	Rn.46324	BI292839	3.96	4.11	4.83	4.32	4.50	5.22	1.30	up	3.81E-01	8.95E-01	-	-
1383866_at	---	---	---	Rn.23675	BI293248	2.81	3.57	2.51	2.99	2.84	4.20	1.30	up	5.16E-01	8.95E-01	-	-
1383167_at	---	---	---	Rn.164405	BM392101	5.85	5.05	5.54	5.93	5.41	6.25	1.30	up	3.25E-01	8.95E-01	-	-
1397558_at	---	---	---	Rn.167597	AW557159	4.79	5.30	4.48	4.91	6.09	4.70	1.30	up	4.86E-01	8.95E-01	-	-
1375006_at	---	---	---	Rn.199480	BE121050	5.95	6.25	6.00	5.92	5.25	5.90	1.30	down	1.86E-01	8.95E-01	-	-
1390599_at	---	---	---	Rn.206084	BE101766	3.87	3.94	3.95	3.35	4.31	5.23	1.30	up	5.23E-01	8.95E-01	-	-
1367685_at	Rps27a	ribosomal protein S27a	81777	Rn.106034	NM_031113	10.52	10.41	10.45	10.47	10.83	11.22	1.30	up	1.57E-01	8.95E-01	-	-
1386905_at	Prkar1a	protein kinase, cAMP dependent regulatory, type I, alpha	25725	Rn.10990	NM_013181	7.44	8.00	8.44	7.84	7.05	7.85	1.30	down	3.91E-01	8.95E-01	-	-
1371938_at	Caprin1	Cell cycle associated protein 1	362173	Rn.22572	AI171369	10.36	10.16	10.68	10.13	9.74	10.19	1.30	down	1.40E-01	8.95E-01	-	-
1379475_at	RGD1563120	similar to RIKEN cDNA 2210009G21	499895	Rn.214487	BF396403	2.40	2.40	2.40	2.61	2.40	3.33	1.30	up	2.52E-01	8.95E-01	-	-
1369070_at	Pex12	peroxisomal biogenesis factor 12	116714	Rn.29982	NM_053921	5.40	5.67	7.23	5.57	5.50	6.08	1.30	down	5.61E-01	8.95E-01	-	-
1373603_at	RGD1565744	similar to RIKEN cDNA 0610007P22	360494	Rn.219246	BG673166	5.48	6.18	6.20	6.21	6.17	6.61	1.30	up	2.39E-01	8.95E-01	-	-
1375342_at	Nfic	Nuclear factor I/C	29228	Rn.86582	BG381296	4.57	4.57	5.30	4.18	4.59	4.54	1.30	down	2.38E-01	8.95E-01	-	-
1388686_at	Rcan1	regulator of calcineurin 1	266766	Rn.12942	AI170193	4.23	2.74	2.49	3.07	2.71	2.54	1.30	down	5.39E-01	8.95E-01	-	-
1367838_at	Cth	cystathionase (cystathionine gamma-lyase)	24962	Rn

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1377608_a_at	Tardbp	TAR DNA binding protein	298648	Rn.2633	BM392298	6.79	7.37	7.42	6.56	6.63	7.27	1.30	down	2.81E-01	8.95E-01	-	-
1378199_at	Luzp5	leucine zipper protein 5	362798	Rn.35615	AI408485	2.40	2.42	2.55	2.41	3.67	2.41	1.30	up	4.26E-01	8.95E-01	-	-
1376241_at	Cul3	Cullin 3	301555	Rn.101949	AA858761	3.36	4.56	4.71	4.23	4.45	5.08	1.30	up	4.92E-01	8.95E-01	-	-
1393287_at	Mov10	Moloney leukemia virus 10	310756	Rn.3508	AW915147	3.52	2.35	2.37	2.36	2.41	2.35	1.30	down	3.88E-01	8.95E-01	-	-
1373090_at	Ssr1	signal sequence receptor, alpha	361233	Rn.123918	AI230697	6.24	7.08	7.31	6.75	7.20	7.80	1.30	up	4.45E-01	8.95E-01	-	-
1371263_a_at	Camk2d	calcium/calmodulin-dependent protein kinase II delta	24246	Rn.87208	X77194	2.70	2.69	2.38	2.70	2.71	3.50	1.30	up	2.58E-01	8.95E-01	-	-
1373830_at	LOC681574	hypothetical protein LOC619574	619574	Rn.162222	AW920524	4.29	4.39	4.16	4.69	4.20	5.07	1.30	up	2.25E-01	8.95E-01	-	-
1389601_at	---	---	---	Rn.40435	BI293610	9.52	9.77	9.06	9.90	9.72	9.86	1.30	up	1.54E-01	8.95E-01	-	-
1384823_at	---	---	---	Rn.216653	AW524486	2.69	2.62	2.70	3.35	2.71	3.08	1.30	up	1.13E-01	8.95E-01	-	-
1370219_at	Cyba	cytochrome b-245, alpha polypeptide	79129	Rn.5859	AI232788	4.20	4.65	5.93	4.43	4.20	5.03	1.30	down	5.50E-01	8.95E-01	-	-
1379419_at	Tmem184c	transmembrane protein 184C	291946	Rn.12069	AA962979	4.12	4.75	2.34	3.44	3.53	5.36	1.30	up	7.14E-01	9.10E-01	-	-
1380705_at	---	---	---	Rn.206215	AW523627	2.50	2.49	3.61	2.48	2.54	2.46	1.30	down	3.71E-01	8.95E-01	-	-
1381764_s_at	Rnf126	ring finger protein 126	314613	Rn.143411	AA819792	8.84	9.41	7.97	9.19	9.12	9.04	1.30	up	4.25E-01	8.95E-01	-	-
1382981_at	Ahi1	Abelson helper integration site 1	308923	Rn.205875	AI138017	7.68	6.59	5.59	6.32	6.60	5.81	1.30	down	5.93E-01	8.95E-01	-	-
1374149_at	---	---	---	Rn.8938	AW144301	2.72	2.71	2.73	2.72	3.87	2.71	1.30	up	3.84E-01	8.95E-01	-	-
1374845_at	---	---	---	Rn.17456	AI176367	6.69	6.28	5.60	6.70	6.01	6.97	1.30	up	4.30E-01	8.95E-01	-	-
1373713_at	---	---	---	Rn.46023	BF393948	2.54	2.51	2.55	2.53	3.68	2.52	1.30	up	3.84E-01	8.95E-01	-	-
1372608_at	LOC313707	similar to exosome component 10	313707	Rn.42519	BM388814	4.05	3.30	2.93	3.25	2.87	3.03	1.30	down	3.43E-01	8.95E-01	-	-
1383953_at	Ercc5	excision repair cross-complementing rodent repair deficiency, complementatic	301382	Rn.208330	BM384968	5.26	4.64	5.66	5.79	5.42	5.48	1.30	up	3.04E-01	8.95E-01	-	-
1384946_at	---	---	---	---	AI070419	2.47	2.49	2.51	3.23	2.89	2.48	1.30	up	1.60E-01	8.95E-01	-	-
1371809_at	Mrps18b	mitochondrial ribosomal protein S18B	294230	Rn.114	BM389296	8.28	8.76	8.71	9.00	8.91	8.96	1.30	up	7.40E-02	8.95E-01	-	-
1374949_at	Zfyve19	zinc finger, FYVE domain containing 19	499871	Rn.37288	BM385443	3.99	3.98	4.00	5.03	4.09	3.97	1.30	up	3.28E-01	8.95E-01	-	-
1385334_at	---	---	---	Rn.8023	AA818166	9.37	9.96	9.31	8.98	9.15	9.38	1.30	down	1.89E-01	8.95E-01	-	-
1377080_at	Nradd	neurotrophin receptor associated death domain	246143	Rn.40224	AI598730	2.21	2.20	2.21	2.21	2.73	2.81	1.30	up	1.19E-01	8.95E-01	-	-
1382959_at	---	---	---	Rn.166477	AA891058	3.50	2.36	2.36	2.35	2.38	2.37	1.30	down	3.80E-01	8.95E-01	-	-
1388499_at	RGD1359380	similar to hypothetical protein MGC7537	303922	Rn.7420	AW531384	7.18	8.19	8.75	7.48	7.29	8.22	1.30	down	5.24E-01	8.95E-01	-	-
1368211_at	Rps14	ribosomal protein S14	29284	Rn.36102	NM_022672	10.95	11.36	10.80	11.20	11.47	11.56	1.30	up	1.31E-01	8.95E-01	-	-
1382762_at	Pgm3	Phosphoglucomutase 3	363109	Rn.24236	AI105359	3.09	2.85	2.66	2.21	2.62	2.65	1.30	down	1.18E-01	8.95E-01	-	-
1375022_at	Afg3l2	AFG3(ATPase family gene 3)-like 2 (yeast)	307350	Rn.8386	AI548730	4.73	4.83	4.21	4.89	4.99	5.00	1.30	up	1.28E-01	8.95E-01	-	-
1375701_at	Mett10d	methyltransferase 10 domain containing	360568	Rn.203131	BF400575	5.77	7.36	8.28	6.89	6.66	6.73	1.30	down	6.37E-01	8.95E-01	-	-
1390960_at	---	---	---	Rn.14812	AA893602	4.11	2.94	2.99	2.95	2.92	3.05	1.30	down	3.84E-01	8.95E-01	-	-
1390959_at	LOC684830	hypothetical protein LOC684830	684830	---	AA925423	2.68	3.70	4.90	3.64	2.81	3.71	1.30	down	6.23E-01	8.95E-01	-	-
1372802_at	Znf512	zinc finger protein 512	313906	Rn.22370	AI172500	2.51	2.49	2.50	2.50	3.60	2.52	1.30	up	3.60E-01	8.95E-01	-	-
1381203_at	Sh3gli1	SH3-domain GRB2-like endophilin B1	292156	Rn.203013	AA819246	5.42	5.58	6.72	6.69	5.29	6.86	1.30	up	5.93E-01	8.95E-01	-	-
1388596_at	Synj1	synaptojanin 1	85238	Rn.22685	BG372397	7.64	7.11	6.11	7.43	7.12	7.44	1.30	up	4.63E-01	8.95E-01	-	-
1368188_at	Hpd	4-hydroxyphenylpyruvate dioxygenase	29531	Rn.3664	NM_017233	9.97	9.53	9.50	9.94	9.93	10.25	1.30	up	1.09E-01	8.95E-01	-	-
1388853_at	Mrpl54	mitochondrial ribosomal protein L54	299628	Rn.20606	BI285231	9.88	10.09	9.97	10.35	10.62	10.10	1.30	up	8.33E-02	8.95E-01	-	-
1387668_at	Ptpn11	protein tyrosine phosphatase, non-receptor type 11	25622	Rn.98209	U05963	5.11	4.68	4.00	4.03	4.12	4.52	1.30	down	3.54E-01	8.95E-01	-	-
1377390_at	Bace2	beta-site APP-cleaving enzyme 2	288227	Rn.38581	BG381587	2.53	2.46	2.48	2.82	3.34	2.43	1.30	up	2.33E-01	8.95E-01	-	-
1389313_at	---	---	---	Rn.199236	AI137972	3.90	3.85	4.37	4.11	3.23	3.65	1.30	down	2.85E-01	8.95E-01	-	-
1370340_x_at	Tpm3	tropomyosin 3, gamma	117557	Rn.37575	BI295970	10.03	10.21	10.58	10.78	10.48	10.67	1.30	up	1.12E-01	8.95E-01	-	-
1372630_at	Rad23a	RAD23 homolog A (S. cerevisiae)	361381	Rn.105419	AA891828	4.71	4.65	4.92	4.34	4.53	4.28	1.30	down	2.75E-02	8.95E-01	-	-
1372710_at	Bet1	blocked early in transport 1 homolog (S. cerevisiae)	29631	Rn.3953	AI175027	5.24	4.95	4.35	5.12	4.97	5.57	1.30	up	3.07E-01	8.95E-01	-	-
1369026_at	Arflp1	ADP-ribosylation factor interacting protein 1	60382	Rn.162603	NM_021763	4.44	4.56	3.82	3.80	5.50	4.84	1.30	up	5.29E-01	8.95E-01	-	-
1395018_at	Lars	leucyl-tRNA synthetase	291624	Rn.7687	BE119004	4.54	4.93	5.00	4.92	5.31	5.37	1.30	up	1.35E-01	8.95E-01	-	-
1381798_at	Lmo7	LIM domain 7	361084	Rn.98417	BE114958	2.37	2.37	2.38	3.50	2.38	2.37	1.30	up	3.75E-01	8.95E-01	-	-
1369234_at	Slc20a2	solute carrier family 20 (phosphate transporter), member 2	29502	Rn.13642	NM_017223	5.06	4.37	4.11	4.28	3.89	4.26	1.30	down	2.97E-01	8.95E-01	-	-
1383954_at	---	---	---	Rn.16559	BI273721	5.94	2.48	5.34	4.32	4.03	4.28	1.30	down	7.44E-01	9.17E-01	-	-
1388531_at	Pgrmc2	progesterone receptor membrane component 2	361940	Rn.7685	BF283382	8.54	8.97	8.82	9.27	8.99	9.19	1.30	up	6.80E-02	8.95E-01	-	-
1383396_at	Fndc3a	fibronectin type III domain containing 3a	306022	Rn.100627	AA894079	7.65	6.99	8.00	7.83	8.19	7.75	1.30	up	3.17E-01	8.95E-01	-	-
1399087_at	RGD1307410	similar to hypothetical protein FLJ31528	360673	Rn.154667	AI179711	3.01	3.39	2.97	3.50	3.99	3.01	1.30	up	2.97E-01	8.95E-01	-	-
1395289_at	Vps26b	vacuolar protein sorting 26 homolog B (S. pombe)	300472	Rn.61419	H33428	4.65	4.62	4.80	3.69	4.26	5.00	1.30	down	3.86E-01	8.95E-01	-	-
1372720_at	Btbd1	BTB (POZ) domain containing 1	293060	Rn.162445	AA848449	7.28	8.35	8.27	8.44	8.30	8.29	1.30	up	3.44E-01	8.95E-01	-	-
1374650_at	Nedd9	neural precursor cell expressed, developmentally down-regulated 9	291044	Rn.8730	BM392374	5.34	4.76	4.22	4.49	5.75	5.19	1.30	up	4.86E-01	8.95E-01	-	-
1381987_at	---	---	---	Rn.203232	AI175803	3.17	3.23	3.26	3.38	3.26	4.13	1.30	up	2.48E-01	8.95E-01	-	-
1380403_at	Rwdd2a	RWD domain containing 2A	363110	Rn.88698	AI408839	3.71	2.74	2.79	2.61	2.78	2.73	1.30	down	3.05E-01	8.95E-01	-	-
1391365_at	---	---	---	Rn.209892	BF416465	2.82	2.54	2.57	2.82	3.76	2.48	1.30	up	3.96E-01	8.95E-01	-	-
1395146_at	Adipor2	adiponectin receptor 2	312670	Rn.101984	BI285808	5.46	4.56	4.87	5.47	3.23	5.07	1.30	down	6.41E-01	8.95E-01	-	-
1368870_at	Id2	inhibitor of DNA binding 2	25587	Rn.3272	NM_013060	7.04	7.54	7.82	6.31	8.03	6.95	1.30	down	5.37E-01	8.95E-01	-	-
1373367_at	---	---	---	Rn.65720	AI556297	9.00	8.74	7.79	8.97	8.54	9.14	1.30	up	4.11E-01	8.95E-01	-	-
1372078_at	Strap	serine/threonine kinase receptor associated protein	297699	Rn.8126	AA891681	6.09	5.79	6.36	6.02	6.81	6.53	1.30	up	2.62E-01	8.95E-01	-	-
1392712_at	---	---	---	Rn.15834	AI044209	2.81	2.55	2.74	2.47	2.26	2.24	1.29	down	2.37E-02	8.95E-01	-	-
1390753_at	---	---	---	Rn.147551	BF419721	2.99	3.14	2.99	3.05	4.16	3.03	1.29	up	3.78E-01	8.95E-01	-	-
1388770_at	Ufm1	ubiquitin-fold modifier 1	365797	Rn.92909	BI275670	7.71	7.71	7.52	8.04	7.43	8.58	1.29	up	3.35E-01	8.95E-01	-	-
1379909_at	Gkap1	G kinase-anchoring protein 1	361202	Rn.2003	AA863315	6.77	6.99	6.07	6.59	7.20	7.14	1.29	up	3.32E-01	8.95E-01	-	-
1391932_at	RGD1308694	similar to hypothetical protein MGC47256	295326	Rn.21161	BI275030	2.60	2.59	2.63	2.61	3.72	2.60	1.29	up	3.76E-01	8.95E-01	-	-
1385336_at	Dok2	docking protein 2	290361	Rn.126595	BF397977	2.49	3.47	2.51	2.47	2.51	2.46	1.29	down	3.59E-01	8.95E-01	-	-
1392858_at	684506 /// LOC68	similar to SMP3 mannosyltransferase /// similar to nuclear cap binding protein	684506 /// 689116	Rn.204538	BM387770	6.71	7.07	7.17	7.16	5.57	7.11	1.29	down	5.28E-01	8.95E-01	-	-
1368668_at	Plaa	phospholipase A2, activating protein	116645	Rn.22250	NM_053866	4.56	4.81	4.69	4.11	5.26	5.80	1.29	up	5.01E-01	8.95E-01	-	-
1387058_at	Pctp	phosphatidylcholine transfer protein	29510	Rn.9487	NM_017225	7.53	7.81	7.63	7.38	8.94	7.77	1.29	up	4.77E-01	8.95E-01	-	-
1392831_at	Pank2	Pantothenate kinase 2 (Hallervorden-Spatz syndrome)	296167	Rn.91999	AA891438	2.57	2.57	2.48	3.65	2.52	2.57	1.29	up	3.70E-01	8.95E-01	-	-
1373009_at	RGD1559786	similar to RIKEN cDNA 0610037L13	298384	Rn.104738	AI176734	8.48	9.14	9.15	9.14	9.08	9.66	1.29	up	2.67E-01	8.95E-01	-	-
1384756_at	Slc43a2	solute carrier family 43, member 2	287532	Rn.204988	BF394311	2.56	2.58	3.45	2.33	4.81	2.57	1.29	up	6.81E-01	9.03E-01	-	-
1369215_a_at	Cpd	carboxypeptidase D	25306	Rn.25905	NM_012836	6.24	7.41	7.24	6.63	7.94	7.43	1.29	up	5.19E-01	8.95E-01	-	-
1398191_at	---	---	---	---	BF403831	2.50	2.52	2.65	3.78	2.35	2.66	1.29	up	4.43E-01	8.95E-01	-	-
1384039_at	RGD1310950	similar to KIAA1078 protein	289400	Rn.92141	BF558912	5.05	4.93	5.03	5.37	5.02	5.73	1.29	up	1.50E-01	8.95E-01	-	-
1370075_at	Dhfr	dihydrofolate reductase	24312	Rn.24681	NM_130400	6.09	6.33	6.15	4.86	6.14	6.46	1.29	down	4.94E-01	8.95E-01	-	-
1382021_at	---	---	---	Rn.199142	AA850650	5.80	5.98	5.69	6.13	6.00	6.44	1.29	up	7.54E-02	8.95E-01	-	-
1382461_at	Prmt7	protein arginine methyltransferase 7	361402	Rn.14954	AI101582	2.71	2.53	2.61	2.48	2.96	3.53	1.29	up	2.93E-01	8.95E-01	-	-
1373389_at	Acad9	acyl-Coenzyme A dehydrogenase family, member 9	294973	Rn.13649	BM391807	5.96	5.39	4.76	5.75	5.49	5.98	1.29	up	3.75E-01	8.95E-01	-	-
1378863_at	---	---	---	Rn.16215	BF412077	4.75	5.79	3.84	3.83	4.82	4.61	1.29	down	5.93E-01	8.95E-01	-	-
1380405_at	08-Sep	septin 8	303135	Rn.23507	BF546570	3.44	4.48	4.85	4.31	3.46	3.88	1.29	down	4.88E-01	8.95E-01	-	-
1376140_at	Abcd1	ATP-binding cassette, sub-family D (ALD), member 1	363516	Rn.163453	BM389221	2.40	3.90	2.38	2.38	2.79	2.39	1.29	down	5.15E-01	8.95E-01	-	-
1370014_at	Stx4	syntaxin 4	81803	Rn.33218	NM_031125	5.82	6.85	7.08	7.72	6.39	6.76	1.29	up	5.38E-01	8.95E-01	-	-
1385505_at	---	---	---	Rn.166280	AI072068	4.05	3.96	5.29	3.05	3.87	5.26	1.29	down	6.57E-01	8.98E-01	-	-
1370910_at	Rfc2	replication factor C (activator 1) 2	116468	Rn.113319	BF283113	5.82	6.98	6.59	5.93	6.41	5.94	1.29	down	3.78E-01	8.95E-01	-	-
1380525_at	Arse	arylsulfatase E (chondrodysplasia punctata 1)	310326	Rn.79118	AA849862	6.83	7.70	7.23	6.77	7.05	6.83	1.29	down	2.33E-01	8.95E-01	-	-
1383807_at	Tbc1d19	TBC1 domain family, member 19	289657	Rn.46324	BG672767	4.70	5.28	4.04	4.60	3.36	4.94	1.29	down	5.69E-01	8.95E-01	-	-
1375071_at	Nup133	nucleoporin 133	292085	---	BE119719	7.25	6.59	6.81	5.93	6.94	6.67	1.29	down	3.58E-01	8.95E-01	-	-
1370305_at	Yif1	Yip1 interacting factor homolog (S. cerevisiae)	171441	Rn.7355	U96490	4.27	5.35	5.42	5.38	5.25	5.53	1.29	up	3.87E-01	8.95E-01	-	-
1378124_at	Ppm1b	protein phosphatase 1B, magnesium dependent, beta isoform	24667	Rn.4143	AI501282	2.52	2.59	2.32	2.74	2.50	3.31	1.29	up	2.18E-01	8.95E-01	-	-
1368944_at	Dlg1	discs, large homolog 1 (Drosophila)	25252	Rn.89331	NM_012788	5.40	4.85	4.08	4.62	3.52	5.08	1.29	down	5.71E-01	8.95E-01	-	-
1388999_at	---	---	---	---	BF397807	7.56	7.45	8.57	7.49	7.27	7.70	1.29	down	3.81E-01	8.95E-01	-	-
1377904_at	---	---	---	---	BE109251	3.71	3.23	3.70	3.68	4.38	3.70	1.29	up	2.56E-01	8.95E-01	-	-
1398468_at	---	---	---	Rn.204861	BE109256	2.33	2.32	2.33	3.44	2.33	2.32	1.29	up	3.75E-01	8.95E-01	-	-
1398185_at	Mfap3l	microfibrillar-associated protein 3-like	306424	Rn.98965	BF410350	2.82	2.71	2.62	2.73	3.95	2.59	1.29	up	4.41E-01	8.95E-01	-	-
1382854_at	---	---	---	Rn.21880	AI232286	2.68	2.36	3.35	2.53	2.38	2.37	1.29	down	2.77E-01	8.95E-01	-	-
1382254_at	---	---	---	Rn.203668	BI295944	6.26	6.27	5.84	6.48	6.27	6.73	1.29	up	1.29E-01	8.95E-01	-	-
1383102_at	---	---	---	Rn.165195	BE110357	4.83	4.36	4.91	4.50	3.70	4.89	1.29	down	3.15E-01	8.95E-01	-	-
1387953_at	Coil	coilin	50998	Rn.203468	AF399643	2.34	2.33	3.49	2.38	2.35	2.33	1.29	down	3.91E-01	8.95E-01	-	-
1376250_at	Nufip1	nuclear fragile X mental retardation protein interacting protein 1	364430	Rn.154742	BI284814	5.47	6.09	5.85	6.09	6.36	6.08	1.29	up	1.44E-01	8.95E-01	-	-
1382067_at	BC363500 /// Ubxn	similar to UBX domain containing 4 /// UBX domain containing 4	363500 /// 685859	Rn.25112	AW434917	8.98	9.22	9.33	9.56	9.58	9.49	1.29	up	2.51E-02	8.95E-01	-	-
1385399_at	---	---	---	Rn.16643	AI071789	3.76	2.62	2.58	2.64	2.70	2.51	1.29	down	3.94E-01	8.95E-01	-	-
1373073_at	Ppp1r7	protein phosphatase 1, regulatory (inhibitor) subunit 7	301618	Rn.19437	BF282816	3.85	4.38	3.06	3.14	3.14	3.90	1.29	down	4.65E-01	8.95E-01	-	-
1395099_at	---	---	---	Rn.209599	AI176297	3.24	3.24	3.13	3.67	2.59	4.47	1.29	up	5.35E-01	8.95E-01	-	-
1368453_at	Fads2	fatty acid desaturase 2	83512	Rn.162483	NM_031344	5.48	4.38	5.31	5.22	5.35	5.71	1.29	up	3.77E-01	8.95E-01	-	-
1386941_at	Plec1	plectin 1	64204	Rn.1085	NM_022401	2.56	2.75	2.82	2.96	2.60	3.69	1.29	up	3.23E-01	8.95E-01	-	-
1371681_at	Tox4	TOX high mobility group box family member 4	286990	Rn.22195	AI145556	6.44	5.95	6.04	5.56	5.87	5.89	1.29	down	1.18E-01	8.95E-01	-	-
1397570_at	---	---	---	Rn.211304	AF410161	4.02	3.50	3.72	3.61	5.03	3.70	1.29	up	4.86E-01	8.95E-01	-	-
1391595_at	Larp6	La ribonucleoprotein domain family, member 6	315731	Rn.33750	AI102304	2.41	2.42	3.54	2.42	2.39	4.29	1.29	up	3.85E-01	8.95E-01	-	-
1396039_at	Slc22a12	solute carrier family 22 (organic anion/urate transporter), member 12	365398	Rn.137035	BG377396	10.28	10.77	10.27	10.68	10.81	10.94	1.29	up	1.09E-01	8.95E-01	-	-
1384084_at	RGD1308106	LOC361719	361719	Rn.16874	AW433952	2.45	2.60	2.32	2.60	3.06	2.82	1.29	up	7.56E-02	8.95E-01	-	-
1390844_at	Fam33a	Family with sequence similarity 33, member A	287598	Rn.203397	AI230329	4.54	3.84	4.34	4.31	5.23	4.29	1.29	up	3.79E-01	8.95E-01	-	-
1376278_at	---	---	---	Rn.154068	BI282100	5.17	5.79	4.14	5.24	5.31	5.65	1.29	up	4.99E-01	8.95E-01	-	-
1376303_a_at	Mbnl	membralin	299608	Rn.37168	BF407469	5.93	6.00	5.89	6.62	6.48	5.82	1.29	up	2.11E-01	8.95E-01	-	-
1384042_at	---	---	---	Rn.24173	BE108303	2.68	2.86	2.85	2.84	3.65	3.01	1.29	up	2.18E-01	8.95E-01	-	-
1372324_at	Znhit3	zinc finger, HIT type 3	497975	Rn.203850	AW253391	3.03	3.28	4.97	2.99	3.01	4.16	1.29	down	6.36E-01	8.95E-01	-	-
1397676_at	---	---	---	---	BF290784	5.31	4.88	3.80	4.97	3.80	4.10	1.29	down	5.52E-01	8.95E-01	-	-
1373633_at	---	---	---	Rn.27327	BF399791	2.91	3.13	3.27	2.65	2.92	2.64	1.29	down	5.48E-02	8.95E-01	-	-
1391190_at	Tnrc6a	trinucleotide repeat containing 6a	308971	Rn.6839	BE117521	7.13	7.58	6.76	6.19	7.33	6.84	1.29	down	4.14E-01	8.95E-01	-	-
1380499_at	---	---	---	Rn.33257	AI029043	3.81	3.87	3.85	3.82	4.96	3.87	1.29	up	3.79E-01	8.95E-01	-	-
1387948_at	Ick	intestinal cell kinase	84411	Rn.3750	D26178	2.76	3.28	3.98	3.26	3.91	3.96	1.29	up	4.29E-01	8.95E-01	-	-
1379283_at	---	---	---	Rn.8634	BE117687	6.05	5.93	6.13	6.17	6.46	6.59	1.29	up	5.53E-02	8.95E-01	-	-
1389063_at	Rbm34	RNA binding motif protein 34	307956	Rn.93968	BM392304	4.31	4.22	4.58	4.47	4.48	5.26	1.29	up	2.62E-01	8.95E-01	-	-
1388429_at	min7 /// LOC4993	gem (nuclear organelle) associated protein 7 /// similar to gem (nuclear organ	499391 /// 685068	Rn.13265	BM384085	2.70	3.37	3.40	2.83	2.84	2.68	1.29	down	1.90E-01	8.95E-01	-	-
1388860_at	Mrpl22	mitochondrial ribosomal protein L22	287302	Rn.13421	AI175327	8.07	8.04	8.07	7.47	7.59	8.02	1.29	down	8.98E-02	8.95E-01	-	-
1377952_at	Adpgk	ADP-dependent glucokinase	315722	Rn.66171	BE102146	2.40	2.85	2.70	3.35	2.69	3.02	1.29	up	1.84E-01	8.95E-01	-	-
1374369_at	Raph1	Ras association (RalGDS/AF-6) and pleckstrin homology domains 1	363239	Rn.16844	BF415686	3.64	2.57	2.68	2.61	2.66	2.51	1.29	down	3.41E-01	8.95E-01	-	-
1374584_at	Stk24	serine/threonine kinase 24 (STE20 homolog, yeast)	361092	Rn.105397	BM388112	10.94	10.68	10.64	10.56	10.11	10.48	1.29	down	9.27E-02	8.95E-01	-	-
1381071_at	---	---	---	Rn.147778	AI112096	3.43	2.52	2.53	3.12	2.63	3.84	1.29	up	4.70E-01	8.95E-01	-	-
1370896_a_at	Myh11	myosin, heavy chain 11, smooth muscle	24582	Rn.94969	X16262	2.90	2.62	2.64	4.02	2.64	2.60	1.29	up	4.79E-01	8.95E-01	-	-
1398846_at	Eif5	eukaryotic translation initiation factor 5	56783	Rn.40123	BE107346	8.13	8.22	7.89	8.05	8.40	8.91	1.29	up	2.40E-01	8.95E-01	-	-
1383839_at	Spg20	spastic paraplegia 20, spartin (Troyer syndrome) homolog (human)	295053	Rn.7964	AI576427	5.47	6.47	7.45	6.96	6.58	6.95	1.29	up	5.62E-01	8.95E-01	-	-
1380213_at	Mbnl1	Muscleblind-like 1 (Drosophila)	282635	Rn.205513	AI599085	7.10	6.17	4.08	6.02	4.88	5.34	1.29	down	7.18E-01	9.11E-01	-	-
1376297_at	Arrdc1	arrestin domain containing 1	366001	Rn.14816	BE112202	2.38	2.38	2.26	3.07	2.39	2.67	1.29	up	1.43E-01	8.95E-01	-	-
1370928_at	Litaf	lipopolysaccharide-induced TNF factor	65161	Rn.6940	BI284739	7.72	7.72	7.97	7.98	7.97	8.57	1.29	up	1.61E-01	8.95E-01	-	-
1370987_at	Spn	sialophorin	24796	Rn.11144	BF550890	2.61	2.50	2.51	2.60	3.35	2.78	1.29	up	1.79E-01	8.95E-01	-	-
1390108_at	RGD1306192	similar to RIKEN cDNA 2310079N02	361443	Rn.19930	AI233162	7.21	6.52	7.63	6.90	6.19	7.17	1.29	down	4.47E-01	8.95E-01	-	-
1373272_at	Plekha5	pleckstrin homology domain containing, family A member 5	246237	Rn.118736	AI009219	6.22	5.79	5.35	6.27	5.60	6.60	1.29	up	3.95E-01	8.95E-01	-	-
1391406_at	---	---	---	Rn.167052	AI169572	8.08	7.22	7.17	7.63	8.02	7.92	1.29	up	3.08E-01	8.95E-01	-	-
1370962_at	Cipc1	castration induced prostatic apoptosis-related protein 1	286894

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1396820_at	Hdac1	histone deacetylase 1	297893	Rn.1863	AW530195	2.60	2.52	3.63	2.61	2.44	2.59	1.29	down	3.69E-01	8.95E-01	-	-
1398773_at	Khdrbs1	KH domain containing, RNA binding, signal transduction associated 1	117268	Rn.162107	NM_130405	6.14	6.17	6.35	6.61	6.48	6.67	1.29	up	1.33E-02	8.95E-01	-	-
1391371_at	Prodh	Proline dehydrogenase	680409	Rn.153570	BE113304	2.59	2.80	2.78	3.66	2.81	2.80	1.29	up	2.79E-01	8.95E-01	-	-
1372650_at	Dnmbp	dynamin binding protein	309362	Rn.11811	BI296334	4.75	4.14	2.73	3.45	3.53	3.54	1.29	down	5.73E-01	8.95E-01	-	-
1373739_at	---	---	---	Rn.210068	BF415431	2.39	2.69	2.41	3.56	2.41	2.63	1.29	up	3.72E-01	8.95E-01	-	-
1369488_at	Ful4	fucosyltransferase 4 (alpha (1,3) fucosyltransferase, myeloid-specific)	60670	Rn.44467	NM_022219	2.30	2.30	2.31	3.41	2.31	2.29	1.29	up	3.78E-01	8.95E-01	-	-
1394003_at	Pole3	polymerase (DNA directed), epsilon 3 (p17 subunit)	298098	Rn.3290	BF522722	6.07	8.12	8.31	7.19	7.40	6.82	1.29	down	6.45E-01	8.95E-01	-	-
1385758_at	Saps1	SAPS domain family, member 1	361502	Rn.138371	BF399333	3.29	3.32	4.00	3.35	2.87	3.29	1.29	down	2.54E-01	8.95E-01	-	-
1371573_at	Rpl36a	ribosomal protein L36a	292964	Rn.23433	AW1420090	11.10	11.43	11.59	11.78	11.57	11.87	1.29	up	9.85E-02	8.95E-01	-	-
1395045_at	Ndufa7	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 7 (B14.5a)	299643	Rn.797	BM384525	6.57	6.71	6.84	6.56	6.78	6.68	1.29	down	2.74E-01	8.95E-01	-	-
1370830_at	Egfr	epidermal growth factor receptor	24329	Rn.37227	M37394	4.85	4.94	4.37	4.50	3.70	4.86	1.29	down	3.95E-01	8.95E-01	-	-
1376177_at	Fam117a	family with sequence similarity 117, member A	497983	Rn.93919	AI179609	4.70	3.66	3.69	3.84	5.10	4.21	1.29	up	5.09E-01	8.95E-01	-	-
1399086_at	Zfp105	zinc finger protein 105	316096	Rn.12040	AI179640	3.29	3.27	2.55	3.28	3.29	3.65	1.29	up	2.47E-01	8.95E-01	-	-
1372748_at	Tbc1d2b	TBC1 domain family, member 2B	315880	Rn.1821	BE113335	3.08	3.07	2.95	3.19	4.10	2.91	1.29	up	3.71E-01	8.95E-01	-	-
1385620_at	Hsph1	heat shock 105kDa/110kDa protein 1	288444	Rn.37805	BF525282	9.65	9.47	9.03	9.07	9.11	8.87	1.29	down	1.39E-01	8.95E-01	-	-
1388880_at	---	---	---	Rn.222017	BI278962	4.79	3.43	4.10	4.58	3.62	3.03	1.29	down	5.74E-01	8.95E-01	-	-
1390814_at	PelI1	pellino 1	305549	Rn.22814	AA848897	5.41	5.86	4.57	5.79	5.39	5.75	1.29	up	4.10E-01	8.95E-01	-	-
1372538_at	Slc25a17	solute carrier family 25 (mitochondrial carrier; peroxisomal membrane protein	300083	Rn.94733	BM389148	8.08	7.92	6.95	7.80	7.88	8.36	1.29	up	4.07E-01	8.95E-01	-	-
1396761_at	---	---	---	Rn.219513	BF404917	2.50	2.50	2.55	3.67	2.53	2.44	1.29	up	4.10E-01	8.95E-01	-	-
1371464_at	Zfand6	zinc finger, AN1-type domain 6	293067	Rn.130357	BI295799	8.29	7.89	8.25	8.31	8.79	8.43	1.29	up	1.30E-01	8.95E-01	-	-
1381364_at	Tnpo1	transportin 1	309126	Rn.56083	BE116070	7.17	6.96	6.44	6.76	5.99	6.72	1.29	down	3.34E-01	8.95E-01	-	-
1397531_at	---	---	---	Rn.38208	BF522208	5.39	5.45	5.22	5.36	6.13	5.68	1.29	up	1.93E-01	8.95E-01	-	-
1379694_at	Epc2	Enhancer of polycomb homolog 2 (Drosophila)	362132	Rn.23462	AI171596	3.43	2.53	4.31	3.72	3.70	3.95	1.29	up	5.20E-01	8.95E-01	-	-
1371863_at	Pgs1	phosphatidylglycerophosphate synthase 1	303898	Rn.50013	BM387059	6.36	5.92	5.92	5.13	6.06	5.91	1.29	down	3.21E-01	8.95E-01	-	-
1374612_at	Papd5	PAP associated domain containing 5	307745	Rn.22363	AI170664	8.08	7.77	8.10	7.68	7.59	7.59	1.29	down	3.08E-02	8.95E-01	-	-
1395556_at	LOC503175	similar to Protein KIAA0280	503175	Rn.120228	BF562964	2.32	3.19	3.16	3.14	3.49	3.13	1.29	up	2.98E-01	8.95E-01	-	-
1387407_at	Nup133	nucleoporin 133	170914	Rn.27765	NM_133402	3.76	3.75	4.63	3.50	3.78	3.76	1.29	down	2.97E-01	8.95E-01	-	-
1368039_at	Synj2bp	synaptojanin 2 binding protein	64531	Rn.6258	BF284821	6.54	6.55	6.91	6.54	5.75	6.63	1.29	down	2.97E-01	8.95E-01	-	-
1378353_at	Setdb1	SET domain, bifurcated 1	689883	Rn.198602	AI180459	2.75	4.67	2.63	2.86	5.51	2.77	1.29	up	7.60E-01	9.22E-01	-	-
1398935_at	---	---	---	Rn.8320	AI009819	7.66	7.54	6.82	7.10	6.56	7.27	1.29	down	3.41E-01	8.95E-01	-	-
1384494_at	---	---	---	Rn.24482	BI303215	10.56	10.61	10.35	10.83	10.92	10.86	1.29	up	1.13E-02	8.95E-01	-	-
1371943_at	Stk40	serine/threonine kinase 40	360230	Rn.4052	BF420075	2.59	2.57	2.58	3.36	2.58	2.90	1.29	up	1.80E-01	8.95E-01	-	-
1393699_at	---	---	---	Rn.172649	BF391905	3.58	2.33	2.42	2.41	2.34	2.49	1.29	down	4.18E-01	8.95E-01	-	-
1381956_at	---	---	---	Rn.123902	AI603497	3.62	3.64	4.06	3.80	3.81	2.61	1.29	down	4.38E-01	8.95E-01	-	-
1367805_at	Gls	glutaminase	24398	Rn.5762	AI577681	5.72	7.00	6.48	6.60	7.33	6.35	1.29	up	4.85E-01	8.95E-01	-	-
1390124_at	Fam98b	family with sequence similarity 98, member B	499866	Rn.24187	AA801136	5.60	6.33	8.47	6.16	6.25	6.89	1.29	down	7.03E-01	9.07E-01	-	-
1383484_at	Msl2l1	male-specific lethal 2-like 1 (Drosophila)	315959	Rn.9626	AW920193	7.10	6.50	5.80	6.64	4.33	7.33	1.29	down	7.28E-01	9.13E-01	-	-
1382197_at	Rhod	ras homolog gene family, member D	293660	Rn.25197	AA955648	5.54	5.95	6.75	5.19	6.02	5.94	1.29	down	4.56E-01	8.95E-01	-	-
1398921_at	Mrpl37	mitochondrial ribosomal protein L37	56281	Rn.3445	BE110549	6.40	7.58	8.17	7.52	7.61	8.12	1.29	up	5.44E-01	8.95E-01	-	-
1392675_at	---	---	---	Rn.166013	AI044784	4.71	3.15	2.86	3.96	2.92	2.74	1.29	down	6.25E-01	8.95E-01	-	-
1398642_at	Mtfr	5-methyltetrahydrofolate-homocysteine methyltransferase reductase	290947	Rn.59092	BI279274	2.69	3.05	2.73	3.43	2.69	3.44	1.29	up	2.52E-01	8.95E-01	-	-
1391836_at	---	---	---	Rn.204050	AI044849	2.42	2.41	3.51	2.41	2.43	2.39	1.29	down	3.73E-01	8.95E-01	-	-
1390389_at	---	---	---	Rn.48789	BM385936	4.79	4.59	4.91	5.20	5.38	4.82	1.29	up	1.29E-01	8.95E-01	-	-
1371666_at	---	---	---	Rn.163668	BM385852	7.02	7.31	8.30	6.91	6.93	7.69	1.29	down	4.79E-01	8.95E-01	-	-
1390408_at	Hccs	holocytochrome c synthetase	317444	Rn.162316	BF405032	5.44	5.22	6.49	4.72	5.57	5.77	1.29	down	5.12E-01	8.95E-01	-	-
1376986_at	Mettl3	methyltransferase-like 3	361035	Rn.139109	BF412656	6.23	7.13	6.51	6.22	5.86	6.69	1.29	down	3.67E-01	8.95E-01	-	-
1398616_at	Ap1a2	adaptor-related protein complex 1, sigma 2 subunit	302671	Rn.17309	AI045228	3.99	3.43	5.78	3.91	4.97	3.24	1.29	down	6.97E-01	9.07E-01	-	-
1379850_at	Psmc6	proteasome (prosome, macropain) 26S subunit, ATPase, 6	289990	Rn.103233	BI296804	8.84	8.36	8.67	7.92	8.43	8.44	1.29	down	1.75E-01	8.95E-01	-	-
1375810_at	RGD1565350	Similar to Shb protein	362513	Rn.84084	AI579708	3.56	3.33	3.70	4.22	3.70	3.77	1.29	up	1.38E-01	8.95E-01	-	-
1387072_at	Wnk1	WNK lysine deficient protein kinase 1	116477	Rn.27409	NM_053794	7.00	6.81	7.77	6.97	7.14	6.38	1.29	down	3.83E-01	8.95E-01	-	-
1388369_at	Tmed9	transmembrane emp24 protein transport domain containing 9	361207	Rn.9386	BM385547	10.64	10.71	11.03	11.27	10.83	11.37	1.29	up	1.49E-01	8.95E-01	-	-
1371859_at	Poldip3	polymerase (DNA-directed), delta interacting protein 3	315170	Rn.3893	D86655	3.64	3.72	3.84	4.57	3.75	3.97	1.29	up	2.25E-01	8.95E-01	-	-
1374980_at	Ccdc130	coiled-coil domain containing 130	304656	Rn.7862	BI282049	3.08	3.20	3.30	4.32	3.03	3.32	1.29	up	4.09E-01	8.95E-01	-	-
1376680_at	Vps37c	vacuolar protein sorting 37 homolog C (S. cerevisiae)	308178	Rn.12915	BG379765	3.32	3.12	2.88	3.24	3.33	3.84	1.29	up	1.84E-01	8.95E-01	-	-
1385025_a_at	Gpr137b	G protein-coupled receptor 137B	288287	Rn.60453	AI235734	5.59	6.96	5.11	6.90	5.36	6.50	1.29	up	6.40E-01	8.95E-01	-	-
1373390_at	Msl1	male-specific lethal 1 homolog (Drosophila)	303514	Rn.22437	AI178783	2.82	2.83	2.74	3.09	3.37	3.02	1.29	up	2.99E-02	8.95E-01	-	-
1377997_at	Agtpbp1	ATP/GTP binding protein 1	290986	Rn.33035	AA943155	7.99	7.90	8.13	8.80	8.43	7.89	1.29	up	2.53E-01	8.95E-01	-	-
1380087_at	---	---	---	Rn.208693	BE119409	2.93	4.16	4.02	4.26	3.98	3.97	1.29	up	4.13E-01	8.95E-01	-	-
1378700_at	---	---	---	Rn.147829	BF403674	2.48	3.51	2.53	2.51	2.46	2.45	1.29	down	3.40E-01	8.95E-01	-	-
1377000_at	Whdc1	WAS protein homology region 2 domain containing 1	293057	Rn.198506	BI297041	2.44	2.38	2.39	2.72	2.68	2.89	1.29	up	5.88E-03	8.95E-01	-	-
1384346_at	---	---	---	Rn.11905	AA864754	3.57	3.87	3.35	3.73	3.81	4.34	1.29	up	2.10E-01	8.95E-01	-	-
1373947_at	Dpt	dermatopontin	289178	Rn.8396	BI278545	8.31	6.39	6.06	7.59	6.65	5.43	1.29	down	7.18E-01	9.11E-01	-	-
1391658_at	Arcn1	archain 1	300674	Rn.2185	BF414061	7.53	7.11	6.99	7.70	7.52	7.49	1.29	up	1.09E-01	8.95E-01	-	-
1396182_at	Pm20d2	peptidase M20 domain containing 2	313130	Rn.43474	BF523195	3.11	2.87	2.52	2.41	2.59	2.42	1.29	down	1.12E-01	8.95E-01	-	-
1389412_at	---	---	---	---	AA800693	10.37	9.70	9.19	10.32	9.74	10.30	1.29	up	4.05E-01	8.95E-01	-	-
1387413_at	Ncf1	neutrophil cytosolic factor 1	114553	Rn.38575	NM_053734	2.52	2.52	2.53	3.65	2.53	2.49	1.29	up	3.95E-01	8.95E-01	-	-
1384724_at	---	---	---	---	AA850766	2.41	3.53	2.37	2.41	2.40	2.41	1.29	down	3.96E-01	8.95E-01	-	-
1368424_at	Ikbkb	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase beta	84351	Rn.19222	NM_053355	2.58	2.82	2.56	3.01	3.22	2.81	1.29	up	6.56E-02	8.95E-01	-	-
1384366_at	---	---	---	Rn.167583	BI283477	3.04	3.73	3.81	3.89	3.56	4.22	1.29	up	3.04E-01	8.95E-01	-	-
1370366_at	Timm10	translocase of inner mitochondrial membrane 10 homolog (yeast)	64464	Rn.8106	AF150091	8.77	9.32	9.53	9.40	9.48	9.83	1.29	up	2.39E-01	8.95E-01	-	-
1376543_at	---	---	---	Rn.129745	BF404136	3.55	3.70	3.72	3.33	3.22	3.32	1.29	down	4.29E-03	8.95E-01	-	-
1373690_at	---	---	---	---	BI290473	3.35	2.37	2.34	2.33	2.33	2.32	1.29	down	3.36E-01	8.95E-01	-	-
1374458_at	---	---	---	Rn.17432	AI600031	4.05	5.14	6.68	4.37	5.18	5.22	1.29	down	6.78E-01	9.02E-01	-	-
1382159_at	---	---	---	Rn.164774	BF386740	4.23	3.98	4.74	4.13	3.37	4.36	1.29	down	3.85E-01	8.95E-01	-	-
1393208_at	Myd11	myc target 1	292264	Rn.55418	BF408465	2.71	2.74	2.74	3.78	2.75	2.86	1.29	up	3.51E-01	8.95E-01	-	-
1372675_at	RGD1306954	similar to RIKEN cDNA 1110004E09	288269	Rn.24386	BI291418	7.69	7.53	5.94	7.43	7.43	7.38	1.29	up	5.52E-01	8.95E-01	-	-
1389010_at	Lta4h	leukotriene A4 hydrolase	299732	Rn.104990	AW918009	5.33	6.49	6.15	5.80	5.58	5.51	1.29	down	3.63E-01	8.95E-01	-	-
1398254_at	Renbp	renin binding protein	81759	Rn.11116	NM_031095	4.78	5.09	4.15	5.33	5.14	4.64	1.29	up	3.53E-01	8.95E-01	-	-
1380154_at	Immt	inner membrane protein, mitochondrial	312444	Rn.47124	BF410417	2.57	2.56	2.59	2.52	3.73	2.56	1.29	up	4.15E-01	8.95E-01	-	-
1389688_at	---	---	---	Rn.154093	BM384373	4.81	4.61	5.24	4.40	3.99	5.19	1.29	down	4.14E-01	8.95E-01	-	-
1383747_at	Ect2	epithelial cell transforming sequence 2 oncogene	361921	Rn.168292	AI578135	2.64	2.59	3.69	2.50	2.74	2.59	1.29	down	3.77E-01	8.95E-01	-	-
1371392_at	Gpi	glucose phosphate isomerase	292804	Rn.84435	BI283882	7.67	7.75	7.22	7.20	7.08	7.27	1.29	down	1.05E-01	8.95E-01	-	-
1389150_at	---	---	---	Rn.169457	AW524559	6.66	7.03	7.37	6.40	6.61	6.96	1.29	down	2.42E-01	8.95E-01	-	-
1391823_at	---	---	---	Rn.211761	AA956842	3.49	2.42	2.45	2.43	2.44	2.41	1.29	down	3.64E-01	8.95E-01	-	-
1381868_at	---	---	---	Rn.211831	BF549366	2.65	2.61	2.65	2.61	3.85	2.54	1.29	up	4.44E-01	8.95E-01	-	-
1383193_at	---	---	---	---	BE112341	2.85	2.83	3.87	2.76	2.85	2.86	1.29	down	3.51E-01	8.95E-01	-	-
1384938_at	Arhgap1	Rho GTPase activating protein 1	311193	Rn.64898	AI535143	3.43	4.01	3.71	3.40	3.35	3.30	1.29	down	1.00E-01	8.95E-01	-	-
1389532_at	Nebl	Nebulette	307189	Rn.7963	AW252250	2.32	2.32	2.37	2.32	2.33	3.44	1.29	up	3.85E-01	8.95E-01	-	-
1398342_at	Tusc2	tumor suppressor candidate 2	501052	Rn.120731	BF546775	5.25	5.31	5.32	4.99	4.25	5.55	1.28	down	3.91E-01	8.95E-01	-	-
1374044_at	LOC688314	similar to stimulated by retinoic acid 13	688314	---	AA850698	3.43	3.24	2.39	3.36	3.23	3.55	1.28	up	3.40E-01	8.95E-01	-	-
1380360_at	Oma1	OMA1 homolog, zinc metallopeptidase (S. cerevisiae)	298282	Rn.14712	AA891814	6.41	6.29	6.72	5.69	6.16	6.49	1.28	down	2.46E-01	8.95E-01	-	-
1378294_at	Fbxl12	F-box and leucine-rich repeat protein 12	313782	Rn.8828	BF282402	3.63	3.52	3.31	3.12	5.09	3.33	1.28	up	5.99E-01	8.95E-01	-	-
1387781_at	Pmpcb	peptidase (mitochondrial processing) beta	64198	Rn.841	NM_022395	7.85	7.99	7.13	7.87	7.86	8.33	1.28	up	3.06E-01	8.95E-01	-	-
1385825_at	Secisbp2l	SECIS binding protein 2-like	296115	Rn.64117	AW920445	6.58	6.62	6.41	6.95	6.65	7.09	1.28	up	6.61E-02	8.95E-01	-	-
1383366_at	---	---	---	Rn.173554	BE107954	2.58	2.74	3.47	2.57	2.58	2.56	1.28	down	2.60E-01	8.95E-01	-	-
1395623_at	Qpctl	glutaminyl-peptide cyclotransferase-like	292687	Rn.100458	AW521959	4.62	3.52	3.21	3.75	4.10	4.59	1.28	up	5.05E-01	8.95E-01	-	-
1377071_at	---	---	---	Rn.146190	BG375652	4.05	3.19	4.16	4.05	4.29	4.14	1.28	up	3.12E-01	8.95E-01	-	-
1372106_at	Ehd4	EH-domain containing 4	192204	Rn.7379	BI284307	3.48	3.60	3.68	4.52	3.74	3.59	1.28	up	2.86E-01	8.95E-01	-	-
1380707_at	RGD1359616	similar to 2010321M09Rik protein	300782	Rn.9525	BE113229	3.90	2.76	2.47	2.78	2.50	2.76	1.28	down	4.65E-01	8.95E-01	-	-
1375417_at	Prkcbp1	protein kinase C binding protein 1	296374	Rn.219272	BM391419	4.58	3.18	2.44	3.71	2.69	2.72	1.28	down	6.38E-01	8.95E-01	-	-
1377949_s_at	Anks1a	ankyrin repeat and sterile alpha motif domain containing 1A	309639	Rn.116614	AA899043	5.18	5.78	4.53	5.64	5.34	5.59	1.28	up	3.89E-01	8.95E-01	-	-
1371333_at	---	---	---	Rn.201378	AI180251	7.07	7.82	8.15	7.69	8.41	8.02	1.28	up	3.98E-01	8.95E-01	-	-
1397913_at	---	---	---	---	AW526277	3.63	5.07	5.00	5.05	5.00	4.73	1.28	up	4.93E-01	8.95E-01	-	-
1382549_at	---	---	---	Rn.149104	AI071736	2.52	2.37	3.98	2.77	2.51	2.51	1.28	down	5.26E-01	8.95E-01	-	-
1372576_at	Exd2	exonuclease 3'-5' domain containing 2	362759	Rn.102	AI232347	5.07	4.97	4.91	5.32	5.07	5.65	1.28	up	1.09E-01	8.95E-01	-	-
1371790_at	Mrpl45	mitochondrial ribosomal protein L45	287656	Rn.107098	BI277658	5.92	5.92	5.28	5.95	5.93	6.33	1.28	up	2.23E-01	8.95E-01	-	-
1373069_at	Mrps30	mitochondrial ribosomal protein S30	294767	Rn.9312	BG378230	6.67	6.25	6.33	6.75	6.75	6.84	1.28	up	5.29E-02	8.95E-01	-	-
1379657_a_at	Znf511	zinc finger protein 511	293586	Rn.118322	BM386837	4.73	4.71	3.95	5.53	3.56	5.38	1.28	up	6.25E-01	8.95E-01	-	-
1382289_at	---	---	---	Rn.205025	BI291954	4.45	4.64	4.91	4.69	4.88	5.52	1.28	up	2.76E-01	8.95E-01	-	-
1373557_at	Mcm4	minichromosome maintenance complex component 4	29728	Rn.8341	AI145081	3.72	3.93	5.02	3.93	3.76	3.90	1.28	down	4.22E-01	8.95E-01	-	-
1390269_at	Tbc1d25	TBC1 domain family, member 25	302552	Rn.34141	BF418593	2.61	2.65	2.31	2.66	3.04	2.95	1.28	up	8.50E-02	8.95E-01	-	-
1370870_at	Met1	malic enzyme 1, NADP(+)-dependent, cytosolic	24552	Rn.3519	M30596	8.32	8.55	8.43	8.51	8.14	7.56	1.28	down	2.74E-01	8.95E-01	-	-
1372589_at	LOC683512	similar to Basic FGF-regressed Zic-binding protein (mbFZb)	683512	Rn.202684	AI177689	4.83	4.46	3.71	4.42	4.95	4.71	1.28	up	3.78E-01	8.95E-01	-	-
1373863_at	Map4k4	mitogen-activated protein kinase kinase kinase kinase 4	301363	Rn.101820	BM388810	3.74	5.38	2.84	4.79	3.74	4.50	1.28	up	6.78E-01	9.02E-01	-	-
1388765_at	Akt2	V-akt murine thymoma viral oncogene homolog 2	25233	Rn.87066	AA946508	5.81	4.95	4.75	4.55	4.80	5.08	1.28	down	3.71E-01	8.95E-01	-	-
1387002_at	Bud31	BUD31 homolog (yeast)	89819	Rn.8172	NM_053556	7.37	7.98	7.57	7.93	8.00	8.07	1.28	up	1.23E-01	8.95E-01	-	-
1381429_at	Mto1	Mitochondrial translation optimization 1 homolog (S. cerevisiae)	300852	Rn.216594	AI059116	2.46	2.44	2.47	2.45	3.58	2.42	1.28	up	4.00E-01	8.95E-01	-	-
1389722_at	---	---	---	Rn.146811	BF408457	3.91	3.60	3.46	3.54	4.32	4.20	1.28	up	2.62E-01	8.95E-01	-	-
1395154_at	Zc3h13	zinc finger CCCH type containing 13	305955	Rn.100827	BI288548	4.66	6.67	5.78	4.72	4.91	6.39	1.28	down	6.69E-01	9.00E-01	-	-
1377692_at	RGD1565310	similar to RIKEN cDNA 1110018J12	362697	Rn.14982	BF556583	3.99	3.76	4.02	3.45	3.56	3.66	1.28	down	2.41E-02	8.95E-01	-	-
1395944_at	RGD1310778	similar to Putative protein C21orf45	288272	Rn.137223	AI548667	3.58	2.41	2.45	2.42	2.54	2.40	1.28	down	4.04E-01	8.95E-01	-	-
1376060_at	---	---	---	Rn.155831	BF416794	5.63	4.71	5.82	6.10	5.55	5.60	1.28	up	4.04E-01	8.95E-01	-	-
1372758_at	---	---	---	Rn.988	BI282978	9.54	9.34	9.52	8.84	9.10	9.37	1.28	down	9.32E-02	8.95E-01	-	-
1383782_at	Spast	spastin	362700	Rn.41645	AI144975	5.09	6.03	5.61	6.29	5.45	6.07	1.28	up	1.89E-01	8.95E-01	-	-
1379140_at	---	---	---	Rn.147337	BF397054	3.67	3.09	3.01	2.79	2.97	2.92	1.28	down	1.71E-01	8.95E-01	-	-
1373240_at	Dhrs3	dehydrogenase/reductase (SDR family) member 3	313689	Rn.12011	BI276935	6.14	5.78	5.82	5.83	5.29	5.54	1.28	down	1.37E-01	8.95E-01	-	-
1392681_at	Rab2a	RAB2A, member RAS oncogene family	65158	Rn.44916	AW522578	9.51	9.65	9.81	10.23	9.86	9.97	1.28	up	6.24E-02	8.95E-01	-	-
1397684_at	Dkk2	dickkopf homolog 2 (Xenopus laevis)	295445	Rn.44861	BF549625	2.51	2.46	2.53	3.48	2.52	2.58	1.28	up	3.15E-01	8.95E-01	-	-
1375814_at	---	---	---	Rn.208440	BG380987	3.34	2.27	2.28	2.27	2.28	2.26	1.28	down	3.70E-01	8.95E-01	-	-
1382058_at	Rras2	related RAS viral (r-ras) oncogene homolog 2	365355	Rn.3271	BI292115	8.05	8.54	7.89	7.59	7.42	8.40	1.28	down	3.73E-01	8.95E-01	-	-
1398822_at	Gdi2	GDP dissociation inhibitor 2	29662	Rn.1441	BM387347	9.55	9.93	9.59	10.15	9.99	10.01	1.28	up	5.11E-02	8.95E-01	-	-
1398397_at	---	---	---	Rn.25061	AI407483	6.37	5.91	4.78	6.12	4.45	5.41	1.28	down	6.24E-01	8.95E-01	-	-
1383121_at	---	---	---	---	BM384218	6.80	6.10	6.70	6.79	7.01	6.88	1.28	up	1.88E-01	8.95E-01	-	-
1388377_at	Copa	coatomer protein complex subunit alpha	304978	Rn.203109	AW142717	8.12	8.17	8.23	8.68	8.91	9.01	1.28	up	3.90E-01	8.95E-01	-	-
1388059_a_at	Slc11a2	solute carrier family 11 (proton-coupled divalent metal ion transporters), memt	25715	Rn.11418	AF029757	3.64	4.39	4.55	4.07	3.33	4.09	1.28	down	3.93E-01	8.95E-01	-	-
1385504_at	Rffl	ring finger and FYVE like domain containing protein	282844	Rn.163140	AW524664	2.54	3.83	2.55	2.54	2.55	2.75	1.28	down	4.55E-01	8.95E-01	-	-
1392747_at	---	---	---	Rn.29397	AI030920	3.23	3.16	2.69	3.03	3.99	3.14	1.28	up	3.56E-01	8.95E-01	-	-
1378229_at	---	---	---	Rn.87338	BE118073	2.24	2.23	2.24	2.24	3.32	2.23	1.28	up	3.77E-01	8.95E-01	-	-
1387231_at	Mrs2	MRS2 magnesium homeostasis factor homolog (S. cerevisiae)	79032	Rn.33647	AF288290	2.47	4.39	2.40	3.04	2.48	2.66	1.28	down	6.21E-01	8.95E-01	-	-
1373443_a_at	Ankra2	ankyrin repeat, family A (RFXANK-like), 2	294679	Rn.161759	AI228292	4.37	4.66	5.60	4.65	4.14	4.76	1.28	down	4.37E-01	8.95E-01	-	-
1386918_at	Oprs1	opioid receptor, sigma 1	29336	Rn.1129	AF087827	4.15	5.71

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1371800_at	Phc2	polyhomeotic homolog 2 (Drosophila)	313038	Rn.2428	AI230538	3.64	4.07	4.29	3.67	3.57	3.69	1.28	down	1.41E-01	8.95E-01	-	-
1385302_at	Gdpd1	glycerophosphodiester phosphodiesterase domain containing 1	303407	Rn.138410	AW528213	2.57	2.50	2.53	3.66	2.53	2.48	1.28	up	4.05E-01	8.95E-01	-	-
1383101_at	Anapc10	anaphase promoting complex subunit 10	361389	Rn.9619	BF556463	3.25	3.27	3.63	3.96	3.87	3.40	1.28	up	1.66E-01	8.95E-01	-	-
1374939_at	Cyfip2	cytoplasmic FMR1 interacting protein 2	303073	Rn.44008	BE112927	3.31	2.57	2.42	2.42	2.43	2.38	1.28	down	2.66E-01	8.95E-01	-	-
1388250_at	Nfib	nuclear factor I/B	29227	Rn.219275	AB012232	6.07	6.70	6.25	6.44	5.38	6.13	1.28	down	3.86E-01	8.95E-01	-	-
1380118_at	Fdxacb1	ferredoxin-fold anticodon binding domain containing 1	315646	Rn.67727	BI275569	6.63	6.74	6.67	7.12	7.35	6.63	1.28	up	1.72E-01	8.95E-01	-	-
1388563_at	Gpbp1	GC-rich promoter binding protein 1	294734	Rn.33325	AI169287	7.51	8.20	7.88	8.34	7.82	8.49	1.28	up	2.80E-01	8.95E-01	-	-
1370809_at	Tubg1	tubulin, gamma 1	252921	Rn.154431	AB015946	4.56	4.03	3.77	3.72	3.77	3.80	1.28	down	1.99E-01	8.95E-01	-	-
1384147_at	Eif1a	eukaryotic translation initiation factor 1A	317163	Rn.3361	AA955540	6.82	6.89	6.91	6.62	7.36	7.72	1.28	up	3.34E-01	8.95E-01	-	-
1393220_at	---	---	---	Rn.204775	AI550323	4.35	3.51	4.95	3.63	3.68	4.42	1.28	down	5.05E-01	8.95E-01	-	-
1380865_at	---	---	---	Rn.211658	BF418059	6.75	6.27	4.64	6.17	6.16	6.39	1.28	up	6.08E-01	8.95E-01	-	-
1372173_at	RGD1309198	similar to U5 snRNP-specific protein (Prp8-binding)	313056	Rn.15351	AI407945	3.50	3.20	3.21	3.21	3.85	3.93	1.28	up	2.24E-01	8.95E-01	-	-
1379422_at	Alg13	asparagine-linked glycosylation 13 homolog (S. cerevisiae)	300284	Rn.29819	AI145871	6.35	7.29	6.85	6.83	7.57	7.16	1.28	up	3.59E-01	8.95E-01	-	-
1391070_at	RGD1566220	similar to hypothetical MGC48595	500892	Rn.20869	AW915526	2.37	3.55	3.27	2.60	2.39	3.14	1.28	down	4.42E-01	8.95E-01	-	-
1392641_at	LOC691543	Hypothetical protein LOC691543	691543	Rn.55420	AA957091	5.99	4.06	3.19	4.07	3.55	4.55	1.28	down	7.04E-01	9.07E-01	-	-
1375289_at	---	---	---	Rn.22461	BM387047	8.71	8.60	9.18	8.60	8.52	8.30	1.28	down	1.47E-01	8.95E-01	-	-
1383321_at	Tpst1	tyrosylprotein sulfotransferase 1	288617	Rn.144004	BG376248	3.73	2.94	2.96	3.19	2.49	2.88	1.28	down	3.39E-01	8.95E-01	-	-
1380079_at	RGD1561472	similar to mKIAA2005 protein	500012	Rn.48221	AW533923	3.31	2.59	2.43	2.42	2.42	2.41	1.28	down	2.57E-01	8.95E-01	-	-
1367644_at	Adcy6	adenylate cyclase 6	25289	Rn.3313	NM_012821	3.71	3.36	3.24	3.11	3.12	3.01	1.28	down	7.00E-02	8.95E-01	-	-
1374782_at	---	---	---	Rn.51810	BF419834	5.57	5.47	5.37	4.63	5.40	5.31	1.28	down	2.26E-01	8.95E-01	-	-
1374045_at	Cog8	component of oligomeric golgi complex 8	291990	Rn.3024	AI598851	4.73	4.25	3.91	3.94	3.94	3.94	1.28	down	2.05E-01	8.95E-01	-	-
1388704_at	---	---	---	---	AA892394	7.55	7.47	7.41	6.71	7.25	7.40	1.28	down	1.67E-01	8.95E-01	-	-
1374622_at	---	---	---	Rn.9546	BE107309	6.18	6.91	6.58	5.93	6.18	6.49	1.28	down	2.51E-01	8.95E-01	-	-
1377714_at	Pvrl3	Poliovirus receptor-related 3	288124	Rn.56373	AI030979	2.79	3.90	4.63	4.78	3.33	4.28	1.28	up	6.30E-01	8.95E-01	-	-
1373004_at	Dnajc2	DnaJ (Hsp40) homolog, subfamily C, member 2	116456	Rn.11908	AA964764	5.99	6.73	6.79	6.01	5.68	6.75	1.28	down	4.33E-01	8.95E-01	-	-
1378096_at	Kif5b	kinesin family member 5B	117550	Rn.4046	AA924572	5.17	5.23	5.55	4.74	4.67	5.47	1.28	down	2.75E-01	8.95E-01	-	-
1388251_at	Prkci	protein kinase C, iota	84026	Rn.1388	AB020615	6.64	6.78	6.11	6.08	5.30	6.08	1.28	down	5.81E-01	8.95E-01	-	-
1376607_a_at	RGD1310414	similar to hypothetical protein FLJ23263	290811	Rn.12987	BG380154	2.74	2.75	3.93	2.76	2.91	2.67	1.28	down	4.23E-01	8.95E-01	-	-
1397854_at	Dpf3	D4, zinc and double PHD fingers, family 3	299186	Rn.38975	BI275309	2.67	2.62	2.73	2.60	3.88	2.61	1.28	up	4.49E-01	8.95E-01	-	-
1392405_at	Tfdp2	transcription factor Dp-2 (E2F dimerization partner 2)	300947	Rn.105731	AI177322	3.52	4.32	4.34	4.55	4.33	4.37	1.28	up	2.72E-01	8.95E-01	-	-
1367777_at	Decr1	2,4-dienoyl CoA reductase 1, mitochondrial	117543	Rn.2854	NM_057197	9.77	9.73	9.93	9.46	9.04	9.87	1.28	down	2.22E-01	8.95E-01	-	-
1392770_at	Neo1	neogenin homolog 1 (chicken)	81735	Rn.10667	BF415817	6.07	7.14	6.57	5.86	6.50	6.36	1.28	down	3.82E-01	8.95E-01	-	-
1392529_at	Spry4	sprouty homolog 4 (Drosophila)	291610	Rn.146922	BI294478	4.37	4.29	4.66	4.57	3.66	4.02	1.28	down	2.82E-01	8.95E-01	-	-
1398778_at	Psma1	proteasome (prosome, macropain) subunit, alpha type 1	29668	Rn.2668	NM_017278	8.55	7.96	8.60	8.07	7.64	8.33	1.28	down	2.83E-01	8.95E-01	-	-
1373936_at	Rnf44	Ring finger protein 44	361212	Rn.21345	AI407107	6.23	6.63	5.53	6.30	6.59	6.57	1.28	up	3.49E-01	8.95E-01	-	-
1368279_at	Mllt3	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila);	114510	Rn.22828	NM_053718	4.76	5.85	6.14	6.53	5.57	5.73	1.28	up	5.27E-01	8.95E-01	-	-
1383639_at	---	---	---	Rn.8327	AA924348	3.32	2.59	2.50	2.42	2.47	2.46	1.28	down	2.42E-01	8.95E-01	-	-
1367754_a_at	Asl	argininosuccinate lyase	59085	Rn.64591	NM_031309	8.76	8.78	7.95	8.92	8.81	8.83	1.28	up	2.65E-01	8.95E-01	-	-
1372581_at	Snf8	SNF8, ESCRT-II complex subunit, homolog (S. cerevisiae)	287645	Rn.162167	BF282487	8.04	9.26	9.46	9.25	9.19	9.38	1.28	up	4.72E-01	8.95E-01	-	-
1380865_at	---	---	---	Rn.147102	BM385284	2.69	3.15	4.08	3.31	3.29	4.38	1.28	up	5.49E-01	8.95E-01	-	-
1376813_at	Lpcat3	lysophosphatidylcholine acyltransferase 3	362434	Rn.19543	BI295855	5.17	3.69	5.00	4.23	3.85	4.71	1.28	down	5.37E-01	8.95E-01	-	-
1371585_at	Gspt1	G1 to S phase transition 1	24420	Rn.72491	BE108192	6.91	7.45	7.39	7.25	7.44	8.12	1.28	up	3.22E-01	8.95E-01	-	-
1385322_at	---	---	---	---	AI602154	3.36	3.90	3.34	3.20	3.13	3.20	1.28	down	1.28E-01	8.95E-01	-	-
1388733_at	Bfar	bifunctional apoptosis regulator	304709	Rn.159939	AI177631	3.65	3.64	3.66	3.39	4.57	4.06	1.28	up	3.55E-01	8.95E-01	-	-
1391304_at	LOC363188	similar to ubiquitin protein ligase E3 component n-recognin 2	363188	Rn.67473	BM388658	2.29	2.28	3.60	2.29	2.29	2.53	1.28	down	4.71E-01	8.95E-01	-	-
1392957_at	Ssbp2	single-stranded DNA binding protein 2	361877	Rn.137445	BF565151	4.43	4.39	4.42	5.11	4.81	4.38	1.28	up	1.67E-01	8.95E-01	-	-
1394778_at	---	---	---	Rn.206780	BE116111	3.22	2.74	2.78	2.74	2.62	2.31	1.28	down	1.48E-01	8.95E-01	-	-
1383414_at	RGD1308117	similar to 9930012K11Rik protein	361066	Rn.104374	BG373072	2.55	2.53	2.46	2.60	2.46	2.46	1.28	down	3.37E-01	8.95E-01	-	-
1369052_at	Zfp111	zinc finger protein 111	170849	Rn.10168	NM_133323	2.96	3.22	2.90	3.22	3.24	3.69	1.28	up	1.21E-01	8.95E-01	-	-
1370026_at	Cryab	crystallin, alpha B	25420	Rn.98208	NM_012935	8.02	11.54	10.50	10.07	10.69	10.35	1.28	up	7.54E-01	9.20E-01	-	-
1380365_at	---	---	---	Rn.147925	BF403932	2.71	2.47	2.70	3.56	2.70	2.68	1.28	up	3.03E-01	8.95E-01	-	-
1382735_at	Atg12	ATG12 autophagy related 12 homolog (S. cerevisiae)	361321	Rn.6224	BF563278	3.59	3.38	4.56	3.79	3.37	3.31	1.28	down	4.18E-01	8.95E-01	-	-
1373315_at	Amt2	aryl hydrocarbon receptor nuclear translocator 2	25243	Rn.10518	AI176425	2.46	2.46	2.49	3.55	2.49	2.43	1.28	up	3.85E-01	8.95E-01	-	-
1374973_at	Med25	mediator complex subunit 25	292889	Rn.23798	AA892531	3.37	3.32	3.25	3.57	4.07	3.36	1.28	up	1.70E-01	8.95E-01	-	-
1373023_at	---	---	---	Rn.221897	BF283704	6.26	6.06	5.95	5.11	5.85	6.26	1.28	down	3.66E-01	8.95E-01	-	-
1375692_at	---	---	---	Rn.163633	AI229025	6.03	5.05	5.25	5.60	5.80	5.99	1.28	up	3.29E-01	8.95E-01	-	-
1382263_at	Odf2l	outer dense fiber of sperm tails 2-like	685425	Rn.139568	AI511280	3.63	4.33	2.62	2.64	3.05	3.82	1.28	down	5.89E-01	8.95E-01	-	-
1371887_at	Hmgb3	high mobility group box 3	305373	Rn.203482	BF398549	6.96	7.71	7.27	7.51	7.98	7.51	1.28	up	2.56E-01	8.95E-01	-	-
1374636_at	Phf17	PHD finger protein 17	310352	Rn.90858	BI298596	5.85	7.55	7.00	7.11	7.04	7.32	1.28	up	5.23E-01	8.95E-01	-	-
1367596_at	Rps26	ribosomal protein S26	27139	Rn.135639	NM_013224	10.35	10.34	10.16	10.42	10.56	10.95	1.28	up	1.06E-01	8.95E-01	-	-
1398981_at	Triap1	TP53 regulated inhibitor of apoptosis 1	691278	Rn.160852	AI171951	7.65	7.88	7.68	7.40	6.95	7.79	1.28	down	2.34E-01	8.95E-01	-	-
1388857_at	Sec23b	Sec23 homolog B (S. cerevisiae)	362226	Rn.8735	BF289044	6.38	6.07	6.23	6.62	6.16	6.96	1.28	up	2.27E-01	8.95E-01	-	-
1389322_at	Pdcd7	programmed cell death 7	363082	Rn.8408	AI013847	6.59	6.59	7.44	6.34	6.37	6.86	1.28	down	3.43E-01	8.95E-01	-	-
1389714_at	---	---	---	Rn.203391	AI103146	5.36	6.00	5.50	6.01	5.59	6.33	1.28	up	2.89E-01	8.95E-01	-	-
1395079_at	---	---	---	Rn.35112	AI454784	3.73	2.94	3.48	3.25	2.55	3.29	1.28	down	3.50E-01	8.95E-01	-	-
1398909_at	LOC301124	hypothetical LOC301124	301124	Rn.4199	AA849634	9.11	9.41	9.31	9.58	9.66	9.66	1.28	up	1.96E-02	8.95E-01	-	-
1373627_at	Inpp5k	Inositol polyphosphate-5-phosphatase K	287533	Rn.7440	BI289104	2.82	3.95	2.57	3.16	4.10	3.15	1.28	up	5.40E-01	8.95E-01	-	-
1370381_at	Pnrc1	proline-rich nuclear receptor coactivator 1	286988	Rn.10967	BF409210	7.29	7.24	7.29	7.18	8.28	7.41	1.28	up	3.48E-01	8.95E-01	-	-
1379010_at	Sfrs3	Splicing factor, arginine/serine-rich 3	361814	Rn.9002	AA956727	2.49	2.69	2.57	3.53	2.63	2.66	1.28	up	3.01E-01	8.95E-01	-	-
1391888_at	Adarb1	adenosine deaminase, RNA-specific, B1	25367	Rn.89675	AW253867	2.43	2.42	2.53	3.59	2.43	2.42	1.28	up	4.16E-01	8.95E-01	-	-
1397014_at	---	---	---	---	BF419776	2.39	2.40	2.48	3.53	2.41	2.40	1.28	up	4.02E-01	8.95E-01	-	-
1392479_at	---	---	---	Rn.202627	AA925694	2.49	2.83	2.67	2.69	2.63	3.73	1.28	up	3.94E-01	8.95E-01	-	-
1379473_at	RGD1307509	similar to RIKEN cDNA 1700108L22	310348	Rn.7988	BI284815	5.97	6.57	7.33	5.92	6.98	5.92	1.28	down	5.39E-01	8.95E-01	-	-
1371904_at	Smyd2	SET and MYND domain containing 2	289372	Rn.7052	BI294698	5.70	6.25	5.78	6.76	5.57	6.45	1.28	up	4.19E-01	8.95E-01	-	-
1373208_at	---	---	---	Rn.9106	BE113371	2.48	2.48	3.56	2.48	2.49	2.49	1.28	down	3.81E-01	8.95E-01	-	-
1375793_at	Mll1	myeloid/lymphoid or mixed-lineage leukemia 1	315606	Rn.62341	BI295700	3.84	3.52	2.93	3.86	3.89	3.60	1.28	up	2.75E-01	8.95E-01	-	-
1386399_at	---	---	---	Rn.133577	H31411	2.55	3.52	2.93	3.56	2.66	3.85	1.28	up	4.80E-01	8.95E-01	-	-
1385871_at	Dhx36	DEAH (Asp-Glu-Ala-His) box polypeptide 36	310461	Rn.2744	AI237532	7.07	5.79	5.80	6.05	5.48	6.06	1.28	down	4.92E-01	8.95E-01	-	-
1369961_at	Pyap2a	phosphatidic acid phosphatase type 2A	64369	Rn.61687	NM_022538	4.43	5.47	3.47	4.35	3.87	4.08	1.28	down	5.82E-01	8.95E-01	-	-
1379395_a_at	Hint2	histidine triad nucleotide binding protein 2	313491	Rn.11657	BI280018	9.63	10.23	10.28	10.45	10.18	10.56	1.28	up	2.14E-01	8.95E-01	-	-
1384536_at	---	---	---	---	BE105669	2.40	2.39	2.43	2.40	3.44	2.46	1.28	up	3.54E-01	8.95E-01	-	-
1398344_at	Med17	mediator complex subunit 17	300367	Rn.17278	BI287962	2.74	4.35	3.31	2.64	3.32	3.38	1.28	down	5.39E-01	8.95E-01	-	-
1373639_at	RGD1565675	similar to RIKEN cDNA 2410022L05	290925	Rn.24956	BE115570	7.70	9.05	8.10	8.59	8.45	8.87	1.28	up	4.46E-01	8.95E-01	-	-
1375529_at	Cbr4	carbonyl reductase 4	359725	Rn.3599	BF404908	7.85	7.83	8.34	8.07	8.26	8.74	1.28	up	2.48E-01	8.95E-01	-	-
1375680_at	---	---	---	---	BG380705	5.09	4.85	5.36	4.77	4.84	4.62	1.28	down	9.11E-02	8.95E-01	-	-
1371687_at	Canx	calnexin	29144	Rn.1762	AA848326	10.20	10.81	11.09	11.06	10.73	11.36	1.28	up	3.30E-01	8.95E-01	-	-
1393325_at	Gtpbp6	GTP binding protein 6 (putative)	363931	Rn.98504	BG378917	3.38	3.97	3.49	3.47	3.48	2.82	1.28	down	2.83E-01	8.95E-01	-	-
1390497_at	---	---	---	Rn.20866	AI175594	3.51	4.51	4.14	4.51	4.53	4.17	1.28	up	3.24E-01	8.95E-01	-	-
1390746_at	---	---	---	Rn.147902	BE112048	2.46	2.54	2.53	2.50	3.19	2.90	1.28	up	1.56E-01	8.95E-01	-	-
1393335_at	Egfl6	EGF-like-domain, multiple 6	317470	Rn.21946	BF418373	3.71	5.51	5.60	4.95	5.37	5.57	1.28	up	6.12E-01	8.95E-01	-	-
1379567_at	Med13	mediator complex subunit 13	303403	Rn.94023	AI105643	5.72	5.04	5.86	4.80	5.07	5.69	1.28	down	3.91E-01	8.95E-01	-	-
1371788_at	Zmat5	zinc finger, matrin type 5	501926	Rn.3249	AI230061	7.23	5.82	5.68	6.00	5.85	5.81	1.28	down	5.17E-01	8.95E-01	-	-
1372932_at	Rrp1	ribosomal RNA processing 1 homolog (S. cerevisiae)	309874	Rn.104084	BI302258	6.74	7.29	7.28	7.48	7.36	7.53	1.28	up	1.34E-01	8.95E-01	-	-
1376499_at	Agap3	ArfGAP with GTPase domain, ankyrin repeat and PH domain 3	362300	Rn.98623	AW252124	3.90	4.15	3.39	2.84	4.18	3.37	1.28	down	4.74E-01	8.95E-01	-	-
1373442_at	Os9	amplified in osteosarcoma	362891	Rn.1579	AI169058	5.90	5.48	6.93	5.53	5.83	5.89	1.28	down	4.70E-01	8.95E-01	-	-
1369278_at	Gna12	guanine nucleotide binding protein, alpha 12	81663	Rn.10497	NM_031034	4.41	4.48	4.39	4.96	4.45	4.92	1.28	up	1.04E-01	8.95E-01	-	-
1390285_at	Efcab4a	EF-hand calcium binding domain 4A	309112	Rn.13220	AI178948	6.25	7.30	6.84	6.43	6.50	6.41	1.28	down	3.14E-01	8.95E-01	-	-
1384302_at	Slc6a17	solute carrier family 6 (neurotransmitter transporter), member 17	613226	Rn.186904	AI712791	4.77	5.65	7.39	6.39	5.71	6.77	1.28	up	6.93E-01	9.05E-01	-	-
1375956_at	Mnat1	menage a trois homolog 1, cyclin H assembly factor (Xenopus laevis)	266713	Rn.15168	AI104569	3.38	3.84	3.78	3.95	3.79	4.31	1.28	up	1.68E-01	8.95E-01	-	-
1393414_at	LOC689176	similar to transmembrane protein 64	689176	---	AW142650	4.67	4.75	5.08	4.69	4.67	5.09	1.28	down	5.02E-01	8.95E-01	-	-
1391029_at	---	---	---	Rn.164691	BF285477	3.86	2.36	2.37	2.83	2.37	2.34	1.28	down	5.37E-01	8.95E-01	-	-
1397122_at	---	---	---	Rn.57978	BF393071	4.17	3.29	3.25	2.62	2.67	4.35	1.28	down	6.13E-01	8.95E-01	-	-
1376228_at	Msl1	male-specific lethal 1 homolog (Drosophila)	303514	Rn.22437	BI285463	3.36	4.44	4.29	3.01	3.64	4.38	1.28	down	5.35E-01	8.95E-01	-	-
1371878_at	Maml1	mastermind like 1 (Drosophila)	303101	Rn.2394	BI294787	2.74	2.74	3.80	2.74	2.75	2.73	1.28	down	3.74E-01	8.95E-01	-	-
1377602_at	Nudt2	nudix (nucleoside diphosphate linked moiety X)-type motif 2	297998	Rn.40265	BF284944	7.76	8.72	7.23	8.05	8.46	8.26	1.28	up	4.77E-01	8.95E-01	-	-
1393910_at	Fam13a1	family with sequence similarity 13, member A1	362378	Rn.47690	BF563968	8.33	8.01	6.14	7.53	7.71	8.30	1.28	up	6.50E-01	8.98E-01	-	-
1376681_at	Rrp8	ribosomal RNA processing 8, methyltransferase, homolog (yeast)	308911	Rn.14828	AI177038	4.21	4.44	3.93	4.09	4.22	5.32	1.28	up	4.43E-01	8.95E-01	-	-
1383369_at	Trim26	tripartite motif-containing 26	309586	Rn.163420	AI028875	3.78	3.92	3.55	3.54	3.11	3.54	1.28	down	1.18E-01	8.95E-01	-	-
1390244_at	Spats2	spermatogenesis associated, serine-rich 2	300221	Rn.52841	AF418231	6.92	7.23	7.36	6.93	6.61	6.91	1.28	down	1.04E-01	8.95E-01	-	-
1384957_at	Atf6	activating transcription factor 6	304962	Rn.15235	AI059385	3.96	3.60	2.77	3.84	2.68	2.75	1.28	down	5.31E-01	8.95E-01	-	-
1386518_at	Irf2	interferon regulatory factor 2	290749	Rn.107887	BI294557	5.17	4.55	2.68	3.99	3.16	4.19	1.28	down	6.87E-01	9.04E-01	-	-
1369027_at	A4galt	alpha 1,4-galactosyltransferase	63888	Rn.48584	NM_022240	3.27	2.86	3.15	2.88	2.90	2.45	1.28	down	1.38E-01	8.95E-01	-	-
1374896_at	---	---	---	Rn.22798	AI101385	6.25	6.42	6.23	6.52	6.63	6.80	1.28	up	2.48E-02	8.95E-01	-	-
1369972_at	Fbxo21	F-box protein 21	360818	Rn.137498	NM_057108	6.11	6.23	6.88	5.58	6.15	6.43	1.28	down	3.66E-01	8.95E-01	-	-
1390157_at	---	---	---	Rn.21816	BI295124	9.23	8.83	8.97	8.54	8.60	8.83	1.28	down	7.37E-02	8.95E-01	-	-
1374000_at	Helz	helicase with zinc finger domain	287773	Rn.19942	BI285893	4.80	2.80	2.36	2.81	3.11	2.78	1.28	down	6.39E-01	8.95E-01	-	-
1386889_at	Scd	stearoyl-CoA desaturase (delta-9-desaturase)	83792	Rn.83595	BE107760	2.34	2.34	2.34	2.45	2.34	3.29	1.28	up	3.04E-01	8.95E-01	-	-
1367854_at	Acly	ATP citrate lyase	24159	Rn.29771	NM_016987	8.77	8.19	8.64	8.20	8.19	8.15	1.28	down	1.19E-01	8.95E-01	-	-
1396086_at	Tmem97	transmembrane protein 97	303330	Rn.20057	H31931	2.95	3.16	3.16	3.13	4.09	3.10	1.28	up	3.50E-01	8.95E-01	-	-
1369956_at	Ifngr1	interferon gamma receptor 1	116465	Rn.19927	NM_053783	4.89	5.60	5.30	5.97	5.45	5.43	1.28	up	2.65E-01	8.95E-01	-	-
1372111_at	Cav1	caveolin 1, caveolae protein	25404	Rn.22518	BI285449	3.99	2.33	2.44	2.45	4.94	2.43	1.28	up	7.40E-01	9.16E-01	-	-
1389427_at	---	---	---	---	BM386487	2.40	2.81	2.94	2.32	2.33	2.44	1.28	down	1.04E-01	8.95E-01	-	-
1384034_at	Vamp4	vesicle-associated membrane protein 4	364033	Rn.105555	D86817	3.90	3.90	3.88	4.15	4.27	4.32	1.28	up	1.89E-03	8.95E-01	-	-
1370236_at	Pptt	palmitoyl-protein thioesterase 1	29411	Rn.1574	AI234353	6.44	6.35	4.45	6.62	5.46	6.22	1.28	up	6.56E-01	8.98E-01	-	-
1394441_at	---	---	---	Rn.168018	AW528593	5.43	5.87	6.18	5.92	6.69	5.93	1.28	up	3.53E-01	8.95E-01	-	-
1387296_at	Cyp2j4	cytochrome P450, family 2, subfamily J, polypeptide 4	65210	Rn.44992	NM_023025	8.37	8.39	8.39	8.73	8.56	8.92	1.28	up	2.63E-02	8.95E-01	-	-
1379098_at	---	---	---	Rn.204304	AI071602	2.89	2.85	2.16	2.85	2.95	3.15	1.28	up	2.35E-01	8.95E-01	-	-
1384489_at	Fbxl11	F-box and leucine-rich repeat protein 11	361700	Rn.12228	BM387189	5.37	6.56	4.78	6.86	4.84	6.06	1.28	up	6.78E-01	9.02E-01	-	-
1367994_at	Dpyd	dihydropyrimidine dehydrogenase	81656	Rn.158382	NM_031027	6.28	6.49	5.34	6.24	5.86	7.07	1.28	up	5.24E-01	8.95E-01	-	-
1377846_a_at	---	---	---	---	AA819391	5.52	6.08	5.92	6.28	6.58	5.72	1.28	up	3.12E-01	8.95E-01	-	-
1390778_at	---	---	---	Rn.220236	AI556731	8.23	7.56	7.95	8.06	8.32	8.41	1.28	up	1.85E-01	8.95E-01	-	-
1389553_at	Clec4a3	C-type lectin domain family 4, member a3	362431	Rn.137522	BF393825	2.53	2.53	4.96	2.65	3.78	2.54	1.28	down	7.17E-01	9.10E-01	-	-
1383556_at	---	---	---	Rn.23397	AI575798	2.40	2.40	3.46	2.40	2.41	2.40	1.28	down	3.75E-01	8.95E-01	-	-
1394163_at	---	---	---	Rn.165314	AA864809	3.40	4.08	3.04	3.19	5.04	3.33	1.28	up	6.27E-01	8.95E-01	-	-
1372369_at	Tmem109	transmembrane protein 109	361732	Rn.1105	AI172075	3.77	3.79	3.40	4.03	3.92	4.07	1.28	up	6.11E-02	8.95E-01	-	-
1393009_at	RGD1309326	similar to RIKEN cDNA 2410002F23	308568	Rn.145001	AI535126	4.33	4.33	3.79	4.52	4.82	4.16	1.28	up	2.56E-01	8.95E-01	-	-
1372276_at	Agpat3	1-acylglycerol-3-phosphate O-acyltransferase 3	294324	Rn.100251	BG378613	5.41	6.21	5.77	5.82	4.59	5.94	1.28	down	5.14E-01	8.95E-01	-	-
1373543_at	---	---	---	Rn.15116	BI296461	3.49	4.16	6.53	4.20	4.73	4.20	1.28	down	7.28E-01	9.13E-01	-	-
1375911_at	RGD735140	hypothetical protein LK44	362219	Rn.11612	AI171772	3.54	3.72	4.26	4.04	4.62	3.91	1.28	up	3.18E-01	8.95E-01	-	-
1393

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1372300_at	Dok4	docking protein 4	361364	Rn.219052	BI288838	5.35	4.59	4.27	4.39	4.25	4.52	1.27	down	3.49E-01	8.95E-01	-	-
1376273_at	Rnasen	ribonuclease type III, nuclear	310159	Rn.41113	BI285089	5.64	5.61	5.11	6.08	5.63	5.71	1.27	up	1.90E-01	8.95E-01	-	-
1376247_at	Pck2	phosphoenolpyruvate carboxykinase 2 (mitochondrial)	361042	Rn.35508	BF403197	2.49	2.40	2.42	3.14	2.50	2.71	1.27	up	1.45E-01	8.95E-01	-	-
1374467_at	Trap1	TNF receptor-associated protein 1	287069	Rn.144695	BM389034	7.64	8.06	6.27	7.32	7.48	8.21	1.27	up	5.95E-01	8.95E-01	-	-
1398450_at	---	---	---	Rn.169451	BI291373	6.87	7.87	6.79	6.48	6.21	7.79	1.27	down	5.93E-01	8.95E-01	-	-
1396251_at	---	---	---	Rn.217043	BM384713	3.83	4.02	4.18	3.72	3.66	3.60	1.27	down	3.29E-02	8.95E-01	-	-
1375388_at	---	---	---	Rn.207831	BF400832	3.23	2.64	2.43	2.42	2.44	2.39	1.27	down	2.23E-01	8.95E-01	-	-
1371089_at	Yc2	glutathione S-transferase Yc2 subunit	494500	Rn.120929	AA945082	2.61	2.57	2.58	3.65	2.57	2.58	1.27	up	3.87E-01	8.95E-01	-	-
1375886_at	---	---	---	Rn.8314	AI236778	7.27	7.08	7.33	6.58	6.94	7.11	1.27	down	1.17E-01	8.95E-01	-	-
1379630_at	---	---	---	Rn.37735	AI105051	3.15	3.99	3.14	3.13	2.97	3.13	1.27	down	2.92E-01	8.95E-01	-	-
1385153_at	Zfp68	zinc finger protein 68	304337	Rn.144939	AI555743	4.65	4.39	4.17	4.04	4.46	5.75	1.27	up	5.50E-01	8.95E-01	-	-
1387659_at	Gda	guanine deaminase	83585	Rn.161897	AF245172	4.33	5.59	5.17	5.23	5.67	5.22	1.27	up	4.33E-01	8.95E-01	-	-
1373655_at	RGD1309888	similar to RIKEN cDNA 1500002O20	365215	Rn.32677	BG371863	5.80	6.41	6.35	7.12	7.86	6.53	1.27	down	7.51E-01	9.19E-01	-	-
1374308_at	Sec14l2	SEC14-like 2 (S. cerevisiae)	116486	Rn.46850	AI576603	3.56	5.82	2.72	2.59	3.81	4.66	1.27	down	7.69E-01	9.24E-01	-	-
1373822_at	309998 /// RGD15	similar to Chain A, Solution Structure Of The Bola-Like Protein From Mus Mu	367088 /// 502367	---	BI275708	10.70	10.48	10.92	11.08	10.86	11.19	1.27	up	9.46E-02	8.95E-01	-	-
1379663_at	---	---	---	Rn.203418	AI010254	4.23	4.47	4.20	5.04	3.93	4.97	1.27	up	3.99E-01	8.95E-01	-	-
1383637_at	---	---	---	Rn.15608	AA925807	3.26	3.08	4.69	3.32	3.27	3.39	1.27	down	5.33E-01	8.95E-01	-	-
1390952_at	Rcor1	REST corepressor 1	314458	Rn.32217	AI144822	3.42	3.48	3.18	3.16	2.87	3.00	1.27	down	4.75E-02	8.95E-01	-	-
1389181_at	---	---	---	Rn.205765	BM389650	4.08	5.63	6.10	6.21	4.63	6.02	1.27	up	6.81E-01	9.03E-01	-	-
1373006_at	Tmem171	transmembrane protein 171	293634	Rn.102124	AI230291	3.47	2.68	2.80	2.58	2.65	2.67	1.27	down	2.31E-01	8.95E-01	-	-
1372172_at	Nphp1	nephronophthisis 1 (juvenile) homolog (human)	296136	Rn.32744	BM386289	4.88	4.19	4.05	3.77	4.03	4.27	1.27	down	3.04E-01	8.95E-01	-	-
1389552_at	Gcc2	GRIP and coiled-coil domain containing 2	309798	Rn.139579	BG371715	6.84	6.54	6.03	6.90	6.60	6.95	1.27	up	2.52E-01	8.95E-01	-	-
1372219_at	Tpm2	tropomyosin 2	500450	Rn.17580	AA012755	6.26	2.80	3.51	5.30	4.40	3.91	1.27	up	7.74E-01	9.26E-01	-	-
1376931_at	RGD1305020	similar to Hepatocellular carcinoma-associated antigen 58 homolog	311575	Rn.38255	BG380736	4.23	4.16	3.88	4.50	4.19	4.63	1.27	up	1.08E-01	8.95E-01	-	-
1383288_at	Mdm2	Mdm2 p53 binding protein homolog (mouse)	314856	Rn.91829	BE117716	7.45	6.07	7.16	6.60	6.39	6.65	1.27	down	4.63E-01	8.95E-01	-	-
1380685_at	---	---	---	Rn.164618	AI103408	5.74	6.22	4.42	5.57	5.47	6.38	1.27	up	6.01E-01	8.95E-01	-	-
1393391_at	Tgs1	trimethylguanosine synthase homolog (S. cerevisiae)	312947	Rn.48378	BF406888	2.81	2.41	3.27	2.81	3.93	2.79	1.27	up	4.85E-01	8.95E-01	-	-
1399069_at	---	---	---	---	AI234008	4.17	5.38	4.92	4.93	5.29	5.29	1.27	up	4.03E-01	8.95E-01	-	-
1386530_at	---	---	---	Rn.205013	AW141081	3.18	2.70	2.48	2.46	2.45	2.41	1.27	down	1.72E-01	8.95E-01	-	-
1398898_at	---	---	---	Rn.203884	BI278623	6.75	7.43	6.86	7.03	7.44	7.61	1.27	up	2.71E-01	8.95E-01	-	-
1376036_at	Flvcr2	feline leukemia virus subgroup C cellular receptor family, member 2	314323	Rn.92663	AI180408	2.35	2.61	2.42	2.56	3.20	2.67	1.27	up	1.77E-01	8.95E-01	-	-
1381234_at	---	---	---	---	BF398454	3.38	2.34	2.35	2.34	2.36	2.32	1.27	down	3.71E-01	8.95E-01	-	-
1381208_at	Hist3h2a	histone cluster 3, H2a	64646	Rn.198869	BE104595	3.65	4.69	4.89	3.94	3.94	4.31	1.27	down	4.37E-01	8.95E-01	-	-
1389645_at	Prodh2	proline dehydrogenase (oxidase) 2	361538	Rn.4247	AI233266	9.95	8.23	8.61	9.44	9.66	8.73	1.27	up	5.91E-01	8.95E-01	-	-
1388514_at	Ppm1g	protein phosphatase 1G (formerly 2C), magnesium-dependent, gamma isofor	259229	Rn.16969	BI285247	5.86	5.76	5.54	5.71	6.69	5.79	1.27	up	3.51E-01	8.95E-01	-	-
1376059_at	---	---	---	---	AI716607	5.88	6.65	5.48	5.40	5.80	5.78	1.27	down	4.00E-01	8.95E-01	-	-
1381381_at	---	---	---	Rn.209652	BF416088	2.53	2.48	2.55	3.52	2.55	2.52	1.27	up	3.54E-01	8.95E-01	-	-
1397557_at	Gtf2h1	general transcription factor IIH, polypeptide 1	361580	Rn.24733	BF524412	2.90	3.36	4.30	3.21	3.11	3.11	1.27	down	4.48E-01	8.95E-01	-	-
1393702_at	Xrn2	5'-3' exoribonuclease 2	362229	Rn.64021	BF397290	6.07	6.15	4.65	5.08	4.74	6.01	1.27	down	6.05E-01	8.95E-01	-	-
1392795_at	Sema6a	Sema domain, transmembrane domain (TM), and cytoplasmic domain, (sema	361324	Rn.203621	AA963069	2.63	3.29	2.47	2.43	2.45	2.46	1.27	down	2.39E-01	8.95E-01	-	-
1379067_at	Gga3	golgi associated, gamma adaptin ear containing, ARF binding protein 3	360658	Rn.198912	AA956006	3.53	4.35	3.23	3.42	4.57	4.15	1.27	up	5.06E-01	8.95E-01	-	-
1382228_at	---	---	---	Rn.24101	BE095590	2.42	2.43	3.63	2.34	2.47	2.62	1.27	down	4.45E-01	8.95E-01	-	-
1398230_at	---	---	---	Rn.207920	BF394178	2.47	2.39	2.47	3.42	2.47	2.47	1.27	up	3.38E-01	8.95E-01	-	-
1370215_at	C1qb	complement component 1, q subcomponent, beta polypeptide	29687	Rn.6702	AW434057	2.48	2.47	2.50	2.47	3.35	2.67	1.27	up	2.61E-01	8.95E-01	-	-
1394450_at	---	---	---	Rn.40570	AI228600	3.20	3.17	2.63	3.20	3.41	3.44	1.27	up	1.57E-01	8.95E-01	-	-
1382470_at	---	---	---	Rn.164958	AA955357	3.03	2.93	2.47	2.43	2.41	2.54	1.27	down	1.23E-01	8.95E-01	-	-
1372862_at	Rab22a	RAB22A, member RAS oncogene family	366265	Rn.37799	BM390237	3.86	4.82	3.72	4.84	4.51	4.08	1.27	up	4.47E-01	8.95E-01	-	-
1383725_at	LOC100192314	hypothetical protein LOC100192314	100192314	Rn.217950	BF552175	2.31	2.44	2.32	3.14	2.32	2.64	1.27	up	2.29E-01	8.95E-01	-	-
1381528_at	St3gal2	ST3 beta-galactoside alpha-2,3-sialyltransferase 2	64442	Rn.33216	BF387076	2.57	2.42	3.82	2.35	2.43	2.99	1.27	down	5.17E-01	8.95E-01	-	-
1384349_at	Pogz	pogo transposable element with ZNF domain	310658	Rn.103975	AI577326	5.86	6.07	5.91	6.79	4.20	5.81	1.27	down	6.72E-01	9.01E-01	-	-
1395989_at	Gfm2	G elongation factor, mitochondrial 2	294672	Rn.219115	BF404121	2.58	3.23	2.52	2.38	2.40	2.51	1.27	down	2.07E-01	8.95E-01	-	-
1398775_at	Rps15a	ribosomal protein S15a	117053	Rn.2890	NM_053982	10.87	10.81	10.93	11.01	11.12	11.52	1.27	up	9.43E-02	8.95E-01	-	-
1375799_at	Tmem121	transmembrane protein 121	691678	Rn.17349	AI763826	2.46	2.44	2.51	2.43	2.95	3.05	1.27	up	1.48E-01	8.95E-01	-	-
1371436_at	Ddah2	dimethylarginine dimethylaminohydrolase 2	294239	Rn.203056	AI176924	5.04	5.14	4.46	4.68	4.35	4.57	1.27	down	2.13E-01	8.95E-01	-	-
1370915_s_at	Dntttip1	deoxynucleotidyltransferase, terminal, interacting protein 1	171437	Rn.82702	BM384112	6.53	6.64	5.82	6.63	6.62	6.77	1.27	up	2.57E-01	8.95E-01	-	-
1380859_at	---	---	---	Rn.11518	AA891931	5.96	5.64	3.83	5.37	5.35	5.74	1.27	up	6.36E-01	8.95E-01	-	-
1376490_at	---	---	---	Rn.165683	BG378933	2.57	2.59	2.62	2.57	2.58	3.67	1.27	up	3.97E-01	8.95E-01	-	-
1379128_at	Arhgef17	Rho guanine nucleotide exchange factor (GEF) 17	308862	Rn.108856	AW229349	2.52	2.48	3.92	2.49	2.59	2.80	1.27	down	5.14E-01	8.95E-01	-	-
1392563_at	Prr5	proline rich 5 (renal)	315189	Rn.30314	AW252517	9.07	9.46	9.01	9.90	9.15	9.53	1.27	up	2.51E-01	8.95E-01	-	-
1393091_at	Mier3	mesoderm induction early response 1, family member 3	310086	Rn.198573	H34096	4.21	4.30	4.61	4.58	4.59	5.00	1.27	up	1.33E-01	8.95E-01	-	-
1382692_at	Clec7a	C-type lectin domain family 7, member a	502902	Rn.15743	AI045955	2.40	2.40	3.75	3.69	3.47	2.43	1.27	up	5.94E-01	8.95E-01	-	-
1371944_at	Ube2l3	ubiquitin-conjugating enzyme E2L 3	363836	Rn.163186	AI407788	8.92	9.44	8.91	9.12	9.75	9.44	1.27	up	2.44E-01	8.95E-01	-	-
1390851_at	Lactb2	Lactamase, beta 2	297768	Rn.1263	AA799676	9.83	9.81	10.20	9.36	9.78	9.67	1.27	down	1.23E-01	8.95E-01	-	-
1377303_at	---	---	---	Rn.204392	BG373000	3.64	4.50	3.57	3.61	3.61	3.46	1.27	down	3.18E-01	8.95E-01	-	-
1390733_at	---	---	---	Rn.210600	BI275867	2.49	2.45	2.51	2.72	3.29	2.48	1.27	up	2.27E-01	8.95E-01	-	-
1371565_at	Kti12	KTI12 homolog, chromatin associated (S. cerevisiae)	685656	Rn.203233	BM390478	5.74	5.44	4.97	4.80	5.10	5.22	1.27	down	2.45E-01	8.95E-01	-	-
1376325_at	Nfrkb	nuclear factor related to kappa B binding protein	315523	Rn.96240	BM388975	4.20	4.21	3.28	3.72	3.47	3.46	1.27	down	3.40E-01	8.95E-01	-	-
1369526_at	Acadsb	acyl-Coenzyme A dehydrogenase, short/branched chain	25618	Rn.44423	NM_013084	5.35	6.95	5.59	6.49	4.88	5.49	1.27	down	6.41E-01	8.95E-01	-	-
1373804_at	Foxp1	forkhead box P1	497480	Rn.33324	AI230954	3.44	3.75	2.97	3.19	2.87	3.06	1.27	down	2.30E-01	8.95E-01	-	-
1372654_at	Eps8l2	EPS8-like 2	361674	Rn.23793	BI285918	8.19	8.79	8.41	8.10	8.22	8.04	1.27	down	1.36E-01	8.95E-01	-	-
1379318_at	LOC498662	similar to RIKEN cDNA 2610019F03	498662	Rn.11716	BI296812	7.30	9.09	9.06	7.81	8.00	8.60	1.27	down	6.18E-01	8.95E-01	-	-
1375910_at	Cdc42ep3	CDC42 effector protein (Rho GTPase binding) 3	313838	Rn.4040	AA874943	3.44	3.42	3.45	3.47	4.40	3.48	1.27	up	3.27E-01	8.95E-01	-	-
1372068_at	Zmynd11	zinc finger, MYND domain containing 11	291259	Rn.38301	BI289543	6.58	6.98	6.89	6.89	7.25	7.35	1.27	up	1.35E-01	8.95E-01	-	-
1387457_at	Dusp12	dual specificity phosphatase 12	64014	Rn.52231	NM_022248	3.40	3.22	5.98	4.48	4.68	4.48	1.27	up	7.20E-01	9.11E-01	-	-
1371781_at	Stat3	signal transducer and activator of transcription 3	25125	Rn.10247	BI285863	3.92	3.86	3.55	4.83	3.77	3.77	1.27	up	4.07E-01	8.95E-01	-	-
1399101_at	Rbm39	RNA binding motif protein 39	362251	Rn.8555	AA849715	8.37	8.26	8.32	7.73	8.00	8.18	1.27	down	6.31E-02	8.95E-01	-	-
1376421_at	---	---	---	Rn.48759	BI278838	5.11	7.00	7.12	6.65	7.02	6.59	1.27	up	6.32E-01	8.95E-01	-	-
1378022_at	Rnf20	ring finger protein 20	313216	Rn.15969	BE113167	4.89	4.87	4.23	5.23	4.98	4.81	1.27	up	2.36E-01	8.95E-01	-	-
1368265_at	Cyp2t1	cytochrome P450 monooxygenase CYP2T1	171380	Rn.144661	NM_134369	3.50	3.70	4.26	3.34	3.68	3.41	1.27	down	2.39E-01	8.95E-01	-	-
1375994_at	---	---	---	Rn.203421	BE107324	5.31	5.54	4.86	4.83	4.84	5.00	1.27	down	1.74E-01	8.95E-01	-	-
1382253_at	Fam118b	family with sequence similarity 118, member B	315549	Rn.129284	BF419062	3.10	3.76	3.09	3.33	3.02	4.63	1.27	up	5.59E-01	8.95E-01	-	-
1389370_at	Phf1	PHD finger protein 1	294287	Rn.24149	AW914993	3.95	4.01	4.19	3.70	3.72	3.69	1.27	down	9.94E-03	8.95E-01	-	-
1372284_at	Trappc3	trafficking protein particle complex 3	362599	Rn.925	AI104319	5.85	6.11	5.91	5.31	5.43	6.11	1.27	down	2.58E-01	8.95E-01	-	-
1394079_at	Tbl1xr1	transducin (beta)-like 1 X-linked receptor 1	365755	Rn.140831	AA944938	4.43	4.37	3.84	3.85	4.72	5.10	1.27	up	4.54E-01	8.95E-01	-	-
1386891_at	Pebp1	phosphatidylethanolamine binding protein 1	29542	Rn.29745	NM_017236	9.56	9.66	9.86	9.45	9.25	9.35	1.27	down	3.05E-02	8.95E-01	-	-
1384210_at	Micall2	MICAL C-terminal like	293180	Rn.30154	BI288809	3.68	2.66	2.68	2.67	2.67	2.65	1.27	down	3.85E-01	8.95E-01	-	-
1393619_at	Cnot6l	CCR4-NOT transcription complex, subunit 6-like	360917	Rn.16306	AI045762	5.95	6.40	6.44	5.48	6.02	6.26	1.27	down	2.87E-01	8.95E-01	-	-
1392876_at	---	---	---	Rn.176368	BG375098	2.69	2.69	2.66	2.69	3.60	2.78	1.27	up	3.02E-01	8.95E-01	-	-
1385319_at	Arhgap27	Rho GTPase activating protein 27	303583	Rn.17895	BE108386	3.41	3.29	4.51	3.89	2.65	3.64	1.27	down	5.59E-01	8.95E-01	-	-
1390503_at	---	---	---	Rn.201878	BI301268	3.25	2.68	3.11	2.68	2.64	2.68	1.27	down	1.13E-01	8.95E-01	-	-
1395058_at	Wdr75	WD repeat domain 75	314545	Rn.38742	AI556441	3.38	4.02	3.90	3.69	4.16	4.48	1.27	up	3.15E-01	8.95E-01	-	-
1376940_at	---	---	---	Rn.220214	BI274420	2.87	2.86	2.87	3.13	3.65	2.86	1.27	up	2.12E-01	8.95E-01	-	-
1380379_at	Fbxo44	F-box protein 44	500587	Rn.24824	AI228000	4.69	5.73	5.09	4.33	6.58	5.62	1.27	up	6.57E-01	8.98E-01	-	-
1378097_at	---	---	---	Rn.21452	AI599593	2.45	2.66	2.75	2.91	2.85	3.13	1.27	up	4.84E-02	8.95E-01	-	-
1368682_at	Sv2a	synaptic vesicle glycoprotein 2a	117559	Rn.11264	NM_057210	2.38	2.37	2.39	3.42	2.39	2.37	1.27	up	3.78E-01	8.95E-01	-	-
1368095_at	Ak3	adenylate kinase 3	26956	Rn.60	NM_013218	8.83	9.01	9.32	8.58	8.44	9.11	1.27	down	2.37E-01	8.95E-01	-	-
1390366_at	Pcdh24	protocadherin 24	291002	Rn.66752	BI291884	8.38	8.58	7.13	7.82	7.37	7.87	1.27	down	5.14E-01	8.95E-01	-	-
1380141_at	Nsun4	NOL1/NOP2/Sun domain family, member 4	298426	Rn.49080	AW526109	2.65	2.73	2.34	2.79	2.88	3.07	1.27	up	7.50E-02	8.95E-01	-	-
1389353_at	Sema6d	sema domain, transmembrane domain (TM), and cytoplasmic domain, (sema	311384	Rn.8257	BM386525	6.90	6.73	5.86	6.65	6.44	7.43	1.27	up	4.82E-01	8.95E-01	-	-
1388995_at	Rnf14	ring finger protein 14	91957	Rn.115357	BF407666	6.94	7.11	6.67	6.79	6.17	6.73	1.27	down	2.17E-01	8.95E-01	-	-
1369454_at	Vdr	vitamin D (1,25- dihydroxyvitamin D3) receptor	24873	Rn.10911	NM_017058	6.07	5.05	5.86	5.97	4.77	5.21	1.27	down	5.05E-01	8.95E-01	-	-
1391890_at	Bcas3	breast carcinoma amplified sequence 3	363662	Rn.203379	AI548031	3.49	2.49	2.51	2.46	2.49	2.51	1.27	down	3.55E-01	8.95E-01	-	-
1380517_at	Zmym3	zinc finger, MYM-type 3	311280	Rn.92967	BI288315	6.44	5.58	6.76	6.17	7.16	6.48	1.27	up	4.97E-01	8.95E-01	-	-
1374364_at	RGD1562335	similar to mKIAA1931 protein	498703	Rn.50677	BI277805	2.91	2.94	3.84	2.90	2.95	2.81	1.27	down	3.29E-01	8.95E-01	-	-
1379548_at	---	---	---	Rn.165198	BF560252	6.42	5.88	5.20	7.27	6.26	5.00	1.27	up	6.70E-01	9.00E-01	-	-
1388960_at	Ppa1	pyrophosphatase (inorganic) 1	294504	Rn.108916	AI412958	6.36	6.13	6.36	5.67	5.74	6.41	1.27	down	2.40E-01	8.95E-01	-	-
1373897_at	Lmnb1	Lamin B1	116685	Rn.11362	AI103106	3.16	4.95	2.81	3.35	3.14	3.39	1.27	down	6.35E-01	8.95E-01	-	-
1396022_at	Zfp322a	Zinc finger protein 322a	680201	Rn.16013	AW534662	3.06	2.74	2.78	2.78	2.87	3.96	1.27	up	4.30E-01	8.95E-01	-	-
1389989_at	Atrx	alpha thalassemia/mental retardation syndrome X-linked (RAD54 homolog, S	246284	Rn.107838	BF397805	5.22	3.96	4.44	3.95	3.75	4.89	1.27	down	5.38E-01	8.95E-01	-	-
1372018_at	Cdc42bpb	CDC42 binding protein kinase beta (DMPK-like)	113960	Rn.105815	BM392107	2.32	2.30	2.31	2.30	2.29	2.27	1.27	down	3.67E-01	8.95E-01	-	-
1380701_at	---	---	---	Rn.210702	BF400722	2.36	2.51	2.45	3.02	2.93	2.40	1.27	up	1.61E-01	8.95E-01	-	-
1369042_at	Pigm	phosphatidylinositol glycan anchor biosynthesis, class M	79112	Rn.163231	NM_024144	5.49	5.53	4.28	4.97	6.03	5.34	1.27	up	5.42E-01	8.95E-01	-	-
1398390_at	Cxcl13	chemokine (C-X-C motif) ligand 13	498335	Rn.6917	AA892854	2.40	2.39	2.41	2.44	2.40	3.38	1.27	up	3.45E-01	8.95E-01	-	-
1375349_at	Sorbs1	sorbin and SH3 domain containing 1	686098	Rn.110441	BI295776	8.33	8.01	6.93	8.09	7.99	8.23	1.27	up	4.69E-01	8.95E-01	-	-
1394590_at	Nkiras1	NFKB inhibitor interacting Ras-like 1	305751	Rn.98363	AA997472	3.41	4.03	4.35	3.85	5.56	3.40	1.27	up	6.56E-01	8.98E-01	-	-
1397692_at	Tia1	TIA1 cytotoxic granule-associated RNA binding protein	312510	Rn.198158	BE104820	2.45	2.44	2.49	2.45	3.53	2.42	1.27	up	4.02E-01	8.95E-01	-	-
1383173_at	---	---	---	---	BI281630	2.45	2.42	3.46	2.44	2.42	2.42	1.27	down	3.74E-01	8.95E-01	-	-
1373243_at	Pmvk	phosphomevalonate kinase	310645	Rn.22202	BG378288	6.44	6.31	6.41	6.06	6.01	6.06	1.27	down	1.55E-03	8.95E-01	-	-
1389580_at	Hltf	helicase-like transcription factor	295568	Rn.161819	BM384827	3.24	3.31	2.59	3.05	2.95	4.16	1.27	up	4.90E-01	8.95E-01	-	-
1388611_at	Tcea3	transcription elongation factor A (SII), 3	298559	Rn.11547	AW252817	11.61	11.61	10.81	11.54	11.85	11.67	1.27	up	2.92E-01	8.95E-01	-	-
1395406_at	Sbno1	Strawberry notch homolog 1 (Drosophila)	304470	Rn.12294	BF552212	8.12	7.92	8.00	7.64	7.56	7.82	1.27	down	2.39E-02	8.95E-01	-	-
1395701_at	Hist1l	Hippocampus abundant transcript-like 1	306687	Rn.204848	BE118561	2.47	3.02	3.27	2.48	2.56	2.69	1.27	down	2.32E-01	8.95E-01	-	-
1372285_at	---	---	---	Rn.12133	BM389061	7.62	6.94	7.48	6.70	7.21	7.11	1.27	down	2.58E-01	8.95E-01	-	-
1389125_at	Mrpl1	mitochondrial ribosomal protein L1	289491	Rn.93038	BI293704	6.30	7.14	6.91	7.24	6.84	7.31	1.27	up	3.04E-01	8.95E-01	-	-
1372954_at	---	---	---	Rn.18889	BF404393	5.17	5.71	5.55	5.07	4.55	5.78	1.27	down	4.34E-01	8.95E-01	-	-
1397957_at	---	---	---	Rn.73491	AA955460	2.98	3.75	3.12	2.99	3.01	2.83	1.27	down	2.31E-01	8.95E-01	-	-
1378137_at	Lrrc59	leucine rich repeat containing 59	287633	Rn.2783	BG379798	2.36	2.61	2.39	2.39	2.76	3.24	1.27	up	2.58E-01	8.95E-01	-	-
1372942_at	Exosc5	exosome component 5	308441	Rn.7400	AA943578	4.52	4.31	4.69	3.95	4.51	4.04	1.27	down	1.71E-01	8.95E-01	-	-
1383510_at	---	---	---	Rn.249	AI230360	7.04	6.56	6.92	6.62	7.63	7.29	1.27	up	3.60E-01	8.95E-01	-	-
1367643_at	Bsg	basigin	25246	Rn.2269	NM_012783	9.16	9.55	8.91	9.34	9.69	9.61	1.27	up	1.86E-01	8.95E-01	-	-
1377321_at	---	---	---	Rn.211515	BF415831	3.49	2.69	2.79	2.65	2.66	2.64	1.27	down	2.43E-01	8.95E-01	-	-
1378883_at	---	---	---	Rn.146629	AI502759	2.39	2.38	2.41	2.38	3.45	2.37	1.27	up	3.93E-01	8.95E-01	-	-
1383083_at	Banp	Btg3 associated nuclear protein	292064	Rn.55281	AI575458	4.57	4.73	4.41	4.98	5.04	4.72	1.27	up	6.42E-02	8.95E-01	-	-
1389559_at	---	---	---	---	AA892872	5.10	4.56	5.74	5.08	4.57	4.74	1.27	down	4.12E-01	8.95E-01	-	-
1397580_at	---	---	---	Rn.27003	AI500809	3.44	2.58	2.54	2.50	2.54	2.50	1.27	down	3.11E-01	8.95E-01	-	-
1383997_at	---	---	---	---	AA874850	3.52	2.44	2.46	2.44	2.45	2.50	1.27	down	3.95E-01	8.95E-01	-	-
1374578_at	---	---	---	Rn.17879	AI409501	2.80	2.90	2.55	3.17	2.93	3.17	1.27	up	5.97E-02	8.95E-01	-	-
1391553_at	---	---	---	Rn.137820	AA956757	3.32	2.92	3.33	3.96	3.59	3.05	1.27	up	3.17E-01	8.95E-01	-	-
1376556_at	---	---	---	Rn.216514	BE111740	2.30	2.30	2.32	3.34	2.30	2.29	1.27	up	3.83E-01	8.95E-01	-	-
1382508_at	Gspt1	G1 to S phase transition 1	24420	Rn.72491	AI228722	5.51	5.90	6.87	5.82	5.44	5.99	1.27	down	4.77E-01	8.95E-01	-	-
1388905_at	---	---	---	---	AI175728	7.82	7.01	7.09	7.31	7.65	7.99	1.27

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1379656_a_at	---	---	---	Rn.98708	AW529016	2.52	2.51	3.55	2.52	2.55	2.50	1.26	down	3.84E-01	8.95E-01	-	-
1372671_at	Rfk	riboflavin kinase	499328	Rn.13360	BI284293	10.10	10.09	10.26	10.02	9.20	10.21	1.26	down	3.42E-01	8.95E-01	-	-
1369501_at	Zfp260	zinc finger protein 260	53982	Rn.98773	NM_017364	3.04	3.42	3.43	3.68	3.13	4.09	1.26	up	3.29E-01	8.95E-01	-	-
1373959_at	Ppp2r1b	protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), beta isofor	315648	Rn.163017	AI411788	8.15	8.49	8.70	8.03	8.13	8.16	1.26	down	1.09E-01	8.95E-01	-	-
1387773_at	Cycs	cytochrome c, somatic	25309	Rn.161841	NM_012839	11.33	11.61	11.83	11.40	11.13	11.23	1.26	down	1.09E-01	8.95E-01	-	-
1395425_at	Cpsf6	cleavage and polyadenylation specific factor 6	299811	Rn.164480	BE099398	6.76	6.37	6.46	5.77	6.35	6.47	1.26	down	2.43E-01	8.95E-01	-	-
1382604_at	Polr3g	polymerase (RNA) III (DNA directed) polypeptide G (32kD)	685465	Rn.147190	BE117925	4.25	4.25	5.79	3.96	4.49	4.82	1.26	down	5.86E-01	8.95E-01	-	-
1386906_a_at	09-Sep	septin 9	83788	Rn.91127	AF180526	5.62	5.23	6.42	6.04	6.17	6.08	1.26	up	3.92E-01	8.95E-01	-	-
1387015_at	Pfn2	profilin 2	81531	Rn.203100	NM_030873	3.00	2.77	3.00	2.92	3.69	3.18	1.26	up	2.33E-01	8.95E-01	-	-
1388945_at	RGD1311307	similar to 1300014I06Rik protein	361238	Rn.6535	BM385779	3.42	2.39	2.42	2.41	2.43	2.36	1.26	down	3.74E-01	8.95E-01	-	-
1368553_at	Acvr1	activin A receptor type II-like 1	25237	Rn.10631	NM_022441	3.13	2.87	2.55	2.51	2.76	2.27	1.26	down	2.00E-01	8.95E-01	-	-
1378186_at	Kif21a	Kinesin family member 21A	300158	Rn.219282	BF408466	4.66	4.82	2.98	4.39	4.80	4.28	1.26	up	6.09E-01	8.95E-01	-	-
1384452_at	Zcchc7	Zinc finger, CCHC domain containing 7	298086	Rn.56971	AA924571	4.74	4.85	4.84	5.58	5.07	4.79	1.26	up	2.22E-01	8.95E-01	-	-
1392745_at	RGD1305713	similar to RIKEN cDNA 3110040N11	293059	Rn.138288	BG380502	3.88	4.43	3.95	3.87	3.54	3.84	1.26	down	1.69E-01	8.95E-01	-	-
1383421_at	---	---	---	Rn.203132	BM386110	7.06	7.00	7.52	6.79	6.93	6.85	1.26	down	1.16E-01	8.95E-01	-	-
1371804_at	Cdadc1	cytidine and dCMP deaminase domain containing 1	361052	Rn.76647	AI172266	5.94	6.18	5.43	5.35	6.50	6.70	1.26	up	5.16E-01	8.95E-01	-	-
1372320_at	Msl3l1	male-specific lethal 3-like 1 (Drosophila)	317464	Rn.7258	BE103894	6.88	7.60	6.99	7.17	7.74	7.57	1.26	up	2.92E-01	8.95E-01	-	-
1376508_at	Lemd2	LEM domain containing 2	361807	Rn.14675	AI044972	2.41	2.49	2.41	2.39	3.53	2.39	1.26	up	4.25E-01	8.95E-01	-	-
1374143_at	Epha2	Eph receptor A2	366492	Rn.23415	AI602491	4.81	4.83	4.89	4.84	3.85	4.83	1.26	down	3.64E-01	8.95E-01	-	-
1376685_at	---	---	---	Rn.40821	AW532489	4.13	5.84	3.56	4.57	4.65	5.31	1.26	up	6.64E-01	8.99E-01	-	-
1394771_at	---	---	---	Rn.208674	BM391898	2.75	2.63	3.22	2.44	2.27	2.87	1.26	down	2.50E-01	8.95E-01	-	-
1388290_at	Dnajc10	DnaJ (Hsp40) homolog, subfamily C, member 10	295690	Rn.8642	AI172034	6.18	5.69	5.39	5.98	5.97	6.32	1.26	up	2.59E-01	8.95E-01	-	-
1374842_at	Cebpz	CCAAT/enhancer binding protein zeta	362686	Rn.204791	BF267009	8.22	7.30	7.07	7.16	6.81	7.61	1.26	down	4.67E-01	8.95E-01	-	-
1398434_at	---	---	---	Rn.8782	BE107465	3.77	3.89	4.66	4.14	3.12	4.05	1.26	down	4.75E-01	8.95E-01	-	-
1378902_at	Tyw1	tRNA-yW synthesizing protein 1 homolog (S. cerevisiae)	304423	Rn.163211	BF413695	8.59	7.56	6.44	7.17	6.60	7.81	1.26	down	6.61E-01	8.98E-01	-	-
1388170_at	Kctd1	potassium channel tetramerisation domain containing 1	291772	Rn.27416	BI285710	2.49	2.46	2.58	2.48	3.60	2.47	1.26	up	4.24E-01	8.95E-01	-	-
1369688_s_at	Ptk2b	PTK2B protein tyrosine kinase 2 beta	50646	Rn.11025	U69101	3.72	4.22	2.24	3.83	3.55	3.80	1.26	up	6.05E-01	8.95E-01	-	-
1372805_at	RGD1310444	LOC363015	363015	Rn.27612	BE328984	2.83	2.53	2.79	3.52	2.83	2.82	1.26	up	2.47E-01	8.95E-01	-	-
1387322_at	Sema6b	sema domain, transmembrane domain (TM), and cytoplasmic domain, (sema	84609	Rn.87343	NM_053471	2.47	2.73	2.47	2.46	3.76	2.45	1.26	up	4.88E-01	8.95E-01	-	-
1396383_at	RGD1311066	similar to RIKEN cDNA 0610011L14 gene	296312	Rn.52749	BE116860	8.15	7.53	7.71	7.12	7.68	7.59	1.26	down	2.52E-01	8.95E-01	-	-
1391611_at	Kif12	Kinesin family member 12	313254	Rn.32294	BI296819	9.54	9.03	8.03	9.38	9.22	9.02	1.26	up	5.00E-01	8.95E-01	-	-
1379827_at	Gps2	G protein pathway suppressor 2	497941	Rn.145424	BG376569	5.80	5.77	5.15	4.23	5.58	5.90	1.26	down	5.75E-01	8.95E-01	-	-
1383701_at	Map2k4	mitogen activated protein kinase kinase 4	287398	Rn.198875	BM385937	2.67	3.99	2.68	2.65	2.68	3.00	1.26	down	4.96E-01	8.95E-01	-	-
1371862_at	Rrm1	ribonucleotide reductase M1	685579	Rn.216762	AI412015	6.19	5.54	4.48	5.19	6.30	5.74	1.26	up	6.01E-01	8.95E-01	-	-
1388828_at	Sidt2	SID1 transmembrane family, member 2	315617	Rn.162997	AI579643	6.42	6.95	5.30	6.93	6.15	6.60	1.26	up	5.62E-01	8.95E-01	-	-
1388174_at	Wnt2b	wingless-type MMTV integration site family, member 2B	116466	Rn.17219	AF204873	2.95	3.14	4.15	3.11	3.00	3.11	1.26	down	4.19E-01	8.95E-01	-	-
1383354_a_at	Fbxo33	F-box protein 33	314157	Rn.222042	BF566664	4.49	5.10	5.02	4.74	3.50	5.36	1.26	down	5.93E-01	8.95E-01	-	-
1385254_at	Xrn1	5'-3' exoribonuclease 1	300944	Rn.13274	BE104427	3.35	3.35	2.55	3.35	3.96	3.55	1.26	up	2.87E-01	8.95E-01	-	-
1373081_at	Baiap2	BAI1-associated protein 2	117542	Rn.95155	AI105000	5.70	5.79	5.32	6.19	6.09	5.53	1.26	up	2.51E-01	8.95E-01	-	-
1380786_at	---	---	---	Rn.168117	BI296185	4.97	4.20	4.23	4.21	4.22	3.96	1.26	down	2.72E-01	8.95E-01	-	-
1376765_at	Mul1	mitochondrial ubiquitin ligase activator of NFKB 1	298576	Rn.152339	BM384731	3.52	3.52	3.66	3.52	2.65	3.51	1.26	down	3.14E-01	8.95E-01	-	-
1378482_at	Mdfic	MyoD family inhibitor domain containing	362325	Rn.18295	AI411065	3.90	4.40	3.90	3.90	2.82	4.48	1.26	down	5.48E-01	8.95E-01	-	-
1391212_at	Tceal1	transcription elongation factor A (SII)-like 1	302593	Rn.41329	BF418812	2.81	3.31	3.34	3.24	3.32	3.91	1.26	up	2.84E-01	8.95E-01	-	-
1389069_at	Rnf8	ring finger protein 8	361815	Rn.12463	BM384061	5.55	5.38	4.76	5.91	5.40	5.40	1.26	up	3.16E-01	8.95E-01	-	-
1384960_at	Cftr	cystic fibrosis transmembrane conductance regulator homolog	24255	Rn.124539	BI281250	3.74	5.09	5.19	4.13	4.37	4.51	1.26	down	5.22E-01	8.95E-01	-	-
1372981_at	RGD1311257	similar to C21orf70 protein	294333	Rn.22122	BI294885	3.70	3.21	3.43	2.98	3.14	3.20	1.26	down	9.98E-02	8.95E-01	-	-
1372794_at	Dapk2	death-associated kinase 2	300799	Rn.98325	BM392203	6.01	6.71	5.07	6.26	6.19	6.35	1.26	up	5.19E-01	8.95E-01	-	-
1370743_a_at	Lnpep	leucyl/cystinyl aminopeptidase	171105	Rn.10614	AY079189	5.16	6.22	5.07	5.22	6.40	5.85	1.26	up	5.39E-01	8.95E-01	-	-
1392342_at	---	---	---	Rn.205559	AI709861	3.02	2.50	2.78	2.51	2.51	2.28	1.26	down	1.18E-01	8.95E-01	-	-
1394473_at	Elk3	ELK3, member of ETS oncogene family	362871	Rn.196088	AI716206	3.17	3.11	2.64	2.68	2.65	2.58	1.26	down	1.17E-01	8.95E-01	-	-
1390237_at	Timm8a1	timm8a1	84383	Rn.162342	BF558361	6.84	7.17	7.33	6.88	6.45	7.00	1.26	down	2.06E-01	8.95E-01	-	-
1390741_at	RGD1304737	similar to KIAA1086 protein	314639	Rn.41117	BI296410	2.37	2.36	2.37	3.38	2.37	2.36	1.26	up	3.76E-01	8.95E-01	-	-
1387964_a_at	Ero1l	ERO1-like (S. cerevisiae)	171562	Rn.64648	AY071924	2.57	2.53	2.54	3.62	2.49	2.52	1.26	up	4.17E-01	8.95E-01	-	-
1379224_at	Mid2	Midline 2	363502	Rn.48869	AA925587	2.56	2.55	3.63	2.61	2.59	2.53	1.26	down	4.02E-01	8.95E-01	-	-
1398856_at	Psma2	proteasome (prosome, macropain) subunit, alpha type 2	29669	Rn.1617	AA801204	9.42	9.84	9.97	9.62	8.98	9.63	1.26	down	2.82E-01	8.95E-01	-	-
1379667_at	Frag1	FGF receptor activating protein 1	116675	Rn.94200	AW527612	2.61	2.59	2.51	2.96	2.64	3.12	1.26	up	8.36E-02	8.95E-01	-	-
1389844_at	Fkbp4	FK506 binding protein 4	260321	Rn.23741	BE113154	8.09	7.26	6.69	6.92	7.12	6.98	1.26	down	4.58E-01	8.95E-01	-	-
1372105_at	Efha1	EF-hand domain family, member A1	171433	Rn.64644	BF284932	7.40	7.53	7.64	7.15	7.02	7.39	1.26	down	5.60E-02	8.95E-01	-	-
1388150_at	Xpo1	exportin 1, CRM1 homolog (yeast)	85252	Rn.34087	AW533924	3.96	4.78	4.62	4.21	5.15	4.99	1.26	up	4.30E-01	8.95E-01	-	-
1389791_at	Cln8	ceroid-lipofuscinosis, neuronal 8	306619	Rn.1924	AI179775	5.46	4.27	3.79	4.75	5.13	4.65	1.26	up	5.49E-01	8.95E-01	-	-
1377550_at	Slc25a23	solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 23	301113	Rn.41	BF405298	4.23	5.28	5.19	5.39	4.23	4.07	1.26	down	5.84E-01	8.95E-01	-	-
1374488_at	Gramd1b	GRAM domain containing 1B	300844	Rn.204239	AI175700	7.37	8.79	7.80	7.80	7.41	7.74	1.26	down	4.85E-01	8.95E-01	-	-
1390253_at	Ankrd9	ankyrin repeat domain 9	314457	Rn.20951	BF395083	2.62	2.49	3.62	2.49	2.62	2.62	1.26	down	4.05E-01	8.95E-01	-	-
1387178_a_at	Cbs	cystathionine beta synthase	24250	Rn.87853	NM_012522	7.59	8.06	7.15	8.14	7.89	7.78	1.26	up	3.00E-01	8.95E-01	-	-
1383180_at	Ppp1r2	protein phosphatase 1, regulatory (inhibitor) subunit 2	192361	Rn.4016	BF288097	4.87	5.05	5.21	5.18	5.21	5.76	1.26	up	1.89E-01	8.95E-01	-	-
1391737_at	Ncf4	neutrophil cytosolic factor 4	500904	Rn.46120	AW526210	2.39	2.37	2.39	2.38	3.41	2.37	1.26	up	3.87E-01	8.95E-01	-	-
1393033_at	Yars2	tyrosyl-tRNA synthetase 2 (mitochondrial)	287924	Rn.163187	BG669575	5.56	5.37	6.82	5.77	4.71	6.25	1.26	down	6.30E-01	8.95E-01	-	-
1381175_at	RGD1307526	similar to modulator of estrogen induced transcription	315792	Rn.49121	BE114469	5.93	5.40	3.27	5.39	5.17	3.04	1.26	down	7.77E-01	9.27E-01	-	-
1368283_at	Ehhadh	enoyl-Coenzyme A, hydratase/3-hydroxyacyl Coenzyme A dehydrogenase	171142	Rn.3673	NM_133606	6.03	6.07	6.19	5.50	5.64	6.15	1.26	down	1.73E-01	8.95E-01	-	-
1399003_at	Ccdc47	coiled-coil domain containing 47	303606	Rn.107772	BE116554	8.30	9.21	8.83	8.90	8.92	9.52	1.26	up	3.73E-01	8.95E-01	-	-
1367830_a_at	Tp53	tumor protein p53	24842	Rn.54443	NM_030989	7.76	8.05	6.85	7.73	7.73	8.21	1.26	up	4.44E-01	8.95E-01	-	-
1396956_at	---	---	---	Rn.173062	BF399606	3.36	2.38	2.41	2.38	2.40	2.37	1.26	down	3.56E-01	8.95E-01	-	-
1371629_at	Cxxc5	CXXC finger 5	291670	Rn.105695	AI105644	7.32	6.92	7.61	7.13	6.66	7.04	1.26	down	2.44E-01	8.95E-01	-	-
1393564_at	RGD1563278	similar to Ubiquitin ligase protein DZIP3 (DAZ-interacting protein 3 homolog)	303963	Rn.162050	BF402371	3.48	2.44	2.46	2.45	2.48	2.44	1.26	down	3.85E-01	8.95E-01	-	-
1398942_at	LOC100125365	hypothetical protein LOC100125365	100125365	Rn.8239	BI278885	9.29	8.68	8.98	9.49	9.36	9.11	1.26	up	1.80E-01	8.95E-01	-	-
1368275_at	Sc4mol	sterol-C4-methyl oxidase-like	140910	Rn.7167	NM_080886	4.70	5.30	5.35	4.69	4.92	4.73	1.26	up	2.06E-01	8.95E-01	-	-
1392311_at	---	---	---	Rn.209618	BF389762	2.47	2.59	2.73	3.61	2.62	2.57	1.26	up	3.90E-01	8.95E-01	-	-
1396233_at	Arsk	arylsulfatase family, member K	365619	Rn.202360	BE114013	2.61	2.59	2.63	2.60	3.59	2.65	1.26	up	3.56E-01	8.95E-01	-	-
1379169_at	Slc25a23	solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 23	301113	Rn.41	BF399958	2.56	2.55	3.84	3.14	2.41	2.40	1.26	down	5.35E-01	8.95E-01	-	-
1390764_at	Zfp324	zinc finger protein 324	365192	Rn.39324	BF420611	2.43	2.40	2.55	2.42	3.52	2.44	1.26	up	4.11E-01	8.95E-01	-	-
1371150_at	Ccnd1	cyclin D1	58919	Rn.22279	X75207	4.12	4.12	4.95	4.03	4.13	4.02	1.26	down	2.94E-01	8.95E-01	-	-
1371377_at	Rps19	ribosomal protein S19	29287	Rn.127775	BG668512	10.04	9.91	9.86	10.12	10.10	10.60	1.26	up	1.21E-01	8.95E-01	-	-
1393761_at	Zfp316	zinc finger protein 316	304293	Rn.40708	BF390194	2.63	2.56	2.81	2.55	3.94	2.52	1.26	up	5.20E-01	8.95E-01	-	-
1388601_at	Abt1	activator of basal transcription 1	306960	Rn.16564	AI598410	4.43	4.33	5.62	4.24	4.22	4.92	1.26	down	5.21E-01	8.95E-01	-	-
1380191_s_at	Txnl1	thioredoxin-like 1	140922	Rn.40430	BF555110	8.50	8.57	8.47	8.82	8.61	9.13	1.26	up	9.58E-02	8.95E-01	-	-
1391623_at	---	---	---	Rn.155925	AI706933	5.47	6.12	5.45	6.05	6.28	5.71	1.26	up	2.95E-01	8.95E-01	-	-
1373270_at	Wipi1	WD repeat domain, phosphoinositide interacting 1	303630	Rn.203725	AI233288	7.01	7.82	6.43	6.97	7.54	7.75	1.26	up	5.11E-01	8.95E-01	-	-
1381070_at	---	---	---	Rn.167036	AI233106	2.57	2.65	2.58	2.37	3.79	2.64	1.26	up	4.87E-01	8.95E-01	-	-
1372815_at	Aoc3	amine oxidase, copper containing 3 (vascular adhesion protein 1)	29473	Rn.198327	AI070137	2.53	2.60	2.64	3.67	2.61	2.50	1.26	up	4.21E-01	8.95E-01	-	-
1391703_at	Orc4l	origin recognition complex, subunit 4-like (yeast)	295596	Rn.144844	BF414253	7.15	6.14	6.61	5.95	6.66	6.29	1.26	down	4.01E-01	8.95E-01	-	-
1383142_at	Klhl26	kelch-like 26 (Drosophila)	290657	Rn.23695	BI289244	4.19	4.19	3.14	4.08	4.23	4.22	1.26	up	3.96E-01	8.95E-01	-	-
1386029_at	---	---	---	---	---	2.56	2.51	4.06	2.56	2.98	2.59	1.26	down	5.59E-01	8.95E-01	-	-
1372099_at	Fam21c	family with sequence similarity 21, member C	297530	Rn.105926	BI303661	7.74	7.82	7.47	8.28	7.77	7.98	1.26	up	1.43E-01	8.95E-01	-	-
1375726_at	Lmo7	LIM domain 7	361084	Rn.98417	BI284480	6.00	6.49	6.02	5.81	5.43	6.27	1.26	down	3.13E-01	8.95E-01	-	-
1398565_at	---	---	---	Rn.207063	AW534457	2.49	2.49	2.52	2.97	2.51	3.03	1.26	up	1.13E-01	8.95E-01	-	-
1367869_at	Oxr1	oxidation resistance 1	117520	Rn.4252	NM_057153	7.76	7.71	7.26	8.39	7.06	8.27	1.26	up	5.02E-01	8.95E-01	-	-
1399130_at	Pigy	phosphatidylinositol glycan anchor biosynthesis, class Y	502782	Rn.204281	AW918690	5.35	5.20	4.90	4.91	5.59	5.95	1.26	up	3.72E-01	8.95E-01	-	-
1378021_at	---	---	---	Rn.89336	AI102035	3.29	2.77	2.58	3.16	3.73	2.75	1.26	up	4.00E-01	8.95E-01	-	-
1397855_at	---	---	---	Rn.31288	BE096287	2.38	2.38	3.39	2.39	2.39	2.37	1.26	down	3.80E-01	8.95E-01	-	-
1389777_at	Ribc1	RIB43A domain with coiled-coils 1	317431	Rn.40643	BF403405	2.65	5.40	6.22	4.35	3.13	5.79	1.26	down	8.14E-01	9.40E-01	-	-
1371951_at	Fhl2	four and a half LIM domains 2	63839	Rn.3849	AA800031	3.83	3.44	3.11	3.15	3.10	3.14	1.26	down	1.83E-01	8.95E-01	-	-
1374479_at	Ino80c	INO80 complex subunit C	291737	Rn.18319	BM390240	3.01	3.77	4.44	2.57	3.56	4.09	1.26	down	6.11E-01	8.95E-01	-	-
1371427_at	Spcs1	signal peptidase complex subunit 1 homolog (S. cerevisiae)	290555	Rn.3761	BG380709	10.03	10.48	10.43	10.62	10.47	10.86	1.26	up	1.40E-01	8.95E-01	-	-
1392497_at	---	---	---	Rn.220443	BE104938	6.33	7.12	6.74	6.97	6.92	7.30	1.26	up	2.64E-01	8.95E-01	-	-
1384264_at	Myh14	myosin, heavy chain 14	308572	Rn.143782	AI578120	4.96	5.16	5.04	4.12	5.08	4.97	1.26	down	3.43E-01	8.95E-01	-	-
1375663_at	Ube2f	ubiquitin-conjugating enzyme E2F (putative)	363284	Rn.62010	AI232346	7.34	7.06	6.75	6.66	6.61	6.88	1.26	down	1.53E-01	8.95E-01	-	-
1394996_at	---	---	---	Rn.173013	BF390127	3.78	4.45	3.03	4.76	3.68	3.83	1.26	up	5.64E-01	8.95E-01	-	-
1381146_at	---	---	---	Rn.148077	AW434387	3.20	2.96	2.53	2.56	2.57	2.55	1.26	down	1.65E-01	8.95E-01	-	-
1399017_at	---	---	---	Rn.13287	AI234040	7.13	7.63	7.87	8.00	7.83	7.79	1.26	up	2.14E-01	8.95E-01	-	-
1370192_at	Stx12	syntaxin 12	65033	Rn.54570	BF283010	6.09	5.45	5.05	5.31	5.25	5.03	1.26	down	3.49E-01	8.95E-01	-	-
1371397_at	Nosip	nitric oxide synthase interacting protein	292894	Rn.146210	AI104068	6.45	6.50	6.59	7.04	7.10	6.40	1.26	up	2.17E-01	8.95E-01	-	-
1384505_at	---	---	---	Rn.50044	BI294773	2.68	2.66	2.68	3.41	3.05	2.56	1.26	up	2.44E-01	8.95E-01	-	-
1391673_at	Arhgap20	Rho GTPase activating protein 20	367085	Rn.20805	AI179083	2.35	2.37	2.36	3.38	2.34	2.36	1.26	up	3.88E-01	8.95E-01	-	-
1396214_at	Kitlg	KIT ligand	60427	Rn.44216	BF562720	4.36	3.31	3.26	3.21	3.42	3.31	1.26	down	4.11E-01	8.95E-01	-	-
1383360_at	RGD7351112	similar to RIKEN cDNA 5830404H04	304055	Rn.107481	AI145787	3.75	5.80	5.01	4.80	3.75	5.01	1.26	down	6.64E-01	8.99E-01	-	-
1370906_at	Bckdhb	branched chain keto acid dehydrogenase E1, beta polypeptide	29711	Rn.15623	BM385109	9.76	9.83	10.12	9.76	9.45	9.50	1.26	down	8.68E-02	8.95E-01	-	-
1398895_at	Golga7	golgi autoantigen, golgin subfamily a, 7	361171	Rn.4102	BM389419	7.15	6.83	7.64	6.97	6.88	6.77	1.26	down	2.45E-01	8.95E-01	-	-
1391289_at	---	---	---	Rn.199652	AW532387	2.39	2.70	2.42	3.11	2.42	2.99	1.26	up	2.31E-01	8.95E-01	-	-
1392976_at	Tpm2	tropomyosin 2	500450	Rn.17580	BF417385	2.31	2.31	2.31	3.56	2.31	2.06	1.26	up	5.12E-01	8.95E-01	-	-
1370995_at	Pou2f1	POU domain, class 2, transcription factor 1	171068	Rn.46300	AW528459	3.57	3.59	4.48	3.50	3.48	3.67	1.26	down	3.39E-01	8.95E-01	-	-
1373748_at	Pdzrn3	PDZ domain containing RING finger 3	312607	Rn.3111	AW532566	6.34	7.10	7.41	6.19	7.01	6.65	1.26	down	4.49E-01	8.95E-01	-	-
1399023_at	Ric8a	resistance to inhibitors of cholinesterase 8 homolog A (C. elegans)	293614	Rn.94796	AA893641	6.49	6.26	7.31	6.51	6.23	6.32	1.26	down	3.68E-01	8.95E-01	-	-
1374789_at	---	---	---	Rn.15476	BF550398	3.05	3.15	2.76	2.76	2.51	2.68	1.26	down	7.22E-02	8.95E-01	-	-
1375553_at	RGD1311742	similar to RIKEN cDNA 5133400G04	291676	Rn.136857	BE096042	4.29	5.25	4.13	4.52	3.92	6.23	1.26	up	6.90E-01	9.05E-01	-	-
1372801_at	Commd10	COMM domain containing 10	361323	Rn.163373	AI171256	6.81	6.52	7.17	6.29	6.59	6.62	1.26	down	1.95E-01	8.95E-01	-	-
1389868_at	RGD1564560	similar to RCK	500988	Rn.222046	AA850780	8.27	8.55	8.63	8.44	9.12	8.89	1.26	up	2.21E-01	8.95E-01	-	-
1373239_at	Nudt18	nudix (nucleoside diphosphate linked moiety X)-type motif 18	361068	Rn.95207	AI145851	6.20	7.27	7.37	6.10	6.49	7.25	1.26	down	5.45E-01	8.95E-01	-	-
1384810_at	Stam2	signal transducing adaptor molecule (SH3 domain and ITAM motif) 2	311030	Rn.161793	BF393740	2.81	3.33	2.84	2.80	2.42	2.77	1.26	down	1.86E-01	8.95E-01	-	-
1393493_at	---	---	---	---	BE117956	6.96	5.35	2.93	6.00	4.02	6.22	1.26	up	8.19E-01	9.42E-01	-	-
1394439_at	RGD1308759	similar to KIAA0892 protein	290668	Rn.49215	AW529321	5.03	5.09	6.74	6.92	5.37	6.58	1.26	up	6.77E-01	9.02E-01	-	-
1372371_at	---	---	---	Rn.164504	BI303031	6.33	7.34	6.51	6.45	5.85	6.88	1.26	down	4.84E-01	8.95E-01	-	-
1373064_at	Dnajc15	DnaJ (Hsp40) homolog, subfamily C, member 15	290370	Rn.8092	BM390416	7.50	5.86	7.40	6.39	6.37	7.01	1.26	down	5.93E-01	8.95E-01	-	-
1372432_at	Prpf3	PRP3 pre-mRNA processing factor 3 homolog (S. cerevisiae)	361995	Rn.116267	BF395125	5.92	6.09	5.10	6.83	5.13	6.14	1.26	up	5.98E-01	8.95E-01	-	-
1374304_at	Xrcc4	X-ray repair complementing defective repair in Chinese hamster cells 4	309995	Rn.40879	AW526081	2.44	2.41	3.46	2.44	2.45	2.44	1.26	down	3.90E-01	8.95E-01	-	-
1396240_at	---	---	---	Rn.38056	AI575096	5.81	4.56	6.75	4.62	5.65	5.85	1.26	down	6.78E-01	9.02E-01	-	-
1387261_at	Ppp3cb	protein phosphatase 3, catalytic subunit, beta isoform	24675	Rn.11063	NM_017042	3.14	3.96	2.91	4.02	3.18	3.80	1.26	up	4.60E-01	8.95E-01	-	-
1387784_at	Psmd10	proteasome (prosome, macropain) 26S subunit, non-ATPase, 10	116722	Rn.18378	NM_053925	7.90	7.75	7.79	8.11	7.94	8.40	1.26	up	7.86E-02	8.95E

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1373278_at	Nfe2l1	nuclear factor, erythroid derived 2,-like 1	360610	Rn.167338	BM391303	5.73	5.73	5.31	6.08	5.80	5.88	1.26	up	1.14E-01	8.95E-01	-	-
1373113_at	08-Mar	membrane-associated ring finger (C3HC4) 8	312656	Rn.48069	AI231778	7.31	7.59	7.72	7.62	7.80	8.19	1.26	up	1.88E-01	8.95E-01	-	-
1379795_at	RGD1306583	similar to RIKEN cDNA 2410002O22 gene	294709	Rn.15285	AA819224	5.17	5.73	5.93	4.95	5.38	5.51	1.26	down	3.10E-01	8.95E-01	-	-
1383984_at	---	---	---	Rn.13480	BM389978	2.99	2.68	6.41	2.82	4.82	3.44	1.26	down	8.17E-01	9.41E-01	-	-
1390917_at	---	---	---	Rn.156828	AI227828	5.28	5.55	5.73	5.37	5.15	5.06	1.26	down	1.11E-01	8.95E-01	-	-
1391254_at	---	---	---	Rn.209982	BF412722	3.42	2.46	2.47	2.43	2.47	2.46	1.26	down	3.57E-01	8.95E-01	-	-
1374692_at	Snx14	sorting nexin 14	315871	Rn.16406	BE107598	5.72	6.55	6.48	6.58	6.48	6.68	1.26	up	2.94E-01	8.95E-01	-	-
1373190_at	Cnot4	CCR4-NOT transcription complex, subunit 4	312227	Rn.203387	AI101401	3.99	4.70	5.77	3.84	4.52	5.11	1.26	down	6.31E-01	8.95E-01	-	-
1392380_at	---	---	---	Rn.209638	BF389979	2.39	2.38	2.40	2.39	3.39	2.38	1.26	up	3.84E-01	8.95E-01	-	-
1388076_at	Serbp1	Serpine1 mRNA binding protein 1	246303	Rn.203108	AF3488527	9.67	10.41	9.77	10.23	10.23	10.37	1.26	up	2.37E-01	8.95E-01	-	-
1393706_at	Steap1	six transmembrane epithelial antigen of the prostate 1	297738	Rn.51773	BE109939	2.42	2.40	2.44	3.41	2.44	2.41	1.26	up	3.73E-01	8.95E-01	-	-
1381350_at	---	---	---	Rn.167745	AI317824	6.10	6.97	6.46	5.88	5.64	7.02	1.26	down	5.41E-01	8.95E-01	-	-
1372539_at	---	---	---	Rn.98484	AA801220	5.22	6.86	4.84	5.35	6.21	6.35	1.26	up	6.60E-01	8.98E-01	-	-
1384088_at	LOC680222	similar to zinc finger protein 748 isoform 2	680222	---	AI070288	3.87	3.70	3.75	3.51	3.26	3.56	1.26	down	3.51E-02	8.95E-01	-	-
1398303_s_at	Tpm3	tropomyosin 3, gamma	117557	Rn.37575	BI295970	6.38	7.02	7.32	6.93	5.72	7.08	1.26	down	5.55E-01	8.95E-01	-	-
1382998_at	---	---	---	Rn.204005	AI044778	2.91	2.52	2.64	3.59	2.75	2.72	1.26	up	3.42E-01	8.95E-01	-	-
1377577_at	Gmps	guanine monphosphate synthetase	295088	Rn.12593	BI283031	8.17	8.08	8.26	8.68	8.16	8.66	1.26	up	1.37E-01	8.95E-01	-	-
1398361_at	Arhgap10	Rho GTPase activating protein 10	688429	Rn.40465	BI295127	4.72	4.89	4.88	4.57	4.70	4.23	1.26	down	9.77E-02	8.95E-01	-	-
1387896_at	Podn /// Scp2	podocan /// sterol carrier protein 2	25541 /// 313483	Rn.31887	M62763	9.12	9.47	9.99	9.04	9.00	9.55	1.26	down	3.46E-01	8.95E-01	-	-
1378595_at	Sfpq	Splicing factor proline/glutamine rich (polypyrimidine tract binding protein ass	252855	Rn.54845	BE113427	6.94	6.68	7.63	7.63	7.54	7.06	1.26	up	3.81E-01	8.95E-01	-	-
1370481_at	Scn1g	sodium channel, nonvoltage-gated 1 gamma	24768	Rn.10360	U37539	2.43	2.43	2.42	3.25	2.41	2.60	1.26	up	2.63E-01	8.95E-01	-	-
1379556_a_at	Ggps1	geranylgeranyl diphosphate synthase 1	291211	Rn.54975	AI105210	8.10	6.70	6.15	6.49	6.74	6.74	1.26	down	6.06E-01	8.95E-01	-	-
1397734_at	---	---	---	Rn.205445	AW524780	4.34	3.47	3.78	4.29	2.58	3.74	1.26	down	5.92E-01	8.95E-01	-	-
1377022_at	Abhd10	abhydrolase domain containing 10	303953	Rn.138774	BF395328	2.47	2.80	3.16	2.41	2.44	2.60	1.26	down	1.90E-01	8.95E-01	-	-
1391222_at	N4bp1	Nedd4 binding protein 1	291921	Rn.137980	AA965076	3.26	4.30	3.36	3.67	4.06	4.18	1.26	up	4.17E-01	8.95E-01	-	-
1376976_at	Sectm1b	secreted and transmembrane 1B	287884	Rn.25030	AI009823	8.56	7.59	7.22	8.15	8.15	8.04	1.26	up	4.59E-01	8.95E-01	-	-
1371551_at	Traf4	Tnf receptor associated factor 4	303285	Rn.3219	BM383323	6.68	6.77	6.58	6.47	6.31	6.27	1.26	down	1.54E-02	8.95E-01	-	-
1372660_at	Tubgcp3	tubulin, gamma complex associated protein 3	306599	Rn.99777	AI180420	2.59	2.78	3.41	2.60	2.59	2.59	1.26	down	2.57E-01	8.95E-01	-	-
1395906_at	Znf652	zinc finger protein 652	497984	Rn.137198	BF290039	3.89	3.61	3.14	3.99	3.77	3.86	1.26	up	2.21E-01	8.95E-01	-	-
1388379_at	Ptpn11	Protein tyrosine phosphatase, non-receptor type 11	25622	Rn.98209	AI172465	5.68	6.64	6.42	6.81	6.08	6.85	1.26	up	4.39E-01	8.95E-01	-	-
1388386_at	Toag1	tolerance-associated gene 1	363169	Rn.20696	AI170759	9.32	9.72	9.55	9.15	9.30	9.14	1.26	down	6.08E-02	8.95E-01	-	-
1379561_at	Atad1	ATPase family, AAA domain containing 1	309532	Rn.54918	AW433567	7.36	7.37	6.45	7.32	7.25	7.59	1.26	up	3.66E-01	8.95E-01	-	-
1377777_at	Brd9	bromodomain containing 9	308067	Rn.23466	BM391018	3.67	5.09	6.30	4.70	4.26	5.11	1.26	down	7.02E-01	9.07E-01	-	-
1368342_at	Ampd3	adenosine monophosphate deaminase 3	25095	Rn.11106	NM_031544	3.22	2.71	2.49	2.48	2.49	2.47	1.26	down	2.04E-01	8.95E-01	-	-
1382641_at	---	---	---	---	BF288390	3.43	2.37	2.38	2.38	2.44	2.37	1.26	down	4.05E-01	8.95E-01	-	-
1380381_at	Alg2	asparagine-linked glycosylation 2, alpha-1,3-mannosyltransferase homolog (S	313231	Rn.98222	AI709513	2.91	3.59	2.42	3.31	3.59	3.00	1.26	up	4.33E-01	8.95E-01	-	-
1376690_at	Medz1	mediator complex subunit 21	312849	Rn.6795	BI296277	5.39	4.79	5.41	5.13	5.76	5.68	1.26	up	3.13E-01	8.95E-01	-	-
1391394_a_at	Pdgfb	platelet derived growth factor receptor, beta polypeptide	24629	Rn.98311	AI071374	3.18	2.72	2.67	2.46	2.73	2.39	1.26	down	1.64E-01	8.95E-01	-	-
1374538_at	Pomgnt1	protein O-linked mannose beta1,2-N-acetylglucosaminyltransferase	362567	Rn.162088	AW915001	4.61	4.08	2.21	3.98	3.69	4.21	1.26	up	6.82E-01	9.03E-01	-	-
1369870_at	Gpr182	G protein-coupled receptor 182	29307	Rn.87119	NM_053302	2.40	2.40	2.41	2.44	3.36	2.40	1.26	up	3.58E-01	8.95E-01	-	-
1385887_at	---	---	---	Rn.203624	AA963272	8.11	7.34	7.48	6.86	8.03	7.06	1.26	down	4.91E-01	8.95E-01	-	-
1393430_at	---	---	---	---	BG668387	4.21	4.18	5.53	3.50	5.24	4.20	1.26	down	6.53E-01	8.97E-01	-	-
1383558_at	Eefsec	eukaryotic elongation factor, selenocysteine-tRNA-specific	500255	Rn.11965	BI290282	6.41	5.23	6.27	5.76	5.65	5.53	1.25	down	4.36E-01	8.95E-01	-	-
1380856_at	---	---	---	Rn.148206	BE120542	2.57	2.54	2.61	2.55	3.64	2.52	1.25	up	4.25E-01	8.95E-01	-	-
1376532_at	Fndc3b	fibronectin type III domain containing 3B	294925	Rn.757	AW533292	2.40	2.46	2.73	2.52	2.39	3.66	1.25	up	4.76E-01	8.95E-01	-	-
1371879_at	Lrrc42	leucine rich repeat containing 42	298309	Rn.98323	BE110542	5.84	5.85	4.89	6.43	5.13	6.00	1.25	up	5.45E-01	8.95E-01	-	-
1371352_at	Hmgn2	high mobility group nucleosomal binding domain 2	114637	Rn.3517	BM391736	8.83	9.14	9.12	9.29	9.26	9.52	1.25	up	6.43E-02	8.95E-01	-	-
1378318_at	Wdr53	WD repeat domain 53	498097	Rn.27313	BF420065	7.24	7.91	7.13	7.99	7.62	7.65	1.25	up	2.93E-01	8.95E-01	-	-
1389153_at	Serbp1	Serpine1 mRNA binding protein 1	246303	Rn.203108	BI296087	6.50	6.83	6.99	6.17	6.21	6.95	1.25	down	3.26E-01	8.95E-01	-	-
1389863_at	Klf1b	Kinesin family member 1B	117548	Rn.6526	AA924554	4.39	6.13	2.41	4.97	4.03	4.90	1.25	up	7.84E-01	9.30E-01	-	-
1372798_at	Zdhhc16	zinc finger, DHHC-type containing 16	654495	Rn.191489	BF282715	5.43	5.48	4.18	5.55	4.83	5.69	1.25	up	5.48E-01	8.95E-01	-	-
1397415_at	Spg3a	spastic paraplegia 3A homolog (human)	362750	Rn.135117	AA851874	2.43	2.42	2.46	3.44	2.45	2.40	1.25	up	3.87E-01	8.95E-01	-	-
1373782_a_at	LOC499770	similar to LOC495800 protein	499770	Rn.154936	AW253957	5.23	5.97	4.52	5.58	5.55	5.58	1.25	up	4.78E-01	8.95E-01	-	-
1391280_at	Mcts2	malignant T cell amplified sequence 2	689500	---	AW529333	5.05	6.09	6.13	5.82	6.25	6.18	1.25	up	4.37E-01	8.95E-01	-	-
1392606_at	---	---	---	Rn.196349	AI030628	3.44	3.88	3.89	4.55	3.35	4.29	1.25	up	4.53E-01	8.95E-01	-	-
1379690_at	---	---	---	Rn.164586	BF420785	4.14	3.94	4.71	3.57	4.20	4.03	1.25	down	3.35E-01	8.95E-01	-	-
1390545_at	---	---	---	Rn.167307	AI178155	6.41	5.52	6.49	6.26	6.42	6.72	1.25	up	3.87E-01	8.95E-01	-	-
1397708_at	LOC288978	hypothetical LOC288978	288978	Rn.32209	BI286555	3.19	3.73	3.58	3.59	3.60	4.30	1.25	up	3.12E-01	8.95E-01	-	-
1368584_a_at	Cplx2	complexin 2	116657	Rn.10134	NM_053878	2.90	2.86	3.02	3.83	2.99	2.94	1.25	up	3.28E-01	8.95E-01	-	-
1384027_a_at	---	---	---	---	AI072042	12.28	12.23	12.46	12.05	11.69	12.25	1.25	down	1.42E-01	8.95E-01	-	-
1379615_at	Klhdc5	kelch domain containing 5	500367	Rn.203842	AI011501	3.35	3.90	3.22	3.78	3.20	4.47	1.25	up	4.80E-01	8.95E-01	-	-
1373898_at	Pan3	PAN3 polyA specific ribonuclease subunit homolog (S. cerevisiae)	360760	Rn.163191	BM387873	6.75	6.56	6.29	6.07	5.60	6.94	1.25	down	4.73E-01	8.95E-01	-	-
1394652_at	Med28	mediator complex subunit 28	305391	Rn.34860	BI285693	3.83	2.85	2.86	2.85	2.86	2.85	1.25	down	3.74E-01	8.95E-01	-	-
1377654_at	Fam3a	family with sequence similarity 3, member A	501664	Rn.12310	BE328936	6.81	6.99	8.65	7.33	6.50	7.65	1.25	down	6.55E-01	8.98E-01	-	-
1379403_at	Fcgrt	Fc fragment of IgG, receptor, transporter, alpha	29558	Rn.15845	BG378210	3.30	2.78	2.48	2.83	2.35	2.40	1.25	down	3.13E-01	8.95E-01	-	-
1390574_at	---	---	---	Rn.216587	BE101126	4.95	5.23	6.15	6.53	5.17	5.62	1.25	up	5.78E-01	8.95E-01	-	-
1370029_at	Ctbp1	C-terminal binding protein 1	29382	Rn.3946	NM_019201	7.24	7.42	7.61	7.20	7.14	6.95	1.25	down	6.54E-02	8.95E-01	-	-
1391935_at	Eif4e3	eukaryotic translation initiation factor 4E member 3	297481	Rn.22407	AI576608	2.62	2.63	3.58	2.62	2.66	2.56	1.25	down	3.64E-01	8.95E-01	-	-
1375144_at	---	---	---	Rn.163612	BM388843	5.02	4.14	4.25	3.36	5.98	3.09	1.25	down	7.52E-01	9.19E-01	-	-
1367557_s_at	apdh /// Gapdh-ps	glyceraldehyde-3-phosphate dehydrogenase /// glyceraldehyde-3-phosphate	24383 /// 689689	Rn.91450	NM_017008	10.98	10.91	11.33	10.83	10.59	10.81	1.25	down	9.66E-02	8.95E-01	-	-
1384890_at	Ezh1	enhancer of zeste homolog 1 (Drosophila)	303547	Rn.154549	AA998678	6.26	5.81	5.97	5.80	5.38	5.88	1.25	down	1.87E-01	8.95E-01	-	-
1372251_at	Rbm5	RNA binding motif protein 5	300996	Rn.17033	BI282892	6.40	6.01	5.72	6.50	4.58	6.08	1.25	down	6.24E-01	8.95E-01	-	-
1380753_at	Patl1	protein associated with topoisomerase II homolog 1 (yeast)	361736	Rn.162495	BF398036	4.13	4.63	4.05	4.89	4.38	4.51	1.25	up	2.40E-01	8.95E-01	-	-
1376196_a_at	Med4	mediator complex subunit 4	306030	Rn.114469	BG375059	4.55	4.07	4.00	4.07	4.99	4.53	1.25	up	3.60E-01	8.95E-01	-	-
1368387_at	Bdh1	3-hydroxybutyrate dehydrogenase, type 1	117099	Rn.36635	NM_053995	7.52	7.06	6.99	6.96	6.53	7.09	1.25	down	2.40E-01	8.95E-01	-	-
1368193_at	Slc26a4	solute carrier family 26, member 4	29440	Rn.11792	NM_019214	4.67	3.23	3.79	4.03	4.04	2.63	1.25	down	6.31E-01	8.95E-01	-	-
1367753_at	Sec31a	SEC31 homolog A (S. cerevisiae)	93646	Rn.6322	NM_033021	8.59	8.59	9.83	9.22	8.24	8.57	1.25	down	5.53E-01	8.95E-01	-	-
1382913_at	Ctnbp2	cortactin binding protein 2	282587	Rn.16244	BE114076	3.38	2.73	2.97	2.95	2.99	4.12	1.25	up	4.87E-01	8.95E-01	-	-
1381400_at	---	---	---	Rn.27550	AI137973	3.09	2.78	3.41	2.77	2.75	2.77	1.25	down	1.50E-01	8.95E-01	-	-
1379706_at	---	---	---	Rn.172391	BF400686	7.83	8.21	8.32	9.06	7.94	8.34	1.25	up	4.13E-01	8.95E-01	-	-
1368474_at	Vcam1	vascular cell adhesion molecule 1	25361	Rn.11267	NM_012889	2.61	2.62	3.72	2.80	2.60	2.58	1.25	down	4.32E-01	8.95E-01	-	-
1397549_at	Agap2	ArfGAP with GTPase domain, ankyrin repeat and PH domain 2	65218	Rn.91094	AW526039	3.36	2.61	2.59	2.54	2.59	2.45	1.25	down	2.74E-01	8.95E-01	-	-
1383992_at	---	---	---	Rn.40467	BM383990	2.41	2.92	4.09	2.93	4.54	2.93	1.25	up	6.80E-01	9.03E-01	-	-
1389390_at	Gatad1	GATA zinc finger domain containing 1	500005	Rn.203407	AI599847	8.20	8.60	9.14	8.85	8.65	9.42	1.25	up	4.13E-01	8.95E-01	-	-
1378002_at	Hspa4l	heat shock protein 4 like	294993	Rn.144829	BF401583	2.66	2.95	3.01	2.49	2.51	2.64	1.25	down	5.19E-02	8.95E-01	-	-
1379627_at	Tm9sf3	transmembrane 9 superfamily member 3	309475	Rn.17150	AW534630	2.91	2.82	2.92	2.96	2.92	3.74	1.25	up	2.93E-01	8.95E-01	-	-
1395560_at	---	---	---	Rn.24173	BF522151	3.71	4.61	4.99	4.36	3.71	4.26	1.25	down	4.93E-01	8.95E-01	-	-
1372027_at	---	---	---	Rn.7760	AI009713	7.52	7.28	5.59	6.39	7.89	7.08	1.25	up	6.85E-01	9.03E-01	-	-
1376604_at	Synm	synemin, intermediate filament protein	308709	Rn.46362	AW553546	2.45	2.43	3.39	2.45	2.45	2.40	1.25	down	3.60E-01	8.95E-01	-	-
1375610_at	Plekha5	Pleckstrin homology domain containing, family A member 5	246237	Rn.118736	AW251839	2.55	4.41	3.10	3.19	2.83	3.06	1.25	down	5.92E-01	8.95E-01	-	-
1399124_at	RGD1310427	similar to KIAA0090 protein	362643	Rn.42115	AI588517	8.84	9.20	9.64	9.03	8.68	8.99	1.25	down	2.74E-01	8.95E-01	-	-
1383920_at	Amt	aminomethyltransferase (glycine cleavage system protein T)	306586	Rn.162376	BF408907	8.45	8.48	8.15	7.96	7.59	8.55	1.25	down	3.36E-01	8.95E-01	-	-
1379484_at	Aven	apoptosis, caspase activation inhibitor	311299	Rn.145049	AA899459	5.20	5.72	5.58	5.78	5.31	6.39	1.25	up	4.06E-01	8.95E-01	-	-
1392621_at	Tcf25	transcription factor 25 (basic helix-loop-helix)	292082	Rn.107920	AI231159	6.72	6.48	5.80	5.75	5.56	6.72	1.25	down	5.10E-01	8.95E-01	-	-
1375425_at	Ift20	intraflagellar transport 20 homolog (Chlamydomonas)	287541	Rn.8370	BF395126	9.23	9.21	8.23	8.92	9.36	9.36	1.25	up	4.21E-01	8.95E-01	-	-
1375554_at	Ddx47	DEAD (Asp-Glu-Ala-Asp) box polypeptide 47	297685	Rn.73790	BM390927	6.42	6.96	5.97	6.66	6.97	6.69	1.25	up	3.44E-01	8.95E-01	-	-
1382749_at	Rbm5	RNA binding motif protein 5	300996	Rn.17033	BI293987	5.02	4.94	3.41	5.47	5.28	3.60	1.25	up	7.02E-01	9.07E-01	-	-
1388680_at	C1galt1c1	C1GALT1-specific chaperone 1	302499	Rn.110010	BM385686	5.96	6.89	7.00	5.78	6.51	6.58	1.25	down	4.81E-01	8.95E-01	-	-
1389430_at	---	---	---	Rn.7039	AI176172	2.75	2.45	3.64	2.46	2.46	2.94	1.25	down	4.54E-01	8.95E-01	-	-
1367462_at	Dnajc8	DnaJ (Hsp40) homolog, subfamily C, member 8	313035	Rn.105212	AI227785	8.86	8.99	9.13	8.55	8.49	8.96	1.25	down	1.26E-01	8.95E-01	-	-
1391851_at	---	---	---	Rn.167459	AI548705	2.82	2.68	2.65	2.69	3.79	2.65	1.25	up	4.37E-01	8.95E-01	-	-
1381623_at	Sfrs4	splicing factor, arginine/serine-rich 4	362612	Rn.63428	BF391476	7.26	7.62	6.52	7.99	6.70	7.68	1.25	up	5.57E-01	8.95E-01	-	-
1385697_at	Ccnt2	cyclin T2	304758	Rn.21407	BI302799	7.87	6.94	7.77	7.16	7.32	7.12	1.25	down	3.40E-01	8.95E-01	-	-
1382724_at	Pigo	phosphatidylinositol glycan anchor biosynthesis, class O	313341	Rn.123611	AW433604	4.15	5.20	2.72	4.27	4.31	4.46	1.25	up	6.76E-01	9.02E-01	-	-
1373440_at	Lyrm2 /// Mdn1	LYR motif containing 2 /// midasin homolog (yeast)	362498 /// 690354	Rn.198716	AI175525	6.81	7.25	7.04	5.75	6.65	7.72	1.25	down	6.07E-01	8.95E-01	-	-
1382628_at	---	---	---	Rn.7963	BE111904	5.46	3.66	2.52	3.58	4.42	4.61	1.25	up	7.40E-01	9.16E-01	-	-
1371044_at	Pde7a	phosphodiesterase 7A	81744	Rn.39142	BF410284	2.47	2.40	3.96	2.92	2.52	2.41	1.25	down	5.76E-01	8.95E-01	-	-
1377896_at	Rab22a	RAB22A, member RAS oncogene family	366265	Rn.37799	BF284914	2.45	2.82	2.98	2.38	2.46	2.43	1.25	down	1.08E-01	8.95E-01	-	-
1376134_at	Mri1	methylthioribose-1-phosphate isomerase homolog (S. cerevisiae)	288912	Rn.16390	BI277596	2.87	4.72	4.10	3.93	4.12	4.61	1.25	up	6.07E-01	8.95E-01	-	-
1375431_at	RGD1306941	similar to CG31122-PA	314406	Rn.1149	AW531861	4.57	3.58	3.29	3.15	4.94	4.31	1.25	up	6.46E-01	8.95E-01	-	-
1388378_at	Eif3c	eukaryotic translation initiation factor 3, subunit C	293484	Rn.4207	AI412236	8.34	8.70	8.56	8.79	8.38	9.40	1.25	up	3.62E-01	8.95E-01	-	-
1369942_at	Actn4	actinin alpha 4	63836	Rn.15777	NM_031675	7.47	8.41	7.88	8.14	8.17	8.41	1.25	up	3.17E-01	8.95E-01	-	-
1381018_s_at	Asap1	ArfGAP with SH3 domain, ankyrin repeat and PH domain 1	314961	Rn.63466	BG378709	3.92	5.42	2.82	6.18	3.32	3.63	1.25	up	7.97E-01	9.34E-01	-	-
1382653_at	---	---	---	Rn.103515	AI136405	7.72	8.30	7.73	7.41	7.55	7.82	1.25	down	2.24E-01	8.95E-01	-	-
1368223_at	Adamts1	ADAM metallopeptidase with thrombospondin type 1 motif, 1	79252	Rn.7897	NM_024400	6.54	5.94	7.35	6.48	5.98	6.40	1.25	down	4.99E-01	8.95E-01	-	-
1370745_at	Slc34a1	solute carrier family 34 (sodium phosphate), member 1	25548	Rn.92022	AB013454	11.15	11.49	11.47	11.65	11.70	11.73	1.25	up	4.52E-02	8.95E-01	-	-
1367002_at	---	---	---	Rn.203419	AA946209	2.57	2.53	2.57	3.57	2.59	2.48	1.25	up	3.99E-01	8.95E-01	-	-
1385856_at	Riok1	RIO kinase 1 (yeast)	291061	Rn.132553	BE096718	7.86	7.96	6.80	8.54	7.45	7.61	1.25	up	5.55E-01	8.95E-01	-	-
1376938_at	---	---	---	Rn.204668	AI717081	2.52	3.55	2.58	2.52	2.63	2.51	1.25	down	3.89E-01	8.95E-01	-	-
1367577_at	Hspb1	heat shock protein 1	24471	Rn.3841	NM_031970	3.53	2.29	3.50	3.43	3.48	3.39	1.25	up	4.72E-01	8.95E-01	-	-
1379810_at	Scye1	small inducible cytokine subfamily E, member 1	114632	Rn.3192	AI454911	7.02	6.27	7.00	6.78	5.94	6.61	1.25	down	4.14E-01	8.95E-01	-	-
1367788_at	Phkg2	phosphorylase kinase, gamma 2 (testis)	140671	Rn.11153	NM_080584	8.12	7.17	5.96	6.80	6.61	6.88	1.25	down	6.34E-01	8.95E-01	-	-
1381058_at	---	---	---	Rn.18180	AI548492	2.52	2.52	2.53	2.48	3.49	2.57	1.25	up	3.70E-01	8.95E-01	-	-
1395010_at	---	---	---	Rn.55326	AI102173	8.35	8.69	8.17	8.24	7.31	8.69	1.25	down	4.96E-01	8.95E-01	-	-
1396473_at	---	---	---	Rn.79500	BM389874	2.69	3.67	2.71	2.70	2.70	2.69	1.25	down	3.72E-01	8.95E-01	-	-
1373657_at	Slc31a2	solute carrier family 31 (copper transporters), member 2	298091	Rn.15570	BF417391	8.03	7.24	7.03	7.91	7.73	7.64	1.25	up	3.64E-01	8.95E-01	-	-
1373561_at	Chpf	chondroitin polymerizing factor	316533	Rn.3794	AI012498	4.40	3.35	3.59	3.34	3.53	3.49	1.25	down	3.71E-01	8.95E-01	-	-
1391021_at	Cgnl1	cingulin-like 1	315795	Rn.120904	BF408587	3.90	4.02	4.73	4.69	5.42	3.51	1.25	up	6.26E-01	8.95E-01	-	-
1399119_at	Znf292	zinc finger protein 292	50552	Rn.106753	BI282030	2.52	3.59	3.14	2.81	3.57	3.84	1.25	up	4.99E-01	8.95E-01	-	-
1373175_at	Pbd1	phosphotriose B domain containing 1	297694	Rn.3413	BI285951	2.39	3.18	2.54	2.38	2.39	2.37	1.25	down	2.56E-01	8.95E-01	-	-
1372871_at	RGD735175	hypothetical protein MGC:72616	316530	Rn.101111	AA891821	6.20	6.69	7.45	7.14	6.70	7.47	1.25	up	4.91E-01	8.95E-01	-	-
1389475_at	Smo	smoothened homolog (Drosophila)	25273	Rn.44429	BF398112	2.37	2.35	2.37	2.37	3.33	2.36	1.25	up	3.75E-01	8.95E-01	-	-
1399077_at	Mtx1	Metaxin 1	295241	Rn.216761	AI411253	5.09	5.62	5.45	5.27	4.84	5.08	1.25	down	1.75E-01	8.95E-01	-	-
1380549_at	Ccar1	cell division cycle and apoptosis regulator 1	361849	Rn.92786	AI555625	8.11	5.71	3.67	6.05	4.56	5.91	1.25	down	8.25E-01	9.44E-01	-	-
1385529_at	FAM3B	family with sequence similarity 3, member B	304050	Rn.219522	BF411402	2.60	2.53	3.71	2.74	2.63	2.50	1.25	down	4.50E-01	8.95E-01	-	-
1393478_at	---	---	---	Rn.147293	AI029492	7.56	8.75	8.83	8.68	8.93	8.50	1.25	up	4.93E-01	8.95E-01	-	-
1383743_at	Lrrc16a	leucine rich repeat containing 16A	360941	Rn.40387	BI275464	5.57	4.51	4.40	4.28	4.73	4.49	1.25	down	4.59E-01	8.95E-01	-	-
1378441_at	---	---	---	Rn.63780	AI176859	4.12	4.48	4.57	4.88	4.62	4.64	1.25	up	1.14E-01	8.95E-01	-	-
1383104_at	RGD1561459	similar to RIK

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1395320_s_at	Rhox9	reproductive homeobox 9	298352	Rn.144519	BI289049	3.40	4.19	3.44	3.38	3.39	3.28	1.25	down	2.83E-01	8.95E-01	-	-
1381252_at	---	---	---	Rn.199756	BE098160	7.45	7.02	7.87	7.82	6.96	6.61	1.25	down	5.00E-01	8.95E-01	-	-
1376812_at	---	---	---	Rn.100323	BF419731	4.25	3.57	2.77	3.59	4.14	3.82	1.25	up	5.19E-01	8.95E-01	-	-
1387268_at	Polr1b	polymerase (RNA) I polypeptide B	83582	Rn.88734	NM_031773	3.79	3.52	3.80	4.26	3.72	4.09	1.25	up	1.53E-01	8.95E-01	-	-
1370569_at	Pde4d	phosphodiesterase 4D, cAMP-specific (phosphodiesterase E3 dunce homolo	24627	Rn.163460	BF565001	4.34	2.97	2.99	2.49	3.48	3.37	1.25	down	5.93E-01	8.95E-01	-	-
1373879_at	---	---	---	Rn.93303	AI234961	5.38	5.96	7.04	6.49	6.28	6.58	1.25	up	5.52E-01	8.95E-01	-	-
1391574_at	---	---	---	---	AW253369	5.51	4.70	5.40	5.21	5.57	5.79	1.25	up	3.52E-01	8.95E-01	-	-
1370957_at	Il6st	interleukin 6 signal transducer	25205	Rn.12138	BM383427	4.76	6.15	5.69	6.33	5.28	5.96	1.25	up	5.63E-01	8.95E-01	-	-
1392698_a_at	Gtf3c4	general transcription factor IIIC, polypeptide 4	685539	Rn.12334	AA899844	7.51	7.25	6.84	7.79	8.04	6.75	1.25	up	5.06E-01	8.95E-01	-	-
1395528_at	Mrpl10	mitochondrial ribosomal protein L10	691075	Rn.204813	BE111618	5.88	6.53	5.55	6.29	6.47	6.17	1.25	up	3.44E-01	8.95E-01	-	-
1389545_at	Tbl1xr1	transducin (beta)-like 1 X-linked receptor 1	365755	Rn.140831	BF281994	7.90	8.50	8.34	8.61	8.60	8.49	1.25	up	1.54E-01	8.95E-01	-	-
1388382_at	LOC361985	similar to NICE-3	361985	Rn.107173	AI407017	8.80	8.98	8.86	9.03	9.35	9.22	1.25	up	3.96E-02	8.95E-01	-	-
1377951_at	---	---	---	Rn.203642	AA964993	3.52	3.80	3.72	3.36	3.35	3.36	1.25	down	1.79E-02	8.95E-01	-	-
1388118_at	Hibadh	3-hydroxyisobutyrate dehydrogenase	63938	Rn.73	AI176586	9.67	9.63	10.06	9.38	9.33	9.89	1.25	down	1.44E-01	8.95E-01	-	-
1375915_at	Irak1bp1	interleukin-1 receptor-associated kinase 1 binding protein 1	300862	Rn.106156	AI073247	5.73	5.50	5.52	5.88	5.80	6.04	1.25	up	3.38E-02	8.95E-01	-	-
1373785_at	Pld4	phospholipase D family, member 4	362792	Rn.6379	AA848738	4.39	2.83	4.53	4.62	2.90	3.27	1.25	down	6.92E-01	9.05E-01	-	-
1372169_at	Mst1	male-specific lethal 1 homolog (Drosophila)	303514	Rn.22437	BE108809	6.14	6.24	5.39	5.96	6.55	6.22	1.25	up	3.68E-01	8.95E-01	-	-
1372379_at	---	---	---	Rn.20397	AI177706	2.67	2.92	3.47	3.18	3.19	3.64	1.25	up	3.19E-01	8.95E-01	-	-
1390779_at	---	---	---	Rn.16562	AA818912	4.49	5.40	4.81	5.03	5.48	5.15	1.25	up	3.43E-01	8.95E-01	-	-
1369494_a_at	Ghrhr	growth hormone releasing hormone receptor	25321	Rn.10936	NM_012850	2.43	2.48	2.52	3.43	2.45	2.52	1.25	up	3.69E-01	8.95E-01	-	-
1370984_at	Zfp46	zinc finger protein 46	298558	Rn.94219	AF151710	3.15	3.28	3.35	3.38	3.35	4.02	1.25	up	2.30E-01	8.95E-01	-	-
1382971_at	Pdcd6ip	programmed cell death 6 interacting protein	501083	Rn.101381	BF389407	8.01	9.25	8.34	8.78	8.78	9.00	1.25	up	4.42E-01	8.95E-01	-	-
1386910_a_at	Apex1	APEX nuclease (multifunctional DNA repair enzyme) 1	79116	Rn.5949	AF311054	7.11	7.06	6.27	7.26	7.06	7.08	1.25	up	3.15E-01	8.95E-01	-	-
1395962_at	Chchd5	coiled-coil-helix-coiled-coil-helix domain containing 5	296147	Rn.8658	BI278980	4.42	3.93	3.56	3.33	4.44	3.18	1.25	down	5.33E-01	8.95E-01	-	-
1374608_at	Tatdn2	TatD DNase domain containing 2	500295	Rn.124135	BF415553	6.84	7.04	7.86	6.80	7.29	6.69	1.25	down	4.24E-01	8.95E-01	-	-
1372185_at	Mettl11a	methyltransferase like 11A	362103	Rn.12306	BF557934	5.41	5.33	5.25	5.24	6.08	5.64	1.25	up	2.66E-01	8.95E-01	-	-
1389640_at	Sh3bgrl2	SH3 domain binding glutamic acid-rich protein like 2	501024	Rn.7595	BM391811	4.26	3.90	4.68	4.09	4.11	3.67	1.25	down	2.97E-01	8.95E-01	-	-
1371876_at	Psmg2	proteasome (prosome, macropain) assembly chaperone 2	291539	Rn.144759	BM387084	5.28	5.31	5.05	4.80	4.53	5.35	1.25	down	2.76E-01	8.95E-01	-	-
1375655_at	---	---	---	Rn.146928	BE107208	2.39	3.52	3.28	2.59	3.90	3.66	1.25	up	5.78E-01	8.95E-01	-	-
1389372_at	RGD1308489	similar to hypothetical protein	313340	Rn.54339	BF394221	5.60	6.29	5.41	4.60	5.77	5.97	1.25	down	5.60E-01	8.95E-01	-	-
1397141_at	---	---	---	Rn.169520	BE097236	2.85	2.57	2.90	2.87	3.51	2.91	1.25	up	2.40E-01	8.95E-01	-	-
1383040_a_at	---	---	---	Rn.155723	AI044098	6.12	6.20	6.23	6.05	7.05	6.41	1.25	up	3.40E-01	8.95E-01	-	-
1377124_at	Mtf1	metal-regulatory transcription factor 1	362591	Rn.20005	AA964824	3.63	4.76	5.43	5.42	3.68	3.75	1.25	down	7.01E-01	9.07E-01	-	-
1370085_at	Rasa1	RAS p21 protein activator (GTPase activating protein) 1	25676	Rn.12223	NM_013135	4.33	5.51	6.33	5.74	4.45	5.02	1.25	down	6.67E-01	8.99E-01	-	-
1398789_at	Rpl37	ribosomal protein L37	81770	Rn.65053	NM_031106	12.72	12.94	12.66	12.97	12.98	13.33	1.25	up	9.48E-02	8.95E-01	-	-
1376571_at	Tmem42	transmembrane protein 42	363171	Rn.161976	BI285997	7.72	8.27	8.67	7.64	8.16	7.90	1.25	down	3.65E-01	8.95E-01	-	-
1398997_at	Phpt1	phosphohistidine phosphatase 1	296517	Rn.74071	AI102252	7.35	8.67	8.24	7.98	9.13	8.11	1.25	up	5.82E-01	8.95E-01	-	-
1377383_at	Efs	embryonal Fyn-associated substrate	290212	Rn.219271	AA897247	2.47	2.46	2.47	2.45	3.46	2.44	1.25	up	3.96E-01	8.95E-01	-	-
1368644_at	Spata6	spermatogenesis associated 6	171413	Rn.8467	AI233848	3.49	3.73	3.57	4.27	3.32	4.16	1.25	up	3.58E-01	8.95E-01	-	-
1396467_at	---	---	---	Rn.219343	BM387106	2.46	2.52	3.95	2.46	2.48	3.04	1.25	down	5.75E-01	8.95E-01	-	-
1388665_at	Ppp4r2	protein phosphatase 4, regulatory subunit 2	297486	Rn.11876	BG378896	7.16	7.22	5.89	7.19	6.36	7.66	1.25	up	6.09E-01	8.95E-01	-	-
1398511_at	Susd2	sushi domain containing 2	294335	Rn.166705	AA901176	7.48	6.52	7.06	6.60	6.73	6.78	1.25	down	3.22E-01	8.95E-01	-	-
1381375_at	RGD1310495	Similar to KIAA1919 protein	309809	Rn.24001	AI232664	5.15	6.47	6.78	6.31	5.27	5.87	1.25	down	6.13E-01	8.95E-01	-	-
1372544_at	---	---	---	Rn.153608	AI410305	6.21	6.75	6.11	6.63	6.66	6.74	1.25	up	1.86E-01	8.95E-01	-	-
1393919_at	Sgms2	sphingomyelin synthase 2	310849	Rn.161863	AW535116	4.91	4.87	4.48	5.31	4.46	5.45	1.25	up	4.01E-01	8.95E-01	-	-
1373820_at	Rfwd2	ring finger and WD repeat domain 2	360860	Rn.8617	AI179107	8.74	9.81	9.07	9.39	9.31	9.87	1.25	up	4.29E-01	8.95E-01	-	-
1389170_at	Casp7	caspase 7	64026	Rn.53995	BF283754	5.55	7.43	7.42	7.07	6.84	7.44	1.25	up	6.50E-01	8.96E-01	-	-
1388594_at	Creld1	cysteine-rich with EGF-like domains 1	312638	Rn.5461	BG371453	3.24	4.06	4.88	3.32	3.93	3.97	1.25	down	5.71E-01	8.95E-01	-	-
1394887_x_at	---	---	---	---	AI407383	4.90	4.67	5.08	4.67	4.68	4.35	1.25	down	1.19E-01	8.95E-01	-	-
1398868_at	Timm13	translocase of inner mitochondrial membrane 13 homolog (yeast)	252928	Rn.2109	AI408157	7.81	8.46	7.85	8.30	8.30	8.47	1.25	up	2.19E-01	8.95E-01	-	-
1399013_at	Tmem85	transmembrane protein 85	296049	Rn.219228	AI412609	7.79	8.58	8.67	8.97	8.34	8.68	1.25	up	3.92E-01	8.95E-01	-	-
1388520_at	Spag9	sperm associated antigen 9	360600	Rn.24583	BI278854	6.41	7.25	7.18	7.44	6.87	7.47	1.25	up	3.94E-01	8.95E-01	-	-
1374136_at	Prmt10	protein arginine methyltransferase 10 (putative)	291947	Rn.199059	BG665121	6.25	7.05	5.36	6.34	6.29	6.99	1.25	up	5.86E-01	8.95E-01	-	-
1386899_at	Ctsh	cathepsin H	25425	Rn.1997	NM_012939	10.03	9.22	9.43	9.36	9.45	8.91	1.25	down	3.39E-01	8.95E-01	-	-
1384940_at	RGD1305314	similar to KIAA0335	309478	Rn.107229	AI136655	2.65	2.55	3.39	2.56	2.58	2.51	1.25	down	2.97E-01	8.95E-01	-	-
1391415_at	Pno1	partner of NOB1 homolog (S. cerevisiae)	289809	Rn.20046	AI043694	6.56	6.96	5.69	6.21	5.88	6.18	1.25	down	4.58E-01	8.95E-01	-	-
1389307_at	Aplp1	amyloid beta (A4) precursor-like protein 1	502317	Rn.114169	AW435479	6.70	6.85	7.71	7.56	7.39	7.25	1.25	up	3.86E-01	8.95E-01	-	-
1398515_at	---	---	---	Rn.146130	BF291177	3.30	2.29	2.32	2.29	2.31	2.35	1.25	down	3.93E-01	8.95E-01	-	-
1385790_at	05-Mar	membrane-associated ring finger (C3HC4) 5	294079	Rn.218003	BF560024	7.73	8.13	7.50	7.75	6.62	8.03	1.25	down	5.34E-01	8.95E-01	-	-
1395537_at	RGD1309228	similar to putative protein, with at least 9 transmembrane domains, of eukaryc	298851	Rn.41348	BF523835	2.60	2.80	3.56	2.78	2.48	2.74	1.25	down	3.62E-01	8.95E-01	-	-
1377917_at	---	---	---	Rn.22974	AI104595	2.41	3.45	2.43	2.40	2.41	2.51	1.25	down	4.08E-01	8.95E-01	-	-
1384330_at	Thg1l	tRNA-histidine guanylyltransferase 1-like (S. cerevisiae)	303067	Rn.160832	AI763467	6.45	6.55	4.50	6.67	5.26	6.53	1.25	up	7.12E-01	9.10E-01	-	-
1372636_at	Rab40c	Rab40c, member RAS oncogene family	359728	Rn.2496	AI007924	3.77	4.50	4.91	3.97	3.82	4.43	1.25	down	4.48E-01	8.95E-01	-	-
1374797_at	Eaf1	ELL associated factor 1	306261	Rn.34587	BM391920	9.31	10.15	9.61	10.01	9.81	10.19	1.25	up	3.01E-01	8.95E-01	-	-
1374124_at	Jmjd8	jumonji domain containing 8	360498	Rn.155261	AA851397	4.77	6.27	7.37	6.62	6.19	6.56	1.25	up	6.99E-01	9.07E-01	-	-
1394093_at	Smarca5	SWI/SNF related, matrix associated, actin dependent regulator of chromatin,	307766	Rn.221918	BF557855	5.44	5.66	5.65	5.38	5.00	5.41	1.25	down	1.02E-01	8.95E-01	-	-
1372520_at	Mcl1	myeloid cell leukemia sequence 1	60430	Rn.161889	AI172056	9.18	9.45	9.91	9.44	8.86	9.29	1.25	down	3.13E-01	8.95E-01	-	-
1398808_at	Impa1	inositol (myo)-1(or 4)-monophosphatase 1	83523	Rn.3975	NM_032057	6.32	6.96	6.90	6.56	6.26	6.42	1.25	down	2.28E-01	8.95E-01	-	-
1382093_at	Ints7	Integrator complex subunit 7	289382	Rn.15180	AI178038	4.01	4.70	4.58	3.92	4.26	4.16	1.25	down	2.50E-01	8.95E-01	-	-
1377043_at	---	---	---	Rn.220193	BF388434	2.54	2.63	2.57	2.86	2.56	3.27	1.25	up	2.02E-01	8.95E-01	-	-
1394795_at	---	---	---	Rn.48834	BE109243	3.55	3.52	3.56	3.71	3.29	4.59	1.25	up	4.53E-01	8.95E-01	-	-
1377408_at	Pla2g6	phospholipase A2, group VI (cytosolic, calcium-independent)	360426	Rn.44692	AW251242	5.71	7.25	7.03	6.41	6.31	6.31	1.25	down	5.45E-01	8.95E-01	-	-
1378324_at	Ttc30b	tetratricopeptide repeat domain 30B	499814	Rn.87109	BE120389	3.26	3.07	3.39	2.95	3.01	2.81	1.25	down	4.39E-02	8.95E-01	-	-
1378255_at	---	---	---	Rn.219459	BE111416	5.51	5.59	6.79	5.91	5.51	5.51	1.25	down	5.07E-01	8.95E-01	-	-
1380844_at	---	---	---	Rn.203445	BE098337	2.49	2.54	2.48	2.72	2.48	3.27	1.25	up	2.50E-01	8.95E-01	-	-
1373284_at	Sav1	salvador homolog 1 (Drosophila)	299116	Rn.14087	AI176607	5.25	5.84	5.78	5.62	5.79	6.41	1.25	up	3.60E-01	8.95E-01	-	-
1373826_at	Ypel5	yippee-like 5 (Drosophila)	298792	Rn.1136	AI170754	9.77	9.55	9.73	9.33	9.37	9.39	1.25	down	1.03E-02	8.95E-01	-	-
1389116_at	Mtmr9	myotubularin related protein 9	282584	Rn.20978	BI111884	2.89	3.96	3.34	2.89	3.09	3.26	1.25	down	3.88E-01	8.95E-01	-	-
1373555_at	---	---	---	Rn.165969	BM392315	7.60	7.89	8.96	8.12	8.59	8.69	1.25	up	5.19E-01	8.95E-01	-	-
1376774_at	Exoc4	Exocyst complex component 4	116654	Rn.221950	BG380482	8.98	8.49	7.85	8.18	8.17	8.03	1.25	down	3.93E-01	8.95E-01	-	-
1395169_at	Zcchc8	zinc finger, CCHC domain containing 8	288661	Rn.144000	BF388779	5.32	5.32	4.55	5.31	5.52	5.31	1.25	up	2.97E-01	8.95E-01	-	-
1370402_at	Eglf7	EGF-like-domain, multiple 7	245963	Rn.144669	AF223678	4.29	4.31	4.94	4.81	4.17	3.62	1.25	down	4.77E-01	8.95E-01	-	-
1385194_at	Rb1cc1	RB1-inducible coiled-coil 1	312927	Rn.33137	BG671668	3.13	3.07	3.91	3.07	3.05	3.04	1.25	down	3.05E-01	8.95E-01	-	-
1376341_at	Ankrd12	Ankyrin repeat domain 12	316775	Rn.94994	BM388895	2.36	2.37	3.34	2.35	2.40	2.38	1.25	down	3.83E-01	8.95E-01	-	-
1388920_at	Bmp6	bone morphogenetic protein 6	25644	Rn.40476	AI230985	3.73	3.79	4.78	3.86	3.80	3.70	1.25	down	4.09E-01	8.95E-01	-	-
1380790_at	Spec1l	SPEC1-like	361828	Rn.63017	BF416414	2.97	2.83	2.46	2.45	2.45	2.40	1.25	down	1.09E-01	8.95E-01	-	-
1384846_at	LOC679610	hypothetical protein LOC679610	679610	Rn.205071	AI453919	3.00	4.54	2.78	3.48	2.78	3.11	1.25	down	6.20E-01	8.95E-01	-	-
1370242_at	Rps23	ribosomal protein S23	124323	Rn.2139	AA848284	11.57	11.92	11.68	12.00	11.87	12.24	1.25	up	1.02E-01	8.95E-01	-	-
1387411_at	Ptprk	protein tyrosine phosphatase, receptor type, K, extracellular region	360302	Rn.216454	NM_020085	4.34	6.30	6.67	5.41	4.94	6.00	1.25	down	7.08E-01	9.08E-01	-	-
1371529_at	Ripk1	receptor (TNFRSF)-interacting serine-threonine kinase 1	306886	Rn.7572	BF289001	3.16	3.71	4.01	3.87	3.85	4.12	1.25	up	2.94E-01	8.95E-01	-	-
1367649_at	Palm	paralemmin	170673	Rn.198776	NM_130829	4.45	4.42	4.32	4.66	4.45	5.04	1.25	up	1.49E-01	8.95E-01	-	-
1390277_at	---	---	---	Rn.210113	BF399451	2.42	2.21	2.41	2.73	2.86	2.38	1.25	up	1.17E-01	8.95E-01	-	-
1391061_at	---	---	---	Rn.205952	BI293100	2.68	2.47	2.44	3.65	2.53	2.37	1.25	up	4.83E-01	8.95E-01	-	-
1373519_at	---	---	---	---	AI412601	6.20	6.20	4.85	5.91	5.97	6.32	1.25	up	5.36E-01	8.95E-01	-	-
1390419_a_at	Tusc3	tumor suppressor candidate 3	290783	Rn.35146	AI454905	6.57	6.70	5.95	6.73	5.99	7.44	1.25	up	5.45E-01	8.95E-01	-	-
1378197_at	KIFC2	kinesin family member C2	300053	Rn.100970	AW433953	5.85	5.72	5.83	6.40	6.13	5.81	1.25	up	1.46E-01	8.95E-01	-	-
1383714_at	RGD1305938	similar to expressed sequence AW549877	310362	Rn.29775	H32348	7.17	7.19	7.23	7.40	6.01	7.24	1.25	down	5.11E-01	8.95E-01	-	-
1373566_at	---	---	---	Rn.216552	AI103026	9.25	8.16	8.64	8.85	9.18	8.97	1.25	up	3.93E-01	8.95E-01	-	-
1393447_at	Kif7 /// LOC498974	kinesin family member 7 /// similar to kinesin family member 7	293047 /// 498974	Rn.145008	BG380625	2.48	2.48	2.51	2.47	3.21	2.45	1.25	up	4.19E-01	8.95E-01	-	-
1372184_at	RGD1309188	similar to hypothetical protein BC011833	315463	Rn.4026	BM392213	7.76	7.88	7.70	8.19	7.60	8.50	1.25	up	3.07E-01	8.95E-01	-	-
1385397_at	Steap4	STEAP family member 4	499991	Rn.16959	AA859085	4.38	3.72	3.71	3.97	3.70	3.20	1.25	down	3.72E-01	8.95E-01	-	-
1371755_at	---	---	---	---	AA799607	7.56	7.39	8.00	7.52	6.75	7.73	1.25	down	4.13E-01	8.95E-01	-	-
1394612_at	LOC500688	Similar to a disintegrin and metalloprotease domain 4	500688	Rn.19779	AW552006	5.12	5.79	7.38	5.49	5.93	5.92	1.25	down	6.68E-01	9.00E-01	-	-
1385567_at	Gtf2f1	general transcription factor IIF, polypeptide 1	316123	Rn.98836	AA955573	4.67	3.84	3.81	3.09	3.90	4.38	1.25	down	5.38E-01	8.95E-01	-	-
1377766_at	RGD1306820	similar to erythroid differentiation-related factor 1	309069	Rn.102186	BI285939	2.46	3.44	2.33	2.32	2.47	2.48	1.25	down	4.21E-01	8.95E-01	-	-
1378259_at	Tardbp	TAR DNA binding protein	298648	Rn.2633	BF396301	5.70	7.70	7.00	6.74	5.25	7.47	1.24	down	7.36E-01	9.15E-01	-	-
1391325_at	---	---	---	Rn.204159	BF397406	2.77	2.84	3.10	3.24	3.09	3.33	1.24	up	6.14E-02	8.95E-01	-	-
1374770_at	Asah1	N-acylsphingosine amidohydrolase (acid ceramidase) 1	84431	Rn.127798	AA800062	5.91	4.97	5.95	6.00	5.96	5.82	1.24	up	3.88E-01	8.95E-01	-	-
1382596_a_at	Tmem214	transmembrane protein 214	362711	Rn.104487	AI230388	6.27	5.54	8.44	6.63	6.09	6.59	1.24	down	7.40E-01	9.16E-01	-	-
1371528_at	Fkbp8	FK506 binding protein 8, 38kDa	296852	Rn.99789	BI274519	5.42	5.03	5.29	4.87	4.83	5.10	1.24	down	9.04E-02	8.95E-01	-	-
1373515_at	Hspc159	galectin-related protein	360983	Rn.17651	BI275737	4.72	4.57	4.75	4.30	5.15	5.54	1.24	up	4.39E-01	8.95E-01	-	-
1383554_at	Rnf128	ring finger protein 128	313511	Rn.7002	AW142796	7.42	7.95	7.79	6.88	7.44	7.89	1.24	down	3.93E-01	8.95E-01	-	-
1381783_at	Akap3	A kinase (PRKA) anchor protein 3	312720	Rn.38091	AI577267	2.55	2.61	3.24	2.87	2.56	2.96	1.24	up	1.84E-01	8.95E-01	-	-
1377069_at	---	---	---	---	BG379055	6.96	7.38	7.53	7.39	7.55	7.86	1.24	up	2.21E-01	8.95E-01	-	-
1367827_at	Ppp2cb	protein phosphatase 2 (formerly 2A), catalytic subunit, beta isoform	24673	Rn.977	NM_017040	7.86	7.29	7.14	7.59	7.64	8.00	1.24	up	2.82E-01	8.95E-01	-	-
1384453_at	---	---	---	Rn.16322	AI045824	2.37	2.36	3.33	2.37	2.38	2.37	1.24	down	3.81E-01	8.95E-01	-	-
1391654_at	---	---	---	---	BF396329	2.74	2.54	3.25	2.55	2.47	2.47	1.24	down	2.13E-01	8.95E-01	-	-
1394014_at	Phf12	PHD finger protein 12	303274	Rn.101513	AA924840	4.40	4.36	5.97	4.49	5.21	4.08	1.24	down	6.41E-01	8.95E-01	-	-
1371373_at	Rnf181	ring finger protein 181	297337	Rn.94883	AI010460	8.97	9.89	9.75	9.98	9.68	9.90	1.24	up	3.51E-01	8.95E-01	-	-
1368840_at	Tmem176b	transmembrane protein 176B	171411	Rn.26876	NM_134390	4.04	5.73	3.70	5.20	3.78	5.44	1.24	up	7.18E-01	9.11E-01	-	-
1385335_at	Trim39	tripartite motif-containing 39	309591	Rn.211560	BF415953	2.54	2.69	4.06	2.89	2.80	2.65	1.24	down	5.53E-01	8.95E-01	-	-
1370899_at	Sfpq	splicing factor proline/glutamine rich (polypyrimidine tract binding protein assc	252855	Rn.54645	BE107056	6.08	6.33	6.21	7.17	5.94	6.46	1.24	up	4.33E-01	8.95E-01	-	-
1383076_at	RGD1308695	similar to RIKEN cDNA 1200016B10	289088	Rn.101917	AA901203	4.26	6.17	4.85	5.59	4.98	5.65	1.24	up	6.29E-01	8.95E-01	-	-
1398858_at	Psmd2	proteasome (prosome, macropain) 26S subunit, non-ATPase, 2	287984	Rn.29909	D37934	8.40	8.77	9.54	8.43	8.66	8.68	1.24	down	4.12E-01	8.95E-01	-	-
1376502_at	RGD1309228	similar to putative protein, with at least 9 transmembrane domains, of eukaryc	298851	Rn.41348	AW523504	6.55	3.77	4.64	5.35	5.02	5.54	1.24	up	7.25E-01	9.13E-01	-	-
1396151_at	Tmcc1	transmembrane and coiled-coil domain family 1	312654	Rn.198698	AA850797	2.49	4.12	3.12	4.14	3.41	3.13	1.24	up	6.05E-01	8.95E-01	-	-
1384009_at	Narf	nuclear prelamin A recognition factor	360681	Rn.162225	AI535383	5.29	5.76	3.86	5.16	5.61	5.07	1.24	up	6.25E-01	8.95E-01	-	-
1374279_at	Scye1	small inducible cytokine subfamily E, member 1	114632	Rn.3192	BI288244	7.00	8.43	8.85	8.24	8.06	8.92	1.24	up	6.37E-01	8.95E-01	-	-
1385761_s_at	---	---	---	Rn.147698	BF400633	4.63	7.13	5.77	6.01	6.08	6.39	1.24	up	6.88E-01	9.04E-01	-	-
1370916_at	Tec	tec protein tyrosine kinase	84492	Rn.11797	AI406496	2.85	2.52	3.19	3.15	3.07	3.38	1.24	up	2.19E-01	8.95E-01	-	-
1388582_at	Psme3	proteasome (prosome, macropain) activator subunit 3	287716	Rn.198325	BM392043	9.14	9.38	9.11	8.50	8.84	9.35	1.24	down	2.93E-01	8.95E-01	-	-
1388806_at	Ttc5	tetratricopeptide repeat domain 5	305837	Rn.16620	AI176039	4.09	4.08	4.54	4.00	3.58	4.19	1.24	down	2.55E-01	8.95E-01	-	-
1372876_at	Sephs2	selenophosphate synthetase 2	308993	Rn.100471	AA799700	9.31	9.81	9.88	8.97	9.38	9.70	1.24	down	3.15E-01	8.95E-01	-	-
1397383_at	Emx1	empty spiracles homeobox 1	500235	Rn.140907	BF391062	4.30	3.67	3.84	3.95	4.52	4.29	1.24	up	2.81E-01	8.95E-01	-	-
1376051_at	Cryl1	crystallin, lambda 1	290277	Rn.57632	BI293393	9.17	9.50	9.68	9.30	9.11	9.00	1.24	down	1.43E-01	8.95E-01	-	-
1372028_at	Nop16	NOP16 nucleolar protein homolog (yeast)	306768	Rn.6090	AA893215	5.33	5.20	5.23	5.40	5.33	5.97	1.24	up	1.99E-01	8.95E-01	-	-
1382820_at	---	---	---	Rn.2633	BF396301	5.70	7.70	7.00	6.74	5.25	7.47	1.24	down	2.43E-01	8.95E-01	-	-
1368762_at	Ubd	ubiquitin D	29168	Rn.18473	NM_053299	2.09	3.77	3.69	2.67	4.24	3.58	1.24	up	6.80E-01	9.03E-01	-	-
1370697_a_at	Nexn	nexilin (F actin binding protein)	246172	Rn.107975	AF056034	4.59	3.58	3.

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1377013_at	---	---	---	---	AI639108	3.87	4.31	4.03	4.76	4.19	4.21	1.24	up	2.41E-01	8.95E-01	-	-
1374563_at	RGD1561004	similar to AMME syndrome candidate gene 1 protein homolog	501539	---	BI301280	2.65	2.65	2.71	3.42	2.85	2.69	1.24	up	2.29E-01	8.95E-01	-	-
1382861_at	Nup160	nucleoporin 160	311182	Rn.21145	AI230642	2.36	2.93	2.31	2.62	2.34	3.58	1.24	up	5.00E-01	8.95E-01	-	-
1392241_at	Ppp2r5a	Protein phosphatase 2, regulatory subunit B', alpha isoform	312754	Rn.104461	AW252634	2.93	2.71	3.31	2.72	2.65	2.65	1.24	down	1.48E-01	8.95E-01	-	-
1371028_at	Tgoln1	trans-golgi network protein	192152	Rn.11349	AW917192	3.89	4.41	5.64	4.42	4.16	4.42	1.24	down	5.85E-01	8.95E-01	-	-
1382840_at	Lrrc19	leucine rich repeat containing 19	680478	Rn.178166	AI232423	7.60	7.58	7.25	7.07	8.08	8.23	1.24	up	4.60E-01	8.95E-01	-	-
1383822_at	Bicd2	bicaudal D homolog 2 (Drosophila)	306809	Rn.103443	AI029990	6.41	6.81	6.87	6.86	6.85	7.32	1.24	up	2.16E-01	8.95E-01	-	-
1395631_at	---	---	---	Rn.123735	BF418465	2.92	2.93	2.94	2.96	3.82	2.94	1.24	up	3.40E-01	8.95E-01	-	-
1372829_at	Rbm8	RNA binding motif protein 8	295284	Rn.37716	BE113079	8.64	8.87	8.81	8.56	7.86	8.96	1.24	down	3.94E-01	8.95E-01	-	-
1387012_at	Sart1	squamous cell carcinoma antigen recognized by T cells	29678	Rn.25144	NM_031596	7.16	7.22	5.81	6.55	7.21	7.36	1.24	up	5.82E-01	8.95E-01	-	-
1375236_at	RGD1563556	similar to mKIAA1377 protein	315409	Rn.141062	BI291246	2.78	2.79	3.72	2.79	2.81	2.76	1.24	down	3.73E-01	8.95E-01	-	-
1368103_at	Abcg1	ATP-binding cassette, sub-family G (WHITE), member 1	85264	Rn.8398	AI712719	2.54	2.49	2.58	2.57	3.41	2.56	1.24	up	3.28E-01	8.95E-01	-	-
1390459_at	---	---	---	Rn.98870	BG670247	2.46	3.30	2.59	2.47	2.46	2.47	1.24	down	2.95E-01	8.95E-01	-	-
1370672_a_at	Dnm3	dynamin 3	171574	Rn.11191	D14076	2.71	3.01	2.41	2.42	2.40	2.37	1.24	down	1.48E-01	8.95E-01	-	-
1388453_at	Myadm	myeloid-associated differentiation marker	369016	Rn.106161	BI296048	6.84	6.47	4.72	7.09	5.93	5.95	1.24	up	7.02E-01	9.07E-01	-	-
1388881_at	Pgp	phosphoglycolate phosphatase	287115	Rn.4311	BG380656	4.19	2.95	2.72	2.66	3.34	2.92	1.24	down	5.65E-01	8.95E-01	-	-
1387267_at	Ntf3	neurotrophin 3	81737	Rn.9715	NM_031073	2.62	3.60	2.63	2.63	2.67	2.62	1.24	down	3.93E-01	8.95E-01	-	-
1371430_at	Dag1	dystroglycan 1 (dystrophin-associated glycoprotein 1)	114489	Rn.36260	AW251326	7.15	6.63	6.17	6.93	6.75	7.21	1.24	up	3.76E-01	8.95E-01	-	-
1383172_at	Ranbp2	RAN binding protein 2	294429	Rn.101115	BF543886	4.46	3.79	3.52	4.18	4.06	4.47	1.24	up	3.65E-01	8.95E-01	-	-
1373729_at	Atpaf1	ATP synthase mitochondrial F1 complex assembly factor 1	313510	Rn.18579	BG376772	6.52	5.58	5.77	5.48	6.52	6.81	1.24	up	5.64E-01	8.95E-01	-	-
1398399_at	RGD1304587	similar to RIKEN cDNA 2310033P09	303180	Rn.21630	AI102518	2.47	2.80	3.87	2.92	2.62	2.68	1.24	down	5.11E-01	8.95E-01	-	-
1377462_at	---	---	---	---	BE111349	2.88	2.83	2.84	2.92	3.34	3.24	1.24	up	6.86E-02	8.95E-01	-	-
1373396_at	Rprd1b	regulation of nuclear pre-mRNA domain containing 1B	311591	Rn.4144	BF283617	4.95	5.43	4.93	5.52	3.92	4.94	1.24	down	5.84E-01	8.95E-01	-	-
1372603_at	Pacsin3	protein kinase C and casein kinase substrate in neurons 3	311187	Rn.15418	BM386892	6.00	6.25	6.65	6.61	6.66	6.57	1.24	up	1.78E-01	8.95E-01	-	-
1371840_at	S1pr1	sphingosine-1-phosphate receptor 1	29733	Rn.109455	BI295971	4.06	2.98	3.75	3.83	3.53	2.50	1.24	down	5.79E-01	8.95E-01	-	-
1380500_s_at	Fkbp2	FK506 binding protein 2	293702	Rn.65866	BF561706	11.83	11.96	11.76	12.10	12.07	12.32	1.24	up	3.09E-02	8.95E-01	-	-
1388428_at	Dtd1	D-tyrosyl-tRNA deacylase 1 homolog (S. cerevisiae)	362227	Rn.23561	BF283022	8.26	8.52	8.04	7.78	9.02	8.97	1.24	up	5.06E-01	8.95E-01	-	-
1374537_at	Chsy1	chondroitin sulfate synthase 1	292999	Rn.13788	AI406533	2.44	2.62	2.47	3.03	2.49	2.94	1.24	up	1.51E-01	8.95E-01	-	-
1387903_at	Pja2	praja 2, RING-H2 motif containing	192256	Rn.18446	D32249	8.27	8.13	7.88	8.30	8.28	8.65	1.24	up	1.33E-01	8.95E-01	-	-
1373313_at	Sel1l	Sel-1 suppressor of lin-12-like (C. elegans)	314352	Rn.20802	BM391570	6.71	6.50	6.74	6.92	6.42	7.54	1.24	up	4.05E-01	8.95E-01	-	-
1370149_at	Asgr1	asialoglycoprotein receptor 1	24210	Rn.44300	NM_012503	4.53	6.74	5.63	5.21	4.68	6.08	1.24	down	7.03E-01	9.07E-01	-	-
1382389_at	---	---	---	Rn.204921	AI179755	4.59	3.61	4.08	4.07	4.79	4.35	1.24	up	4.27E-01	8.95E-01	-	-
1390465_at	---	---	---	---	AW534554	4.68	5.56	5.75	6.02	5.13	5.78	1.24	up	5.02E-01	8.95E-01	-	-
1372834_at	Vps4b	vacuolar protein sorting 4 homolog B (S. cerevisiae)	360834	Rn.25893	BI304063	9.02	8.88	8.89	8.17	8.89	8.79	1.24	down	2.44E-01	8.95E-01	-	-
1385074_at	Smarca2	SWI/SNF related, matrix associated, actin dependent regulator of chromatin,	361745	Rn.94939	BE102268	7.99	8.86	8.37	8.66	7.45	8.17	1.24	down	5.11E-01	8.95E-01	-	-
1393818_s_at	RGD1311142	similar to hypothetical protein FLJ32796	361564	Rn.82375	BE102234	2.67	2.66	2.60	2.61	3.59	2.66	1.24	up	3.83E-01	8.95E-01	-	-
1372988_at	Cnot10	CCR4-NOT transcription complex, subunit 10	316034	Rn.23825	BF397012	7.05	6.86	5.89	6.26	6.27	6.33	1.24	down	4.33E-01	8.95E-01	-	-
1392881_at	St3gal4	ST3 beta-galactoside alpha-2,3-sialyltransferase 4	363040	Rn.24125	BF284899	2.37	2.37	2.38	2.37	2.31	2.37	1.24	up	3.78E-01	8.95E-01	-	-
1388328_at	Eif3i	eukaryotic translation initiation factor 3, subunit I	682390	Rn.162577	BM392200	10.52	10.33	10.22	10.70	10.56	10.75	1.24	up	4.02E-02	8.95E-01	-	-
1397915_at	---	---	---	Rn.46323	AW526790	2.34	2.54	2.60	2.55	3.32	2.53	1.24	up	3.15E-01	8.95E-01	-	-
1368236_at	Mep1a	meprin 1 alpha	25684	Rn.16265	NM_013143	9.50	10.18	9.94	9.37	9.27	10.04	1.24	down	3.76E-01	8.95E-01	-	-
1379686_at	Spsb3	spla/ryanodine receptor domain and SOCS box containing 3	302981	Rn.20038	AI170880	3.37	2.37	2.42	2.40	2.47	2.36	1.24	down	3.96E-01	8.95E-01	-	-
1372415_at	Gtf2h3	general transcription factor IIH, polypeptide 3	288651	Rn.203542	BM385649	6.29	7.26	7.87	7.67	7.04	7.65	1.24	up	5.70E-01	8.95E-01	-	-
1371945_at	Ube2i3	ubiquitin-conjugating enzyme E2L 3	363836	Rn.163186	AI407788	6.76	7.83	8.42	7.18	7.30	7.60	1.24	down	5.69E-01	8.95E-01	-	-
1390603_at	---	---	---	Rn.216449	AA856317	5.86	6.67	5.37	5.98	4.35	6.64	1.24	down	7.10E-01	9.09E-01	-	-
1379043_at	---	---	---	Rn.155414	BI284837	5.08	5.05	4.95	4.52	4.71	4.91	1.24	down	5.88E-02	8.95E-01	-	-
1391003_at	Fam178a	family with sequence similarity 178, member A	499360	Rn.113020	BE117528	4.28	4.20	3.58	3.26	5.65	4.08	1.24	up	6.94E-01	9.06E-01	-	-
1388492_at	Tnip1	TNFAIP3 interacting protein 1	363599	Rn.113408	AW919111	7.92	8.17	8.43	7.81	8.51	8.14	1.24	up	2.92E-01	8.95E-01	-	-
1391318_x_at	Usp49	ubiquitin specific peptidase 49	316211	Rn.147913	AW252553	3.13	2.58	3.02	2.65	2.62	2.53	1.24	down	1.43E-01	8.95E-01	-	-
1371604_at	Mrpl34	mitochondrial ribosomal protein L34	290632	Rn.2509	AA858969	6.91	7.66	6.22	7.50	6.70	7.53	1.24	up	5.66E-01	8.95E-01	-	-
1374399_at	Eh4	EH-domain containing 4	192204	Rn.7376	AA801107	3.21	3.08	3.20	2.91	2.89	2.77	1.24	down	6.45E-03	8.95E-01	-	-
1390179_at	Ankrd52	ankyrin repeat domain 52	362811	Rn.8972	BE107540	4.23	3.50	3.22	3.32	3.35	3.34	1.24	down	3.58E-01	8.95E-01	-	-
1377493_at	Mto1	mitochondrial translation optimization 1 homolog (S. cerevisiae)	300852	Rn.216594	BM386301	6.77	6.55	5.13	5.30	6.17	6.05	1.24	down	6.20E-01	8.95E-01	-	-
1381970_at	Lsm14a	LSM14A, SCD6 homolog A (S. cerevisiae)	361554	Rn.2370	AA945865	8.09	7.83	8.88	7.91	7.74	8.23	1.24	down	4.20E-01	8.95E-01	-	-
1396220_at	---	---	---	Rn.203110	BI302034	3.36	2.55	2.56	2.51	2.56	2.47	1.24	down	3.14E-01	8.95E-01	-	-
1397540_at	---	---	---	Rn.167715	BF398168	3.91	4.21	4.24	4.24	4.51	4.51	1.24	down	6.21E-01	8.95E-01	-	-
1388633_at	RGD1309313	similar to RIKEN cDNA 4930538D17	309454	Rn.8265	BM388921	2.47	2.91	2.81	2.88	3.18	3.06	1.24	up	1.21E-01	8.95E-01	-	-
1370162_at	Ppp4r1	protein phosphatase 4, regulatory subunit 1	140943	Rn.16065	AI536553	5.14	4.52	5.14	6.06	4.87	5.00	1.24	down	5.28E-01	8.95E-01	-	-
1393273_at	---	---	---	Rn.108008	AW533027	4.35	3.43	2.83	3.48	2.93	3.27	1.24	down	5.44E-01	8.95E-01	-	-
1397381_at	---	---	---	Rn.27184	AI136603	2.56	4.22	3.52	4.32	3.44	3.46	1.24	up	6.10E-01	8.95E-01	-	-
1371614_at	Atg12	ATG12 autophagy related 12 homolog (S. cerevisiae)	361321	Rn.6224	AI169001	6.26	6.52	7.12	6.60	5.84	6.53	1.24	down	4.29E-01	8.95E-01	-	-
1390067_at	---	---	---	Rn.208140	BF403821	3.29	2.36	2.37	2.36	2.38	2.35	1.24	down	3.74E-01	8.95E-01	-	-
1375179_at	---	---	---	---	AI231282	2.80	2.59	3.62	3.81	2.88	3.26	1.24	up	4.98E-01	8.95E-01	-	-
1392386_at	---	---	---	Rn.205478	AI578435	7.94	6.92	6.50	6.57	7.73	7.99	1.24	up	6.38E-01	8.95E-01	-	-
1372422_at	---	---	---	Rn.17376	AI175506	7.58	8.57	8.49	8.58	8.63	8.36	1.24	up	3.98E-01	8.95E-01	-	-
1390199_at	---	---	---	Rn.166352	BM389647	5.76	6.45	5.79	5.77	5.83	5.47	1.24	down	2.87E-01	8.95E-01	-	-
1389047_at	Bag2	Bcl2-associated athanogene 2	690038	Rn.163913	AI009167	2.39	2.75	2.77	2.85	2.98	3.01	1.24	up	7.97E-02	8.95E-01	-	-
1387765_at	Mbl1	mannose-binding lectin (protein A) 1	24548	Rn.10273	NM_012599	3.51	3.20	2.46	3.34	3.28	3.49	1.24	up	3.83E-01	8.95E-01	-	-
1390813_at	Msi2	Musashi homolog 2 (Drosophila)	360596	Rn.43808	AI236624	7.74	8.05	7.75	8.16	7.91	8.40	1.24	up	1.50E-01	8.95E-01	-	-
1391936_a_at	---	---	---	Rn.45026	BI289110	9.15	7.99	7.95	7.93	7.66	8.57	1.24	down	5.51E-01	8.95E-01	-	-
1388635_at	---	---	---	Rn.216610	BF542301	2.44	2.80	2.50	2.43	3.52	2.73	1.24	up	4.17E-01	8.95E-01	-	-
1372358_at	LOC686590	similar to IQ motif and Sec7 domain 1	686590	---	AI012613	5.24	5.49	4.51	5.67	5.08	5.42	1.24	up	4.16E-01	8.95E-01	-	-
1392932_at	Leng8	leukocyte receptor cluster (LRC) member 8	361506	Rn.217745	BI279191	8.80	7.54	6.84	8.65	8.48	6.98	1.24	up	7.12E-01	9.10E-01	-	-
1399031_at	Dda1	DET1 and DDB1 associated 1	688813	Rn.86998	BM391360	3.02	3.69	3.75	3.73	3.75	3.89	1.24	up	2.66E-01	8.95E-01	-	-
1372582_at	Csnk1g3	casein kinase 1, gamma 3	64823	Rn.10084	AI407847	6.38	6.14	5.78	6.35	6.25	6.62	1.24	up	2.12E-01	8.95E-01	-	-
1398990_at	---	---	---	Rn.163564	BI281754	7.88	7.66	8.16	7.86	8.13	8.64	1.24	up	3.19E-01	8.95E-01	-	-
1382275_at	Pak1ip1	PAK1 interacting protein 1	361232	Rn.115052	AI236989	3.38	3.60	3.47	3.61	4.23	3.52	1.24	up	2.53E-01	8.95E-01	-	-
1393400_at	Zap70	zeta-chain (TCR) associated protein kinase	301348	Rn.17862	BM387946	3.30	2.38	2.38	2.38	2.38	2.37	1.24	down	3.70E-01	8.95E-01	-	-
1379393_at	Vil1	villin 1	316521	Rn.220408	AI231564	7.63	8.02	7.48	7.72	7.05	7.45	1.24	down	2.85E-01	8.95E-01	-	-
1373813_at	Dnajc10	DnaJ (Hsp40) homolog, subfamily C, member 10	295690	Rn.8642	AI172034	6.99	6.56	6.12	6.71	6.72	7.16	1.24	up	3.49E-01	8.95E-01	-	-
1383236_at	Fxr1	fragile X mental retardation, autosomal homolog 1	361927	Rn.94652	BE118678	7.48	7.60	7.49	7.32	6.81	7.53	1.24	down	2.29E-01	8.95E-01	-	-
1372662_at	Fbxo34	F-box protein 34	305830	Rn.137885	AI176698	3.76	4.75	5.13	5.33	4.14	5.09	1.24	up	6.01E-01	8.95E-01	-	-
1393209_at	Bsnd	Bartter syndrome, infantile, with sensorineural deafness (Bartin)	192675	Rn.22715	AI547423	3.44	3.11	2.61	4.33	3.39	2.35	1.24	up	6.45E-01	8.95E-01	-	-
1388678_at	---	---	---	Rn.2368	AI176695	6.44	6.77	6.92	7.07	6.96	7.02	1.24	up	9.94E-02	8.95E-01	-	-
1382987_at	---	---	---	Rn.74539	AA874945	2.57	3.09	3.95	3.02	2.99	2.68	1.24	down	4.98E-01	8.95E-01	-	-
1376181_at	Ncoa5	nuclear receptor coactivator 5	296372	Rn.8482	BG688724	6.48	7.07	6.33	6.39	6.24	6.32	1.24	down	2.48E-01	8.95E-01	-	-
1394346_at	Arhgef12	Rho guanine nucleotide exchange factor (GEF) 12	367072	Rn.129752	BF545496	6.33	6.79	7.20	6.59	7.35	7.30	1.24	up	4.28E-01	8.95E-01	-	-
1389879_at	Sp3	Sp3 transcription factor	367846	---	AA875516	7.16	6.49	4.41	7.09	5.70	6.19	1.24	up	7.54E-01	9.20E-01	-	-
1371533_at	Dctn6	dynactin 6	290798	Rn.3642	BI282273	7.75	7.15	7.62	7.88	7.95	7.61	1.24	up	2.13E-01	8.95E-01	-	-
1376143_at	Ddx54	DEAD (Asp-Glu-Ala-Asp) box polypeptide 54	360815	Rn.41869	BG380619	2.60	4.64	2.71	2.69	4.51	3.68	1.24	up	7.34E-01	9.15E-01	-	-
1384252_at	RGD1309095	similar to hypothetical protein BC015148	301381	Rn.40282	AI603103	5.69	5.36	5.07	5.00	5.08	5.11	1.24	down	1.62E-01	8.95E-01	-	-
1372670_at	RGD1307682	similar to hypothetical protein FLJ21827	300675	Rn.13688	BI281686	6.45	7.74	7.65	7.05	7.32	6.55	1.24	down	5.51E-01	8.95E-01	-	-
1373484_at	Klhl13	kelch-like 13 (Drosophila)	313445	Rn.24229	AI179828	2.73	2.74	2.62	2.66	3.09	3.26	1.24	up	1.69E-01	8.95E-01	-	-
1374766_at	---	---	---	Rn.220207	BE103616	6.39	5.68	5.80	6.45	4.39	6.11	1.24	down	6.70E-01	9.00E-01	-	-
1377797_at	Emg1	EMG1 nucleolar protein homolog (S. cerevisiae)	312706	Rn.162786	AI071470	4.07	5.74	6.04	5.54	3.79	5.58	1.24	down	7.35E-01	9.15E-01	-	-
1386946_at	Cpt1a	carnitine palmitoyltransferase 1a, liver	25757	Rn.2856	NM_031559	8.26	8.37	8.24	8.41	8.59	8.81	1.24	up	6.82E-02	8.95E-01	-	-
1379673_at	Uap1l1	UDP-N-acteylglucosamine pyrophosphorylase 1-like 1	296560	Rn.23051	AI230747	3.35	2.43	2.45	2.47	2.43	2.41	1.24	down	3.66E-01	8.95E-01	-	-
1388801_at	RGD1305469	Similar to RIKEN cDNA 9030221M09 gene	305466	Rn.198970	AA945103	4.66	5.04	3.63	4.74	4.46	5.05	1.24	up	5.35E-01	8.95E-01	-	-
1377815_at	Rpp14	ribonuclease P 14 subunit (human)	361020	Rn.43524	BE102535	7.54	8.13	7.77	7.77	6.55	8.20	1.24	down	5.87E-01	8.95E-01	-	-
1375030_at	B3galt5	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 5	288161	Rn.28077	AI639289	9.12	9.02	8.95	9.09	8.11	8.96	1.24	down	3.97E-01	8.95E-01	-	-
1397539_at	Incenp	inner centromere protein	293733	Rn.92193	H34382	7.57	7.07	7.35	7.81	7.13	6.13	1.24	down	5.77E-01	8.95E-01	-	-
1379410_at	---	---	---	Rn.164226	AA925019	6.83	5.89	4.53	6.18	6.35	5.65	1.24	up	6.82E-01	9.03E-01	-	-
1369939_at	Cycs	cytochrome c, somatic	25309	Rn.161841	NM_012839	12.43	12.22	12.52	12.05	12.01	12.18	1.24	down	3.60E-02	8.95E-01	-	-
1397682_at	---	---	---	Rn.203421	AW917689	3.44	3.49	3.56	3.03	4.11	4.27	1.24	up	4.77E-01	8.95E-01	-	-
1385905_at	Hnrnpf	Heterogeneous nuclear ribonucleoprotein F	64200	Rn.144596	AI178616	6.47	6.01	6.26	6.09	5.36	6.36	1.24	down	3.99E-01	8.95E-01	-	-
1371568_at	Nisch	nischarin	306255	Rn.96234	BI282284	6.48	5.35	5.51	6.10	5.63	5.33	1.24	down	3.34E-01	8.95E-01	-	-
1397907_at	LOC501546	Hypothetical protein LOC501546	501546	Rn.12130	BF553760	2.44	2.46	2.47	3.37	2.47	2.46	1.24	up	3.64E-01	8.95E-01	-	-
1369683_at	Bid	BH3 interacting domain death agonist	64625	Rn.31142	AF136282	2.42	2.41	3.34	2.42	2.42	2.41	1.24	down	3.75E-01	8.95E-01	-	-
1398863_at	Gnb2	guanine nucleotide binding protein (G protein), beta polypeptide 2	81667	Rn.1155	AF277892	2.77	4.00	2.81	3.18	2.69	2.78	1.24	down	5.14E-01	8.95E-01	-	-
1397533_at	Mpp5	membrane protein, palmitoylated 5 (MAGUK p55 subfamily member 5)	314259	Rn.8181	BF555544	7.63	7.03	7.30	6.64	7.00	7.39	1.24	down	3.31E-01	8.95E-01	-	-
1372077_at	Strap	serine/threonine kinase receptor associated protein	297699	Rn.8126	AA891681	7.88	7.76	6.30	7.75	7.50	7.61	1.24	up	5.81E-01	8.95E-01	-	-
1368817_at	Psme4	proteasome (prosome, macropain) activator subunit 4	498433	Rn.163607	NM_023986	8.18	8.05	7.44	7.66	7.41	7.67	1.24	down	2.76E-01	8.95E-01	-	-
1393447_at	Jam2	junctional adhesion molecule 2	619374	Rn.6473	BI290037	2.56	4.30	2.57	2.57	2.55	3.37	1.24	down	6.55E-01	8.97E-01	-	-
1377662_at	Pir	pirin (iron-binding nuclear protein)	363465	Rn.103685	AI176041	3.11	3.07	3.11	3.10	3.11	4.01	1.24	up	3.63E-01	8.95E-01	-	-
1376644_at	Med19	mediator complex subunit 19	311165	Rn.218981	BG380933	4.22	2.91	2.86	2.94	2.90	3.22	1.24	down	5.38E-01	8.95E-01	-	-
1376598_at	Paxip1	PAX interacting (with transcription-activation domain) protein 1	311944	Rn.136961	AI179993	4.31	4.93	4.94	5.29	4.93	4.87	1.24	up	2.81E-01	8.95E-01	-	-
1389038_at	Etf1	eukaryotic translation termination factor 1	307503	Rn.98549	BF285387	7.02	6.31	8.01	6.26	6.97	7.19	1.24	down	6.15E-01	8.95E-01	-	-
1398841_at	Rab1	RAB1, member RAS oncogene family	81754	Rn.106743	AI411122	10.16	10.38	10.20	10.53	10.51	10.63	1.24	up	1.67E-02	8.95E-01	-	-
1370309_a_at	Hnrnpab	heterogeneous nuclear ribonucleoprotein A/B	83498	Rn.1427	AJ238854	9.04	9.31	8.88	9.29	9.47	9.40	1.24	up	8.83E-02	8.95E-01	-	-
1380577_at	Abcg2	ATP-binding cassette, sub-family G (WHITE), member 2	312382	Rn.1313	AI175616	9.55	10.15	9.73	9.17	9.48	9.85	1.24	down	3.11E-01	8.95E-01	-	-
1379846_at	Acer2	alkaline ceramidase 2	313339	Rn.6387	AI500753	3.38	2.43	2.50	2.48	2.48	2.43	1.24	down	3.71E-01	8.95E-01	-	-
1385063_at	---	---	---	Rn.212077	BG377323	5.22	5.31	4.28	5.21	5.12	5.40	1.24	up	4.14E-01	8.95E-01	-	-
1371578_at	Prkaca	protein kinase, cAMP-dependent, catalytic, alpha	25636	Rn.20	AW915101	7.59	7.93	8.04	8.61	7.61	8.27	1.24	up	3.96E-01	8.95E-01	-	-
1385273_at	---	---	---	Rn.203057	AA859665	5.51	4.37	3.93	4.28	4.25	4.36	1.24	down	5.52E-01	8.95E-01	-	-
1367579_a_at	Tuba1b /// Tuba1c /// Tu	tubulin, alpha 1A /// tubulin, alpha 1B /// tubulin, alpha 1C	418 /// 500929 /// 6	Rn.154526	BI285434	9.37	9.44	9.56	9.18	8.79	9.49	1.24	down	2.19E-01	8.95E-01	-	-
1373828_at	Crtc2	CREB regulated transcription coactivator 2	310615	Rn.13599	AI412614	5.14	5.55	4.71	5.45	5.43	5.44	1.24	up	2.77E-01	8.95E-01	-	-
1379845_at	---	---	---	Rn.11990	AI237283	3.79	3.82	2.95	3.18	3.16	3.31	1.24	down	3.50E-01	8.95E-01	-	-
1379601_at	Alkbh5	alkB, alkylation repair homolog 5 (E. coli)	303193	Rn.146441	AI030982	4.98	4.78	7.01	5.23	5.45	5.16	1.24	down	6.90E-01	9.05E-01	-	-
1379679_at	---	---	---	Rn.55946	BF290584	4.75	5.84	5.43	5.70	5.64	5.61	1.24	up	3.88E-01	8.95E-01	-	-
1395197_at	---	---	---	Rn.203900	BI293027	2.40	2.40	2.43	2.42	3.05	2.68	1.24	up	1.66E-01	8.95E-01	-	-
1396301_x_at	Afmid	aryiformamidase	688283	Rn.216742	BI277442	7.26	7.69	7.52	7.19	7.25	7.10	1.24	down	8.39E-02	8.95E-01	-	-
1376078_at	---	---	---	Rn.22415	BI296274	9.87	10.12	9.89	9.17	10.01	9.78	1.24	down	3.07E-01	8.95E-01	-	-
1372811_at	Ktn1	kinectin 1	361029	Rn.66508	BI289779	4.11	4.20	4.09	4.15	4.09	5.08	1.24	up	3.94E-01	8.95E-01	-	-
1376257_at	Znf629	zinc finger protein 629	308998	Rn.44885	AW520814	2.80	2.80	3.75	2.77	2.45	3.20	1.24	down	4.69E-01	8.95E-01	-	-
1381996_at	---	---	---	Rn.8057	BG666712	2.41	2.87	2.83	2.39	2.41	2.38	1.24	down	1.04E-01	8.95E-01	-	-
1377367_at	Kazald1	Kazal-type serine peptidase inhibitor domain 1	293997	Rn.138194	BE099439	2.50	2.55	2.54	2.50	3.50	2.51	1.24	up	4.08E-01	8.95E-01	-	-
1389379_at	---	---	---	Rn.165738	AI011967	2.48	2.55	2.51	2.53	3.43	2.51	1.24	up	3.71E-01	8.95E-01	-	-
1397267_at	Rimbp2	RIM binding protein 2	266780	Rn.207562	BF410275	2.48	2.47	2.48

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1376824_at	---	---	---	Rn.205314	AI408131	6.31	6.78	5.71	6.64	6.14	6.95	1.24	up	4.77E-01	8.95E-01	-	-
1393162_at	Slc39a6	solute carrier family 39 (metal ion transporter), member 6	291733	Rn.99415	AI502079	2.71	2.81	3.27	2.72	2.44	2.72	1.24	down	1.94E-01	8.95E-01	-	-
1373565_at	Smarca4	SWI/SNF related, matrix associated, actin dependent regulator of chromatin,	171379	Rn.23417	BE329013	5.61	6.40	6.64	6.24	6.47	6.85	1.24	up	4.43E-01	8.95E-01	-	-
1399000_at	Atp9b	ATPase, class II, type 9B	291411	Rn.217953	AI233289	3.26	3.59	3.29	3.53	3.54	3.98	1.24	up	1.71E-01	8.95E-01	-	-
1382625_at	---	---	---	Rn.19235	BE101437	2.33	2.31	2.32	2.32	3.05	2.50	1.24	up	2.37E-01	8.95E-01	-	-
1393180_at	Ctdsp1	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phos	363249	Rn.163070	AI011492	6.11	5.80	5.62	5.25	5.69	5.67	1.24	down	2.09E-01	8.95E-01	-	-
1373391_at	Tmoc1	transmembrane and coiled-coil domains 1	289196	Rn.86308	BM390343	4.01	3.89	4.17	3.90	4.10	4.98	1.24	up	4.23E-01	8.95E-01	-	-
1368099_at	Clasp2	cytoplasmic linker associated protein 2	114514	Rn.19943	NM_053722	4.21	4.19	5.13	4.13	4.21	4.28	1.23	down	3.87E-01	8.95E-01	-	-
1368091_at	Oplah	5-oxoprolinase (ATP-hydrolysing)	116684	Rn.3066	NM_053904	7.36	7.97	7.02	7.18	6.79	7.46	1.23	down	4.21E-01	8.95E-01	-	-
1369742_at	Herc1	hect (homologous to the E6-AP (UBE3A) carboxyl terminus) domain and RCC	315771	Rn.77185	NM_031610	7.49	7.51	5.79	7.13	6.91	7.67	1.23	up	6.45E-01	8.95E-01	-	-
1373353_at	Brpf1	bromodomain and PHD finger containing, 1	679713	Rn.160093	BE097309	2.82	2.89	3.55	2.70	2.84	2.81	1.23	down	2.66E-01	8.95E-01	-	-
1388635_at	Tmem127	transmembrane protein 127	311405	Rn.19881	BE113372	9.50	9.45	10.09	10.27	9.81	9.87	1.23	up	2.94E-01	8.95E-01	-	-
1389805_at	---	---	---	---	BF400933	3.79	4.75	4.12	4.48	4.52	4.56	1.23	up	3.43E-01	8.95E-01	-	-
1394833_at	---	---	---	Rn.163688	BE120930	2.65	3.00	2.66	3.97	2.65	2.60	1.23	up	5.48E-01	8.95E-01	-	-
1378610_at	---	---	---	Rn.147204	BG378206	2.92	3.33	3.56	2.58	3.06	3.27	1.23	down	3.38E-01	8.95E-01	-	-
1373922_at	---	---	---	Rn.18449	BG377024	5.61	5.11	5.55	5.85	5.91	5.42	1.23	up	2.42E-01	8.95E-01	-	-
1390351_at	---	---	---	Rn.81527	AI231225	7.79	9.15	8.03	7.46	7.85	8.56	1.23	up	7.68E-01	9.24E-01	-	-
1368839_at	Wfs1	Wolfram syndrome 1 homolog (human)	83725	Rn.16015	NM_031823	5.09	2.42	2.40	3.98	3.22	3.62	1.23	up	7.57E-01	9.21E-01	-	-
1393236_at	Riok3	RIO kinase 3 (yeast)	361293	Rn.203135	AI137233	9.05	8.95	8.72	8.98	9.70	8.95	1.23	up	3.19E-01	8.95E-01	-	-
1378790_at	---	---	---	---	AW535379	2.61	2.56	2.61	2.57	2.60	3.54	1.23	up	3.94E-01	8.95E-01	-	-
1367787_at	Ica1	islet cell autoantigen 1	81024	Rn.1379	NM_030844	2.30	2.29	3.24	2.30	2.33	2.29	1.23	down	3.88E-01	8.95E-01	-	-
1397601_at	---	---	---	Rn.55540	BI289709	2.33	2.33	2.34	3.25	2.33	2.33	1.23	up	3.77E-01	8.95E-01	-	-
1387663_at	Gmfb	glia maturation factor, beta	81661	Rn.10454	NM_031032	6.58	7.35	6.81	6.78	7.42	7.46	1.23	up	3.90E-01	8.95E-01	-	-
1375057_at	Tspan18	tetraspanin 18	311210	Rn.219380	BG377313	4.85	3.49	3.92	4.53	4.51	4.13	1.23	up	5.11E-01	8.95E-01	-	-
1378181_at	Rpp40	ribonuclease P 40 subunit (human)	291071	Rn.23660	BI279714	3.80	3.76	3.78	3.88	3.86	4.51	1.23	up	2.31E-01	8.95E-01	-	-
1382113_at	MGC72612	Similar to expressed sequence AI449175	494340	Rn.17914	BF398543	3.44	2.62	2.78	2.75	2.60	2.58	1.23	down	3.04E-01	8.95E-01	-	-
1382760_at	---	---	---	Rn.22915	AA899481	4.34	3.23	3.42	3.41	3.41	3.27	1.23	down	4.28E-01	8.95E-01	-	-
1387050_s_at	s1 /// Xng1l1 /// Kn	kininogen 1 /// kininogen 1-like 1 /// kininogen 2	03 /// 25087 /// 288	Rn.44576	NM_012696	3.42	2.62	2.64	2.62	2.55	2.60	1.23	down	3.16E-01	8.95E-01	-	-
1368843_at	Yme1l1	YME1-like 1 (S. cerevisiae)	114217	Rn.8153	NM_053682	7.74	8.64	8.66	7.36	8.55	8.22	1.23	down	5.53E-01	8.95E-01	-	-
1389730_at	---	---	---	Rn.20365	AI176502	8.78	9.39	9.17	8.58	8.87	8.97	1.23	down	2.28E-01	8.95E-01	-	-
1367745_at	Dgkz	diacylglycerol kinase zeta	81221	Rn.11208	NM_031143	4.73	5.15	4.73	4.48	4.39	4.83	1.23	down	1.97E-01	8.95E-01	-	-
1389293_at	Cpsf2	cleavage and polyadenylation specific factor 2	299256	Rn.8038	BM390250	6.99	6.88	6.64	7.29	7.12	7.02	1.23	up	7.90E-02	8.95E-01	-	-
1372840_at	Zbed4	zinc finger, BED-type containing 4	315211	Rn.162962	AI170289	4.20	5.57	5.78	4.76	5.04	4.85	1.23	down	5.80E-01	8.95E-01	-	-
1367601_at	Ctkd2	CTD/kinase-interacting transactivator, with Glu/Asp-rich carboxy-terminal domai	114490	Rn.31765	AI013390	5.40	5.40	5.71	5.29	5.13	5.18	1.23	down	5.65E-02	8.95E-01	-	-
1395198_at	Rnf114	Ring finger protein 114	362277	Rn.49925	BE099956	3.50	2.57	2.60	2.57	2.62	2.57	1.23	down	3.77E-01	8.95E-01	-	-
1367654_at	Fat1	FAT tumor suppressor homolog 1 (Drosophila)	83720	Rn.8633	NM_031819	8.94	9.79	8.19	9.41	8.92	9.50	1.23	up	5.73E-01	8.95E-01	-	-
1368418_a_at	Cp	ceruloplasmin	24268	Rn.32777	AF202115	4.29	3.62	3.55	3.37	3.75	3.42	1.23	down	3.17E-01	8.95E-01	-	-
1374444_at	Plxnb1	plexin B1	316009	Rn.26773	BI285540	4.13	4.70	3.44	4.36	4.36	4.45	1.23	up	4.52E-01	8.95E-01	-	-
1385656_at	Tmem174	transmembrane protein 174	499516	Rn.122955	AI043676	10.28	9.77	10.22	9.64	9.86	9.86	1.23	down	1.63E-01	8.95E-01	-	-
1377033_at	Serpinf2	serine (or cysteine) peptidase inhibitor, clade F, member 2	287527	Rn.15774	BG377997	10.67	10.72	10.88	10.25	10.37	10.74	1.23	down	1.34E-01	8.95E-01	-	-
1367948_a_at	Kdr	kinase insert domain protein receptor	25589	Rn.88869	U93307	6.15	5.78	6.56	6.44	5.88	5.25	1.23	down	5.01E-01	8.95E-01	-	-
1374241_at	---	---	---	Rn.147629	AI406271	6.18	7.20	7.11	7.19	6.27	7.94	1.23	up	6.30E-01	8.95E-01	-	-
1371203_at	Prkci	protein kinase C, iota	84006	Rn.1388	AB020615	9.44	9.43	8.66	9.51	9.69	9.24	1.23	up	3.53E-01	8.95E-01	-	-
1381255_at	---	---	---	Rn.31236	AA956474	4.63	2.67	2.49	2.68	2.79	3.43	1.23	down	6.98E-01	9.07E-01	-	-
1384309_at	---	---	---	Rn.7284	BF393535	2.49	3.01	3.18	2.62	2.55	2.61	1.23	down	2.22E-01	8.95E-01	-	-
1384410_at	---	---	---	Rn.203671	AA964404	2.91	2.89	2.79	3.73	2.95	2.82	1.23	up	3.51E-01	8.95E-01	-	-
1374603_at	Setmar	SET domain and mariner transposase fusion gene	500281	Rn.7640	AA943793	2.50	2.50	3.44	2.50	2.50	2.53	1.23	down	3.89E-01	8.95E-01	-	-
1387003_at	Luzp1	leucine zipper protein 1	79428	Rn.154410	NM_030830	4.81	4.73	2.99	4.72	3.93	4.79	1.23	up	6.68E-01	9.00E-01	-	-
1390416_at	Slc25a30	Solute carrier family 25, member 30	361074	Rn.19440	H35736	10.14	10.86	10.50	10.13	10.15	10.33	1.23	down	2.36E-01	8.95E-01	-	-
1389264_at	Ankrd54	ankyrin repeat domain 54	362957	Rn.28758	BI278594	5.28	5.04	3.64	4.90	4.70	5.27	1.23	up	6.06E-01	8.95E-01	-	-
1393351_at	Rdh10	Retinol dehydrogenase 10 (all-trans)	353252	Rn.16968	BE109501	6.75	7.84	8.27	7.51	7.49	6.95	1.23	down	5.70E-01	8.95E-01	-	-
1371984_at	---	---	---	Rn.219218	AI598442	2.45	2.43	2.45	2.44	3.37	2.43	1.23	up	3.88E-01	8.95E-01	-	-
1390549_at	Adipor2	adiponectin receptor 2	312670	Rn.101984	AA859796	2.74	4.30	3.30	3.34	4.15	3.75	1.23	up	5.88E-01	8.95E-01	-	-
1374492_at	---	---	---	Rn.234	AI102666	2.38	2.40	2.37	2.35	3.34	2.36	1.23	up	4.10E-01	8.95E-01	-	-
1371335_at	Atp5l	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit G	300677	Rn.107458	AA944393	10.11	10.20	9.97	10.16	10.48	10.54	1.23	up	9.05E-02	8.95E-01	-	-
1397675_at	Eif4h	eukaryotic translation initiation factor 4H	288599	Rn.79423	H31800	7.32	7.38	7.92	6.99	6.97	7.75	1.23	down	3.98E-01	8.95E-01	-	-
1398448_at	---	---	---	Rn.199585	BE108346	5.77	5.64	6.60	6.08	6.38	6.44	1.23	up	4.02E-01	8.95E-01	-	-
1377011_at	Fry	furry homolog (Drosophila)	304244	Rn.36184	BF415061	2.52	2.57	2.35	2.85	3.04	2.46	1.23	up	1.77E-01	8.95E-01	-	-
1390783_at	Abca8a	ATP-binding cassette, sub-family A (ABC1), member 8a	303638	Rn.22789	BG671264	2.67	2.32	3.01	2.38	2.40	2.31	1.23	down	2.08E-01	8.95E-01	-	-
1374062_x_at	Mapre3	microtubule-associated protein, RP/EB family, member 3	298848	Rn.154513	AA946204	4.76	3.91	6.23	4.69	4.70	4.61	1.23	down	6.79E-01	9.02E-01	-	-
1377837_at	Rnf113a2	ring finger protein 113A2	314313	Rn.18838	AI231532	6.12	6.89	5.41	5.96	6.54	6.81	1.23	up	5.77E-01	8.95E-01	-	-
1392984_at	Cpne3	copine III	313387	Rn.4034	BG671686	8.13	8.20	8.56	7.39	8.08	8.51	1.23	down	4.41E-01	8.95E-01	-	-
1383255_at	Gpkow	G patch domain and KOW motifs	679890	Rn.147981	BE116202	4.68	3.96	3.45	3.39	4.04	3.76	1.23	down	4.97E-01	8.95E-01	-	-
1384001_at	---	---	---	Rn.212894	AW143174	5.63	5.50	4.24	3.59	5.68	5.20	1.23	down	7.17E-01	9.10E-01	-	-
1378326_at	Trub2	Trub2 pseudouridine (psi) synthase homolog 2 (E. coli)	366012	Rn.105581	AW435059	6.73	6.90	6.76	7.79	6.64	6.87	1.23	up	4.43E-01	8.95E-01	-	-
1367986_at	Ptgfrn	prostaglandin F2 receptor negative regulator	29602	Rn.6332	NM_019243	4.49	5.06	5.54	5.26	5.33	5.40	1.23	up	3.79E-01	8.95E-01	-	-
1376512_at	Ftsj2	FtsJ homolog 2 (E. coli)	304323	Rn.198939	BI290160	4.97	5.39	3.52	5.19	4.56	5.03	1.23	up	6.42E-01	8.95E-01	-	-
1372851_at	---	---	---	Rn.164907	AI412931	3.12	3.16	2.86	3.09	3.69	3.26	1.23	up	2.12E-01	8.95E-01	-	-
1397942_at	---	---	---	Rn.172388	BF552711	7.30	7.29	7.63	7.97	7.49	7.65	1.23	up	1.70E-01	8.95E-01	-	-
1377121_at	Dlg5	discs, large homolog 5 (Drosophila)	305645	Rn.154574	AW520410	6.80	6.39	6.74	6.83	7.03	6.97	1.23	up	9.94E-02	8.95E-01	-	-
1380762_at	LOC290577	hypothetical LOC290577	290577	Rn.8014	BG378362	3.37	2.46	2.48	2.48	2.47	2.45	1.23	down	3.73E-01	8.95E-01	-	-
1391990_at	---	---	---	Rn.161414	BF405569	3.68	2.57	2.83	3.89	2.90	3.19	1.23	up	5.38E-01	8.95E-01	-	-
1384251_at	Lrrc27	leucine rich repeat containing 27	499281	Rn.33049	AI137873	2.29	2.29	2.41	2.27	2.31	3.31	1.23	up	4.28E-01	8.95E-01	-	-
1392389_at	---	---	---	Rn.212622	BF389942	3.24	2.43	2.50	2.42	2.42	2.42	1.23	down	3.09E-01	8.95E-01	-	-
1384633_at	Slc18a2	Solute carrier family 18 (vesicular monoamine), member 2	25549	Rn.9686	BF545691	6.42	6.21	7.10	6.56	5.59	6.88	1.23	down	5.30E-01	8.95E-01	-	-
1376733_at	Igsf11	immunoglobulin superfamily, member 11	303926	Rn.154553	AI407898	8.10	7.71	7.96	7.72	7.55	7.59	1.23	down	7.10E-02	8.95E-01	-	-
1392227_at	LOC298018	hypothetical LOC298018	298018	Rn.204460	BI288917	5.74	5.94	6.94	5.98	5.76	5.99	1.23	down	4.73E-01	8.95E-01	-	-
1377811_at	Ankrd12	ankyrin repeat domain 12	316775	Rn.94994	AI577496	2.48	2.49	3.53	2.42	2.49	2.69	1.23	down	4.46E-01	8.95E-01	-	-
1372948_at	Mrpl63	mitochondrial ribosomal protein 63	691814	Rn.22630	BG376781	9.20	9.36	8.81	9.26	9.42	9.58	1.23	up	1.83E-01	8.95E-01	-	-
1393823_at	Polh	polymerase (DNA directed), eta	316235	Rn.53711	BE121014	3.20	3.32	2.47	3.20	3.47	3.22	1.23	up	3.41E-01	8.95E-01	-	-
1394241_at	Clip1	CAP-GLY domain containing linker protein 1	65201	Rn.22069	BF401902	3.23	4.92	4.93	5.97	2.89	5.12	1.23	up	7.94E-01	9.34E-01	-	-
1385753_at	---	---	---	Rn.172804	AI395818	4.02	6.32	4.41	6.70	4.18	4.77	1.23	up	7.87E-01	9.31E-01	-	-
1388090_at	Wrnip1	Werner helicase interacting protein 1	282835	Rn.8783	BI284350	5.57	6.29	6.09	5.54	5.19	6.31	1.23	down	4.88E-01	8.95E-01	-	-
1373708_at	Tut1	terminal uridylyl transferase 1, U6 snRNA-specific	499314	Rn.129389	BG378168	4.80	4.51	3.60	4.54	3.25	4.22	1.23	down	6.01E-01	8.95E-01	-	-
1369387_at	Vav1	vav 1 guanine nucleotide exchange factor	25156	Rn.48861	NM_012759	2.77	2.76	2.86	2.83	3.75	2.70	1.23	up	4.17E-01	8.95E-01	-	-
1390534_at	Smc5	structural maintenance of chromosomes 5	293867	Rn.127947	BG374727	3.88	4.28	4.42	4.35	4.77	4.23	1.23	up	2.32E-01	8.95E-01	-	-
1367542_at	Gpbp1l1	GC-rich promoter binding protein 1-like 1	313519	Rn.6789	AI411793	8.17	8.98	8.50	8.68	9.00	8.87	1.23	up	2.98E-01	8.95E-01	-	-
1384792_at	Prpf40a	PRP40 pre-mRNA processing factor 40 homolog A (S. cerevisiae)	295607	Rn.95204	BE107114	2.43	2.53	2.48	2.53	2.53	3.29	1.23	up	3.03E-01	8.95E-01	-	-
1392778_at	---	---	---	Rn.159231	AA891634	4.60	3.63	4.01	3.61	3.23	4.50	1.23	down	5.58E-01	8.95E-01	-	-
1369689_at	Nsf	N-ethylmaleimide-sensitive factor	60355	Rn.13345	AI547471	5.83	5.49	6.50	5.98	5.19	5.76	1.23	down	4.73E-01	8.95E-01	-	-
1374680_at	Rdh13	Retinol dehydrogenase 13 (all-trans/9-cis)	361504	Rn.2371	AA858731	6.27	5.65	6.55	6.40	5.33	5.84	1.23	down	5.02E-01	8.95E-01	-	-
1379427_at	Pgrmc2	progesterone receptor membrane component 2	361940	Rn.7685	AI137488	7.71	6.96	5.24	7.05	6.15	7.60	1.23	up	7.40E-01	9.16E-01	-	-
1388449_at	Eef1b2	eukaryotic translation elongation factor 1 beta 2	363241	Rn.3910	AI175551	10.00	10.72	10.37	10.50	10.45	11.04	1.23	up	3.44E-01	8.95E-01	-	-
1371621_at	---	---	---	Rn.63551	BF419441	3.24	2.35	2.37	2.36	2.36	2.34	1.23	down	3.63E-01	8.95E-01	-	-
1395499_at	---	---	---	Rn.30310	BF392443	6.91	7.27	8.39	6.43	8.02	7.21	1.23	down	6.63E-01	8.99E-01	-	-
1383153_at	---	---	---	Rn.23647	AI555284	2.31	2.29	2.31	3.19	2.32	2.29	1.23	up	3.67E-01	8.95E-01	-	-
1374640_at	Them4	thioesterase superfamily member 4	361992	Rn.12625	BE112158	2.48	2.49	3.38	2.47	2.49	2.48	1.23	down	3.72E-01	8.95E-01	-	-
1387111_at	Ddah1	dimethylarginine dimethylaminohydrolase 1	64157	Rn.7398	NM_022297	10.19	9.99	10.19	9.90	9.37	10.21	1.23	down	3.03E-01	8.95E-01	-	-
1397596_at	Trim2	tripartite motif-containing 2	361970	Rn.16973	H31511	7.14	5.80	5.68	5.79	5.84	6.09	1.23	down	5.64E-01	8.95E-01	-	-
1376853_at	Rpap3	RNA polymerase II associated protein 3	300189	Rn.49051	BG380641	4.81	4.93	4.99	4.75	4.76	4.32	1.23	down	1.19E-01	8.95E-01	-	-
1382131_at	---	---	---	Rn.166138	AW523674	5.51	6.21	6.87	6.32	6.49	6.68	1.23	up	5.02E-01	8.95E-01	-	-
1368008_at	Prom1	prominin 1	60357	Rn.144589	NM_021751	11.20	11.59	11.55	11.66	11.55	12.03	1.23	up	1.94E-01	8.95E-01	-	-
1368177_at	Acsl3	acyl-CoA synthetase long-chain family member 3	114024	Rn.54820	NM_057107	6.34	6.42	6.44	6.23	5.65	6.42	1.23	down	2.73E-01	8.95E-01	-	-
1371140_a_at	Accn1	amiloride-sensitive cation channel 1, neuronal	25364	Rn.37523	Y14635	2.41	2.41	3.51	2.63	2.41	2.38	1.23	down	4.70E-01	8.95E-01	-	-
1395534_at	Rasl10b	RAS-like, family 10, member B	303382	Rn.8804	AW919370	4.16	5.37	4.83	5.49	3.18	4.79	1.23	down	7.16E-01	9.10E-01	-	-
1398408_at	---	---	---	---	AI948410	3.04	3.35	4.28	2.41	3.64	3.72	1.23	down	6.24E-01	8.95E-01	-	-
1397288_at	---	---	---	Rn.199263	BM390376	3.98	3.32	3.67	4.35	3.23	4.29	1.23	up	5.07E-01	8.95E-01	-	-
1374331_at	Rqcd1	rcd1 (required for cell differentiation) homolog 1 (S. pombe)	301513	Rn.18033	AI178068	4.59	3.03	3.05	3.35	3.04	3.37	1.23	down	6.01E-01	8.95E-01	-	-
1385545_at	Klf12	Kruppel-like factor 12	306110	Rn.61602	BF403922	2.37	2.21	2.48	2.98	2.42	2.57	1.23	up	1.82E-01	8.95E-01	-	-
1375627_at	Sfxn5	sideroflexin 5	261737	Rn.161851	AI575254	4.50	4.09	2.96	3.81	3.82	4.81	1.23	up	6.27E-01	8.95E-01	-	-
1376590_at	---	---	---	Rn.163592	AA818732	5.80	6.02	5.39	5.72	5.76	6.63	1.23	up	4.38E-01	8.95E-01	-	-
1378898_at	---	---	---	Rn.208048	BE109293	3.38	2.61	2.63	2.66	2.61	2.46	1.23	down	3.16E-01	8.95E-01	-	-
1370848_at	Slc2a1	solute carrier family 2 (facilitated glucose transporter), member 1	24778	Rn.3205	BI284218	8.57	9.48	8.19	8.88	9.27	8.99	1.23	up	4.95E-01	8.95E-01	-	-
1372531_at	Ppfibp2	PTPRF interacting protein, binding protein 2 (liprin beta 2)	308918	Rn.2971	BE106488	3.87	4.86	4.67	3.92	4.26	4.33	1.23	down	4.13E-01	8.95E-01	-	-
1374853_at	Bod1	biorientation of chromosomes in cell division 1	287173	Rn.144696	AI137833	7.70	7.12	6.79	7.02	6.62	7.06	1.23	down	3.73E-01	8.95E-01	-	-
1398945_at	---	---	---	Rn.114358	AA851439	7.41	7.63	8.04	7.65	8.13	8.20	1.23	up	3.02E-01	8.95E-01	-	-
1395203_at	Tfdp2	transcription factor Dp-2 (E2F dimerization partner 2)	300947	Rn.105731	AI177311	3.97	4.16	3.65	3.95	4.14	4.60	1.23	up	2.86E-01	8.95E-01	-	-
1377510_at	---	---	---	Rn.208269	BE114170	2.48	3.28	2.48	2.47	2.49	2.37	1.23	down	3.30E-01	8.95E-01	-	-
1388838_at	Chmp4b	chromatin modifying protein 4B	312254	---	AA943752	5.29	4.91	3.29	5.38	3.92	5.10	1.23	up	7.14E-01	9.10E-01	-	-
1382227_at	Agpat3	1-acylglycerol-3-phosphate O-acyltransferase 3	294324	Rn.100251	AW533203	4.62	5.23	4.25	4.98	4.73	5.28	1.23	up	4.13E-01	8.95E-01	-	-
1379843_at	Vps36	Vacuolar protein sorting 36 homolog (S. cerevisiae)	290851	Rn.12707	AA998346	6.31	8.27	8.51	8.15	7.84	8.00	1.23	up	6.92E-01	9.05E-01	-	-
1380813_at	---	---	---	---	AA891239	7.37	7.98	7.73	7.02	7.42	7.75	1.23	down	3.37E-01	8.95E-01	-	-
1371978_at	Osbpl9	oxysterol binding protein-like 9	298369	Rn.61554	AI406375	7.49	7.27	7.50	7.17	6.73	7.47	1.23	down	2.61E-01	8.95E-01	-	-
1379764_at	---	---	---	Rn.205036	AI555029	2.68	2.64	2.66	2.65	3.61	2.61	1.23	up	4.11E-01	8.95E-01	-	-
1369552_at	Samsn1	SAM domain, SH3 domain and nuclear localization signals, 1	170637	Rn.81187	NM_130821	3.51	2.86	2.92	2.87	2.87	2.65	1.23	down	2.46E-01	8.95E-01	-	-
1370613_s_at	Ugt1a5 /// Ugt1a6	UDP glucuronosyltransferase 1 family, polypeptide A1 /// UDP glucuronosyltra	01595 /// 396527	Rn.26489	AF461738	10.90	10.20	11.34	10.61	10.48	10.46	1.23	down	4.24E-01	8.95E-01	-	-
1373509_at	Naun4	NOL1/NOP2/Sun domain family, member 4	298426	Rn.49080	BE113288	3.76	3.60	4.06	3.76	4.09	4.47	1.23	up	2.89E-01	8.95E-01	-	-
1378231_at	---	---	---	Rn.76515	BI300425	2.41	2.38	2.38	2.92	2.58	2.56	1.23	up	6.33E-02	8.95E-01	-	-
1372152_at	Alg14	asparagine-linked glycosylation 14 homolog (S. cerevisiae)	362031	Rn.136923	BI275874	6.43	7.51	7.54	7.65	6.99	7.73	1.23	up	5.30E-01	8.95E-01	-	-
1389519_at	Psmd8	proteasome (prosome, macropain) 26S subunit, non-ATPase, 8	292766	Rn.137673	BI275955	6.15	6.34	5.61	6.37	6.06	6.57	1.23	up	3.23E-01	8.95E-01	-	-
1369099_at	Slc30a1	solute carrier family 30 (zinc transporter), member 1	58976	Rn.10120	NM_022853	5.52	5.46	5.73	5.51	6.17	5.93	1.23	up	2.27E-01	8.95E-01	-	-
1379540_at	---	---	---	Rn.96103	BM383595	2.82	2.81	2.74	3.64	2.83	2.81	1.23	up	3.41E-01	8.95E-01	-	-
1373035_at	---	---	---	---	AI031032	4.49	4.97	4.91	4.73	3.93	4.81	1.23	down	4.04E-01	8.95E-01	-	-
1386681_at	LOC497934	similar to hypothetical protein FLJ20014	497934	Rn.45766	BF567176	2.50	2.51	2.36	3.15	2.56	2.54	1.23	up	2.23E-01	8.95E-01	-	-
1375317_at	Ddc	dopa decarboxylase (aromatic L-amino acid decarboxylase)	24311	Rn.11064	BI296559	2.53	2.42	2.43	3.42	2.44	2.41	1.23	up	4.25E-01	8.95E-01	-	-
1387918_at	Tpm3	tropomyosin 3, gamma	117557	Rn.37575	BI295970	8.21	8.28	8.89	8.93	8.60	8.74	1.23	up	2.75E-01	8.95E-01	-	-
1372522_at	RGD1310061	similar to hypothetical protein FLJ10154	290912	Rn.108929	AI556235	9.35	7.76	7.50	8.12	7.41	8.19	1.23	down	6.60E-01	8.98E-01	-	-
1391828_at	---	---	---	Rn.18608	AI030836	3.36	3.00	2.94	2.85	2.93	2.62	1.23	down	1.35E-01	8.95E-01	-	-
1387685_at	Freq	frequenin homolog (Drosophila)	65153	Rn.62653	NM_024366	6.95	6.82	6.87

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1382894_at	LOC691396	similar to Zinc finger protein 551 (Zinc finger protein KOX23)	691396	Rn.38959	BF415011	2.36	2.39	3.42	2.35	2.36	2.56	1.23	down	4.53E-01	8.95E-01	-	-
1371475_at	Rnase4	ribonuclease, RNase A family 4	56759	Rn.1742	BI284831	2.43	2.40	3.32	2.43	2.44	2.40	1.23	down	3.80E-01	8.95E-01	-	-
1390998_at	Glis1	GLIS family zinc finger 1	298732	Rn.104223	BI295528	4.81	5.40	4.84	4.74	4.85	4.58	1.23	down	2.27E-01	8.95E-01	-	-
1391157_at	---	---	---	Rn.201712	BE104457	3.17	4.74	3.92	3.62	3.89	3.43	1.23	down	5.66E-01	8.95E-01	-	-
1397157_at	---	---	---	Rn.200177	BF411716	2.51	3.37	2.52	2.56	2.52	2.44	1.23	down	3.62E-01	8.95E-01	-	-
1381414_at	---	---	---	Rn.165086	AA964872	4.14	3.98	4.18	3.82	3.86	3.73	1.23	down	1.65E-02	8.95E-01	-	-
1392411_at	Tinag	tubulointerstitial nephritis antigen	300846	Rn.43851	AI411848	8.91	9.24	9.50	9.20	8.35	9.21	1.23	down	4.23E-01	8.95E-01	-	-
1377385_at	Arhgap27	Rho GTPase activating protein 27	303583	Rn.17895	BE100015	6.01	4.50	5.08	5.10	4.81	4.79	1.23	down	5.47E-01	8.95E-01	-	-
1370052_at	P4pk1	3-phosphoinositide dependent protein kinase-1	81745	Rn.10905	NM_031081	5.39	6.88	6.68	6.60	6.48	6.75	1.23	up	5.65E-01	8.95E-01	-	-
1369932_a_at	Raf1	v-raf-leukemia viral oncogene 1	24703	Rn.33282	NM_012639	5.18	4.86	4.61	5.16	5.19	5.18	1.23	up	1.51E-01	8.95E-01	-	-
1371684_at	Pelo	pelota homolog (Drosophila)	294754	Rn.3842	AA799330	4.46	4.77	3.21	4.42	4.37	4.54	1.23	up	5.69E-01	8.95E-01	-	-
1380553_at	Osgin2	oxidative stress induced growth inhibitor family member 2	313085	Rn.211931	BM390497	4.33	3.48	3.50	3.28	5.55	3.36	1.23	up	7.28E-01	9.13E-01	-	-
1381443_at	Hapln4	hyaluronan and proteoglycan link protein 4	361129	Rn.98362	AI716459	3.23	2.43	2.44	2.43	2.44	2.35	1.23	down	3.31E-01	8.95E-01	-	-
1390254_at	---	---	---	Rn.48878	BG380253	3.36	2.44	2.47	2.46	2.47	2.45	1.23	down	3.80E-01	8.95E-01	-	-
1390294_at	---	---	---	Rn.26694	BE100986	6.19	5.61	5.64	5.57	5.34	5.65	1.23	down	2.34E-01	8.95E-01	-	-
1375751_at	---	---	---	---	BE098727	4.72	4.08	5.26	6.05	5.79	3.11	1.23	up	7.82E-01	9.29E-01	-	-
1399064_at	---	---	---	Rn.13922	AI009591	3.79	4.20	3.95	3.69	3.67	3.70	1.23	down	7.17E-02	8.95E-01	-	-
1374163_at	Anapc4	anaphase promoting complex subunit 4	305420	Rn.41255	BM389995	8.25	8.56	7.97	8.41	8.55	8.71	1.23	up	1.99E-01	8.95E-01	-	-
1395826_at	Ppp2r5e	protein phosphatase 2, regulatory subunit B', epsilon isoform	299147	Rn.24394	BG664036	5.41	4.68	5.06	4.94	6.26	4.83	1.23	up	5.91E-01	8.95E-01	-	-
1389648_at	Ripk4	receptor-interacting serine-threonine kinase 4	304053	Rn.28403	AI170382	7.54	7.96	8.23	8.19	8.17	8.26	1.23	up	2.22E-01	8.95E-01	-	-
1367988_at	Cyp2c23	cytochrome P450, family 2, subfamily c, polypeptide 23	83780	Rn.2184	U04733	11.41	11.09	10.91	11.41	11.59	11.30	1.23	up	1.56E-01	8.95E-01	-	-
1374063_at	Sfrs3	splicing factor, arginine/serine-rich 3	361814	Rn.9002	AI579288	8.20	8.19	8.26	7.93	7.57	8.26	1.23	down	2.14E-01	8.95E-01	-	-
1384200_at	RGD1307234	similar to RIKEN cDNA 4931400A14	316732	Rn.162279	BE107328	2.75	2.66	2.79	2.72	2.96	3.41	1.23	up	2.27E-01	8.95E-01	-	-
1382230_at	Klhdc8a	kelch domain containing 8A	305096	Rn.44339	BI296330	2.97	2.51	2.53	2.52	3.87	2.50	1.23	up	5.69E-01	8.95E-01	-	-
1372925_at	Sirt3	sirtuin (silent mating type information regulation 2 homolog) 3 (S. cerevisiae)	293615	Rn.24698	AI233135	5.59	5.47	6.17	5.03	5.79	5.51	1.23	down	3.93E-01	8.95E-01	-	-
1373611_at	Il17ra	interleukin 17 receptor A	312679	Rn.106209	BI279744	6.94	7.62	6.31	7.25	7.30	7.20	1.23	up	4.79E-01	8.95E-01	-	-
1385503_at	LOC678772	similar to O-acetyltransferase	678772	---	BM387442	8.08	8.01	9.14	8.61	8.14	7.59	1.23	down	5.63E-01	8.95E-01	-	-
1375181_at	LOC499782	similar to 60S ribosomal protein L12	499782	Rn.128979	AI170643	10.85	10.83	10.80	10.96	10.95	11.46	1.23	up	1.54E-01	8.95E-01	-	-
1398551_at	Ttc25	tetratricopeptide repeat domain 25	303534	Rn.12620	AA997115	5.49	6.44	6.43	7.30	3.53	6.65	1.23	down	8.19E-01	9.42E-01	-	-
1390027_at	Usp8	ubiquitin specific peptidase 8	296121	Rn.52174	AI137190	5.38	6.51	6.00	5.80	6.84	6.14	1.23	up	5.44E-01	8.95E-01	-	-
1375401_at	Mvk	mevalonate kinase	81727	Rn.6995	BE118400	2.38	3.14	3.12	2.44	2.43	2.88	1.23	down	3.66E-01	8.95E-01	-	-
1390412_at	Slc40a1	solute carrier family 39 (iron-regulated transporter), member 1	170840	Rn.15324	AI229664	5.64	5.37	5.61	6.09	5.41	6.00	1.23	up	2.70E-01	8.95E-01	-	-
1392847_at	Cbll1	Cas-Br-M (murine) ecotropic retroviral transforming sequence-like 1	314028	Rn.92651	BE118227	3.87	4.90	3.68	4.42	4.57	4.35	1.23	up	4.86E-01	8.95E-01	-	-
1384831_at	Slc7a13	solute carrier family 7, (cationic amino acid transporter, y+ system) member 13	313089	Rn.22708	AI233155	12.85	13.13	13.00	12.64	12.65	12.82	1.23	down	4.07E-02	8.95E-01	-	-
1383647_a_at	Crb3	crumbs homolog 3 (Drosophila)	301112	Rn.14560	BI283883	6.67	6.68	8.13	7.72	5.83	7.05	1.23	down	7.09E-01	9.09E-01	-	-
1374085_at	Mxd4	Max dimerization protein 4	360961	Rn.3279	BI274201	5.88	4.65	4.74	5.13	5.93	5.09	1.23	up	5.72E-01	8.95E-01	-	-
1394496_at	---	---	---	Rn.147672	AI408614	2.42	2.41	3.26	2.40	2.41	2.39	1.23	down	3.57E-01	8.95E-01	-	-
1385649_at	Itga5	integrin alpha 5 (fibronectin receptor alpha)	315346	Rn.100796	AI385152	2.52	2.50	2.50	2.50	3.41	2.49	1.23	up	3.90E-01	8.95E-01	-	-
1384103_at	RGD1561416	similar to novel protein (HT036)	500536	Rn.162825	BE106350	5.41	6.09	6.54	5.71	5.71	5.73	1.23	down	4.19E-01	8.95E-01	-	-
1389684_at	Prpf39	PRP39 pre-mRNA processing factor 39 homolog (S. cerevisiae)	314171	Rn.12521	AA850679	6.94	6.84	6.73	6.40	6.59	6.63	1.23	down	3.40E-02	8.95E-01	-	-
1375666_at	Dmtf1	cyclin D binding myb-like transcription factor 1	114485	Rn.116028	BE098802	6.95	6.73	6.35	5.83	6.41	6.90	1.23	down	4.50E-01	8.95E-01	-	-
1381297_at	Arhgef5	Rho guanine nucleotide exchange factor (GEF) 5	140898	Rn.89839	BI292668	4.68	5.93	5.42	5.80	5.42	5.69	1.23	up	4.79E-01	8.95E-01	-	-
1380098_at	---	---	---	Rn.170134	AW535324	2.95	2.94	3.71	2.95	2.95	2.82	1.23	down	3.22E-01	8.95E-01	-	-
1374857_at	Nola1	nucleolar protein family A, member 1 (H/ACA small nucleolar RNPs)	499709	Rn.15522	AI579021	7.89	7.64	6.69	7.89	7.24	7.97	1.23	up	5.32E-01	8.95E-01	-	-
1383499_at	Amigo1	adhesion molecule with Ig like domain 1	295365	Rn.116338	BG371995	2.75	2.76	2.84	3.74	2.76	2.73	1.23	up	4.24E-01	8.95E-01	-	-
1388184_at	Icmt	isoprenylcysteine carboxyl methyltransferase	170818	Rn.48709	BM391649	5.40	5.94	7.11	5.66	6.05	5.86	1.23	down	5.99E-01	8.95E-01	-	-
1388441_at	LOC689574	hypothetical protein LOC689574	689574	Rn.64564	BG379987	8.93	9.18	8.76	9.33	9.09	9.33	1.23	up	1.15E-01	8.95E-01	-	-
1373001_at	Chchd4	coiled-coil-helix-coiled-coil-helix domain containing 4	312559	Rn.16427	AA817990	6.94	7.09	7.10	6.37	6.56	7.32	1.23	down	3.75E-01	8.95E-01	-	-
1393233_at	Armc6	armadillo repeat containing 6	306352	Rn.162263	BG381676	3.09	3.07	4.04	3.07	3.09	3.15	1.23	down	4.12E-01	8.95E-01	-	-
1369725_at	Adap2	ArfGAP with dual PH domains 2	56826	Rn.203877	NM_020101	6.13	6.62	5.64	6.88	6.65	5.74	1.23	up	5.47E-01	8.95E-01	-	-
1383393_at	---	---	---	Rn.167071	AA858485	10.37	8.92	8.78	9.73	9.28	9.95	1.23	up	6.19E-01	8.95E-01	-	-
1385926_at	---	---	---	Rn.23216	BF550565	2.29	2.61	2.61	2.61	3.14	2.64	1.23	up	2.20E-01	8.95E-01	-	-
1374161_at	Ipo11	importin 11	310056	Rn.196126	AI104686	2.26	3.93	4.08	3.50	3.51	4.13	1.23	up	6.61E-01	8.98E-01	-	-
1383108_at	Taf13	TAF13 RNA polymerase II, TATA box binding protein (TBP)-associated factor	310784	Rn.15054	BE120513	2.78	5.86	5.53	4.24	3.73	5.32	1.23	down	7.99E-01	9.35E-01	-	-
1374865_at	RGD1562618	similar to RIKEN cDNA 6030419C18 gene	501007	Rn.45705	AW523682	8.24	5.76	5.49	6.59	5.95	6.06	1.23	down	7.60E-01	9.22E-01	-	-
1378766_at	---	---	---	Rn.25554	AI236320	5.41	6.10	5.45	5.37	5.22	5.48	1.23	down	2.82E-01	8.95E-01	-	-
1396369_at	---	---	---	Rn.62044	BF412269	3.85	3.55	3.40	3.37	3.61	2.93	1.23	down	2.84E-01	8.95E-01	-	-
1381999_at	Camsap1	calmodulin regulated spectrin-associated protein 1	296580	Rn.203213	BE096370	3.94	3.70	4.13	3.62	3.67	3.59	1.23	down	8.03E-02	8.95E-01	-	-
1374326_at	Ppan	peter pan homolog (Drosophila)	298699	Rn.144881	AI178019	4.56	4.97	4.28	5.01	4.04	5.65	1.23	up	5.96E-01	8.95E-01	-	-
1372316_at	Sgk493	protein kinase-like protein SgK493	313860	Rn.27	BM384131	3.57	3.96	3.52	3.60	3.07	3.49	1.23	down	2.42E-01	8.95E-01	-	-
1393455_at	---	---	---	Rn.216496	AA998007	4.13	4.12	4.94	4.13	4.19	3.99	1.23	down	3.50E-01	8.95E-01	-	-
1393172_at	Nab1	Ngfi-A binding protein 1	64824	Rn.10099	AA848648	3.19	4.27	5.33	4.67	3.53	5.46	1.23	up	7.42E-01	9.17E-01	-	-
1367494_at	RGD1310899	similar to CGI-35 protein	299198	Rn.1198	AW523764	8.40	8.79	8.87	8.92	8.78	9.23	1.23	up	2.11E-01	8.95E-01	-	-
1392434_at	---	---	---	Rn.173421	AI410789	2.92	2.70	2.42	2.40	2.38	2.37	1.23	down	1.10E-01	8.95E-01	-	-
1391270_at	Cnnm3	cyclin M3	301345	Rn.50710	BE112177	5.14	4.70	4.61	3.17	7.01	5.14	1.23	up	8.07E-01	9.38E-01	-	-
1382670_at	Larp1	La ribonucleoprotein domain family, member 1	303158	Rn.98804	BF394189	5.14	4.34	4.22	4.53	5.68	4.38	1.23	up	5.89E-01	8.95E-01	-	-
1385872_at	Dhx36	DEAH (Asp-Glu-Ala-His) box polypeptide 36	310461	Rn.2744	AI237532	7.79	6.46	6.26	6.61	6.04	6.97	1.23	down	6.22E-01	8.95E-01	-	-
1369414_at	Stxbp3	syntaxin binding protein 3	114095	Rn.211988	NM_053637	7.77	8.48	8.36	7.89	7.72	8.12	1.23	down	3.01E-01	8.95E-01	-	-
1395393_at	---	---	---	Rn.147243	BG671174	2.38	3.56	2.67	2.62	2.94	3.93	1.23	up	8.10E-01	8.95E-01	-	-
1382063_at	Gla	galactosidase, alpha	363494	Rn.98982	BM385090	4.72	5.24	4.67	4.23	4.60	4.92	1.23	down	3.41E-01	8.95E-01	-	-
1379793_at	Sfrs12ip1	SFRS12-interacting protein 1	361888	Rn.15726	AW535749	6.31	7.48	7.19	7.53	6.98	7.36	1.23	up	4.91E-01	8.95E-01	-	-
1374589_at	Vezt	vezatin, adherens junctions transmembrane protein	299738	Rn.16786	AI235367	3.21	3.15	4.28	3.05	4.62	3.84	1.23	up	6.41E-01	8.95E-01	-	-
1368078_at	Esm1	endothelial cell-specific molecule 1	64536	Rn.6376	NM_022604	5.06	4.14	5.85	5.37	5.29	3.51	1.23	down	7.27E-01	9.13E-01	-	-
1390656_at	---	---	---	Rn.161410	BF389473	7.89	8.24	8.49	8.58	8.29	8.62	1.23	up	2.24E-01	8.95E-01	-	-
1388464_at	LOC680835	similar to cullin 7	680835	Rn.91915	AI598527	2.91	2.54	2.31	2.30	2.30	2.29	1.23	down	1.70E-01	8.95E-01	-	-
1367931_a_at	Ptbp1	polypyrimidine tract binding protein 1	29497	Rn.64440	X60790	6.12	6.91	6.55	5.87	6.36	6.47	1.23	down	3.76E-01	8.95E-01	-	-
1386078_at	Slc35a1	solute carrier family 35 (CMP-sialic acid transporter), member A1	313139	Rn.24337	AI228537	4.52	3.96	4.61	4.61	4.69	4.66	1.23	up	2.27E-01	8.95E-01	-	-
1371741_at	Actr1a	ARP1 actin-related protein 1 homolog A, centractin alpha (yeast)	294010	Rn.32312	AI409891	8.14	7.58	6.90	7.55	7.11	7.08	1.23	down	4.93E-01	8.95E-01	-	-
1379660_at	---	---	---	Rn.43341	BG672127	4.43	3.26	3.32	3.42	3.30	3.42	1.23	down	4.87E-01	8.95E-01	-	-
1369003_at	Dedd	death effector domain-containing	83631	Rn.203286	NM_031800	6.25	6.79	5.72	6.91	6.20	6.53	1.23	up	4.71E-01	8.95E-01	-	-
1383333_at	RGD735112	similar to RIKEN cDNA 5830404H04	304055	Rn.107481	BI281419	2.40	2.39	2.41	2.40	3.28	2.39	1.23	up	3.77E-01	8.95E-01	-	-
1386191_a_at	Lhfpl2	lipoma HMGIC fusion partner-like 2	294643	Rn.203042	AI231089	2.50	2.51	2.54	2.52	2.68	3.23	1.23	up	2.43E-01	8.95E-01	-	-
1378250_at	H13	Histocompatibility 13	311545	Rn.12102	BE104756	4.75	3.50	3.17	3.53	3.05	3.97	1.23	down	6.22E-01	8.95E-01	-	-
1382629_at	Far1	fatty acyl CoA reductase 1	293173	Rn.211975	BM383809	6.80	6.83	6.61	5.98	7.13	6.26	1.23	down	4.54E-01	8.95E-01	-	-
1379115_at	---	---	---	Rn.207241	BF407646	2.32	2.55	2.39	2.49	2.54	3.11	1.22	up	2.38E-01	8.95E-01	-	-
1388744_at	Mcm7	minichromosome maintenance deficient 7 (S. cerevisiae)	288532	Rn.113	AI599678	7.72	7.44	7.14	7.49	6.59	7.35	1.22	down	4.19E-01	8.95E-01	-	-
1389025_at	Taf11	TAF11 RNA polymerase II, TATA box binding protein (TBP)-associated factor	309638	Rn.11920	BI278688	8.02	7.00	6.70	6.89	6.92	7.03	1.22	down	5.06E-01	8.95E-01	-	-
1369256_at	Bace1	beta-site APP cleaving enzyme 1	29392	Rn.207201	NM_019204	3.58	3.66	3.54	4.27	3.86	3.53	1.22	up	2.48E-01	8.95E-01	-	-
1371480_at	RGD1561797	similar to RIKEN cDNA 2610528K03	499655	Rn.119060	AI407985	3.06	3.22	3.25	3.36	3.38	3.67	1.22	up	6.49E-02	8.95E-01	-	-
1374431_at	Atp6v1a	ATPase, H+ transporting, lysosomal V1 subunit A	685232	Rn.1431	BE120644	10.23	10.05	10.29	9.59	10.35	9.74	1.22	down	2.97E-01	8.95E-01	-	-
1398514_at	Hgd	homogentisate 1, 2-dioxygenase	360719	Rn.24631	AI232328	11.65	11.79	11.81	11.37	11.30	11.70	1.22	down	9.51E-02	8.95E-01	-	-
1384184_at	---	---	---	Rn.89498	BE117485	2.70	2.68	2.72	2.69	3.19	3.10	1.22	up	1.30E-01	8.95E-01	-	-
1389850_at	Arid1a	AT rich interactive domain 1A (SWI-like)	297867	Rn.61077	AA800926	6.23	5.96	6.64	6.55	5.54	5.87	1.22	down	4.57E-01	8.95E-01	-	-
1382309_at	---	---	---	Rn.122118	BI286390	4.57	4.70	3.90	4.20	3.81	4.28	1.22	down	3.68E-01	8.95E-01	-	-
1391196_at	---	---	---	Rn.171297	BE112135	3.23	2.36	2.39	2.37	2.38	2.35	1.22	down	3.64E-01	8.95E-01	-	-
1369515_s_at	Insrr	insulin receptor-related receptor	60663	Rn.44446	NM_022212	3.17	2.29	2.30	2.30	2.30	2.29	1.22	down	3.71E-01	8.95E-01	-	-
1373095_at	RGD1307597	similar to mKIAA0317 protein	299197	Rn.93564	AI408081	6.30	7.37	7.41	7.26	7.70	7.00	1.22	up	5.23E-01	8.95E-01	-	-
1398835_at	Actb	actin, beta	81822	Rn.94978	NM_031144	12.26	12.09	12.10	12.05	11.73	11.80	1.22	down	5.88E-02	8.95E-01	-	-
1378313_at	---	---	---	Rn.65153	BI296600	2.30	2.30	2.31	2.30	3.19	2.29	1.22	up	3.84E-01	8.95E-01	-	-
1380537_at	Nckap1l	NCK associated protein 1 like	315348	Rn.149002	BI293796	2.75	2.71	3.39	2.71	2.75	2.51	1.22	down	2.78E-01	8.95E-01	-	-
1396041_at	---	---	---	Rn.168479	AW252694	5.88	2.90	3.52	3.94	3.56	3.92	1.22	down	7.66E-01	9.23E-01	-	-
1375369_at	RGD1305793	similar to hypothetical protein FLJ20154	309456	Rn.105679	Z83035	4.79	5.44	5.88	5.83	5.89	5.26	1.22	up	4.77E-01	8.95E-01	-	-
1396921_at	---	---	---	Rn.201869	AI555158	2.70	2.69	3.28	2.52	2.78	2.49	1.22	down	2.49E-01	8.95E-01	-	-
1375548_at	RGD1310351	similar to RIKEN cDNA 4732418C07	298425	Rn.23067	BI296537	7.12	6.80	7.25	6.84	6.20	7.26	1.22	down	4.35E-01	8.95E-01	-	-
1372437_at	Skp1	S-phase kinase-associated protein 1	287280	Rn.3477	BM390921	12.26	12.18	12.45	12.03	11.93	12.05	1.22	down	2.93E-02	8.95E-01	-	-
1383838_at	---	---	---	---	BI296294	3.75	3.61	3.50	3.56	2.79	3.63	1.22	down	3.58E-01	8.95E-01	-	-
1380824_at	Hook3	Hook homolog 3 (Drosophila)	306548	Rn.203282	AI501458	4.88	4.62	3.70	4.73	3.72	3.87	1.22	down	5.73E-01	8.95E-01	-	-
1386195_x_at	---	---	---	Rn.227	AI176775	2.46	2.45	2.50	2.46	3.38	2.44	1.22	up	3.99E-01	8.95E-01	-	-
1376658_at	Raph1	Ras association (RalGDS/AF-6) and pleckstrin homology domains 1	363239	Rn.16844	BF391087	3.10	5.31	2.90	5.24	2.94	4.01	1.22	up	7.89E-01	9.32E-01	-	-
1391891_at	Agtpbp1	ATP/GTP binding protein 1	299986	Rn.33035	AI711114	5.92	5.07	4.59	5.64	4.05	5.02	1.22	down	6.54E-01	8.97E-01	-	-
1367916_at	Plcd1	phospholipase C, delta 1	24655	Rn.12324	NM_017035	2.98	2.57	2.99	2.98	3.31	3.13	1.22	up	1.57E-01	8.95E-01	-	-
1398247_at	Lonp1	lon peptidase 1, mitochondrial	170916	Rn.146805	NM_133404	6.15	6.32	5.91	6.26	6.01	6.98	1.22	up	4.04E-01	8.95E-01	-	-
1392287_at	---	---	---	Rn.18215	AW523201	3.98	3.76	4.49	3.25	4.39	3.71	1.22	down	5.02E-01	8.95E-01	-	-
1368412_a_at	Ptpro	protein tyrosine phosphatase, receptor type, O	50677	Rn.10163	D45412	3.52	2.71	2.70	2.68	2.69	2.68	1.22	up	3.45E-01	8.95E-01	-	-
1378282_at	Csnk2a2	casein kinase 2, alpha prime polypeptide	307641	Rn.24013	BI290750	4.48	6.46	6.06	5.80	6.37	3.95	1.22	down	7.74E-01	9.26E-01	-	-
1393502_at	RGD1306153	similar to predicted CDS, putative protein of bilaterial origin (4J193)	361410	Rn.20683	AI071962	5.85	5.04	5.26	5.02	5.23	5.03	1.22	down	3.09E-01	8.95E-01	-	-
1373773_at	Gpm6a	glycoprotein m6a	306439	Rn.34376	BF394166	8.04	8.64	8.03	8.16	8.19	8.49	1.22	down	3.98E-01	8.95E-01	-	-
1398819_at	Dnaja1	DnaJ (Hsp40) homolog, subfamily A, member 1	65028	Rn.64562	NM_022934	10.71	10.90	10.76	10.58	10.26	10.65	1.22	down	9.44E-02	8.95E-01	-	-
1368233_at	Gtf2f2	general transcription factor IIF, polypeptide 2	81674	Rn.11000	NM_031042	5.71	4.74	3.24	5.57	2.95	4.31	1.22	down	7.94E-01	9.34E-01	-	-
1381349_at	LOC363188	similar to ubiquitin protein ligase E3 component n-recognin 2	363188	Rn.67473	AI231906	7.23	6.67	7.85	6.08	7.15	7.64	1.22	down	6.38E-01	8.95E-01	-	-
1376892_at	Gria3	glutamate receptor, ionotrophic, AMPA 3	29628	Rn.74049	AI102061	3.32	2.49	2.52	2.49	2.52	2.44	1.22	up	3.45E-01	8.95E-01	-	-
1383430_at	Tsen2	tRNA splicing endonuclease 2 homolog (S. cerevisiae)	312649	Rn.206216	BF414509	4.88	4.96	5.16	5.96	4.68	5.22	1.22	up	4.85E-01	8.95E-01	-	-
1398896_at	Arcn1	archain 1	300674	Rn.2185	AA892567	7.78	7.38	8.14	7.82	6.79	7.81	1.22	down	5.11E-01	8.95E-01	-	-
1388797_at	U2af2	U2 small nuclear ribonucleoprotein auxiliary factor (U2AF) 2	308335	Rn.15383	AI232163	3.67	3.76	3.54	4.34	3.58	3.92	1.22	up	2.74E-01	8.95E-01	-	-
1388099_a_at	Tfpt	TCF3 (E2A) fusion partner	85423	Rn.12922	AB029495	5.42	5.57	5.24	5.20	4.75	5.41	1.22	down	2.51E-01	8.95E-01	-	-
1368877_at	Zfp354a	zinc finger protein 354A	24522	Rn.11049	NM_052798	8.64	7.79	9.26	9.42	8.25	8.89	1.22	up	6.22E-01	8.95E-01	-	-
1377551_at	---	---	---	Rn.22576	BE116580	2.38	2.37	2.38	3.26	2.39	2.36	1.22	up	3.82E-01	8.95E-01	-	-
1379541_at	---	---	---	Rn.183922	BE329099	4.79	4.47	6.50	5.33	4.93	4.62	1.22	down	6.84E-01	9.03E-01	-	-
1397358_at	Ccdc39	coiled-coil domain containing 39	310315	Rn.219691	AI105407	2.48	2.84	2.95	2.46	2.51	2.41	1.22	down	1.14E-01	8.95E-01	-	-
1396302_at	---	---	---	Rn.79053	BM389727	2.40	3.33	2.45	2.44	2.47	2.39	1.22	down	3.89E-01	8.95E-01	-	-
1395444_at	---	---	---	Rn.209942	BF412266	2.51	2.50	2.51	3.10	2.81	2.49	1.22	up	1.76E-01	8.95E-01	-	-
1393259_at	---	---	---	Rn.154223	AI044342	3.31	3.39	3.61	2.55	5.38	3.26	1.22	up	7.50E-01	9.19E-01	-	-
1388809_at	Smpdl3a	sphingomyelin phosphodiesterase, acid-like 3A	294422	Rn.8142	BM389498	4.31	3.80	4.42	4.64	4.46	4.30	1.22	up	2.47E-01	8.95E-01	-	-
1373451_at	Ponx3	pregnancy-like 3 (Drosophila)	309167	Rn.19007	BE105268	2.56	2.38	2.72	2.60	2.63	3.30	1.22	up	3.09E-01	8.95E-01	-	-
1384391_at	Rdh10	retinol dehydrogenase 10 (all-trans)	353252	Rn.16968	BE096510	7.80	6.07	3.61	6.28	5.35	4.99	1.22	down	8.31E-01	9.47E-01	-	-
1370324_at	Atp7b	ATPase, Cu++ transporting, beta polypeptide	24218	Rn.10025	AF120492	2.88	2.87	2.89	2.88	3.77	2.87	1.22	up	3.85E-01	8.95E-01	-	-
1373463_at	---	---	---	Rn.164998	AI172281	2.48	2.59	2.46	2.42	2.46	3.53	1.22	up	4.73E-01	8.95E-01	-	-
1376714_at	Amn1	antagonist of mitotic exit network 1 homolog (S. cerevisiae)	302032	Rn.104

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1374656_at	Exoc3	exocyst complex component 3	252881	Rn.6753	AA851443	5.88	5.69	5.90	5.33	5.65	5.63	1.22	down	7.65E-02	8.95E-01	-	-
1368348_at	Slc6a4	solute carrier family 6 (neurotransmitter transporter, serotonin), member 4	25553	Rn.1663	NM_013034	2.95	3.69	2.88	2.93	2.94	2.77	1.22	down	3.36E-01	8.95E-01	-	-
1373791_at	RGD1359127	similar to RIKEN cDNA 2310011J03	299612	Rn.39052	BI283399	6.17	6.16	5.73	5.55	6.66	6.71	1.22	up	5.17E-01	8.95E-01	-	-
1383644_at	---	---	---	Rn.21471	BM385202	3.04	2.79	3.42	2.83	2.94	2.61	1.22	down	2.34E-01	8.95E-01	-	-
1368467_at	Cyp4f1	cytochrome P450, family 4, subfamily f, polypeptide 1	56266	Rn.5722	NM_019623	10.88	10.41	11.00	10.53	10.30	10.58	1.22	down	2.24E-01	8.95E-01	-	-
1372523_at	Gclc	glutamate-cysteine ligase, catalytic subunit	25283	Rn.8365	AA892770	12.36	12.60	12.58	12.10	12.20	12.38	1.22	down	6.28E-02	8.95E-01	-	-
1377190_at	---	---	---	Rn.202637	AI010237	2.80	2.72	2.91	2.79	3.36	3.15	1.22	up	1.75E-01	8.95E-01	-	-
1382438_at	---	---	---	Rn.169101	BF393639	3.09	2.56	2.44	2.54	2.42	2.27	1.22	down	2.54E-01	8.95E-01	-	-
1373638_at	---	---	---	---	BG380827	3.58	3.76	3.86	3.69	4.09	4.28	1.22	up	2.06E-01	8.95E-01	-	-
1397923_at	---	---	---	Rn.209744	BF390621	2.61	2.59	2.77	2.89	3.20	2.76	1.22	up	1.14E-01	8.95E-01	-	-
1393739_at	---	---	---	---	BE108371	8.72	8.47	8.66	9.23	9.09	8.39	1.22	up	3.45E-01	8.95E-01	-	-
1382993_at	Bbc3	Bcl-2 binding component 3	317673	Rn.25176	AI236152	2.95	2.60	2.88	3.31	3.04	2.93	1.22	up	1.36E-01	8.95E-01	-	-
1374737_at	Tsen54	tRNA splicing endonuclease 54 homolog (S. cerevisiae)	690308	Rn.198903	AW528218	2.36	2.35	2.39	3.10	2.40	2.46	1.22	up	2.67E-01	8.95E-01	-	-
1378758_at	---	---	---	Rn.147368	BG380223	3.25	2.40	2.42	2.40	2.45	2.35	1.22	down	3.62E-01	8.95E-01	-	-
1388474_at	Ube2i	Ubiquitin-conjugating enzyme E2I	25573	Rn.2274	AI104523	5.65	6.38	6.68	6.37	6.46	6.75	1.22	up	4.29E-01	8.95E-01	-	-
1393352_at	Copa3	COP9 constitutive photomorphogenic homolog subunit 3 (Arabidopsis)	287367	Rn.3963	BF282468	4.98	5.63	5.09	5.23	4.57	5.03	1.22	down	3.60E-01	8.95E-01	-	-
1390717_at	Crls1	cardiolipin synthase 1	366196	Rn.35982	BM391963	6.52	7.46	6.35	7.54	6.65	7.00	1.22	up	5.42E-01	8.95E-01	-	-
1383523_at	Arhgef18	rho/rac guanine nucleotide exchange factor (GEF) 18	304193	Rn.100250	BE110369	3.88	3.90	4.82	3.73	3.73	4.27	1.22	down	4.66E-01	8.95E-01	-	-
1373042_at	Chmp2a	chromatin modifying protein 2A	365191	Rn.203178	AW434104	8.31	8.42	7.70	8.38	8.21	8.69	1.22	up	3.34E-01	8.95E-01	-	-
1367591_at	Prdx3	peroxiredoxin 3	64371	Rn.2011	NM_022540	8.39	8.46	8.78	8.04	7.94	8.80	1.22	down	3.89E-01	8.95E-01	-	-
1384101_at	Wasl	Wiskott-Aldrich syndrome-like	682507	---	BM388523	8.39	8.96	8.98	9.05	8.79	9.34	1.22	up	3.15E-01	8.95E-01	-	-
1376632_at	Lmcd1	LIM and cysteine-rich domains 1	494021	Rn.20476	AI602501	6.88	6.19	4.79	6.21	6.73	5.79	1.22	up	6.90E-01	9.05E-01	-	-
1391205_at	Heatr2	HEAT repeat containing 2	304332	Rn.16461	AA818139	5.86	6.14	4.63	6.07	4.91	6.52	1.22	up	6.88E-01	9.04E-01	-	-
1371444_at	Lass2	LAG1 homolog, ceramide synthase 2	310667	Rn.1448	BI284504	5.72	5.33	5.07	5.49	5.60	5.90	1.22	up	2.70E-01	8.95E-01	-	-
1391286_at	---	---	---	---	AA818116	6.63	7.10	7.21	7.60	7.18	7.02	1.22	up	3.10E-01	8.95E-01	-	-
1372817_at	Zfp260	zinc finger protein 260	53982	Rn.98773	BI291616	2.96	3.41	4.29	3.40	2.98	3.42	1.22	down	5.29E-01	8.95E-01	-	-
1368545_at	Cflar	CASP8 and FADD-like apoptosis regulator	117279	Rn.204752	NM_057138	4.19	5.50	4.98	4.46	5.43	5.65	1.22	up	6.16E-01	8.95E-01	-	-
1367730_at	Uso1	USO1 homolog, vesicle docking protein (yeast)	56042	Rn.4746	NM_019379	8.55	8.65	8.22	8.41	8.72	9.16	1.22	up	3.16E-01	8.95E-01	-	-
1390145_at	---	---	---	Rn.160159	AW524532	8.19	8.75	8.89	8.10	8.19	8.68	1.22	down	3.64E-01	8.95E-01	-	-
1376476_at	Telo2	TEL2, telomere maintenance 2, homolog (S. cerevisiae)	302986	Rn.34729	BI279598	2.63	3.21	2.62	2.50	2.56	2.53	1.22	down	2.18E-01	8.95E-01	-	-
1376085_at	Tmem185a	transmembrane protein 185A	309357	Rn.6505	AA849731	5.22	5.03	5.03	4.07	5.05	5.30	1.22	down	4.93E-01	8.95E-01	-	-
1391181_at	---	---	---	Rn.7583	BF390734	2.41	2.41	2.42	2.41	2.42	3.27	1.22	up	3.72E-01	8.95E-01	-	-
1393310_at	---	---	---	Rn.165497	BG672309	6.06	6.10	4.68	5.93	5.42	6.35	1.22	up	6.23E-01	8.95E-01	-	-
1371018_at	Celsr2	cadherin, EGF LAG seven-pass G-type receptor 2 (flamingo homolog, Drosop	83465	Rn.2912	BF417765	2.91	3.38	2.98	2.90	4.35	2.88	1.22	up	6.01E-01	8.95E-01	-	-
1390188_at	Mrpl51	mitochondrial ribosomal protein L51	297601	Rn.154504	BF419327	7.04	7.17	6.77	7.67	6.96	7.22	1.22	up	2.96E-01	8.95E-01	-	-
1378382_at	Pgam5	Phosphoglycerate mutase family member 5	288731	Rn.23489	AI230014	9.07	8.05	8.56	8.25	8.22	8.35	1.22	down	3.90E-01	8.95E-01	-	-
1395645_at	---	---	---	---	BF408105	5.09	5.44	2.82	5.37	4.43	4.40	1.22	up	7.61E-01	9.22E-01	-	-
1373524_at	---	---	---	Rn.202394	AA946482	6.99	7.57	6.65	6.70	6.31	7.33	1.22	down	5.12E-01	8.95E-01	-	-
1398225_at	Chd6	chromodomain helicase DNA binding protein 6	311607	Rn.43055	BF413591	2.26	2.25	2.27	2.26	2.26	3.12	1.22	up	3.75E-01	8.95E-01	-	-
1378952_at	Tmem101	transmembrane protein 101	303564	Rn.94772	H31535	4.07	4.02	4.03	4.46	4.50	4.01	1.22	up	1.42E-01	8.95E-01	-	-
1394984_at	Tnfrc6a	tetranucleotide repeat containing 6a	308971	Rn.6833	BI297127	6.65	6.05	4.80	5.96	5.55	5.14	1.22	down	6.53E-01	8.97E-01	-	-
1389581_at	Il33	interleukin 33	361749	Rn.106849	BF390510	9.45	10.27	9.60	9.94	10.08	10.17	1.22	up	3.35E-01	8.95E-01	-	-
1391052_at	Dom3z	DOM-3 homolog Z (C. elegans)	361799	Rn.20463	BI289847	4.32	3.75	4.26	4.75	4.13	4.31	1.22	up	3.27E-01	8.95E-01	-	-
1371111_at	RT1-Aw2	RT1 class Ib, locus Aw2	24737	Rn.219983	X82669	3.61	2.57	2.44	2.59	2.59	2.57	1.22	down	4.82E-01	8.95E-01	-	-
1373536_at	---	---	---	---	AW525196	10.45	10.93	11.21	10.63	10.32	10.79	1.22	down	3.36E-01	8.95E-01	-	-
1374320_at	F5	coagulation factor V (proaccelerin, labile factor)	304929	Rn.82910	AI717113	2.34	2.32	2.35	2.34	2.35	3.19	1.22	up	3.66E-01	8.95E-01	-	-
1367481_at	Vps28	vacuolar protein sorting 28 homolog (S. cerevisiae)	300052	Rn.36912	BI278301	4.53	5.01	4.58	4.52	4.95	5.53	1.22	up	4.35E-01	8.95E-01	-	-
1378874_at	Cdk2	cyclin dependent kinase 2	362817	Rn.104460	AI012076	2.86	3.25	3.19	2.81	2.87	2.75	1.22	down	8.32E-02	8.95E-01	-	-
1371563_at	Rcc2	regulator of chromosome condensation 2	298594	Rn.98282	BE109154	6.36	6.41	5.94	6.06	6.09	7.42	1.22	up	5.78E-01	8.95E-01	-	-
1374387_at	Arl6ip5	ADP-ribosylation-like factor 6 interacting protein 5	66028	Rn.64512	BG662580	7.34	8.63	8.29	8.45	7.68	8.99	1.22	up	6.26E-01	8.95E-01	-	-
1388182_at	Prim1	DNA primase, p49 subunit	246327	Rn.92497	BE108911	2.58	2.54	4.17	2.82	2.61	3.00	1.22	down	6.29E-01	8.95E-01	-	-
1389632_at	Rhobtb1	Rho-related BTB domain containing 1	309722	Rn.3782	AA799294	10.99	11.24	11.09	11.52	11.16	11.50	1.22	up	1.03E-01	8.95E-01	-	-
1395710_at	Mier1	mesoderm induction early response 1 homolog (Xenopus laevis)	313418	Rn.36542	BI275003	4.32	5.19	4.75	4.92	5.28	4.92	1.22	up	3.64E-01	8.95E-01	-	-
1398836_s_at	Actb	actin, beta	81822	Rn.94978	NM_031144	11.49	11.84	11.43	12.00	10.79	11.10	1.22	down	4.99E-01	8.95E-01	-	-
1393687_at	---	---	---	Rn.148946	BE113870	3.37	3.40	3.55	4.15	3.27	3.77	1.22	up	3.34E-01	8.95E-01	-	-
1373768_at	Bms1	BMS1 homolog, ribosome assembly protein (yeast)	362426	An.41094	AI406390	5.49	6.79	7.37	6.86	6.07	5.86	1.22	down	6.76E-01	9.01E-01	-	-
1374150_at	---	---	---	Rn.114558	AA875425	5.51	6.46	5.66	5.74	4.66	6.38	1.22	down	6.49E-01	8.96E-01	-	-
1394467_at	---	---	---	Rn.175328	AI511367	5.35	5.69	3.88	5.33	4.82	5.62	1.22	up	6.59E-01	8.98E-01	-	-
1382307_at	Ppp1r12a	protein phosphatase 1, regulatory (inhibitor) subunit 12A	116670	Rn.162937	BF406594	5.38	5.13	4.73	5.74	5.66	4.71	1.22	up	4.94E-01	8.95E-01	-	-
1389833_at	---	---	---	---	BF285924	5.12	6.22	6.50	6.04	5.22	5.72	1.22	down	5.87E-01	8.95E-01	-	-
1367696_at	Ifitm2	interferon induced transmembrane protein 2	114709	Rn.108174	NM_030833	7.52	8.34	7.28	7.87	7.58	8.55	1.22	up	5.42E-01	8.95E-01	-	-
1386311_at	---	---	---	---	AI008479	2.47	2.54	2.66	3.39	2.56	2.57	1.22	up	3.68E-01	8.95E-01	-	-
1388698_at	Ecm1	extracellular matrix protein 1	116662	Rn.97792	AI407838	5.19	2.99	2.54	3.20	2.64	4.02	1.22	down	7.69E-01	9.25E-01	-	-
1388584_at	---	---	---	Rn.8097	AI598881	4.21	4.13	4.31	4.13	3.63	4.03	1.22	down	1.54E-01	8.95E-01	-	-
1373116_at	Kpna3	Karyopherin (importin) alpha 3	361055	Rn.18504	AA945320	4.89	5.22	4.92	5.31	4.95	5.62	1.22	up	2.65E-01	8.95E-01	-	-
1386912_at	Pcolce	procollagen C-endopeptidase enhancer	29569	Rn.2910	NM_019237	3.31	2.39	2.40	2.46	2.40	2.38	1.22	down	4.07E-01	8.95E-01	-	-
1367628_at	Lgals1	lectin, galactoside-binding, soluble, 1	56646	Rn.57	NM_019904	3.28	2.72	2.86	2.68	2.73	2.59	1.22	down	1.73E-01	8.95E-01	-	-
1387833_at	Tmprss2	transmembrane protease, serine 2	156435	Rn.81082	NM_130424	4.45	2.93	2.92	3.64	2.91	2.89	1.22	down	6.40E-01	8.95E-01	-	-
1388567_at	Thump1	THUMP domain containing 1	309041	Rn.12345	BF282947	8.24	9.28	8.57	8.71	8.52	9.71	1.22	up	5.85E-01	8.95E-01	-	-
1395554_at	---	---	---	Rn.203908	BF405684	2.68	3.36	2.82	2.68	2.72	2.61	1.22	down	2.44E-01	8.95E-01	-	-
1395610_at	Tspan33	tetraspanin 33	500065	Rn.1696	AI600124	2.88	2.60	2.90	3.46	2.89	2.88	1.22	up	2.51E-01	8.95E-01	-	-
1397572_at	---	---	---	Rn.51538	BE109994	6.48	6.17	6.80	6.83	6.52	6.96	1.22	up	2.74E-01	8.95E-01	-	-
1383189_at	---	---	---	Rn.133346	AA818143	4.60	3.67	3.73	4.15	3.49	3.49	1.22	down	4.85E-01	8.95E-01	-	-
1388581_at	Hn1	hematological and neurological expressed 1	287828	Rn.198910	AI317868	4.96	6.63	7.02	6.59	5.91	6.96	1.22	up	7.05E-01	9.08E-01	-	-
1376067_at	Cnot2	CCR4-NOT transcription complex, subunit 2	299805	Rn.99836	AA800637	6.49	5.48	6.36	5.66	5.64	6.17	1.22	down	4.76E-01	8.95E-01	-	-
1393235_at	---	---	---	Rn.166309	AI059968	4.91	4.39	4.79	4.68	5.59	4.68	1.22	up	4.50E-01	8.95E-01	-	-
1374760_at	---	---	---	Rn.30593	BG374448	2.91	4.46	3.59	3.74	2.93	3.43	1.22	down	6.04E-01	8.95E-01	-	-
1389982_at	Lhx1	LIM homeobox 1	257634	Rn.127825	BF419586	4.95	4.89	5.56	5.40	5.26	5.60	1.22	up	2.93E-01	8.95E-01	-	-
1368142_at	Anxa7	annexin A7	155423	Rn.106184	AI013802	2.40	2.42	2.38	2.41	3.29	1.22	up	3.94E-01	8.95E-01	-	-
1374406_at	Klhdc2	kelch domain containing 2	299113	Rn.129179	AA925512	6.80	7.43	7.77	7.37	7.98	7.50	1.22	up	4.48E-01	8.95E-01	-	-
1387364_at	Folh1	folate hydrolase	85309	Rn.89278	AF040256	2.54	2.42	3.17	2.43	2.44	2.41	1.22	down	2.92E-01	8.95E-01	-	-
1399075_at	Map3k7	Mitogen activated protein kinase kinase kinase 7	313121	Rn.24019	AI146037	6.28	6.07	6.44	6.55	6.79	6.31	1.22	up	1.76E-01	8.95E-01	-	-
1390463_at	---	---	---	Rn.63780	BG378294	2.69	2.64	2.68	3.45	2.69	2.73	1.22	up	3.13E-01	8.95E-01	-	-
1383700_at	Pppde2	PPPDE peptidase domain containing 2	315160	Rn.198242	AA965075	3.68	3.76	3.26	3.99	3.76	3.81	1.22	up	1.75E-01	8.95E-01	-	-
1398589_at	Plra	paired immunoglobin-like type 2 receptor alpha	288568	Rn.94103	AW434602	2.54	2.53	2.73	2.75	3.38	2.53	1.22	up	3.39E-01	8.95E-01	-	-
1397121_at	RT1-T24-2	RT1 class I, T24, gene 2	416557	---	BI298734	2.76	2.80	2.75	3.72	2.76	2.69	1.22	up	4.39E-01	8.95E-01	-	-
1369409_at	Nab1	Ngfi-A binding protein 1	64824	Rn.10099	NM_022856	3.12	3.50	2.70	2.74	3.15	4.30	1.22	up	6.13E-01	8.95E-01	-	-
1398555_at	---	---	---	Rn.39287	AI549027	4.32	4.82	3.31	3.70	3.84	5.77	1.22	up	7.40E-01	9.16E-01	-	-
1376977_at	Ptger3	Prostaglandin E receptor 3 (subtype EP3)	24929	Rn.10361	AI411541	4.04	4.45	4.39	4.16	5.18	4.40	1.22	up	4.40E-01	8.95E-01	-	-
1374193_at	---	---	---	Rn.167718	BI303636	4.93	4.57	4.40	4.16	4.98	5.61	1.22	up	5.58E-01	8.95E-01	-	-
1382906_at	MGC114529	similar to melanoma antigen family A, 10	317590	Rn.8063	BI288264	3.28	2.38	2.40	2.38	2.39	2.44	1.22	down	3.92E-01	8.95E-01	-	-
1398810_at	Pdap1	PDGFA associated protein 1	64527	Rn.6158	NM_022595	8.26	7.80	7.10	8.18	7.36	8.47	1.22	up	5.77E-01	8.95E-01	-	-
1368742_at	C5ar1	complement component 5a receptor 1	113959	Rn.10680	NM_053619	3.92	2.32	2.32	3.06	2.32	2.32	1.22	down	6.55E-01	8.97E-01	-	-
1379243_at	Ndufa6	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 6 (B14)	315167	Rn.4013	AA819547	7.95	9.26	9.51	9.04	9.14	9.40	1.22	up	5.95E-01	8.95E-01	-	-
1390451_at	Wdr41	WD repeat domain 41	361879	Rn.146022	BM390195	2.48	2.35	2.38	2.37	2.33	3.35	1.22	up	4.45E-01	8.95E-01	-	-
1376887_at	Zfp445	zinc finger protein 445	301076	Rn.100996	AI555799	4.51	5.46	5.34	4.95	5.50	5.72	1.22	up	4.92E-01	8.95E-01	-	-
1382024_at	1138 /// LOC69018	DnaJ (Hsp40) homolog, subfamily B, member 6 /// similar to DnaJ (Hsp40) ho	362283 /// 681138	Rn.129050	BM383877	9.40	9.34	9.54	9.02	9.08	9.32	1.22	down	5.90E-02	8.95E-01	-	-
1374854_at	Pinx1	PIN2-interacting protein 1	305963	Rn.15365	AA924658	2.36	3.29	2.40	2.41	2.39	2.39	1.22	down	4.06E-01	8.95E-01	-	-
1392062_a_at	rCG_34541	hexosaminidase (glycosyl hydrolase family 20, catalytic domain) containing	100216475	Rn.16928	BE097702	3.23	3.58	3.55	4.00	3.67	3.54	1.22	up	1.70E-01	8.95E-01	-	-
1368954_at	Pld2	phospholipase D2	250937	Rn.9798	NM_033299	3.07	3.06	2.49	3.06	3.36	3.06	1.22	up	2.57E-01	8.95E-01	-	-
1392952_at	Acsf2	acyl-CoA synthetase family member 2	619561	Rn.146366	BI277131	6.73	4.35	4.37	5.67	5.83	4.80	1.22	up	7.56E-01	9.20E-01	-	-
1390380_at	---	---	---	Rn.164798	BE116633	6.13	6.69	5.63	6.00	5.85	5.74	1.22	down	4.15E-01	8.95E-01	-	-
1381424_at	---	---	---	---	AI636231	3.11	2.96	3.46	2.73	2.93	3.03	1.22	down	1.74E-01	8.95E-01	-	-
1393674_at	---	---	---	---	BF396736	3.06	3.38	3.75	3.24	3.09	3.01	1.22	down	2.48E-01	8.95E-01	-	-
1385259_at	Ube2k	ubiquitin-conjugating enzyme E2K (UBC1 homolog, yeast)	289623	Rn.203330	AI112792	4.78	3.89	2.30	3.94	3.63	4.25	1.22	up	7.23E-01	9.12E-01	-	-
1372712_at	Tlc1	tetratricopeptide repeat domain 1	287208	Rn.81253	BG380294	7.74	7.83	7.69	7.75	8.04	8.12	1.22	up	7.17E-02	8.95E-01	-	-
1369773_at	Bmp3	bone morphogenetic protein 3	25667	Rn.208979	NM_017105	4.67	5.75	6.44	4.55	5.90	5.55	1.22	down	6.87E-01	9.04E-01	-	-
1383791_at	RGD1566155	similar to 2610030H06Rik protein	501658	Rn.108094	BG664616	5.08	4.66	4.64	4.64	5.49	5.11	1.22	up	3.75E-01	8.95E-01	-	-
1386895_at	Maged1	melanoma antigen, family D, 1	84469	Rn.54596	NM_053409	9.35	8.36	8.35	8.27	8.51	8.43	1.22	down	4.48E-01	8.95E-01	-	-
1394692_at	Mbd4	Methyl-CpG binding domain protein 4	680915	Rn.179073	AA850656	2.38	2.37	3.23	2.38	2.38	2.37	1.22	down	3.75E-01	8.95E-01	-	-
1380053_at	Tm9sf3	transmembrane 9 superfamily member 3	309475	Rn.17150	BF397371	5.41	6.05	4.22	5.16	3.46	6.22	1.22	down	7.83E-01	9.30E-01	-	-
1383218_at	---	---	---	Rn.203822	BF286009	2.39	2.37	2.39	2.38	3.26	2.37	1.22	up	3.88E-01	8.95E-01	-	-
1379763_at	Smg7	Smg-7 homolog, nonsense mediated mRNA decay factor (C. elegans)	360855	Rn.60213	BE111542	7.29	7.22	5.62	7.23	7.36	6.88	1.22	up	6.92E-01	9.05E-01	-	-
1372768_at	---	---	---	Rn.22240	AW251331	6.39	6.73	6.25	6.84	6.60	6.78	1.22	up	1.49E-01	8.95E-01	-	-
1399034_at	Pcnx	pecanex homolog (Drosophila)	314288	Rn.23381	AI009650	4.98	5.05	5.18	5.37	4.71	5.98	1.22	up	4.87E-01	8.95E-01	-	-
1379898_at	---	---	---	Rn.95640	AI030607	3.39	3.44	3.39	3.86	2.95	4.26	1.22	up	5.05E-01	8.95E-01	-	-
1398362_at	Notch2	Notch homolog 2 (Drosophila)	29492	Rn.65930	AI011448	3.52	6.26	4.98	4.90	4.43	6.28	1.22	up	7.84E-01	9.30E-01	-	-
1376107_at	---	---	---	Rn.163970	BI294839	4.75	4.55	3.95	4.72	3.20	4.47	1.22	down	6.21E-01	8.95E-01	-	-
1383361_at	LOC690183	similar to DnaJ homolog subfamily B member 6 (Heat shock protein J2) (HSJ	690183	---	BM383741	11.03	10.91	10.90	10.51	10.71	10.77	1.22	down	3.54E-02	8.95E-01	-	-
1377375_at	Asss	aminoacylate-semisaldehyde synthase	298925	Rn.198671	AA944898	8.99	8.74	9.42	9.12	8.99	9.89	1.22	up	4.58E-01	8.95E-01	-	-
1373432_at	LOC294446	similar to Myristoylated alanine-rich C-kinase substrate (MARCKS) (ACAMP-	294446	---	BE111604	6.56	6.26	6.56	5.90	6.53	6.11	1.22	down	2.51E-01	8.95E-01	-	-
1382500_at	---	---	---	---	BF408533	5.69	5.79	5.85	5.95	5.98	6.26	1.22	up	6.23E-02	8.95E-01	-	-
1383096_at	Aplp2	amyloid beta (A4) precursor-like protein 2	64312	Rn.1423	AI235240	5.37	4.38	5.53	4.77	5.27	4.39	1.22	down	5.56E-01	8.95E-01	-	-
1394786_at	Sorl1	sortilin-related receptor, LDLR class A repeats-containing	300852	Rn.92871	AW526831	5.44	5.02	5.44	5.45	5.27	6.03	1.22	up	3.54E-01	8.95E-01	-	-
1393441_at	Cdkn2d	similar to cyclin-dependent kinase inhibitor 2D	494444	Rn.185816	BI395605	2.31	3.16	2.32	2.31	2.32	2.31	1.22	down	3.71E-01	8.95E-01	-	-
1390450_s_at	Ogn	osteoglycin	291015	Rn.103114	AA945955	3.58	3.50	3.51	3.46	3.50	2.79	1.22	down	2.91E-01	8.95E-01	-	-
1375678_at	---	---	---	---	AI412430	9.71	9.59	9.71	9.83	9.91	10.12	1.22	up	4.16E-02	8.95E-01	-	-
1372806_at	Vps35	vacuolar protein sorting 35 homolog (S. cerevisiae)	25479	Rn.161720	AA955295	7.32	7.38	7.55	6.94	7.05	7.42	1.22	down	1.52E-01	8.95E-01	-	-
1389589_at	---	---	---	Rn.22273	BI105898	4.30	4.20	4.32	4.07	4.13	3.78	1.22	down	7.17E-02	8.95E-01	-	-
1387329_at	Rnf38	ring finger protein 38	171501	Rn.82699	NM_134467	4.86	6.37	6.60	5.47	6.66	6.55	1.22	up	6.92E-01	9.05E-01	-	-
1373300_at	RGD1306151	similar to hypothetical protein DKFZp761D0211	362455	Rn.147512	BI296249	2.48	2.48	2.49	3.34	2.49	2.47	1.22	up	3.81E-01	8.95E-01	-	-
1398832_at	Ncl	nucleolin	25135	Rn.144561	NM_012749	9.64	10.13	10.29	10.15	10.34	10.42	1.22	up	2.52E-01	8.95E-01	-	-
1380055_at	Il34	interleukin 34	498951	Rn.16799	BI296368	5.10	5.73	4.99	5.03	5.01	4.93	1.22	down	2.92E-01	8.95E-01	-	-
1373167_at	Lrrc20	leucine rich repeat containing 20	499430	Rn.156423	BI295165	2.80	2.84	2.81	2.98	3.53	2.79	1.22	up	2.74E-01	8.95E-01	-	-
1397362_at	---	---	---	Rn.153635	AI071343	6.36	6.94	6.30	6.79	6.76	6.91	1.22	up	2.48E-01	8.95E-01	-	-
1372725_at	Plscr2	phospholipid scramblase 2	315883	Rn.105328	AI411594	8.35	8.89	9.13	8.38	8.76	8.38	1.22	down	3.38E-01	8.95E-01	-	-
1387325_at	Slc27a5	solute carrier family 27 (fatty acid transporter), member 5	29111	Rn.207898	NM_024143	2.35	2.35	2.37	3.19	2.38	2.35	1.22	up	3.66E-01	8.95E-01	-	-
1392552_at	Gatad2b	GATA zinc finger domain containing 2B	310614	Rn.133230	BE109744	5.06	5.94	4.39	5.06	5.84	5.33	1.22	up	6.05E-01	8.95E-01	-	-
1395963_at	---	---	---	Rn.166627	BI303658	5.76	5.56	5.61	6.28	5.99	5.51	1.22	up	2.89E-01	8.95E-01	-	-
1396163_at	Iglp	interferon gamma induced GTPase	303163	Rn.220163	BF563316	2.43	2.42	2

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicats)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1393240_at	Efemp2	EGF-containing fibulin-like extracellular matrix protein 2	293677	Rn.16151	AI112299	2.62	2.35	2.72	3.58	2.46	2.49	1.21	up	5.04E-01	8.95E-01	-	-
1393131_at	Fiz1	FLT3-interacting zinc finger 1	292584	Rn.18880	AI112338	2.63	4.41	4.29	4.41	3.18	4.58	1.21	up	7.19E-01	9.11E-01	-	-
1372796_at	---	---	---	Rn.7339	AA894188	6.76	6.52	6.76	6.43	6.43	6.33	1.21	down	3.25E-02	8.95E-01	-	-
1387771_a_at	Mapk3	mitogen activated protein kinase 3	50689	Rn.2592	AF155236	3.01	3.54	2.81	2.83	2.81	2.89	1.21	down	2.67E-01	8.95E-01	-	-
1376167_at	---	---	---	Rn.4292	AA799347	2.30	2.40	2.41	2.41	2.60	2.95	1.21	up	1.63E-01	8.95E-01	-	-
1370970_at	Kcnj14	potassium inwardly-rectifying channel, subfamily J, member 14	276720	Rn.154434	AI717104	3.28	2.40	2.41	2.39	2.46	2.40	1.21	down	3.93E-01	8.95E-01	-	-
1370577_at	Zfp455	zinc finger protein 455	286979	Rn.10864	U67083	2.40	2.55	2.55	2.51	2.59	3.23	1.21	up	2.94E-01	8.95E-01	-	-
1387869_s_at	Rabggta	Rab geranylgeranyltransferase, alpha subunit	58983	Rn.29434	AI410860	2.93	3.57	2.80	3.27	2.80	4.08	1.21	up	5.62E-01	8.95E-01	-	-
1395419_at	Mll1	myeloid/lymphoid or mixed-lineage leukemia 1	315606	Rn.62341	AA965060	3.47	5.03	5.38	4.12	5.22	3.69	1.21	down	7.25E-01	9.13E-01	-	-
1367868_at	Adrm1	adhesion regulating molecule 1	65138	Rn.9320	NM_031708	5.73	6.33	6.18	5.70	5.83	5.87	1.21	down	2.11E-01	8.95E-01	-	-
1386573_a_at	---	---	---	Rn.18516	BF546904	2.33	2.32	2.32	3.10	2.34	2.37	1.21	up	3.24E-01	8.95E-01	-	-
1370190_at	H3f3b	H3 histone, family 3B	117056	Rn.198918	AI177503	9.90	9.98	9.99	10.20	10.12	10.39	1.21	up	2.95E-02	8.95E-01	-	-
1372841_at	Reep6	receptor accessory protein 6	362835	Rn.9353	BG376982	5.29	5.96	4.81	5.86	5.23	5.81	1.21	up	5.11E-01	8.95E-01	-	-
1392761_at	---	---	---	Rn.154345	BM389886	3.04	3.50	3.64	3.56	3.59	3.87	1.21	up	2.48E-01	8.95E-01	-	-
1395363_at	Mars	methionine-tRNA synthetase	299851	Rn.140163	AI102047	3.77	3.11	2.83	2.65	2.97	3.25	1.21	down	4.41E-01	8.95E-01	-	-
1373894_at	Rab31	RAB31, member RAS oncogene family	246324	Rn.28921	BF410946	2.53	2.61	3.00	2.39	2.53	2.38	1.21	down	1.44E-01	8.95E-01	-	-
1394695_at	Fam46a	family with sequence similarity 46, member A	300870	Rn.788	BE111700	2.34	2.35	2.36	2.60	2.35	2.93	1.21	up	1.70E-01	8.95E-01	-	-
1392422_at	Alg9	asparagine-linked glycosylation 9, alpha-1,2-mannosyltransferase homolog (S	367083	Rn.135879	AI236397	4.74	5.75	4.75	4.72	4.21	5.47	1.21	down	6.02E-01	8.95E-01	-	-
1378120_at	Mrto4	mRNA turnover 4 homolog (S. cerevisiae)	298586	Rn.219376	BI280303	3.13	3.28	3.89	3.23	2.96	3.26	1.21	down	3.30E-01	8.95E-01	-	-
1377093_at	---	---	---	Rn.16399	BE106555	3.25	3.25	3.27	3.29	4.10	3.23	1.21	up	3.76E-01	8.95E-01	-	-
1389132_at	Hip1	huntingtin interacting protein 1	192154	Rn.839	AW253339	3.93	5.41	5.80	4.18	5.73	4.06	1.21	up	7.27E-01	9.13E-01	-	-
1389990_at	---	---	---	---	BE329244	5.13	5.05	4.83	5.08	5.17	3.92	1.21	down	5.35E-01	8.95E-01	-	-
1372042_at	Cmtm3	CKLF-like MARVEL transmembrane domain containing 3	291813	Rn.15332	BI294844	2.30	2.29	3.14	2.30	2.30	2.29	1.21	down	3.75E-01	8.95E-01	-	-
1367662_at	Hsd17b10	hydroxysteroid (17-beta) dehydrogenase 10	63864	Rn.2700	NM_031682	11.60	11.48	11.71	11.30	11.12	11.53	1.21	down	1.05E-01	8.95E-01	-	-
1398012_at	---	---	---	---	BF412119	2.27	2.26	2.27	2.27	3.12	2.26	1.21	up	3.79E-01	8.95E-01	-	-
1370018_at	Hspb2	heat shock protein 2	161476	Rn.22486	NM_130431	2.43	3.60	2.42	2.42	2.46	2.72	1.21	down	5.25E-01	8.95E-01	-	-
1376054_at	Sfrs16	splicing factor, arginine/serine-rich 16	499390	Rn.17553	AI102054	4.15	4.07	4.17	4.14	4.98	4.11	1.21	up	3.84E-01	8.95E-01	-	-
1383907_at	---	---	---	Rn.19231	BE117969	8.43	8.78	8.70	8.36	8.28	8.42	1.21	down	7.11E-02	8.95E-01	-	-
1380203_at	Znf512b	zinc finger protein 512B	311721	Rn.160649	BI285498	3.20	3.14	2.61	3.27	3.25	3.27	1.21	up	2.11E-01	8.95E-01	-	-
1392555_at	Etv1	Ets variant 1	362733	Rn.76536	AI112936	6.67	5.34	7.17	7.08	6.88	6.06	1.21	up	6.80E-01	9.03E-01	-	-
1369984_at	Cox17	cytochrome c oxidase, subunit XVII assembly protein homolog (S. cerevisiae)	89786	Rn.19207	NM_053540	9.23	9.66	9.43	9.37	9.00	9.13	1.21	down	1.63E-01	8.95E-01	-	-
1376923_at	---	---	---	Rn.205674	AI717053	5.03	4.63	5.22	4.71	4.62	4.71	1.21	down	1.88E-01	8.95E-01	-	-
1398759_at	Tsc22d1	TSC22 domain family, member 1	498545	Rn.3545	NM_013043	11.15	11.30	11.58	11.53	11.67	11.67	1.21	up	1.10E-01	8.95E-01	-	-
1374979_at	Wnt5b	wingless-type MMTV integration site family, member 5B	282582	Rn.58724	BF392911	2.39	2.40	2.41	3.22	2.46	2.37	1.21	up	3.59E-01	8.95E-01	-	-
1394070_at	---	---	---	---	AA893087	3.97	3.63	5.89	4.23	3.35	5.07	1.21	down	7.62E-01	9.22E-01	-	-
1388368_at	Med28	mediator complex subunit 28	305391	Rn.34860	BM389891	7.48	8.95	8.08	8.64	7.99	8.72	1.21	up	5.97E-01	8.95E-01	-	-
1393966_at	Pbx1	pre-B-cell leukemia homeobox 1	304947	Rn.205189	AW530825	4.76	4.46	4.12	4.21	3.99	4.31	1.21	down	2.51E-01	8.95E-01	-	-
1374148_at	---	---	---	Rn.20316	BI296414	4.36	4.01	3.40	4.03	3.78	4.80	1.21	up	5.40E-01	8.95E-01	-	-
1383601_at	Bclaf1	BCL2-associated transcription factor 1	293017	Rn.202401	BI295614	2.79	3.04	2.52	2.50	2.51	2.49	1.21	down	1.37E-01	8.95E-01	-	-
1399028_at	RGD1308290	Similar to RIKEN cDNA 5730454B08	360845	Rn.73695	AI171954	7.64	7.81	7.22	8.01	7.72	7.77	1.21	up	2.29E-01	8.95E-01	-	-
1385765_at	/// LOC360868	lin9 homolog (C. elegans) /// similar to lin-9 homolog (C. elegans)	360868 /// 689523	Rn.214693	BF406563	5.25	4.12	5.25	4.26	4.72	4.81	1.21	down	5.36E-01	8.95E-01	-	-
1373299_at	Ubxn1	UBX domain protein 1	293719	Rn.198539	BI295816	7.51	8.97	8.48	8.33	8.31	9.15	1.21	up	6.13E-01	8.95E-01	-	-
1385016_at	RGD1560784	similar to RIKEN cDNA B630019K06	363449	---	AI136882	2.47	2.53	2.50	3.29	2.53	2.52	1.21	up	3.36E-01	8.95E-01	-	-
1398574_a_at	Cdc25	cell division cycle 2-like 5 (cholinesterase-related cell division controller)	306998	Rn.23420	AI170890	3.96	4.30	4.76	3.82	5.56	4.49	1.21	up	6.42E-01	8.95E-01	-	-
1395821_at	Cbfb	core-binding factor, beta subunit	361391	Rn.7308	BF524120	6.76	6.78	6.64	7.24	6.80	6.98	1.21	up	1.08E-01	8.95E-01	-	-
1387086_at	Camlg	calcium modulating ligand	81715	Rn.63999	NM_053334	4.04	4.11	4.46	4.84	3.12	3.81	1.21	down	6.17E-01	8.95E-01	-	-
1384950_at	Pi4k2b	phosphatidylinositol 4-kinase type 2 beta	305419	Rn.21189	AI060149	6.02	5.56	3.34	4.93	3.08	6.08	1.21	down	8.28E-01	9.46E-01	-	-
1397178_at	---	---	---	Rn.32366	AA899041	3.91	4.45	4.01	2.91	4.23	4.40	1.21	down	6.06E-01	8.95E-01	-	-
1389582_at	LOC683983	similar to Nucleoporin Nup43	683983	Rn.216533	AI407405	2.54	2.54	2.55	2.86	2.55	3.05	1.21	up	1.31E-01	8.95E-01	-	-
1371705_at	Vps26a	Vacuolar protein sorting 26 homolog A (S. pombe)	361846	Rn.3673	BI285508	6.33	6.45	6.19	5.77	6.19	6.18	1.21	down	1.48E-01	8.95E-01	-	-
1394419_at	Arhgap11a	Rho GTPase activating protein 11A	296080	Rn.51673	BE109109	2.44	2.49	2.45	2.43	3.06	2.73	1.21	up	2.03E-01	8.95E-01	-	-
1382778_at	Dusp6	Dual specificity phosphatase 6	116663	Rn.4313	AI231350	7.73	7.59	7.79	7.13	8.51	8.32	1.21	up	5.58E-01	8.95E-01	-	-
1391584_at	---	---	---	Rn.164498	AA850595	6.93	6.15	7.02	6.97	5.62	6.67	1.21	down	6.03E-01	8.95E-01	-	-
1393451_at	Cenpn	centromere protein N	361416	Rn.65502	BI295149	4.17	4.16	3.61	3.99	4.19	4.59	1.21	up	3.36E-01	8.95E-01	-	-
1378394_at	Mppe1	metallophosphoesterase 1	361344	Rn.64185	BE113263	4.23	4.52	4.08	3.96	3.31	4.72	1.21	down	5.48E-01	8.95E-01	-	-
1395461_at	Apc2	adenomatosis polyposis coli 2	299611	Rn.168155	BI294552	2.42	2.35	2.36	3.26	3.27	2.35	1.21	up	4.13E-01	8.95E-01	-	-
1389108_at	Tbcd	tubulin-specific chaperone d	360683	---	AI710235	8.57	8.73	8.59	7.90	8.68	8.48	1.21	down	3.13E-01	8.95E-01	-	-
1383141_a_at	Cpsf7	cleavage and polyadenylation specific factor 7, 59kDa	365407	Rn.98627	AI236700	7.62	7.64	7.85	7.41	7.56	7.31	1.21	down	5.36E-02	8.95E-01	-	-
1385830_at	RGD1561507	similar to hypothetical protein FLJ31606	292078	Rn.206669	BE110287	5.76	5.95	4.75	5.99	4.56	6.74	1.21	up	7.26E-01	9.13E-01	-	-
1375962_at	---	---	---	Rn.48946	BE102925	5.86	5.83	5.74	5.85	6.30	6.11	1.21	up	1.09E-01	8.95E-01	-	-
1374476_at	---	---	---	Rn.40468	AA866267	6.93	6.92	7.20	7.07	6.54	6.61	1.21	down	2.16E-01	8.95E-01	-	-
1386885_at	Ech1	enoyl coenzyme A hydratase 1, peroxisomal	64526	Rn.6148	AI45056	9.41	10.18	9.50	9.41	9.25	9.60	1.21	down	3.51E-01	8.95E-01	-	-
1368533_at	Heph	hephaestin	117240	Rn.43849	NM_133304	2.63	2.63	2.58	2.63	3.50	2.55	1.21	up	4.12E-01	8.95E-01	-	-
1383157_at	Mrpl44	mitochondrial ribosomal protein L44	301552	Rn.3298	AW520344	8.06	8.55	7.69	8.49	8.23	8.42	1.21	up	3.44E-01	8.95E-01	-	-
1387777_at	Itk	integrin linked kinase	170922	Rn.95042	NM_133409	8.30	6.77	8.69	6.67	8.68	7.25	1.21	up	7.44E-01	9.17E-01	-	-
1398587_at	---	---	---	Rn.43360	AA860035	7.94	5.46	6.25	5.68	5.90	7.22	1.21	down	7.66E-01	9.24E-01	-	-
1375864_at	Cc2d1b	coiled-coil and C2 domain containing 1B	313478	Rn.3265	BI274151	5.87	5.71	4.29	4.68	4.90	5.46	1.21	down	6.42E-01	8.95E-01	-	-
1378998_at	---	---	---	Rn.20558	AI071538	2.71	2.70	2.67	2.69	3.52	2.70	1.21	up	3.72E-01	8.95E-01	-	-
1390474_at	Npal2	NIPA-like domain containing 2	362899	Rn.242	AA859508	3.70	3.30	2.54	2.78	2.75	3.17	1.21	down	4.88E-01	8.95E-01	-	-
1374900_at	Gosr2	golgi SNAP receptor complex member 2	64154	Rn.13518	BM388807	7.25	7.44	7.34	7.79	7.10	7.97	1.21	up	3.61E-01	8.95E-01	-	-
1393194_at	Baz1b	bromodomain adjacent to zinc finger domain, 1B	368002	Rn.7043	BF558732	3.49	4.50	2.60	3.47	2.88	5.08	1.21	up	7.62E-01	9.22E-01	-	-
1392437_at	Alg2	asparagine-linked glycosylation 2, alpha-1,3-mannosyltransferase homolog (S	313231	Rn.98222	AI070159	3.19	2.32	2.34	2.35	2.34	2.32	1.21	down	3.85E-01	8.95E-01	-	-
1395510_at	Abhd1	abhydrolase domain containing 1	313917	Rn.162847	AW916573	3.83	4.07	4.11	4.20	3.02	3.95	1.21	down	4.93E-01	8.95E-01	-	-
1367520_at	Apoa1bp	apolipoprotein A-I binding protein	295229	Rn.14886	AI231050	7.55	8.38	7.86	8.22	8.10	8.30	1.21	up	3.24E-01	8.95E-01	-	-
1396408_at	LOC688319	similar to RAS-related C3 botulinum substrate 3	688319	---	BE108736	3.45	2.86	2.87	2.86	2.87	2.61	1.21	down	2.63E-01	8.95E-01	-	-
1379500_at	Ccdc117	coiled-coil domain containing 117	498404	Rn.20126	AA860044	4.73	5.06	4.94	5.15	5.62	4.80	1.21	up	3.39E-01	8.95E-01	-	-
1370365_at	Gss	glutathione synthetase	25458	Rn.1692	L38615	10.98	11.30	11.25	10.88	10.84	10.99	1.21	down	6.49E-02	8.95E-01	-	-
1398065_at	Sobpl	sine oculis-binding protein homolog-like (Drosophila)	309860	Rn.208930	BF394331	2.83	2.55	2.84	3.22	3.01	2.82	1.21	up	1.37E-01	8.95E-01	-	-
1372546_at	Mapkapk3	mitogen-activated protein kinase-activated protein kinase 3	315994	Rn.8789	BM390276	4.00	4.49	4.66	5.13	4.37	4.48	1.21	up	4.16E-01	8.95E-01	-	-
1374514_at	---	---	---	Rn.17185	BG671893	6.34	6.59	5.76	6.05	5.30	6.49	1.21	down	5.52E-01	8.95E-01	-	-
1379592_at	Slc25a13	solute carrier family 25, member 13 (citrin)	362322	Rn.14686	AI045151	6.72	7.29	6.73	6.32	6.58	7.00	1.21	down	3.68E-01	8.95E-01	-	-
1387177_at	Vipr2	vasoactive intestinal peptide receptor 2	29555	Rn.10011	NM_017238	2.93	2.30	2.47	2.26	2.31	2.29	1.21	down	2.21E-01	8.95E-01	-	-
1392665_at	Exosc3	exosome component 3	313243	Rn.219381	BF285589	3.82	3.29	3.60	3.31	3.32	3.24	1.21	down	1.50E-01	8.95E-01	-	-
1382636_at	---	---	---	Rn.164585	AA899383	4.13	4.16	5.43	4.08	4.02	4.79	1.21	down	6.04E-01	8.95E-01	-	-
1367483_at	RGD1309148	similar to RIKEN cDNA 3110001D03	298147	Rn.2448	AI170657	4.42	4.42	5.37	4.32	4.63	4.41	1.21	down	4.48E-01	8.95E-01	-	-
1389570_at	Inpp5k	inositol polyphosphate-5-phosphatase K	287533	Rn.7440	AA860657	3.56	3.64	2.77	3.19	2.77	3.18	1.21	down	4.20E-01	8.95E-01	-	-
1372892_at	Znf213	Zinc finger protein 213	287094	Rn.98676	BE109668	4.20	3.61	3.63	3.43	3.37	3.80	1.21	down	3.03E-01	8.95E-01	-	-
1373682_at	Ddx51	DEAD (Asp-Glu-Ala-Asp) box polypeptide 51	304570	Rn.15921	BI290764	3.22	4.53	4.63	3.72	4.17	3.66	1.21	down	5.96E-01	8.95E-01	-	-
1385565_at	Rad50	RAD50 homolog (S. cerevisiae)	64012	Rn.51136	BF564092	2.54	2.48	2.49	2.85	2.52	2.97	1.21	up	1.09E-01	8.95E-01	-	-
1389479_at	Klf3	Kruppel-like factor 3 (basic)	114845	Rn.218431	AI233750	5.26	6.08	5.32	5.62	5.13	6.74	1.21	up	6.38E-01	8.95E-01	-	-
1367573_at	Rps6	ribosomal protein S6	29304	Rn.34341	NM_017160	11.68	11.71	11.59	11.79	11.92	12.11	1.21	up	4.97E-02	8.95E-01	-	-
1394479_at	Afmid	aryformamidase	688283	Rn.216742	BI288580	6.97	6.62	6.98	6.78	6.51	6.45	1.21	down	1.49E-01	8.95E-01	-	-
1388716_at	Ehmt2	euchromatic histone lysine N-methyltransferase 2	361798	Rn.116518	BE109525	6.13	6.25	4.77	5.50	6.21	6.28	1.21	up	6.33E-01	8.95E-01	-	-
1378668_at	---	---	---	Rn.164437	BG672426	6.90	6.59	6.43	6.15	5.86	7.07	1.21	down	5.16E-01	8.95E-01	-	-
1376749_at	Ogn	osteoglycin	291015	Rn.103114	AA945955	3.20	2.55	2.45	2.51	2.45	2.41	1.21	down	3.05E-01	8.95E-01	-	-
1376600_at	---	---	---	Rn.2868	BI289616	6.12	6.45	6.26	6.02	7.02	6.63	1.21	up	4.15E-01	8.95E-01	-	-
1372408_at	Gga2	golgi associated, gamma adaptin ear containing, ARF binding protein 2	293455	Rn.18248	BI278620	5.39	4.67	3.40	4.64	5.01	4.64	1.21	up	6.65E-01	8.99E-01	-	-
1395147_at	---	---	---	Rn.216560	BE116565	4.39	3.74	3.97	4.12	3.93	4.88	1.21	up	4.71E-01	8.95E-01	-	-
1371993_at	Cpne3	copine III	313087	Rn.4034	AI237636	3.65	3.97	3.16	3.36	3.28	3.31	1.21	down	3.06E-01	8.95E-01	-	-
1370474_at	Thrb	thyroid hormone receptor beta	24831	Rn.88692	J03933	3.06	4.45	3.46	3.55	2.46	4.12	1.21	down	6.87E-01	9.04E-01	-	-
1389814_at	LOC501546	hypothetical protein LOC501546	501546	Rn.12130	BI299841	8.63	8.96	7.63	8.05	7.74	8.59	1.21	down	5.88E-01	8.95E-01	-	-
1367834_at	Srm	spermidine synthase	84596	Rn.22258	NM_053464	4.98	4.68	4.24	4.98	4.40	5.34	1.21	up	4.89E-01	8.95E-01	-	-
1367867_at	Gfer	growth factor, augmenter of liver regeneration	24705	Rn.11039	NM_013222	5.42	6.83	6.13	6.80	6.13	6.28	1.21	up	5.76E-01	8.95E-01	-	-
1373489_at	Chaf1a	chromatin assembly factor 1, subunit A (p150)	363333	Rn.12758	AI012664	2.50	2.52	2.28	2.64	2.55	2.94	1.21	up	1.19E-01	8.95E-01	-	-
1383879_at	---	---	---	---	BG377332	7.71	8.02	7.95	7.80	7.08	7.97	1.21	down	3.92E-01	8.95E-01	-	-
1375916_at	Pcmt1l	protein-L-isoaspartate (D-aspartate) O-methyltransferase domain containing 2	311726	Rn.96446	AA895163	4.55	4.45	4.49	4.46	4.79	5.07	1.21	up	1.99E-01	8.95E-01	-	-
1389738_at	Ung	uracil-DNA glycosylase	304577	Rn.104379	AA848420	8.17	8.49	7.99	8.25	7.24	8.34	1.21	down	5.09E-01	8.95E-01	-	-
1371710_at	Etnk1	Ethanolamine kinase 1	312828	Rn.7630	BM391283	9.56	10.28	10.02	9.43	9.77	9.84	1.21	down	3.22E-01	8.95E-01	-	-
1375416_at	Fam104a	family with sequence similarity 104, member A	619573	Rn.98587	AI231165	4.59	4.76	4.29	4.58	5.23	4.67	1.21	up	3.23E-01	8.95E-01	-	-
1392594_at	Sudd2	sushi domain containing 2	294335	Rn.166705	AI136409	2.36	2.35	2.38	2.36	3.21	2.35	1.21	up	3.87E-01	8.95E-01	-	-
1378652_at	---	---	---	Rn.52308	BE111540	3.29	2.52	2.46	2.68	2.46	2.30	1.21	down	3.91E-01	8.95E-01	-	-
1379270_at	---	---	---	Rn.154043	AI171163	2.82	2.87	2.86	3.68	2.86	2.83	1.21	up	3.75E-01	8.95E-01	-	-
1370406_a_at	Cd55	Cd55 molecule	64036	Rn.18841	AB032395	2.33	3.14	2.34	2.33	2.34	2.32	1.21	down	3.58E-01	8.95E-01	-	-
1382784_at	Angel2	angel homolog 2 (Drosophila)	305035	Rn.62	AI058332	4.06	4.78	4.87	4.92	4.37	5.25	1.21	up	4.88E-01	8.95E-01	-	-
1396642_at	LOC360990	similar to ubiquitin specific protease 34	360990	Rn.16057	BF403725	2.52	3.40	2.52	2.52	2.51	2.59	1.21	down	4.02E-01	8.95E-01	-	-
1395159_at	---	---	---	---	BE121256	2.36	2.35	2.37	2.35	3.20	2.36	1.21	up	3.84E-01	8.95E-01	-	-
1377679_at	Gpr125	G protein-coupled receptor 125	305408	Rn.217999	BI295085	4.48	5.18	5.28	5.58	4.38	5.81	1.21	up	4.18E-01	8.95E-01	-	-
1392882_at	RGD1305110	similar to KIAA1841 protein	305579	Rn.57428	BF391198	6.24	5.23	3.64	4.67	4.29	5.31	1.21	down	7.51E-01	9.19E-01	-	-
1374203_at	---	---	---	---	BM385279	3.81	4.66	4.14	4.39	4.37	4.68	1.21	up	3.59E-01	8.95E-01	-	-
1381296_at	---	---	---	Rn.163597	AA819045	2.84	2.83	2.24	2.86	2.95	2.93	1.21	up	2.42E-01	8.95E-01	-	-
1387081_at	Rcn2	reticulocalbin 2, EF-hand calcium binding domain	29218	Rn.6133	NM_017132	6.70	6.01	6.59	6.72	6.64	6.76	1.21	up	2.73E-01	8.95E-01	-	-
1394094_at	---	---	---	Rn.160465	AI412196	3.44	2.57	2.49	2.59	2.53	2.56	1.21	down	4.18E-01	8.95E-01	-	-
1380022_at	Rrn3	RRN3 RNA polymerase I transcription factor homolog (S. cerevisiae)	304714	Rn.159763	BE119114	4.92	4.72	5.26	4.78	4.65	4.65	1.21	down	1.66E-01	8.95E-01	-	-
1368122_at	Rnf103	ring finger protein 103	84508	Rn.45685	NM_053438	7.56	8.69	8.47	8.20	8.26	9.08	1.21	up	5.71E-01	8.95E-01	-	-
1392211_at	Sec24b	SEC24 family, member B (S. cerevisiae)	295461	Rn.102003	BF408070	4.58	5.43	7.24	5.99	6.38	5.70	1.21	up	7.50E-01	9.19E-01	-	-
1387676_at	Mark1	MAP/microtubule affinity-regulating kinase 1	117016	Rn.21430	NM_053947	2.48	2.48	3.33	2.48	2.49	2.49	1.21	down	3.84E-01	8.95E-01	-	-
1371616_at	---	---	---	Rn.23024	AW524495	5.26	4.96	6.33	5.85	5.93	5.49	1.21	up	5.66E-01	8.95E-01	-	-
1397092_at	Armc9	armadillo repeat containing 9	301579	Rn.27285	AI145850	3.28	2.59	2.79	2.60	2.67	2.55	1.21	down	2.59E-01	8.95E-01	-	-
1374146_at	Madl2l	MAD2 mitotic arrest deficient-like 2 (yeast)	313702	Rn.27237	BF419366	5.47	5.93	5.94	6.65	5.58	5.94	1.21	up	4.77E-01	8.95E-01	-	-
1382273_at	Bcl2l14	Bcl2-like 14 (apoptosis facilitator)	500348	Rn.162775	BF283609	2.34	2.31	2.32	2.31	2.32	3.16	1.21	up	3.85E-01	8.95E-01	-	-
1379506_at	---	---	---	Rn.12150	AA863909	5.27	6.69	6.35	5.35	5.49	6.63	1.21	down	6.64E-01	8.99E-01	-	-
1377645_at	LOC360479	similar to hypothetical protein	360479	Rn.3653	AA892331	2.54	2.53	2.55	2.54	3.36	2.54	1.21	up	3.70E-01	8.95E-01	-	-
1367485_a_at	Ppp2r2a	protein phosphatase 2 (formerly 2A), regulatory subunit B, alpha isoform	117104	Rn.81155	M83297	5.70	6.21	5.69	6.45	5.80	6.17	1.21	up	3.42E-01	8.95E-01	-	-
1387129_at	Xrcc1	X-ray repair complementing defective repair in Chinese hamster cells 1	84495	Rn.13754	NM_053435	4.97	5.04	5.51	5.05	5.49	4.16	1.21	down	5.51E-01	8.95E-01	-	-
1382644_at	---	---	---	Rn.97119	AA875527	4.32	4.72	4.75	4.75	4.37	5.49	1.21	up	4.82E-01	8.95E-01	-	-
1384747_at	Gpr137b	G protein-coupled receptor 137B	289287	Rn.60453	BF404188	7.11	7.32	7.45	7.44	7.32	7.95	1.21	up	2.77E-01	8.95E-01	-	-
1370492_a_at	Flt1	fms-related tyrosine kinase 1	54251	Rn.10239	AF116795	3.70	3.79	3.79	3.77	3.53	3.16	1.21	down	2.00E-01	8.95E-01	-	-
1399032_at	Ercc1	excision repair cross-complementing rodent repair deficiency, complementatic	292673	Rn.7320	AA892791	4.54	4.64	4.46	5.35	4.32	4.80	1.21	up	4.13E-01	8.95E-01	-	-
1368295_at	Slco2b1	solute carrier organic anion transporter family, member 2b1	140860	Rn.44538	AF169410	2.50	2.41

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicats)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1388110_at	1a1 /// RGD15662	eukaryotic translation elongation factor 1 alpha 1 /// similar to eukaryotic trans	171361 /// 310360	Rn.965	X61043	11.89	11.85	11.75	12.03	12.05	12.23	1.21	up	2.29E-02	8.95E-01	-	-
1383474_at	Irak2	interleukin-1 receptor-associated kinase 2	362418	Rn.17123	BI274988	5.55	6.16	6.76	6.64	6.28	6.38	1.21	up	4.98E-01	8.95E-01	-	-
1375706_at	---	---	---	---	AI230273	8.15	7.97	7.36	7.96	8.10	8.24	1.21	up	3.36E-01	8.95E-01	-	-
1374527_at	Echdc2	enoyl Coenzyme A hydratase domain containing 2	298381	Rn.1408	AI172274	7.02	7.04	7.29	6.70	6.70	7.13	1.21	down	1.79E-01	8.95E-01	-	-
1391454_at	RGD1565584	similar to tyrosine kinase-associated leucine zipper protein LAZIpII	293112	Rn.35776	BF286105	2.59	5.16	5.61	4.30	4.92	4.98	1.21	up	7.91E-01	9.33E-01	-	-
1368885_at	---	---	---	---	AI009808	2.41	2.39	3.21	2.40	2.41	2.38	1.21	down	3.68E-01	8.95E-01	-	-
1368542_at	Zfp423	zinc finger protein 423	94188	Rn.9981	NM_053583	2.37	2.35	3.00	2.36	3.84	2.34	1.21	up	6.39E-01	8.95E-01	-	-
1372338_at	LOC687395	similar to CG9240-PA	687395	---	AI599079	6.96	7.55	7.35	7.49	7.63	7.55	1.21	up	2.01E-01	8.95E-01	-	-
1390177_at	---	---	---	Rn.6397	AI233857	3.67	2.62	2.62	2.62	2.62	2.86	1.21	down	4.87E-01	8.95E-01	-	-
1370618_at	Optn	optineurin	246294	Rn.63435	AB066907	4.61	4.24	4.17	4.47	4.77	4.60	1.21	up	1.64E-01	8.95E-01	-	-
1398588_at	Slu7	SLU7 splicing factor homolog (S. cerevisiae)	303057	Rn.137183	BE098532	4.78	4.89	5.86	5.13	6.02	5.20	1.21	up	5.75E-01	8.95E-01	-	-
1390634_at	RGD1566314	similar to KIAA1407	288106	Rn.140653	BF400831	2.89	2.58	2.36	2.34	2.35	2.33	1.21	down	1.50E-01	8.95E-01	-	-
1368277_at	Ppp3ca	protein phosphatase 3 (formerly 2B), catalytic subunit, alpha isoform	24674	Rn.6866	NM_017041	7.15	7.87	8.32	7.30	7.60	7.62	1.21	down	4.88E-01	8.95E-01	-	-
1375339_at	Enth	enthoprotin	360515	Rn.222041	BI296679	9.35	8.82	8.52	8.93	9.36	9.23	1.21	up	3.77E-01	8.95E-01	-	-
1384767_at	Usp42	ubiquitin specific peptidase 42	288482	Rn.25011	BF404275	3.81	3.65	2.78	3.66	4.00	3.38	1.21	up	4.96E-01	8.95E-01	-	-
1383544_at	Fchsd1	FCH and double SH3 domains 1	307482	Rn.100014	AI385372	2.31	2.30	3.22	2.32	2.38	2.38	1.21	down	4.23E-01	8.95E-01	-	-
1373872_at	Mgat4a	mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase	367252	Rn.145359	BE096535	3.12	3.08	3.09	3.25	2.88	3.98	1.21	up	4.47E-01	8.95E-01	-	-
1381522_at	---	---	---	---	BI280528	2.42	2.40	2.43	3.13	2.42	2.51	1.21	up	2.92E-01	8.95E-01	-	-
1369471_at	Fnbp1	formin binding protein 1	192348	Rn.20445	NM_138914	4.48	4.61	5.33	4.41	4.25	4.95	1.21	down	4.66E-01	8.95E-01	-	-
1396403_at	RGD1311595	similar to KIAA2026 protein	309307	Rn.96138	BE107859	6.36	7.03	6.96	6.88	7.28	7.00	1.21	up	3.21E-01	8.95E-01	-	-
1368051_at	Hsd17b12	hydroxysteroid (17-beta) dehydrogenase 12	84013	Rn.203283	NM_032066	8.45	9.44	10.14	8.92	8.91	9.38	1.21	down	6.24E-01	8.95E-01	-	-
1376103_at	---	---	---	Rn.53230	AA946360	3.24	2.72	2.43	2.87	2.36	2.33	1.21	down	4.06E-01	8.95E-01	-	-
1393040_at	---	---	---	Rn.137593	BE097656	4.27	2.58	3.29	3.61	2.54	3.18	1.21	down	6.64E-01	8.99E-01	-	-
1377593_at	Dpm1	dolichyl-phosphate mannosyltransferase polypeptide 1, catalytic subunit	296394	Rn.7840	BI284172	8.45	8.81	8.63	8.70	8.97	9.04	1.21	up	1.38E-01	8.95E-01	-	-
1377237_at	---	---	---	Rn.204414	AI137274	2.74	3.86	3.05	3.03	2.37	3.43	1.21	down	5.82E-01	8.95E-01	-	-
1373548_at	---	---	---	Rn.3104	BE107518	7.10	7.84	7.94	7.01	7.59	7.46	1.21	down	4.37E-01	8.95E-01	-	-
1379838_at	---	---	---	Rn.199539	BE100444	5.90	5.11	5.11	5.11	5.11	5.09	1.21	down	3.61E-01	8.95E-01	-	-
1371997_at	Akr1cl2	aldo-keto reductase family 1, member C-like 2	307091	Rn.108718	BM390833	8.75	9.34	9.19	9.09	9.49	9.51	1.21	up	2.93E-01	8.95E-01	-	-
1371494_at	---	---	---	Rn.14639	BE110614	5.19	6.43	6.20	5.86	6.08	6.69	1.21	up	5.82E-01	8.95E-01	-	-
1398044_at	---	---	---	Rn.208757	BF392326	3.51	3.20	3.52	3.64	3.94	3.47	1.21	up	1.90E-01	8.95E-01	-	-
1382010_at	LOC691750	hypothetical protein LOC691750	691750	Rn.2425	AI711537	2.94	2.44	2.44	2.33	2.33	3.98	1.21	up	6.61E-01	8.98E-01	-	-
1377646_at	---	---	---	Rn.3093	AI177360	6.50	4.34	4.87	5.08	5.56	4.26	1.21	down	7.35E-01	9.15E-01	-	-
1368365_at	Aldh3a2	aldehyde dehydrogenase 3 family, member A2	65183	Rn.9113	NM_031731	7.17	6.85	6.08	6.69	6.66	7.56	1.21	up	5.88E-01	8.95E-01	-	-
1371767_at	Smarcd1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin,	363002	Rn.21196	BG380270	5.15	2.77	2.81	3.07	4.34	4.14	1.21	up	7.72E-01	9.28E-01	-	-
1371393_at	Clstn1	calsyntenin 1	313717	Rn.99876	AA851222	5.96	6.50	7.07	6.79	6.67	6.88	1.21	up	4.51E-01	8.95E-01	-	-
1375377_at	Igsf3	immunoglobulin superfamily, member 3	295325	---	BE098713	3.00	2.84	2.58	3.65	2.39	3.19	1.21	up	5.23E-01	8.95E-01	-	-
1372274_at	Mll5	Myeloid/lymphoid or mixed-lineage leukemia 5 (trithorax homolog, Drosophila	311968	Rn.106040	AI009727	8.15	7.10	7.61	7.27	7.49	7.28	1.21	down	4.32E-01	8.95E-01	-	-
1389789_at	Mxd1	Max dimerization protein 1	362391	Rn.19241	AI059602	6.19	6.17	6.41	6.01	6.31	5.63	1.21	down	2.70E-01	8.95E-01	-	-
1370397_at	Cyp4a3	cytochrome P450, family 4, subfamily a, polypeptide 3	298423	Rn.33492	M33936	11.48	11.52	11.89	11.27	11.41	11.39	1.21	down	1.20E-01	8.95E-01	-	-
1392534_at	Pmepa1	prostate transmembrane protein, androgen induced 1	311676	Rn.28828	BI274101	5.03	4.95	4.32	4.96	4.96	5.20	1.21	up	3.23E-01	8.95E-01	-	-
1389136_at	Pknlr	protein-kinase, interferon-inducible double stranded RNA dependent inhibitor,	308845	Rn.161856	AI462380	6.20	6.72	6.02	5.75	6.18	6.20	1.21	down	3.49E-01	8.95E-01	-	-
1369597_at	Vapb	VAMP (vesicle-associated membrane protein)-associated protein B and C	60431	Rn.52500	NM_021847	5.78	5.76	6.68	5.73	5.75	5.92	1.21	down	4.29E-01	8.95E-01	-	-
1388849_at	Aup1	ancient ubiquitous protein 1	680423	Rn.198163	BG375145	10.07	10.19	9.91	10.51	10.12	10.34	1.21	up	1.24E-01	8.95E-01	-	-
1375083_at	---	---	---	Rn.42082	BM387126	4.33	6.03	6.42	5.03	5.12	5.82	1.21	down	7.14E-01	9.10E-01	-	-
1370200_at	Glud1	glutamate dehydrogenase 1	24399	Rn.55106	AW916644	8.93	9.41	9.46	8.84	9.10	9.04	1.21	down	2.22E-01	8.95E-01	-	-
1372813_at	RGD1306682	similar to RIKEN cDNA 1810046J19	360617	Rn.143893	AA858862	8.60	8.87	9.19	8.57	8.58	8.70	1.21	down	2.00E-01	8.95E-01	-	-
1378476_at	Aars2	alanyl-tRNA synthetase 2, mitochondrial (putative)	301254	Rn.109849	BM390047	4.07	4.49	5.78	5.28	3.29	4.96	1.21	down	7.53E-01	9.20E-01	-	-
1375525_at	Mapre1	microtubule-associated protein, RP/EB family, member 1	114764	Rn.7652	BI294783	5.84	5.99	6.50	6.31	6.00	6.84	1.21	up	4.38E-01	8.95E-01	-	-
1369663_at	Ephx2	epoxide hydrolase 2, cytoplasmic	65030	Rn.54495	NM_022936	3.64	2.54	2.49	2.53	2.48	2.84	1.21	down	5.24E-01	8.95E-01	-	-
1376772_at	RGD1308299	Similar to chromosome 6 open reading frame 130; hypothetical 9.7 kDa prote	367214	Rn.136283	BM386583	2.66	3.21	3.95	3.61	2.96	4.07	1.21	up	6.12E-01	8.95E-01	-	-
1383313_at	Chfr	checkpoint with forkhead and ring finger domains	288734	Rn.15515	BE120149	2.51	3.14	2.52	2.47	2.51	3.99	1.21	up	6.43E-01	8.95E-01	-	-
1382581_at	Ehf	ets homologous factor	295965	Rn.220252	BF417773	2.55	2.63	2.58	2.63	3.06	2.88	1.21	up	9.59E-02	8.95E-01	-	-
1377697_at	Apbb2	amyloid beta (A4) precursor protein-binding, family B, member 2	305338	Rn.24283	BI275738	7.98	8.10	7.69	8.35	8.23	8.00	1.21	up	1.62E-01	8.95E-01	-	-
1387959_at	Aspg	asparaginase homolog (S. cerevisiae)	246266	Rn.29979	AB009372	6.91	7.38	6.66	7.23	6.94	7.59	1.21	up	3.90E-01	8.95E-01	-	-
1370269_at	Cyp1a1	cytochrome P450, family 1, subfamily a, polypeptide 1	24296	Rn.10352	X00469	6.34	8.92	8.78	7.83	5.98	7.42	1.21	down	7.95E-01	9.34E-01	-	-
1386947_at	Cdh1	cadherin 1	83502	Rn.1303	NM_031334	4.87	5.86	5.17	5.58	5.42	5.72	1.21	up	4.25E-01	8.95E-01	-	-
1375378_at	Qk	quaking	499022	Rn.85462	BE108882	4.44	4.26	3.74	4.55	4.26	4.44	1.21	up	2.94E-01	8.95E-01	-	-
1394240_at	RGD1305158	Similar to RIKEN cDNA 1810030N24	297971	Rn.16772	AI014154	4.58	4.32	5.45	4.32	4.59	4.63	1.21	down	4.90E-01	8.95E-01	-	-
1392232_at	Rps13	ribosomal protein S13	161477	Rn.198625	AI030983	2.51	3.06	2.40	2.40	2.37	2.38	1.21	down	2.55E-01	8.95E-01	-	-
1370383_s_at	RT1-Db1	RT1 class II, locus Db1	294270	Rn.33311	BI279526	8.14	6.28	3.43	7.30	4.99	6.37	1.21	up	8.68E-01	9.59E-01	-	-
1386114_at	---	---	---	Rn.217345	BF550033	2.70	3.24	2.96	2.73	2.71	2.64	1.21	down	1.60E-01	8.95E-01	-	-
1381115_at	---	---	---	---	AW536039	4.63	4.90	4.75	5.20	4.52	5.37	1.21	up	3.77E-01	8.95E-01	-	-
1392830_at	Chd1	chromodomain helicase DNA binding protein 1	308215	Rn.218360	BF396625	3.83	3.44	3.46	3.41	4.40	3.74	1.21	up	4.44E-01	8.95E-01	-	-
1367998_at	GD1563818 /// SI	similar to secretory leukocyte protease inhibitor /// secretory leukocyte peptid	296356 /// 84386	Rn.144851	NM_053372	2.41	2.72	2.41	2.41	3.55	2.40	1.21	up	5.30E-01	8.95E-01	-	-
1373899_at	RGD1309829	similar to cDNA2G6.1.1 (novel protein)	299190	Rn.98718	BI275244	6.69	7.97	8.04	7.30	7.65	8.56	1.21	up	6.64E-01	8.99E-01	-	-
1395061_at	Dpf2	D4, zinc and double PHD fingers family 2	361711	Rn.17281	BE111797	4.13	3.26	3.33	3.86	3.03	3.02	1.21	down	5.30E-01	8.95E-01	-	-
1399079_at	---	---	---	---	AI101659	9.84	9.69	9.75	9.25	9.44	9.21	1.21	down	1.64E-01	8.95E-01	-	-
1368064_a_at	Ddc	dopa decarboxylase (aromatic L-amino acid decarboxylase)	24311	Rn.11064	U31884	5.15	5.14	4.46	5.25	5.15	5.16	1.21	up	3.02E-01	8.95E-01	-	-
1389052_at	Ttc13	tetratricopeptide repeat domain 13	292095	Rn.98912	BI278584	4.81	4.81	5.97	4.51	5.10	5.17	1.21	down	5.71E-01	8.95E-01	-	-
1387995_a_at	Ifitm3	interferon induced transmembrane protein 3	361673	Rn.145191	BI285494	5.63	5.62	5.70	5.81	5.40	4.93	1.21	down	3.52E-01	8.95E-01	-	-
1384386_at	Rasa2	RAS p21 protein activator 2	25597	Rn.161946	BF287084	3.39	2.49	2.57	2.55	2.58	2.50	1.21	down	4.01E-01	8.95E-01	-	-
1387947_at	Mafb	v-maf musculoaponeurotic fibrosarcoma oncogene homolog B (avian)	54264	Rn.10725	U56241	3.16	2.45	2.51	2.42	2.46	2.43	1.21	down	3.01E-01	8.95E-01	-	-
1376130_a_at	Dtnb	dystrobrevin, beta	362715	Rn.61275	BM390663	4.82	3.91	6.55	5.95	5.55	4.59	1.21	up	7.72E-01	9.26E-01	-	-
1370367_at	Slc1a1	solute carrier family 1 (neuronal/epithelial high affinity glutamate transporter, s	25550	Rn.6384	U39555	10.03	9.89	9.91	9.67	9.68	9.66	1.21	down	3.13E-03	8.95E-01	-	-
1382111_at	Glod5	glyoxalase domain containing 5	302554	Rn.19978	AI459436	8.45	8.50	8.23	8.67	8.39	8.94	1.21	up	2.06E-01	8.95E-01	-	-
1376168_at	Tmem32	transmembrane protein 32	302864	Rn.64172	BE100946	8.74	8.50	6.95	8.73	7.61	8.67	1.21	up	7.07E-01	9.08E-01	-	-
1396031_at	---	---	---	Rn.173127	BF401497	2.90	2.90	2.91	3.69	2.89	2.94	1.21	up	3.56E-01	8.95E-01	-	-
1376966_at	---	---	---	Rn.124042	BE108930	6.09	4.91	5.02	4.80	4.79	5.61	1.21	down	5.92E-01	8.95E-01	-	-
1389222_at	LOC687992	similar to Serum amyloid A-3 protein precursor	687992	---	BI282847	3.30	3.50	3.33	3.27	3.31	2.75	1.21	down	2.28E-01	8.95E-01	-	-
1387405_at	Garnl1	GTPase activating Rap/RanGAP domain-like 1	56785	Rn.86984	NM_020083	3.05	3.22	2.94	3.48	3.45	3.08	1.21	up	1.49E-01	8.95E-01	-	-
1385924_at	---	---	---	Rn.167831	AI454060	4.42	3.13	5.44	5.69	3.71	2.79	1.21	down	8.15E-01	9.41E-01	-	-
1379076_at	---	---	---	Rn.12349	BE328961	5.57	5.25	6.27	6.31	5.93	5.67	1.21	up	4.87E-01	8.95E-01	-	-
1371715_at	MGC112883	LOC500651	500651	Rn.203250	AI012212	5.83	6.50	6.08	6.36	6.18	6.69	1.21	up	3.35E-01	8.95E-01	-	-
1383098_at	Fyttd1	forty-two-three domain containing 1	360726	Rn.13677	BG667845	4.63	4.56	5.06	4.38	4.45	4.61	1.21	down	1.89E-01	8.95E-01	-	-
1382366_at	OC685626 /// Pik3	similar to Phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic subunit alp	170911 /// 685626	Rn.190480	AI578786	6.08	5.98	6.05	5.97	6.69	6.26	1.21	up	2.71E-01	8.95E-01	-	-
1381542_at	Ubxn4	UBX domain protein 4	304766	Rn.2022	AI704885	9.34	9.25	9.45	9.67	9.29	9.89	1.21	up	2.14E-01	8.95E-01	-	-
1376550_at	---	---	---	Rn.160393	BF405084	3.34	2.51	2.57	2.56	2.60	2.45	1.21	down	3.75E-01	8.95E-01	-	-
1394989_at	---	---	---	---	BI294446	3.11	2.30	2.32	2.31	2.31	2.30	1.21	down	3.68E-01	8.95E-01	-	-
1392223_at	Epn2	epsin 2	60443	Rn.44273	AW521110	2.64	2.63	2.49	2.64	3.24	2.69	1.21	up	2.47E-01	8.95E-01	-	-
1382179_at	Rdh14	retinol dehydrogenase 14 (all-trans/9-cis/11-cis)	500629	Rn.12697	AW534743	7.08	7.02	7.30	7.24	7.54	7.43	1.21	up	9.48E-02	8.95E-01	-	-
1385097_at	Dab1	disabled homolog 1 (Drosophila)	266729	Rn.206534	AW527993	2.41	3.15	2.46	2.40	2.41	2.40	1.21	down	3.19E-01	8.95E-01	-	-
1389468_at	Rpia	ribose 5-phosphate isomerase A	362383	Rn.12446	BF393902	4.90	4.24	4.55	4.14	4.38	4.37	1.21	down	2.59E-01	8.95E-01	-	-
1390394_at	LOC500034	similar to CG3570-PA	500034	Rn.17799	AW251900	6.48	5.87	5.62	6.17	5.91	5.09	1.21	down	5.49E-01	8.95E-01	-	-
1376807_at	Rabl3	RAB, member of RAS oncogene family-like 3	360720	Rn.162058	BF417476	6.76	6.47	7.85	6.82	6.97	6.48	1.21	down	5.77E-01	8.95E-01	-	-
1373448_at	Acyp1	acylphosphatase 1, erythrocyte (common) type	299203	Rn.3465	AI413052	9.85	10.03	9.62	9.45	9.72	9.52	1.21	down	1.32E-01	8.95E-01	-	-
1371870_at	Tcf25	transcription factor 25 (basic helix-loop-helix)	292082	Rn.107920	AI169493	8.14	7.75	8.95	7.86	8.09	7.69	1.21	up	5.07E-01	8.95E-01	-	-
1381167_at	Tiam1	T-cell lymphoma invasion and metastasis 1	304109	Rn.204561	BF390767	2.66	2.48	2.60	2.80	3.16	2.58	1.21	up	1.99E-01	8.95E-01	-	-
1369703_at	Epas1	endothelial PAS domain protein 1	29452	Rn.55138	NM_023090	6.09	4.51	4.02	5.06	4.99	3.76	1.21	down	7.38E-01	9.16E-01	-	-
1391776_at	Cmc1	COX assembly mitochondrial protein homolog (S. cerevisiae)	361162	Rn.60294	BF403524	4.69	4.88	5.61	4.62	5.35	6.02	1.21	up	6.14E-01	8.95E-01	-	-
1380236_at	Itga9	integrin alpha 9	685004	Rn.198229	BM390141	7.29	6.13	4.48	6.11	6.56	6.04	1.21	up	7.62E-01	9.22E-01	-	-
1385953_at	Mllt3	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila);	114510	Rn.22828	AI454608	3.49	3.44	3.59	4.46	3.46	3.40	1.21	up	4.79E-01	8.95E-01	-	-
1391094_at	---	---	---	Rn.166703	BM387077	4.65	5.19	6.65	5.24	4.66	5.78	1.21	down	7.12E-01	9.10E-01	-	-
1374401_at	Snx2	sorting nexin 2	291464	Rn.106877	AI549249	9.21	9.19	9.07	9.37	9.62	9.29	1.21	up	6.46E-02	8.95E-01	-	-
1367963_at	Mlst8	MTOR associated protein, LST8 homolog (S. cerevisiae)	64226	Rn.9444	NM_022404	4.64	4.07	3.56	4.93	3.05	3.49	1.21	down	7.00E-01	9.07E-01	-	-
1392920_at	Eli3	Elongation factor RNA polymerase II-like 3	296102	Rn.162689	BE109672	7.32	7.18	6.99	6.35	7.06	7.28	1.21	down	4.17E-01	8.95E-01	-	-
1382125_at	07-Mar	membrane-associated ring finger (C3HC4) 7	311059	Rn.117620	AI072976	3.54	3.75	4.79	3.76	3.30	4.22	1.20	down	5.97E-01	8.95E-01	-	-
1398620_at	Samd4a	Sterile alpha motif domain containing 4A	305826	Rn.32662	BF397903	2.71	3.55	2.69	2.62	2.72	2.81	1.20	down	4.06E-01	8.95E-01	-	-
1383527_at	---	---	---	Rn.17773	BF418522	2.56	2.46	2.49	3.45	2.48	2.38	1.20	up	4.77E-01	8.95E-01	-	-
1379274_at	---	---	---	Rn.164403	AW535515	2.65	2.42	2.53	2.56	3.43	2.42	1.20	up	4.54E-01	8.95E-01	-	-
1376115_at	---	---	---	Rn.203665	AA864244	3.35	3.69	2.78	3.20	2.62	3.19	1.20	down	4.58E-01	8.95E-01	-	-
1384270_at	---	---	---	Rn.117830	BG375371	2.87	3.26	3.16	2.75	2.68	3.05	1.20	down	1.75E-01	8.95E-01	-	-
1379390_at	St6galnac2	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosami	303692	Rn.53257	AA891414	6.08	5.62	6.01	5.55	5.92	5.43	1.20	down	2.65E-01	8.95E-01	-	-
1388976_at	Bola3	bolA homolog 3 (E. coli)	297388	Rn.13809	AI178272	8.00	8.00	8.57	7.74	8.07	7.94	1.20	down	2.76E-01	8.95E-01	-	-
1381099_at	---	---	---	Rn.211784	AI236843	3.06	2.69	2.50	2.49	2.50	2.46	1.20	down	1.78E-01	8.95E-01	-	-
1386166_at	Atp6v1g3	ATPase, H+ transporting, lysosomal V1 subunit G3	289407	Rn.14800	AA892881	3.58	2.47	2.75	2.48	3.14	2.38	1.20	down	5.48E-01	8.95E-01	-	-
1374486_at	RGD1309453	Similar to hypothetical protein FLJ32884	310689	Rn.105776	AI412491	4.38	5.10	5.09	5.30	5.31	4.77	1.20	up	4.19E-01	8.95E-01	-	-
1371190_at	---	---	---	---	BG153272	11.10	10.81	11.05	11.25	11.36	11.16	1.20	up	6.27E-02	8.95E-01	-	-
1388337_at	---	---	---	Rn.7972	AA946032	6.08	5.91	5.75	6.01	6.41	6.12	1.20	up	1.55E-01	8.95E-01	-	-
1383443_at	LOC498685	similar to UPF0308 protein C9orf21	498685	Rn.24906	AI146079	7.95	7.60	8.40	7.61	8.49	8.65	1.20	up	5.39E-01	8.95E-01	-	-
1374316_at	LOC686980	similar to arsenate resistance protein 2	686980	---	AI229612	6.82	6.86	5.47	5.96	6.75	5.62	1.20	down	6.60E-01	8.98E-01	-	-
1376178_at	---	---	---	Rn.209963	BF403703	2.63	2.65	2.64	3.47	2.64	2.62	1.20	up	3.94E-01	8.95E-01	-	-
1372143_at	Ube2v2	ubiquitin-conjugating enzyme E2 variant 2	287927	Rn.3933	AA849958	6.90	7.40	7.71	6.76	7.05	7.40	1.20	down	4.23E-01	8.95E-01	-	-
1374340_at	---	---	---	Rn.17175	AA848536	4.60	5.01	5.02	3.76	5.10	4.96	1.20	down	5.80E-01	8.95E-01	-	-
1395866_at	LOC503192	Zinc finger protein ZFP	503192	Rn.69744	BF543899	5.94	5.04	4.87	4.97	5.25	4.83	1.20	down	4.91E-01	8.95E-01	-	-
1375456_at	Fam108b1	Family with sequence similarity 108, member B1	309399	Rn.7522	AI007882	2.91	4.45	2.93	3.30	2.79	3.40	1.20	down	6.48E-01	8.96E-01	-	-
1394746_at	Herc1	hect (homologous to the E6-AP (UBE3A) carboxyl terminus) domain and RCC	315771	Rn.77165	AI180352	4.85	6.00	5.47	5.45	6.21	5.46	1.20	up	5.57E-01	8.95E-01	-	-
1373302_at	Acer2	alkaline ceramidase 2	313339	Rn.6387	BM387041	3.85	3.10	3.12	3.12	3.10	3.04	1.20	down	3.42E-01	8.95E-01	-	-
1367705_at	Glrx1	glutaredoxin 1 (thioltransferase)	64045	Rn.1484	NM_022278	5.24	5.61	5.20	5.54	4.32	5.38	1.20	down	5.45E-01	8.95E-01	-	-
1384352_at	Papd4	PAP associated domain containing 4	361878	Rn.98477	AI547390	4.99	5.12	4.66	5.47	5.00	5.11	1.20	up	2.42E-01	8.95E-01	-	-
1398938_at	Acp1	acid phosphatase 1, soluble	24161	Rn.108187	AI170780	8.57	8.34	8.86	8.23	8.09	8.65	1.20	down	3.02E-01	8.95E-01	-	-
1367726_at	Thra	thyroid hormone receptor alpha	81812	Rn.11307	NM_031134	2.78	2.83	2.74	2.80	3.43	2.93	1.20	up	2.38E-01	8.95E-01	-	-
1391642_at	Zbtb39	zinc finger and BTB domain containing 39	299510	Rn.62592	AA819563	2.38	2.37	3.16	2.38	2.39	2.35	1.20	down	3.66E-01	8.95E-01	-	-
1369438_at	N5	DNA binding protein N5	64825	Rn.202953	NM_022857	3.28	3.38	2.74	3.13	2.74	2.73	1.20	down	3.25E-01	8.95E-01	-	-
1369307_at	Ep300	E1A binding protein p300	170915	Rn.12447	NM_133403	2.44	2.44	2.19	2.76	2.45	2.67	1.20	up	9.60E-02	8.95E-01	-	-
1382214_at	Nhlrc2	NHL repeat containing 2	307986	Rn.161909	AI029201	4.20	4.50	4.27	4.21	5.39	4.18	1.20	up	5.48E-01	8.95E-01	-	-
1374014_at	Nsmaf	neutral sphingomyelinase (N-SMase) activation associated factor	353233	Rn.32919	AI410079	4.44	3.86	3.40	3.39	3.48	4.03	1.20	down	4.98E-01	8.95E-01	-	-
1387644_at	Btc	betacellulin	64022	Rn.53987	NM_022256	5.38	4.13	4.38	3

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1370565_at	---	---	---	---	AF057564	4.41	4.77	5.21	4.56	4.43	4.60	1.20	down	3.28E-01	8.95E-01	-	-
1380962_at	Ace2	Angiotensin I converting enzyme (peptidyl-dipeptidase A) 2	302668	Rn.129779	BE098785	8.17	8.91	8.03	7.55	8.12	8.63	1.20	down	5.55E-01	8.95E-01	-	-
1379481_at	Pabpn1	poly(A) binding protein, nuclear 1	116697	Rn.39199	AW525583	8.51	8.28	8.17	8.10	8.17	7.89	1.20	down	1.14E-01	8.95E-01	-	-
1386976_at	Cd82	Cd82 molecule	83628	Rn.3022	NM_031797	5.67	5.42	5.37	5.47	4.83	5.36	1.20	down	2.92E-01	8.95E-01	-	-
1387048_at	Ddx39	DEAD (Asp-Glu-Ala-Asp) box polypeptide 39	89827	Rn.161716	NM_053563	3.15	4.39	2.47	3.32	2.69	3.21	1.20	down	6.77E-01	9.02E-01	-	-
1379518_at	---	---	---	Rn.203790	AI029126	7.49	7.04	6.60	7.17	6.42	6.74	1.20	down	4.75E-01	8.95E-01	-	-
1381347_at	---	---	---	Rn.203789	AI178745	2.56	2.56	2.56	2.92	2.63	2.93	1.20	up	5.55E-02	8.95E-01	-	-
1384628_at	Iyd	iodotyrosine deiodinase	308129	Rn.34836	AI549292	8.06	8.80	8.74	8.07	8.22	8.51	1.20	down	3.83E-01	8.95E-01	-	-
1394228_at	Tmigd1	transmembrane and immunoglobulin domain containing 1	363654	Rn.13478	AA893147	9.64	10.31	9.24	9.54	10.14	10.31	1.20	up	5.32E-01	8.95E-01	-	-
1377678_at	---	---	---	Rn.11630	BI283757	2.37	2.37	3.17	2.37	2.38	2.36	1.20	down	3.79E-01	8.95E-01	-	-
1373311_at	Phf3	PHD finger protein 3	363210	Rn.21075	BF405581	6.67	6.41	5.98	5.68	6.04	6.55	1.20	down	4.58E-01	8.95E-01	-	-
1373665_at	RGD1563106	similar to novel protein	303238	Rn.203763	AI588689	4.96	5.07	4.32	5.52	4.35	5.28	1.20	up	5.67E-01	8.95E-01	-	-
1374891_at	Brf2	BRF2, subunit of RNA polymerase III transcription initiation factor, BRF1-like	306542	Rn.163328	BF406144	2.47	2.45	3.50	2.44	2.45	2.72	1.20	down	4.99E-01	8.95E-01	-	-
1389415_at	Rabn1	round spermatid basic protein 1	310749	Rn.38954	BI289649	3.54	3.82	4.91	4.16	3.91	3.39	1.20	down	6.05E-01	8.95E-01	-	-
1372999_at	Dcun1d5	DCN1, defective in cullin neddylation 1, domain containing 5 (S. cerevisiae)	315405	Rn.103938	AI171216	7.22	7.97	8.37	7.43	7.38	7.95	1.20	down	5.29E-01	8.95E-01	-	-
1383110_at	Klhl24	kelch-like 24 (Drosophila)	303803	Rn.163189	BM385908	5.61	5.88	5.57	5.78	6.17	5.90	1.20	up	1.55E-01	8.95E-01	-	-
1398669_at	---	---	---	---	AA893160	2.64	2.87	2.87	3.69	2.65	2.83	1.20	up	4.65E-01	8.95E-01	-	-
1398815_at	Apeh	N-acylaminoacyl-peptide hydrolase	24206	Rn.11057	NM_012500	7.36	7.96	7.01	7.57	7.64	7.90	1.20	up	4.17E-01	8.95E-01	-	-
1387415_a_at	Stxbp5	syntaxin binding protein 5 (tomosyn)	81022	Rn.96029	AF118889	3.37	3.23	2.77	2.62	2.75	3.19	1.20	down	3.49E-01	8.95E-01	-	-
1371135_at	Xylt1	xylosyltransferase 1	64133	Rn.162460	AJ295748	3.21	2.62	2.64	2.63	2.63	2.42	1.20	down	2.68E-01	8.95E-01	-	-
1368536_at	Enpp2	ectonucleotide pyrophosphatase/phosphodiesterase 2	84050	Rn.20403	NM_057104	7.32	7.50	7.15	7.45	7.50	7.82	1.20	up	1.63E-01	8.95E-01	-	-
1375344_at	Zfp36l2	Zinc finger protein 36, C3H type-like 2	298765	Rn.22055	AF188884	3.91	4.09	4.13	3.52	3.92	3.91	1.20	down	1.45E-01	8.95E-01	-	-
1390309_a_at	---	---	---	---	BG372822	2.57	2.53	2.65	3.03	2.77	2.74	1.20	up	5.41E-02	8.95E-01	-	-
1386864_at	Pgam1	phosphoglycerate mutase 1 (brain)	24642	Rn.1383	NM_053290	11.29	11.15	11.44	11.05	10.86	11.17	1.20	down	9.36E-02	8.95E-01	-	-
1382084_at	RGD1562988	Similar to EHM2	500464	Rn.21106	AA850264	3.70	3.94	4.64	3.26	3.21	5.03	1.20	down	7.09E-01	9.09E-01	-	-
1391474_at	Med14	mediator complex subunit 14	317343	Rn.17025	AA858511	7.04	5.93	6.60	5.57	6.33	6.87	1.20	down	6.22E-01	8.95E-01	-	-
1380422_at	RGD1560686	similar to sidekick 1	304297	---	BG376951	3.18	2.41	2.44	2.41	2.43	2.39	1.20	down	3.56E-01	8.95E-01	-	-
1387513_at	Cyth3	cytohesin 3	116693	Rn.10673	NM_053912	2.36	2.35	2.37	2.36	3.17	2.35	1.20	up	3.87E-01	8.95E-01	-	-
1398363_at	Wdr54	WD repeat domain 54	500226	Rn.222011	AI178206	4.26	4.05	4.49	4.33	4.26	5.00	1.20	up	3.79E-01	8.95E-01	-	-
1381384_at	---	---	---	Rn.168043	AW530069	6.04	5.89	6.23	5.20	5.98	6.19	1.20	down	4.54E-01	8.95E-01	-	-
1397780_at	---	---	---	---	BE096283	2.33	3.10	2.35	2.33	2.34	2.32	1.20	down	3.58E-01	8.95E-01	-	-
1382219_at	RGD1307509	similar to RIKEN cDNA 1700108L22	310348	Rn.7988	AA945904	6.78	8.32	8.57	8.19	8.13	8.14	1.20	up	6.62E-01	8.98E-01	-	-
1379075_at	Mboat2	membrane bound O-acyltransferase domain containing 2	313997	Rn.35322	AI501287	4.05	2.67	2.56	3.33	2.56	2.59	1.20	down	6.50E-01	8.96E-01	-	-
1373526_at	Atg5	ATG5 autophagy related 5 homolog (S. cerevisiae)	365601	Rn.98385	AI105153	2.45	4.51	3.67	3.65	3.67	4.10	1.20	up	6.90E-01	9.05E-01	-	-
1387626_at	Dck	deoxycytidine kinase	79127	Rn.10058	NM_024158	2.35	2.55	3.55	2.55	2.56	2.55	1.20	down	5.16E-01	8.95E-01	-	-
1390091_at	RGD1565257	Similar to zinc finger protein 650	311115	Rn.16154	AI409724	2.33	2.68	2.35	2.95	2.88	2.33	1.20	up	3.07E-01	8.95E-01	-	-
1382899_at	---	---	---	Rn.161883	AI409173	2.46	3.14	2.56	2.48	2.43	2.46	1.20	down	2.83E-01	8.95E-01	-	-
1374931_at	Mrpl40	mitochondrial ribosomal protein L40	287962	Rn.3831	AA943496	2.98	4.16	4.94	3.30	4.42	3.56	1.20	down	7.10E-01	9.09E-01	-	-
1377007_at	---	---	---	Rn.165337	AI409696	3.54	4.02	4.78	3.74	3.24	4.57	1.20	down	6.45E-01	8.95E-01	-	-
1377866_a_at	Ggps1	geranylgeranyl diphosphate synthase 1	291211	Rn.54975	AI232147	5.36	5.28	4.69	5.53	5.26	5.33	1.20	up	3.04E-01	8.95E-01	-	-
1382565_at	---	---	---	Rn.207539	BE108260	2.66	2.65	2.66	2.88	3.36	2.52	1.20	up	3.38E-01	8.95E-01	-	-
1389615_at	Derl1	Der1-like domain family, member 1	362912	Rn.110990	BI284801	6.84	6.89	7.16	6.99	7.07	7.62	1.20	up	2.97E-01	8.95E-01	-	-
1383310_at	---	---	---	Rn.165414	AI030892	6.11	6.14	6.92	6.21	5.49	6.68	1.20	down	5.77E-01	8.95E-01	-	-
1387367_at	Glg1	golgi apparatus protein 1	29476	Rn.89086	NM_017211	3.08	4.75	6.50	4.86	3.96	4.71	1.20	down	8.09E-01	9.38E-01	-	-
1385227_at	Trps1	trichorhinophalangeal syndrome I homolog (human)	299897	Rn.164578	BF398245	7.73	6.88	7.13	7.15	6.69	7.10	1.20	down	4.18E-01	8.95E-01	-	-
1372081_at	---	---	---	Rn.220292	BI299305	3.52	3.22	3.00	3.50	3.64	3.39	1.20	up	1.91E-01	8.95E-01	-	-
1378616_a_at	Osbp	oxysterol binding protein	365410	Rn.107910	AI175488	2.60	3.35	2.96	3.70	2.62	3.38	1.20	up	5.33E-01	8.95E-01	-	-
1394283_at	---	---	---	Rn.191093	AW144132	6.75	6.52	6.67	6.70	7.78	8.25	1.20	up	5.95E-01	8.95E-01	-	-
1374668_at	Sf3a1	splicing factor 3a, subunit 1	305479	Rn.114913	AI230180	4.01	3.85	4.24	3.82	3.64	3.84	1.20	down	1.13E-01	8.95E-01	-	-
1384795_at	Zfml	zinc finger, matrin-like	312491	Rn.15272	BE116205	6.17	5.77	5.24	6.04	6.00	5.93	1.20	up	3.87E-01	8.95E-01	-	-
1373234_at	---	---	---	Rn.34796	BI277492	6.48	6.86	6.28	6.59	5.94	6.30	1.20	down	3.58E-01	8.95E-01	-	-
1373003_at	Sart3	squamous cell carcinoma antigen recognized by T-cells 3	304582	Rn.101480	BF414266	7.18	7.13	6.59	6.55	6.97	6.59	1.20	down	3.18E-01	8.95E-01	-	-
1392238_at	---	---	---	Rn.166611	AI112241	2.48	2.47	2.67	2.82	2.76	2.84	1.20	up	1.67E-02	8.95E-01	-	-
1395850_at	Pus3	pseudouridylate synthase 3	315554	Rn.22763	AA894165	5.30	5.40	5.22	5.21	5.89	5.61	1.20	up	2.66E-01	8.95E-01	-	-
1371239_s_at	Tpm3	tropomyosin 3, gamma	117557	Rn.37575	AF053361	10.33	10.59	10.82	11.03	10.64	10.89	1.20	up	2.06E-01	8.95E-01	-	-
1375088_at	---	---	---	Rn.154299	BF404846	4.40	2.56	2.88	2.98	2.70	3.36	1.20	down	6.83E-01	9.03E-01	-	-
1390442_at	Urb2	URB2 ribosome biogenesis 2 homolog (S. cerevisiae)	292087	Rn.6429	BF284171	3.53	3.80	4.36	3.32	4.07	3.52	1.20	down	4.71E-01	8.95E-01	-	-
1373080_at	Papola	poly (A) polymerase alpha	314417	Rn.3455	BI284622	7.88	7.44	7.46	7.87	8.06	7.64	1.20	up	2.31E-01	8.95E-01	-	-
1375986_at	LOC680262	hypothetical protein LOC680262	680262	Rn.144586	AW914928	3.52	2.81	2.47	2.46	3.34	3.79	1.20	up	6.25E-01	8.95E-01	-	-
1380544_at	---	---	---	Rn.222034	BF396688	4.53	6.17	7.89	7.33	4.58	5.89	1.20	down	8.44E-01	9.51E-01	-	-
1377741_at	---	---	---	Rn.129730	BF389042	6.65	6.21	5.63	5.80	6.84	6.64	1.20	up	5.76E-01	8.95E-01	-	-
1377037_at	Acot4	acyl-CoA thioesterase 4	681337	Rn.203185	AI411493	5.67	5.67	7.13	4.80	6.50	6.28	1.20	down	7.38E-01	9.16E-01	-	-
1381919_at	Hps6	Hermansky-Pudlak syndrome 6	309446	Rn.69203	BI290986	7.27	6.31	3.71	5.61	4.49	6.40	1.20	down	8.37E-01	9.49E-01	-	-
1393225_at	LOC314655	Similar to a disintegrin-like and metalloprotease (reprolysin type) with thrombo	314655	Rn.135600	BE115446	2.49	2.57	2.74	3.36	2.70	2.52	1.20	up	3.78E-01	8.95E-01	-	-
1390517_at	---	---	---	Rn.94086	BM392260	3.52	3.54	3.56	4.06	3.37	3.99	1.20	up	2.96E-01	8.95E-01	-	-
1368079_at	Pdk1	pyruvate dehydrogenase kinase, isozyme 1	116551	Rn.11185	NM_053826	3.30	3.68	2.57	3.29	3.31	3.74	1.20	up	5.02E-01	8.95E-01	-	-
1374073_at	Slc46a1	solute carrier family 46, member 1	303333	Rn.153975	BI285135	2.30	2.29	2.31	2.34	2.32	3.03	1.20	up	3.21E-01	8.95E-01	-	-
1385059_at	Znf655	zinc finger protein 655	360764	Rn.6840	AI136696	2.88	2.86	2.43	3.29	2.66	3.01	1.20	up	3.22E-01	8.95E-01	-	-
1397228_at	---	---	---	Rn.204790	AI103063	2.74	2.65	3.47	2.69	2.70	2.67	1.20	down	3.65E-01	8.95E-01	-	-
1379367_at	RGD1308251	similar to RIKEN cDNA 2810405K02	362676	Rn.27527	BF388220	6.44	6.01	6.33	6.69	6.53	6.36	1.20	up	1.75E-01	8.95E-01	-	-
1395549_at	Saps2	SAPS domain family, member 2	300146	Rn.135331	BF402983	2.42	2.78	2.43	2.42	3.59	2.40	1.20	up	5.57E-01	8.95E-01	-	-
1390160_at	---	---	---	Rn.156118	AW534222	2.30	2.30	2.31	2.30	3.11	2.29	1.20	up	3.86E-01	8.95E-01	-	-
1384431_at	---	---	---	Rn.204230	AI070150	5.91	5.89	5.51	5.89	6.28	5.93	1.20	up	2.12E-01	8.95E-01	-	-
1379597_at	---	---	---	Rn.199253	AI011037	3.01	3.14	3.44	3.95	3.23	3.20	1.20	up	3.94E-01	8.95E-01	-	-
1398487_at	Pbx1	pre-B-cell leukemia homeobox 1	304947	Rn.205189	BF419639	7.09	7.01	7.02	7.09	7.82	7.01	1.20	up	3.66E-01	8.95E-01	-	-
1371605_at	Ndufa12	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 12	299739	Rn.86466	AI710281	10.70	9.93	10.68	9.97	10.48	10.08	1.20	down	4.28E-01	8.95E-01	-	-
1372797_at	Pqbp1	polyglutamine binding protein 1	302557	Rn.11769	BM383862	7.72	8.04	8.01	8.45	8.00	8.11	1.20	up	1.95E-01	8.95E-01	-	-
1392023_at	---	---	---	Rn.207129	AW434002	2.45	2.46	3.26	2.44	2.48	2.46	1.20	down	3.83E-01	8.95E-01	-	-
1384364_at	Fbxo4	F-box protein 4	310363	Rn.45165	AW521356	4.82	6.29	5.54	6.42	4.58	6.44	1.20	up	7.43E-01	9.17E-01	-	-
1393334_at	---	---	---	Rn.17664	AW528448	2.52	2.74	2.69	3.51	2.52	2.71	1.20	up	4.45E-01	8.95E-01	-	-
1390722_at	---	---	---	---	AW531272	8.39	9.03	9.28	8.97	9.06	9.46	1.20	up	4.36E-01	8.95E-01	-	-
1397551_at	Ddx27	DEAD (Asp-Glu-Ala-Asp) box polypeptide 27	362274	Rn.206923	BG373974	4.80	6.89	8.01	6.62	6.76	7.11	1.20	up	7.96E-01	9.34E-01	-	-
1397956_at	RGD1311273	Similar to RIKEN cDNA 9530058B02	685545	Rn.106191	AI703949	2.35	3.21	2.35	2.45	2.34	2.33	1.20	down	4.18E-01	8.95E-01	-	-
1383463_at	Zfp91	Zinc finger protein 91	246282	Rn.1772	AW918514	5.75	5.59	5.70	4.55	5.62	6.08	1.20	down	5.94E-01	8.95E-01	-	-
1399135_at	Rpap3	RNA polymerase II associated protein 3	300189	Rn.49051	BI290646	8.05	8.91	8.93	8.60	8.14	8.37	1.20	down	4.58E-01	8.95E-01	-	-
1390659_at	---	---	---	Rn.167124	BI302830	2.51	2.51	2.54	2.56	2.93	2.87	1.20	up	8.70E-02	8.95E-01	-	-
1382829_at	---	---	---	Rn.23530	AI137187	2.65	2.79	4.28	3.68	2.58	4.25	1.20	up	7.32E-01	9.14E-01	-	-
1370220_at	Scpep1	serine carboxypeptidase 1	114861	Rn.2108	BI283159	8.71	7.82	8.29	7.84	8.38	7.81	1.20	down	4.57E-01	8.95E-01	-	-
1376869_at	---	---	---	Rn.53972	BE108193	5.60	5.75	5.89	5.54	5.35	5.55	1.20	down	7.12E-02	8.95E-01	-	-
1398641_at	Plekha3	pleckstrin homology domain-containing, family A (phosphoinositide binding sp	295674	Rn.204132	AI058924	3.63	3.85	5.00	3.76	3.56	4.37	1.20	down	6.20E-01	8.95E-01	-	-
1373253_at	Acbd4	acyl-Coenzyme A binding domain containing 4	303577	Rn.18284	BE111646	12.09	11.53	11.79	11.98	10.88	11.76	1.20	down	5.22E-01	8.95E-01	-	-
1377757_at	Shprh	SNF2 histone linker PHD RING helicase	308282	Rn.2515	AA858978	3.62	3.82	3.85	3.41	3.42	3.67	1.20	down	8.01E-02	8.95E-01	-	-
1376802_at	Tchp	trichoplein, keratin filament binding	304547	Rn.19337	AW915558	4.97	4.70	2.86	4.48	4.90	3.94	1.20	up	7.34E-01	9.15E-01	-	-
1380719_at	---	---	---	Rn.58552	BF396220	3.88	3.16	3.22	3.17	3.07	3.24	1.20	down	3.29E-01	8.95E-01	-	-
1379555_at	---	---	---	Rn.49292	AI233902	7.53	7.37	6.98	7.35	7.41	7.91	1.20	up	3.37E-01	8.95E-01	-	-
1367506_at	mrpl11	mitochondrial ribosomal protein L11	293666	Rn.3762	BF283488	8.63	8.79	9.11	8.34	8.53	8.87	1.20	down	2.81E-01	8.95E-01	-	-
1370237_at	Hadh	hydroxyacyl-Coenzyme A dehydrogenase	113965	Rn.92789	AA799574	9.04	8.89	8.72	8.55	8.66	8.66	1.20	down	5.51E-02	8.95E-01	-	-
1389907_at	Zbtb8os	zinc finger and BTB domain containing 8 opposite strand	297885	---	AI169317	9.27	9.49	9.52	8.89	9.07	9.54	1.20	down	2.77E-01	8.95E-01	-	-
1399048_at	Carm1	coactivator-associated arginine methyltransferase 1	363026	Rn.219328	BI274121	3.94	3.28	3.10	3.59	3.09	4.42	1.20	up	6.03E-01	8.95E-01	-	-
1377157_at	RGD1309747	similar to KIAA0947 protein	306965	Rn.137376	BI273812	2.62	3.35	2.63	3.58	2.82	2.99	1.20	up	4.76E-01	8.95E-01	-	-
1373214_at	Kdelc1	KDEL (Lys-Asp-Glu-Leu) containing 1	316370	Rn.7848	AA945238	3.91	4.40	3.26	4.11	3.92	4.33	1.20	up	4.97E-01	8.95E-01	-	-
1379259_at	---	---	---	Rn.146603	AW534671	2.52	2.60	2.60	2.76	3.02	2.73	1.20	up	5.41E-02	8.95E-01	-	-
1381344_at	---	---	---	Rn.147544	BF394536	3.28	3.18	3.24	3.11	2.41	3.40	1.20	down	4.26E-01	8.95E-01	-	-
1383043_at	Sfrs2ip	Splicing factor, arginine/serine-rich 2, interacting protein	312030	Rn.199124	AA955140	4.68	6.50	5.86	5.88	5.73	6.22	1.20	up	6.60E-01	8.98E-01	-	-
1377742_at	LOC366300	hypothetical LOC366300	366300	Rn.203101	AI170706	6.14	6.30	6.55	6.01	6.06	6.14	1.20	down	1.01E-01	8.95E-01	-	-
1384107_at	---	---	---	Rn.20525	AI071397	6.04	5.37	5.84	5.30	5.67	5.50	1.20	down	3.11E-01	8.95E-01	-	-
1388036_a_at	Mll4	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila);	26955	Rn.58	U83231	8.23	8.06	7.35	8.27	7.65	6.93	1.20	down	6.10E-01	8.95E-01	-	-
1384376_at	---	---	---	Rn.25329	AA818641	4.74	3.49	3.72	4.54	3.16	3.46	1.20	down	6.69E-01	9.00E-01	-	-
1387453_at	Zbtb10	zinc finger and BTB domain containing 10	80338	Rn.162568	NM_024489	5.56	5.31	5.00	5.54	5.24	5.87	1.20	up	3.40E-01	8.95E-01	-	-
1383924_at	LOC688765	hypothetical protein LOC688765	688765	Rn.54726	BF397684	2.77	3.21	2.25	2.41	3.18	3.43	1.20	up	5.61E-01	8.95E-01	-	-
1395212_at	---	---	---	Rn.156727	BE105805	3.52	2.52	2.48	2.48	2.56	2.69	1.20	down	4.90E-01	8.95E-01	-	-
1384934_at	Slc41a2	Solute carrier family 41, member 2	362861	Rn.7329	AA893454	3.27	3.13	2.40	2.45	2.39	3.18	1.20	down	5.21E-01	8.95E-01	-	-
1389873_at	Pycard	PYD and CARD domain containing	282817	Rn.7817	BI282953	5.02	4.34	3.91	4.43	5.48	4.15	1.20	up	6.40E-01	8.95E-01	-	-
1371928_at	Cdca8	cell division cycle associated 8	500545	Rn.14970	BG380355	5.36	4.58	4.59	4.59	4.59	4.58	1.20	down	3.69E-01	8.95E-01	-	-
1370356_at	Rbm10	RNA binding motif protein 10	64510	Rn.8822	DB3948	7.60	6.37	6.67	6.66	6.67	6.53	1.20	down	5.22E-01	8.95E-01	-	-
1393371_at	---	---	---	Rn.176450	BG378781	2.84	2.83	2.81	3.40	3.05	2.82	1.20	up	1.98E-01	8.95E-01	-	-
1395343_at	Tm9sf3	transmembrane 9 superfamily member 3	309475	Rn.17150	BF545305	7.51	7.72	8.20	7.91	7.95	8.36	1.20	up	3.55E-01	8.95E-01	-	-
1373019_at	---	---	---	Rn.22316	AI172468	7.58	7.94	7.23	7.16	6.73	8.06	1.20	down	5.87E-01	8.95E-01	-	-
1389880_at	Foxk2	Forkhead box K2	303753	Rn.44253	AW525701	4.63	4.93	3.34	4.00	4.24	3.88	1.20	down	6.29E-01	8.95E-01	-	-
1378063_at	---	---	---	Rn.147728	AW524795	2.27	2.26	3.05	2.27	2.27	2.26	1.20	down	3.71E-01	8.95E-01	-	-
1396286_at	---	---	---	Rn.207519	BG372956	5.51	5.59	4.81	5.50	5.48	5.70	1.20	up	3.68E-01	8.95E-01	-	-
1391902_at	---	---	---	Rn.206411	AW527377	2.60	3.35	2.60	2.56	2.65	2.56	1.20	down	3.56E-01	8.95E-01	-	-
1389616_at	---	---	---	Rn.203217	BF403163	3.83	3.86	3.92	4.75	4.04	3.61	1.20	up	4.77E-01	8.95E-01	-	-
1388933_at	Lama5	laminin, alpha 5	140433	Rn.62612	BI274917	7.53	6.55	3.60	7.03	4.95	6.48	1.20	up	6.55E-01	8.95E-01	-	-
1380545_at	Asap1	ArfGAP with SH3 domain, ankyrin repeat and PH domain 1	314961	Rn.63466	BF419027	2.44	2.39	3.28	2.40	2.55	2.38	1.20	down	4.26E-01	8.95E-01	-	-
1388779_at	Zfp180	zinc finger protein 180	246279	Rn.14669	BG381516	6.59	6.43	5.50	6.35	6.36	6.61	1.20	up	4.97E-01	8.95E-01	-	-
1373784_at	Cct8	chaperonin containing Tcp1, subunit 8 (theta)	288305	Rn.98524	BF406759	5.06	4.68	4.37	3.80	4.70	4.83	1.20	down	5.29E-01	8.95E-01	-	-
1373337_at	Grhpr	glyoxylate reductase/hydroxypyruvate reductase	680021	Rn.7815	AI412065	11.89	11.72	11.44	11.96	11.80	12.08	1.20	up	1.67E-01	8.95E-01	-	-
1371661_at	Mrps23	mitochondrial ribosomal protein S23	360594	Rn.198893	AI411153	7.19	7.08	6.78	7.20	7.30	7.33	1.20	up	1.14E-01	8.95E-01	-	-
1389451_at	Gpr172b	G protein-coupled receptor 172B	362942	Rn.29304	AI179502	2.79	3.04	2.92	3.48	2.86	3.20	1.20	up	2.44E-01	8.95E-01	-	-
1390352_at	Pcgf1	polycomb group ring finger 1	312480	Rn.203514	AA926371	6.48	6.15	5.49	5.38	5.92	6.04	1.20	down	5.03E-01	8.95E-01	-	-
1386916_at	Aco1	aconitase 1, soluble	50655	Rn.35934	NM_017321	9.03	9.46	9.03	8.90	8.75	9.09	1.20	down	2.07E-01	8.95E-01	-	-
1374662_at	Slc35a1	solute carrier family 35 (CMP-sialic acid transporter), member A1	313139	Rn.24337	AA891848	8.53	8.96	9.57	8.24	8.66	9.37	1.20	down	5.90E-01	8.95E-01	-	-
1367612_at	Mgst1	microsomal glutathione S-transferase 1	171341	Rn.2583	NM_134349	11.06	10.90	11.28	11.29	11.18	11.56	1.20	up	1.78E-01	8.95E-01	-	-
1369040_at	Cdc42bpa	CDC42 binding protein kinase alpha	114116	Rn.10871	NM_053657	2.73	2.82	2.42	2.40	2.40	2.39	1.20	down	1.04E-01	8.95E-01	-	-
1392788_at	---	---	---	Rn.165858	AA944323	2.55	2.62	2.51	2.76	2.93	2.77	1.20	up	1.41E-02	8.95E-01	-	-
1382061_at	Ldhd	lactate dehydrogenase D	307858	Rn.204989	AI501131	9.84	10.82	10.76	10.45	10.53	11.21	1.20	up	5.51E-01	8.95E-01	-	-
1377018_at	---	---	---	Rn.33642	BF284124	7.95	8.09	7.02	7.66	7.02	7.60	1.20	down	5.46E-01	8.95E-01	-	-
1371296_at	Sdhd	succinate dehydrogenase complex, subunit D, integral membrane protein	363061	Rn.3040	AI176608	9.18	10.02	9.78	9.58	9.16	9.47	1.20	down	4.02E-01	8.95E-01	-	-
1373455_at	Paf1	Paf1, RNA polymerase II associated factor, homolog (S. cerevisiae)	361531	Rn.161558	BE115648	9.31	9.24	8.83	9.21	8.30	9.09	1.20	down	4.63E-01	8.95E-01	-	-
1372791_at	Wnk1	WNK lysine deficient protein kinase 1	116477

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1371039_at	Cacnb4	calcium channel, voltage-dependent, beta 4 subunit	58942	Rn.9863	L02315	4.25	4.26	3.91	3.28	3.29	5.08	1.20	down	6.94E-01	9.06E-01	-	-
1388947_at	Eif5b	eukaryotic translation initiation factor 5B	308306	Rn.107482	BI291654	6.81	7.97	7.29	7.24	6.25	7.80	1.20	down	6.71E-01	9.00E-01	-	-
1371584_at	Tpo4ap	transient receptor potential cation channel, subfamily C, member 4 associated	362247	Rn.100109	BM390843	4.54	4.89	4.86	4.67	4.89	3.95	1.20	down	4.43E-01	8.95E-01	-	-
1372916_at	Mrps27	mitochondrial ribosomal protein S27	361883	Rn.203126	BI295139	5.40	4.23	4.28	5.09	4.92	4.67	1.20	up	5.56E-01	8.95E-01	-	-
1370567_at	Adra2b	adrenergic, alpha-2B-, receptor	24174	Rn.10296	M32061	5.97	5.90	5.93	5.49	5.63	5.91	1.20	down	1.08E-01	8.95E-01	-	-
1384141_at	Zfp84	zinc finger protein 84	308482	Rn.203644	BI289930	6.35	6.63	5.57	6.96	5.72	6.64	1.20	up	6.24E-01	8.95E-01	-	-
1375929_at	Mrlr	max binding protein	287521	Rn.30696	BI289109	5.38	5.72	5.28	6.29	5.22	5.63	1.20	up	4.88E-01	8.95E-01	-	-
1390053_at	LOC684996	similar to chromosome 7 open reading frame 11	684996	Rn.30	BE099903	2.40	3.58	2.40	2.39	2.40	2.82	1.20	down	5.71E-01	8.95E-01	-	-
1396845_at	Fbxl20	F-box and leucine-rich repeat protein 20	64039	Rn.18281	AW526217	2.38	3.29	2.40	2.39	2.54	2.37	1.20	down	4.46E-01	8.95E-01	-	-
1381508_at	---	---	---	Rn.49769	BE098143	2.65	2.64	3.45	2.65	2.67	2.66	1.20	down	3.92E-01	8.95E-01	-	-
1376025_at	Prmt2	protein arginine methyltransferase 2	499420	Rn.145566	BG670963	2.44	2.45	3.25	2.45	2.46	2.45	1.20	down	3.89E-01	8.95E-01	-	-
1369757_at	Itpkb	inositol 1,4,5-trisphosphate 3-kinase B	54260	Rn.22498	NM_019312	2.44	2.43	2.45	2.43	3.24	2.43	1.20	up	3.93E-01	8.95E-01	-	-
1369626_at	Ide	insulin degrading enzyme	25700	Rn.45029	BI291249	4.97	4.96	4.58	5.33	4.99	4.95	1.20	up	2.15E-01	8.95E-01	-	-
1382935_at	RGD7735029	SEL1 domain containing protein RGD735029	307480	Rn.12899	BE113823	8.86	8.64	8.59	8.70	8.36	8.25	1.20	down	1.79E-01	8.95E-01	-	-
1374702_at	---	---	---	Rn.12186	BI291393	7.20	7.36	7.14	7.08	7.58	7.82	1.20	up	3.20E-01	8.95E-01	-	-
1389317_at	Tmem127	transmembrane protein 127	311405	Rn.19881	BF417627	5.60	5.80	5.30	5.50	4.49	5.94	1.20	down	6.01E-01	8.95E-01	-	-
1397206_at	---	---	---	Rn.149155	AI548120	3.69	4.50	4.41	5.01	4.46	3.90	1.20	up	5.64E-01	8.95E-01	-	-
1372200_at	Gpsm3	G-protein signaling modulator 3 (AGS3-like, C. elegans)	406163	Rn.7475	BI273727	3.17	2.67	2.45	3.69	2.72	2.66	1.20	up	5.51E-01	8.95E-01	-	-
1372949_at	11-Sep	Septin 11	305227	Rn.27798	BG663067	7.44	6.78	6.90	7.37	7.29	7.24	1.20	up	2.79E-01	8.95E-01	-	-
1382365_at	Nlk	Nemo like kinase	497961	Rn.113514	AA997745	5.01	5.91	6.57	6.06	5.91	6.30	1.20	up	6.11E-01	8.95E-01	-	-
1385671_at	---	---	---	Rn.199202	AA956689	4.47	4.46	3.52	4.46	4.51	4.65	1.20	up	2.44E-01	8.95E-01	-	-
1392149_at	---	---	---	Rn.165448	AA997766	9.55	9.68	9.26	9.45	9.74	10.07	1.20	up	3.02E-01	8.95E-01	-	-
1395026_at	Fmo4	flavin containing monooxygenase 4	246247	Rn.216582	BI293319	8.45	8.67	8.18	7.95	8.29	8.30	1.20	down	2.30E-01	8.95E-01	-	-
1372741_at	Sccpdh	saccharopine dehydrogenase (putative)	305021	Rn.23989	AI412013	7.71	8.25	8.06	7.54	7.79	7.92	1.20	down	2.58E-01	8.95E-01	-	-
1393061_at	Ttc36	tetratricopeptide repeat domain 36	300676	Rn.107180	AI030103	6.42	7.48	7.17	6.98	6.69	6.63	1.20	down	4.82E-01	8.95E-01	-	-
1380932_at	---	---	---	Rn.155230	BG373573	3.23	3.19	2.60	3.21	2.50	2.54	1.20	down	4.49E-01	8.95E-01	-	-
1372487_at	Fam104a	family with sequence similarity 104, member A	619573	Rn.98587	BI296006	5.78	5.06	4.87	4.81	4.90	5.23	1.20	down	4.47E-01	8.95E-01	-	-
1395226_at	Aftph	aftiphilin	305544	Rn.105388	BI274777	6.13	5.93	4.49	5.49	5.62	6.20	1.20	up	6.70E-01	9.00E-01	-	-
1371707_at	Tnpo2	transportin 2 (importin 3, karyopherin beta 2b)	304670	Rn.222029	AI235431	6.72	5.97	5.93	6.42	6.65	6.33	1.20	up	4.03E-01	8.95E-01	-	-
1373331_at	Lrsam1	leucine rich repeat and sterile alpha motif containing 1	311866	Rn.61607	BM383310	3.34	2.60	2.62	2.59	2.61	2.58	1.20	down	3.53E-01	8.95E-01	-	-
1367911_at	Idh3a	isocitrate dehydrogenase 3 (NAD+) alpha	114996	Rn.95104	NM_053638	6.54	5.98	6.81	6.61	6.99	6.51	1.20	up	4.18E-01	8.95E-01	-	-
1388690_at	Brms1l	breast cancer metastasis-suppressor 1-like	299053	Rn.95406	AI105439	3.86	4.17	3.96	3.72	5.03	4.02	1.20	up	5.62E-01	8.95E-01	-	-
1388961_at	Itgb1bp2	integrin beta 1 binding protein 2	317258	Rn.39792	BF407194	2.48	2.48	2.51	2.51	3.26	2.47	1.20	up	3.76E-01	8.95E-01	-	-
1389422_at	---	---	---	Rn.124369	AI180400	7.98	8.93	9.13	8.54	8.95	9.32	1.19	up	5.73E-01	8.95E-01	-	-
1367455_at	Vcp	valosin-containing protein	116643	Rn.98891	NM_053864	9.60	10.18	9.74	9.36	9.19	10.21	1.19	down	5.15E-01	8.95E-01	-	-
1373594_at	---	---	---	Rn.22692	BE097279	2.37	2.32	3.16	2.44	2.32	2.31	1.19	down	4.07E-01	8.95E-01	-	-
1389091_at	Usp3	ubiquitin specific peptidase 3	363084	Rn.16420	AI411205	4.61	4.70	5.41	5.23	5.09	5.17	1.19	up	3.71E-01	8.95E-01	-	-
1380455_at	---	---	---	Rn.29821	BM389422	2.43	3.22	2.44	2.45	2.43	2.43	1.19	down	3.81E-01	8.95E-01	-	-
1392246_at	---	---	---	Rn.164046	AA900645	4.42	3.52	4.35	4.11	4.30	4.65	1.19	up	4.78E-01	8.95E-01	-	-
1390125_at	Tm9sf1	transmembrane 9 superfamily member 1	361043	Rn.12071	BE098998	4.34	5.42	4.90	4.65	3.77	5.47	1.19	down	6.82E-01	9.03E-01	-	-
1380009_at	Vrk1	vaccinia related kinase 1	362779	Rn.92083	BM392230	3.81	4.22	4.26	4.69	4.37	4.00	1.19	up	3.55E-01	8.95E-01	-	-
1384542_at	---	---	---	Rn.148318	BE103021	6.49	5.43	5.36	4.81	5.90	5.79	1.19	down	6.37E-01	8.95E-01	-	-
1384508_at	---	---	---	Rn.202662	AI576469	5.63	4.79	5.66	5.76	5.44	5.66	1.19	up	4.40E-01	8.95E-01	-	-
1378275_at	Upf3a	UPF3 regulator of nonsense transcripts homolog A (yeast)	361176	Rn.56460	BG377170	7.09	7.07	6.25	6.97	6.04	6.64	1.19	down	5.45E-01	8.95E-01	-	-
1390509_a_at	Mrpl51	mitochondrial ribosomal protein L51	297601	Rn.154504	BI294880	8.24	7.85	7.11	7.65	6.87	7.92	1.19	down	6.06E-01	8.95E-01	-	-
1378020_at	---	---	---	Rn.13852	AI060205	6.57	5.88	6.12	6.61	6.22	6.51	1.19	up	3.33E-01	8.95E-01	-	-
1389596_at	Cox18	COX18 cytochrome c oxidase assembly homolog (S. cerevisiae)	289522	Rn.24568	BM389642	5.76	5.67	4.87	5.56	5.27	6.23	1.19	up	5.56E-01	8.95E-01	-	-
1394900_at	---	---	---	Rn.161123	BF413876	2.93	3.26	2.73	4.30	2.75	2.64	1.19	up	6.69E-01	9.00E-01	-	-
1388877_at	Mrps5	mitochondrial ribosomal protein S5	296134	Rn.9035	BM386940	5.06	4.85	5.10	5.53	4.87	5.39	1.19	up	2.99E-01	8.95E-01	-	-
1398040_at	---	---	---	Rn.79834	BI300326	2.67	3.08	2.52	2.50	2.56	2.45	1.19	down	2.10E-01	8.95E-01	-	-
1385166_at	---	---	---	Rn.200081	BF398185	3.88	3.50	5.56	4.96	3.47	3.75	1.19	down	7.56E-01	9.21E-01	-	-
1375336_at	Hsp90ab1	heat shock protein 90kDa alpha (cytosolic), class B member 1	301252	Rn.98667	AI237389	11.66	11.93	11.69	11.61	11.41	11.49	1.19	down	6.70E-02	8.95E-01	-	-
1388058_at	Taf6	TAF6 RNA polymerase II, TATA box binding protein (TBP)-associated factor	288533	Rn.102447	D49446	2.63	2.47	2.71	3.28	2.66	2.64	1.19	up	3.14E-01	8.95E-01	-	-
1381847_at	RGD1561413	Similar to BC021442 protein	500585	Rn.162129	AI137632	2.72	2.99	3.01	2.98	3.04	3.48	1.19	up	2.35E-01	8.95E-01	-	-
1367544_at	Rnf111	ring finger protein 111	300813	Rn.82537	BE120556	5.54	4.99	5.27	4.51	5.35	5.16	1.19	down	4.42E-01	8.95E-01	-	-
1377457_a_at	Sorl1	sortilin-related receptor, LDLR class A repeats-containing	300652	Rn.92871	AA850618	8.24	6.97	5.68	7.99	6.67	7.00	1.19	up	7.76E-01	9.27E-01	-	-
1386057_at	---	---	---	Rn.98448	BF289233	2.72	2.67	2.80	3.82	2.73	2.40	1.19	up	5.84E-01	8.95E-01	-	-
1391915_at	LOC295778 /// LO	heat shock protein 9 /// similar to Stress-70 protein, mitochondrial precursor (371 /// 295778 /// 50		Rn.7535	BE120145	3.46	2.55	2.64	2.68	2.63	2.57	1.19	down	4.31E-01	8.95E-01	-	-
1371949_at	Bzw1	basic leucine zipper and W2 domains 1	363232	Rn.96215	AI229287	8.28	8.15	8.06	7.74	7.80	8.18	1.19	down	1.72E-01	8.95E-01	-	-
1388332_at	Rac1	Ras-related C3 botulinum toxin substrate 1	363875	Rn.29157	AA799542	9.75	10.02	9.74	10.42	9.98	9.87	1.19	up	2.50E-01	8.95E-01	-	-
1374500_at	Prpf38b	PRP38 pre-mRNA processing factor 38 (yeast) domain containing B	499691	Rn.7210	AI011571	4.96	5.36	6.30	5.58	5.19	5.09	1.19	down	5.81E-01	8.95E-01	-	-
1378665_at	---	---	---	Rn.33908	AA818867	2.99	3.09	4.76	2.87	2.90	4.30	1.19	down	7.48E-01	9.18E-01	-	-
1384135_at	---	---	---	Rn.165616	AI575629	3.38	3.51	2.67	4.04	2.81	3.48	1.19	up	5.93E-01	8.95E-01	-	-
1375266_at	---	---	---	Rn.163726	BG380633	3.35	3.73	3.53	3.28	4.03	2.52	1.19	down	5.98E-01	8.95E-01	-	-
1393869_at	---	---	---	---	AA859589	2.43	2.43	2.45	3.22	2.44	2.42	1.19	up	3.87E-01	8.95E-01	-	-
1367828_at	Acads	acyl-Coenzyme A dehydrogenase, C-2 to C-3 short chain	64304	Rn.1167	NM_022512	6.36	6.28	6.34	6.41	5.47	6.33	1.19	down	4.41E-01	8.95E-01	-	-
1389767_at	RGD1304924	similar to hypothetical protein FLJ31364	302982	Rn.34400	BE115349	4.90	3.81	4.00	4.20	3.63	4.11	1.19	down	5.37E-01	8.95E-01	-	-
1376464_at	---	---	---	Rn.167440	BE102505	3.45	2.92	2.96	3.03	2.70	2.84	1.19	down	2.63E-01	8.95E-01	-	-
1378519_at	---	---	---	Rn.210193	BF398120	2.64	2.52	2.42	2.87	2.67	2.81	1.19	up	4.12E-02	8.95E-01	-	-
1369255_at	Il1r1	interleukin 1 receptor, type I	25663	Rn.9758	NM_013123	2.39	3.03	2.34	2.33	2.34	2.33	1.19	down	3.12E-01	8.95E-01	-	-
1388843_at	---	---	---	Rn.205072	BI296771	8.18	7.49	7.75	7.52	7.56	7.57	1.19	down	2.77E-01	8.95E-01	-	-
1394931_at	Mbnl2	muscleblind-like 2	680445	Rn.1940	AI180361	7.88	7.17	6.96	7.38	7.54	7.85	1.19	up	4.56E-01	8.95E-01	-	-
1378114_at	---	---	---	Rn.209761	BF415965	2.39	3.20	2.40	2.45	2.40	2.38	1.19	down	3.95E-01	8.95E-01	-	-
1374294_at	Srcap	Snf2-related CREBBP activator protein	361652	Rn.62858	AW534851	3.17	3.23	2.51	3.19	3.30	3.19	1.19	up	3.35E-01	8.95E-01	-	-
1377209_at	Klhl25	kelch-like 25 (Drosophila)	293023	Rn.16545	BI283664	5.63	5.58	6.37	5.74	5.79	5.27	1.19	down	4.48E-01	8.95E-01	-	-
1392989_at	---	---	---	Rn.25467	BI295986	7.71	8.06	7.91	8.01	8.19	8.25	1.19	up	1.11E-01	8.95E-01	-	-
1388754_at	---	---	---	Rn.202341	AI176839	10.03	9.57	9.93	9.97	9.91	10.42	1.19	up	2.96E-01	8.95E-01	-	-
1389961_at	Sdccag3	serologically defined colon cancer antigen 3	306322	Rn.110254	AA900261	7.45	6.84	7.09	7.56	7.47	7.12	1.19	up	3.10E-01	8.95E-01	-	-
1389577_at	Cirh1a	cirrhosis, autosomal recessive 1A (human)	291987	Rn.106235	AI101160	7.01	5.48	4.85	5.42	5.49	5.67	1.19	down	7.12E-01	9.10E-01	-	-
1391252_at	Rnf41	ring finger protein 41	362814	Rn.74790	BI290717	4.29	5.07	4.95	5.68	3.80	4.07	1.19	down	7.09E-01	9.09E-01	-	-
1372849_at	---	---	---	Rn.163674	AI229183	6.78	5.35	5.82	6.40	6.02	6.29	1.19	up	5.90E-01	8.95E-01	-	-
1397821_at	---	---	---	Rn.171764	BF523355	4.16	4.16	4.25	3.40	4.16	4.23	1.19	down	3.95E-01	8.95E-01	-	-
1383208_at	Pole3	polymerase (DNA directed), epsilon 3 (p17 subunit)	298098	Rn.3290	AW142350	6.96	7.18	7.57	7.02	7.14	6.78	1.19	down	2.83E-01	8.95E-01	-	-
1382587_at	---	---	---	Rn.203429	AA901257	2.45	3.52	2.55	2.66	2.63	2.46	1.19	down	5.01E-01	8.95E-01	-	-
1394105_at	Samd4b	sterile alpha motif domain containing 4B	308473	Rn.40291	AA859633	7.50	7.18	7.52	8.27	7.88	6.82	1.19	up	5.99E-01	8.95E-01	-	-
1374713_at	---	---	---	Rn.24383	AI228970	3.17	2.82	2.49	2.66	2.34	2.71	1.19	down	3.26E-01	8.95E-01	-	-
1373285_at	---	---	---	Rn.1395	AI406624	4.42	2.73	2.61	2.73	2.74	3.52	1.19	down	7.11E-01	9.09E-01	-	-
1382293_at	Tmem213	transmembrane protein 213	689748	Rn.24723	BG377109	5.75	4.30	4.03	5.07	4.57	3.67	1.19	down	7.24E-01	9.12E-01	-	-
1376053_at	---	---	---	Rn.89299	BM385144	2.41	2.43	2.45	2.42	2.44	3.19	1.19	up	3.73E-01	8.95E-01	-	-
1389113_at	Slc45a3	solute carrier family 45, member 3	304785	Rn.9239	AI598307	3.10	3.70	3.98	3.13	3.43	3.45	1.19	down	4.12E-01	8.95E-01	-	-
1392101_s_at	---	---	---	Rn.24732	AI175670	2.91	2.96	2.82	3.00	2.78	3.67	1.19	up	3.98E-01	8.95E-01	-	-
1370843_at	Gng8	guanine nucleotide binding protein (G protein), gamma 8	245986	Rn.11233	BM391912	3.14	3.29	3.15	4.07	3.14	3.13	1.19	up	4.63E-01	8.95E-01	-	-
1372220_at	---	---	---	Rn.8959	BI278846	7.15	7.29	6.98	7.18	7.54	7.46	1.19	up	1.46E-01	8.95E-01	-	-
1370375_at	Gls2	glutaminase 2 (liver, mitochondrial)	192268	Rn.10202	J05499	3.09	2.40	2.41	2.39	2.41	2.33	1.19	down	3.30E-01	8.95E-01	-	-
1374495_at	Lrba	LPS-responsive vesicle trafficking, beach and anchor containing	361975	Rn.2120	BM388121	5.08	5.01	4.97	4.92	5.20	5.70	1.19	up	3.28E-01	8.95E-01	-	-
1373459_at	Stk11ip	serine/threonine kinase 11 interacting protein	301535	Rn.17056	AI100051	3.42	3.52	3.37	3.96	2.68	4.44	1.19	up	6.55E-01	8.98E-01	-	-
1376376_at	---	---	---	Rn.167909	AI501923	3.43	3.39	2.82	3.41	3.61	3.38	1.19	up	2.95E-01	8.95E-01	-	-
1391863_at	---	---	---	Rn.48944	BE106361	3.19	2.25	2.29	2.29	2.40	2.28	1.19	down	4.55E-01	8.95E-01	-	-
1370482_at	Scn1b	sodium channel, nonvoltage-gated 1 beta	24767	Rn.9807	U35174	2.98	2.28	2.33	2.27	2.29	2.27	1.19	down	3.22E-01	8.95E-01	-	-
1372275_at	---	---	---	Rn.11436	BI296757	5.96	4.36	4.93	4.77	5.13	4.58	1.19	down	3.63E-01	8.95E-01	-	-
1398772_at	Nsfl1c	NSFL1 (p97) cofactor (p47)	83809	Rn.2771	NM_031981	6.65	6.79	7.61	7.40	7.75	7.14	1.19	down	6.90E-01	9.05E-01	-	-
1394865_at	Rtp3	receptor (chemosensory) transporter protein 3	316018	Rn.198821	AI709592	2.45	3.23	2.46	2.51	2.45	2.41	1.19	down	3.85E-01	8.95E-01	-	-
1396535_at	---	---	---	Rn.63089	BF388500	2.40	2.38	2.46	2.39	3.23	2.38	1.19	up	4.20E-01	8.95E-01	-	-
1373598_at	Ubn1	ubinuclein 1	302935	Rn.49741	BE116948	6.37	6.60	6.98	6.57	6.31	6.30	1.19	down	2.71E-01	8.95E-01	-	-
1369200_at	Nt5e	5' nucleotidase, ecto	58813	Rn.40132	NM_021576	4.56	5.46	5.49	4.64	4.97	5.14	1.19	down	4.94E-01	8.95E-01	-	-
1379526_at	---	---	---	Rn.129894	BI294017	6.67	7.57	7.29	7.33	7.47	7.50	1.19	up	4.00E-01	8.95E-01	-	-
1375062_at	RGD1561490	similar to Adaptor-related protein complex 1, mu 2 subunit (AP1M2)	367038	Rn.216511	BM392237	2.50	4.68	2.84	3.72	2.92	2.62	1.19	down	7.53E-01	9.20E-01	-	-
1367456_at	Ube2d3	ubiquitin-conjugating enzyme E2D 3 (UBC4/5 homolog, yeast)	81920	Rn.2778	NM_031237	11.28	11.27	11.71	11.15	11.10	11.25	1.19	down	1.68E-01	8.95E-01	-	-
1394800_at	---	---	---	---	BF290090	3.27	3.26	2.55	3.36	3.31	3.17	1.19	up	3.60E-01	8.95E-01	-	-
1387906_a_at	Gnas	GNAS complex locus	24896	Rn.31	AF107845	2.38	3.09	2.42	2.38	2.38	2.37	1.19	down	3.32E-01	8.95E-01	-	-
1384958_at	Ube2j1	Ubiquitin-conjugating enzyme E2, J1	297961	Rn.18843	BI279112	7.01	6.59	6.40	6.58	6.82	7.36	1.19	up	4.36E-01	8.95E-01	-	-
1375883_at	LOC501515	similar to Zinc finger CCHC domain-containing protein 6	501515	Rn.16458	BI298766	4.58	3.90	4.18	3.90	4.01	3.98	1.19	down	2.68E-01	8.95E-01	-	-
1376738_at	Ttc23	tetratricopeptide repeat domain 23	308708	Rn.16924	BF284579	2.77	2.74	2.79	3.02	2.78	3.25	1.19	up	1.38E-01	8.95E-01	-	-
1385210_at	Dock5	dedicator of cytokinesis 5	305987	Rn.209596	BF389450	3.45	4.44	2.51	3.41	3.45	4.30	1.19	up	7.06E-01	9.08E-01	-	-
1373067_at	Clnnb1	Catenin (cadherin associated protein), beta 1	84353	Rn.112601	AI102738	11.26	10.86	10.85	10.65	10.85	10.70	1.19	down	1.57E-01	8.95E-01	-	-
1372427_at	Raver1	ribonucleoprotein, PTB-binding 1	298705	Rn.105739	AI170542	5.04	5.35	3.47	4.46	5.04	5.13	1.19	up	7.02E-01	9.07E-01	-	-
1395007_at	Znf23	zinc finger protein 23 (KOX 16)	307839	Rn.6479	BE120572	4.30	4.46	4.17	4.65	4.17	4.88	1.19	up	3.20E-01	8.95E-01	-	-
1377202_at	Smc6l1	SMC6 structural maintenance of chromosomes 6-like 1 (yeast)	313961	Rn.7047	AI172197	6.72	5.83	5.11	6.00	6.48	5.94	1.19	up	6.35E-01	8.95E-01	-	-
1381201_at	---	---	---	Rn.199766	BI280967	2.32	2.33	2.34	2.33	2.33	3.09	1.19	up	3.74E-01	8.95E-01	-	-
1385540_at	Pias1	Protein inhibitor of activated STAT, 1	300772	Rn.24369	AI044916	10.07	8.57	8.15	9.13	9.42	9.01	1.19	up	6.91E-01	9.05E-01	-	-
1368106_at	Plk2	polo-like kinase 2 (Drosophila)	83722	Rn.12100	NM_031821	2.74	2.48	2.74	3.18	2.77	2.78	1.19	up	1.88E-01	8.95E-01	-	-
1376818_at	Wtip	Wilms tumor 1 interacting protein	361552	Rn.137669	BI291177	3.86	4.62	3.86	3.85	3.37	4.35	1.19	down	5.41E-01	8.95E-01	-	-
1376295_at	---	---	---	Rn.34626	BE119676	4.10	4.16	5.23	4.48	4.09	4.16	1.19	down	5.47E-01	8.95E-01	-	-
1398437_at	---	---	---	Rn.218014	BF412792	2.86	3.44	2.77	2.91	2.59	2.81	1.19	down	3.32E-01	8.95E-01	-	-
1367742_at	Cpt1b	carnitine palmitoyltransferase 1b, muscle	25756	Rn.6028	NM_013200	3.19	2.53	2.57	2.53	2.53	2.47	1.19	down	3.00E-01	8.95E-01	-	-
1374208_at	Zc3h7a	zinc finger CCCH type containing 7 A	360466	Rn.15835	BE116569	7.72	7.86	7.59	7.87	7.87	8.20	1.19	up	1.38E-01	8.95E-01	-	-
1392086_at	Mtss1	Metastasis suppressor 1	362918	Rn.38488	BE115673	3.49	3.42	3.41	4.26	3.56	3.25	1.19	up	4.45E-01	8.95E-01	-	-
1382124_at	Cnnm3	cyclin M3	301345	Rn.50710	BE105042	7.92	7.98	7.67	6.93	7.91	7.96	1.19	down	5.09E-01	8.95E-01	-	-
1388863_at	Ube2a	ubiquitin-conjugating enzyme E2A, RAD6 homolog (S. cerevisiae)	298317	Rn.8585	BE111651	6.88	7.03	7.42	6.53	7.06	6.98	1.19	down	3.33E-01	8.95E-01	-	-
1373344_at	RGD1562200	similar to GS2 gene	363471	Rn.16693	AI412541	4.20	2.85	2.78	2.82	3.54	4.50	1.19	down	6.47E-01	8.95E-01	-	-
1378960_at	---	---	---	Rn.210646	BF399697	4.15	3.73	3.76	3.79	3.70	3.39	1.19	down	2.36E-01	8.95E-01	-	-
1393275_at	---	---	---	---	BM390444	2.48	2.63	3.43	2.75	2.49	2.54	1.19	down	4.52E-01	8.95E-01	-	-
1396294_at	---	---	---	Rn.166172	BE106134	3.33	2.41	2.41	2.39	4.16	2.37	1.19	up	7.23E-01	9.12E-01	-	-
1391410_at	---	---	---	Rn.199616	BM393239	2.89	3.54	2.31	2.64	2.19	3.15	1.19	down	6.03E-01	8.95E-01	-	-
1391433_at	Acot2	acyl-CoA thioesterase 2	192272	Rn.37524	AA899721	10.67	10.86	10.23	10.54	10.73	11.27	1.19	up	4.29E-01	8.95E-01	-	-
1390625_at	RGD1304879	similar to Zinc finger protein 398 (Zinc finger DNA binding protein p52/p71)	312301	Rn.40881	BG381711	2.75	2.39	2.80	2.39	2.40	2.38	1.19	down	1.23E-01	8.95E-01	-	-
1373881_at	Arhgdib	Rho, GDP dissociation inhibitor (GDI) beta	362456	Rn.15842	BF286771	2.45	3.12	2.45	2.45	2.28	2.54	1.19	down	3.46E-01	8.95E-01	-	-
1373112_at	RGD1306873	Similar to RIKEN cDNA 2210010N04 gene	304285	Rn.162096	BE110870	2.96	3.72	4.41	4.07	4.10	3.67	1.19	up	5.98E-01	8.95E-01	-	-
1386054_at	C1ql3	Complement component 1, q subcomponent-like 3	680404	Rn.13498	AA893351	4.66	4.99	4.99	5.09	5.06	5.26	1.19	up	1.19E-01	8.95E-01	-	-
1373020_at	Magmas	mitochondria-associated protein involved in granulocyte-macrophage colony-	679907	Rn.144694	BG379323	10.57	10.47	10.24	10.64	10.70	10.69	1.19	up	6.64E-02	8.95E-01	-	-
1372

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicats)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1395737_at	Cd276	Cd276 molecule	315716	Rn.76129	AW143901	2.38	2.34	2.35	2.45	2.38	2.98	1.19	up	2.55E-01	8.95E-01	-	-
1368297_at	Gata2	GATA binding protein 2	25159	Rn.34322	NM_033442	3.07	2.32	2.32	2.32	2.33	2.31	1.19	down	3.70E-01	8.95E-01	-	-
1369316_s_at	Snap29	synaptosomal-associated protein 29	116500	Rn.17902	NM_053810	5.53	6.45	6.55	6.46	6.48	6.33	1.19	up	4.86E-01	8.95E-01	-	-
1370155_at	Col1a2	collagen, type I, alpha 2	84352	Rn.107239	BI282748	3.53	2.92	2.61	3.67	3.07	3.06	1.19	up	4.96E-01	8.95E-01	-	-
1396373_at	---	---	---	Rn.209180	BF416860	2.47	2.43	2.49	2.47	3.22	2.46	1.19	up	3.76E-01	8.95E-01	-	-
1375480_at	RGD1566399	similar to MYST histone acetyltransferase monocytic leukemia 4	305681	Rn.221977	AI703713	3.25	2.35	2.37	2.43	2.40	2.38	1.19	down	4.43E-01	8.95E-01	-	-
1393551_at	---	---	---	Rn.131538	AI044529	9.49	9.51	9.01	9.60	9.53	9.63	1.19	up	2.03E-01	8.95E-01	-	-
1387878_at	Glud1	glutamate dehydrogenase 1	24399	Rn.55106	AW916644	10.54	10.89	10.66	10.43	10.29	10.61	1.19	down	1.44E-01	8.95E-01	-	-
1391481_at	---	---	---	---	BE104424	8.53	8.36	7.66	8.58	8.88	7.85	1.19	up	5.68E-01	8.95E-01	-	-
1397272_at	Kif13a	kinesin family member 13A	308173	Rn.41333	BI297130	2.50	3.65	3.02	2.72	2.73	2.97	1.19	down	5.04E-01	8.95E-01	-	-
1368109_at	St3gal5	ST3 beta-galactoside alpha-2,3-sialyltransferase 5	83505	Rn.22706	NM_031337	7.74	7.71	7.63	8.26	7.84	7.73	1.19	up	2.01E-01	8.95E-01	-	-
1367848_at	Dctn1	dynactin 1	29167	Rn.11284	NM_024130	3.22	4.36	3.71	3.52	3.51	3.51	1.19	down	4.88E-01	8.95E-01	-	-
1382434_at	Entpd5	ectonucleoside triphosphate diphosphohydrolase 5	314312	Rn.63533	AI059015	9.76	10.02	10.46	10.19	9.38	9.92	1.19	down	4.66E-01	8.95E-01	-	-
1373807_at	Vegfa	vascular endothelial growth factor A	83785	Rn.1923	AI175732	7.11	5.88	6.20	6.94	6.68	6.32	1.19	up	5.72E-01	8.95E-01	-	-
1381149_at	---	---	---	Rn.56934	BI293484	3.88	3.55	3.25	3.27	3.26	3.38	1.19	down	2.47E-01	8.95E-01	-	-
1368669_at	Ucp2	uncoupling protein 2 (mitochondrial, proton carrier)	54315	Rn.13333	NM_019354	3.95	3.74	3.30	4.43	3.60	3.71	1.19	up	4.79E-01	8.95E-01	-	-
1372221_at	---	---	---	Rn.21816	BM389079	5.62	5.79	4.95	4.65	5.10	5.85	1.19	down	5.92E-01	8.95E-01	-	-
1372880_at	Zbtb17	zinc finger and BTB domain containing 17	313666	Rn.15582	BF285118	3.53	2.93	4.02	3.24	3.25	3.23	1.19	down	4.72E-01	8.95E-01	-	-
1391107_at	Xrn1	5'-3' exoribonuclease 1	300944	Rn.13214	BI275784	3.68	2.20	3.36	3.40	2.21	2.88	1.19	down	6.80E-01	9.03E-01	-	-
1389363_at	Adi1	acireductone dioxygenase 1	298934	Rn.12694	AA997430	6.30	6.14	6.64	6.14	5.97	6.22	1.19	down	2.00E-01	8.95E-01	-	-
1389536_at	Hus1	HUS1 checkpoint homolog (S. pombe)	498411	Rn.12812	BF281854	8.09	8.02	8.05	8.04	7.11	8.24	1.19	down	5.11E-01	8.95E-01	-	-
1374362_at	Znf821	zinc finger protein 821	307834	Rn.18256	BF412970	3.72	4.73	4.60	3.65	3.67	4.98	1.19	down	6.67E-01	8.99E-01	-	-
1373274_at	---	---	---	---	BI282039	3.82	2.44	2.36	2.58	2.59	2.70	1.19	down	6.25E-01	8.95E-01	-	-
1372652_at	Foxo4	forkhead box O4	302415	Rn.19646	BM386443	4.37	5.35	5.71	4.53	5.07	5.08	1.19	down	6.00E-01	8.95E-01	-	-
1382832_at	Rcc2	regulator of chromosome condensation 2	298594	Rn.98282	AI236185	2.51	2.46	2.46	3.33	2.38	2.47	1.19	up	4.52E-01	8.95E-01	-	-
1371130_at	Slc1a3	solute carrier family 1 (glial high affinity glutamate transporter), member 3	29483	Rn.34134	X63744	3.52	2.54	2.87	2.81	2.75	2.63	1.19	down	4.40E-01	8.95E-01	-	-
1373470_at	Ctnnb1	catenin (cadherin associated protein), beta 1	84353	Rn.112601	BM388896	11.61	11.37	11.44	11.24	11.40	11.03	1.19	down	1.24E-01	8.95E-01	-	-
1374525_at	Raph1	Ras association (RalGDS/AF-6) and pleckstrin homology domains 1	363239	Rn.16844	BF284017	2.97	2.70	3.11	2.67	2.71	2.64	1.19	down	1.09E-01	8.95E-01	-	-
1389546_at	Amotl2	angiomotin like 2	65157	Rn.25101	BF418582	8.52	9.16	7.16	8.34	7.55	8.20	1.19	down	7.14E-01	9.10E-01	-	-
1396363_at	---	---	---	Rn.160241	BF399356	2.45	3.13	2.44	2.43	2.43	2.40	1.19	down	3.32E-01	8.95E-01	-	-
1383711_at	Nmt1	N-myristoyltransferase 1	259274	Rn.830	BE126380	5.28	5.28	4.99	5.12	5.67	5.50	1.19	up	2.54E-01	8.95E-01	-	-
1372073_at	Gatad2a	GATA zinc finger domain containing 2A	290669	Rn.8522	AI008814	6.18	6.80	5.53	6.03	6.49	6.74	1.19	up	5.84E-01	8.95E-01	-	-
1378739_at	Cldec	cell death-inducing DFFA-like effector c	500292	Rn.33794	AA818135	7.16	7.46	8.17	7.59	6.89	7.55	1.19	down	5.40E-01	8.95E-01	-	-
1377897_at	Whsc1l1	Wolf-Hirschhorn syndrome candidate 1-like 1 (human)	290831	Rn.163332	AI231330	4.93	4.99	4.61	5.21	4.93	5.13	1.19	up	1.61E-01	8.95E-01	-	-
1379312_at	Pprc1	peroxisome proliferator-activated receptor gamma, coactivator-related 1	294007	Rn.9484	AI706508	4.06	3.43	3.35	4.33	3.17	4.09	1.19	up	5.82E-01	8.95E-01	-	-
1371586_at	Mrpl48	mitochondrial ribosomal protein L48	293149	Rn.107172	AF209972	7.38	7.46	7.28	7.14	6.82	7.41	1.19	down	2.34E-01	8.95E-01	-	-
1367527_at	---	---	---	---	AI600258	6.70	7.45	7.31	6.75	6.49	7.46	1.19	down	5.36E-01	8.95E-01	-	-
1367737_at	Fuca1	fucosidase, alpha-L- 1, tissue	24375	Rn.3469	NM_012562	7.78	8.63	7.83	8.24	8.11	8.65	1.19	up	4.78E-01	8.95E-01	-	-
1373366_at	Ganab	glucosidase, alpha; neutral AB	293721	Rn.99241	BM389337	7.64	7.94	7.27	7.78	7.53	8.29	1.19	up	4.46E-01	8.95E-01	-	-
1378305_at	Tm4sf1	transmembrane 4 L six family member 1	295061	Rn.24712	AI578087	2.67	2.63	3.28	2.57	2.69	2.58	1.19	down	3.07E-01	8.95E-01	-	-
1376861_at	/// Mosc	similar to motile sperm domain containing 1 /// motile sperm domain containin	312312 /// 686087	Rn.163261	AW525240	4.56	4.84	5.75	5.01	4.53	4.86	1.19	down	5.53E-01	8.95E-01	-	-
1374186_at	Lrrc47	leucine rich repeat containing 47	362672	Rn.160689	BE109362	8.05	8.29	8.32	8.29	7.66	7.95	1.19	down	2.83E-01	8.95E-01	-	-
1398891_at	Mrpl15	mitochondrial ribosomal protein L15	297799	Rn.1122	AI103129	8.16	8.42	8.04	8.02	7.27	8.58	1.19	down	5.61E-01	8.95E-01	-	-
1379252_at	---	---	---	Rn.164080	AW522833	7.61	7.51	6.49	6.96	7.44	7.96	1.19	up	6.13E-01	8.95E-01	-	-
1374440_at	Hsd17b11	hydroxysteroid (17-beta) dehydrogenase 11	289456	Rn.102059	BE098506	7.54	7.64	7.27	7.94	7.23	8.02	1.19	up	4.13E-01	8.95E-01	-	-
1380375_at	---	---	---	Rn.107976	BE097519	2.54	2.52	2.56	3.30	2.55	2.51	1.19	up	3.86E-01	8.95E-01	-	-
1396172_at	Cdc16	CDC16 cell division cycle 16 homolog (S. cerevisiae)	290875	Rn.66098	BG671873	3.48	3.38	3.49	3.57	3.71	3.82	1.19	up	3.26E-02	8.95E-01	-	-
1383191_at	Ppp1r1a	protein phosphatase 1, regulatory (inhibitor) subunit 1A	58977	Rn.9756	BE097583	4.51	3.61	3.63	3.61	3.78	3.60	1.19	down	4.54E-01	8.95E-01	-	-
1390930_at	---	---	---	Rn.199428	BF406924	3.12	2.88	3.10	3.15	3.41	3.30	1.19	up	8.03E-02	8.95E-01	-	-
1397105_at	Sin3a	SIN3 homolog A, transcription regulator (yeast)	363067	Rn.63749	BE095920	4.22	3.67	2.30	3.68	3.63	3.62	1.19	up	6.83E-01	9.03E-01	-	-
1371389_at	Pdhb	pyruvate dehydrogenase (lipoamide) beta	289950	Rn.102424	BM389223	10.81	10.86	11.16	10.59	10.84	10.65	1.19	down	1.34E-01	8.95E-01	-	-
1371639_at	Vps29	vacuolar protein sorting 29 homolog (S. cerevisiae)	288666	Rn.2547	BF291006	9.88	9.75	10.38	9.74	9.89	9.64	1.19	down	2.91E-01	8.95E-01	-	-
1368432_a_at	Ros1	c-ros oncogene 1 , receptor tyrosine kinase	25346	Rn.87436	NM_012874	3.59	4.35	3.83	4.18	3.78	4.56	1.19	up	4.74E-01	8.95E-01	-	-
1383449_at	---	---	---	Rn.203241	AA801218	4.81	3.63	4.26	4.83	2.61	4.51	1.19	down	7.63E-01	9.22E-01	-	-
1374524_at	Sdy	dimenoxysterone lyase	363285	Rn.23854	BM384384	8.53	8.25	7.91	8.05	7.93	7.94	1.19	down	2.41E-01	8.95E-01	-	-
1396079_at	RGD1311429	similar to KIAA1267 protein	360642	Rn.24932	BF558358	4.76	5.39	6.38	6.04	4.63	5.12	1.19	down	7.10E-01	9.09E-01	-	-
1375574_at	Gga3	golgi associated, gamma adaptin ear containing, ARF binding protein 3	360658	Rn.198912	BE112983	4.76	4.90	4.64	4.94	5.11	4.99	1.19	up	4.91E-02	8.95E-01	-	-
1390807_at	Car5b	carbonic anhydrase 5b, mitochondrial	302669	Rn.22441	BG375352	8.57	9.38	8.89	8.41	8.64	9.03	1.19	down	4.48E-01	8.95E-01	-	-
1388659_at	Carhsp1	calcium regulated heat stable protein 1	260416	Rn.14584	BI295783	5.44	6.37	5.99	6.23	6.05	6.26	1.19	up	4.22E-01	8.95E-01	-	-
1394957_at	Nisch	nischarin	306255	Rn.96234	BE108587	2.81	3.76	2.82	3.14	2.69	2.81	1.19	down	5.08E-01	8.95E-01	-	-
1374754_at	---	---	---	Rn.12700	BF400833	2.55	2.54	2.40	2.99	2.55	2.69	1.19	up	1.47E-01	8.95E-01	-	-
1374675_at	Tmem9b	TMEM9 domain family, member B	293415	Rn.219247	BG374992	3.74	4.71	4.64	4.11	3.54	4.68	1.19	down	6.13E-01	8.95E-01	-	-
1368794_at	Haao	3-hydroxyanthranilate 3,4-dioxygenase	56823	Rn.48675	NM_020076	10.50	10.77	10.33	10.19	10.15	10.52	1.19	down	2.24E-01	8.95E-01	-	-
1382251_at	Kpna1	karyopherin (importin) alpha 1	288064	Rn.6272	BE120157	4.20	4.56	4.22	3.78	4.22	4.23	1.19	down	2.56E-01	8.95E-01	-	-
1397838_at	RGD1564792	RGD1564792	499976	---	BF522792	3.12	3.09	3.12	3.11	3.86	3.10	1.19	up	3.77E-01	8.95E-01	-	-
1385645_at	---	---	---	Rn.130556	AA875088	3.16	2.47	2.52	2.47	2.48	2.46	1.19	down	3.29E-01	8.95E-01	-	-
1396009_at	---	---	---	---	BE108258	3.44	3.05	3.12	3.08	2.99	2.79	1.19	down	1.63E-01	8.95E-01	-	-
1378360_at	---	---	---	---	BF397301	4.32	3.73	4.37	4.19	4.45	4.52	1.19	up	3.34E-01	8.95E-01	-	-
1381530_at	---	---	---	---	AI599482	7.02	7.29	6.41	7.12	7.12	7.23	1.19	up	3.99E-01	8.95E-01	-	-
1388759_at	---	---	---	Rn.104756	BM389875	9.37	9.47	9.39	8.96	9.17	9.35	1.19	down	1.05E-01	8.95E-01	-	-
1374976_a_at	Soat1	Sterol O-acyltransferase 1	81782	Rn.59	AI548897	3.24	3.96	5.63	3.25	3.72	5.12	1.19	down	7.97E-01	9.34E-01	-	-
1387071_a_at	Mapt	microtubule-associated protein tau	29477	Rn.2455	BE107978	4.25	5.69	4.88	4.40	4.51	5.17	1.19	down	6.33E-01	8.95E-01	-	-
1368461_at	Slc22a8	solute carrier family 22 (organic anion transporter), member 8	83500	Rn.23348	NM_031332	9.65	8.57	7.55	9.78	8.44	8.29	1.19	up	7.63E-01	9.22E-01	-	-
1373446_at	Phf13	PHD finger protein 13	313742	Rn.162136	AI102512	4.48	4.56	5.85	4.88	4.51	4.77	1.19	down	6.14E-01	8.95E-01	-	-
1394029_at	RGD1566155	similar to 2610030H06Rik protein	501658	Rn.108094	BF283049	5.48	5.12	5.03	4.06	5.22	5.60	1.19	down	6.33E-01	8.95E-01	-	-
1398941_at	Pcbp2	poly(rC) binding protein 2	363005	Rn.106644	AI170413	8.33	8.80	8.86	8.87	8.80	9.06	1.19	up	2.51E-01	8.95E-01	-	-
1390335_at	---	---	---	Rn.168533	AW252589	6.46	6.47	7.75	6.57	6.57	6.79	1.19	down	5.98E-01	8.95E-01	-	-
1390343_at	Ccnc	cyclin C	114839	Rn.106758	AA998893	6.97	7.34	7.80	6.60	7.42	7.33	1.19	down	5.21E-01	8.95E-01	-	-
1371488_at	659845 /// RGD15	similar to SPBPJ4664.02 /// RGD1562079	308494 /// 499125	Rn.3527	AW915978	7.52	7.89	7.96	7.64	7.17	7.82	1.19	down	3.54E-01	8.95E-01	-	-
1374127_at	Znf18	zinc finger protein 18	303226	Rn.93963	BM392050	2.60	4.00	2.35	3.29	2.32	2.58	1.19	down	6.95E-01	9.06E-01	-	-
1395990_at	Srcap	Snf2-related CREBBP activator protein	361652	Rn.62858	AA819145	5.46	4.84	4.86	5.86	4.86	5.18	1.19	up	5.28E-01	8.95E-01	-	-
1372365_at	Rin2	Ras and Rab interactor 2	311494	Rn.34193	BM392293	8.88	9.27	8.68	8.95	9.19	9.42	1.19	up	3.22E-01	8.95E-01	-	-
1372331_at	Eif1ay	eukaryotic translation initiation factor 1A, Y-linked	302697	Rn.106940	BM386033	10.70	10.11	10.53	10.11	10.24	10.24	1.19	down	2.40E-01	8.95E-01	-	-
1394535_at	Kif16b	kinesin family member 16B	311478	Rn.7029	BF397930	3.19	5.94	2.40	4.66	2.40	3.72	1.19	down	8.53E-01	9.54E-01	-	-
1388833_at	Pole3	polymerase (DNA directed), epsilon 3 (p17 subunit)	298098	Rn.3290	AA892270	6.45	6.38	5.83	5.92	5.89	6.10	1.19	down	2.99E-01	8.95E-01	-	-
1391948_at	Bcl11b	B-cell CLL/lymphoma 11B (zinc finger protein)	314423	Rn.162897	BM390227	2.34	2.34	2.35	2.34	3.09	2.33	1.19	up	3.79E-01	8.95E-01	-	-
1367668_a_at	Scd	stearoyl-CoA desaturase (delta-9-desaturase)	83792	Rn.83595	BE107760	2.99	3.29	4.46	3.30	2.96	3.74	1.19	down	6.48E-01	8.96E-01	-	-
1386039_x_at	---	---	---	---	BF288392	3.63	2.74	2.75	2.94	2.74	2.70	1.19	down	4.58E-01	8.95E-01	-	-
1383155_at	Fam117b	family with sequence similarity 117, member B	363236	Rn.8070	AA945854	3.74	3.89	4.17	3.81	3.61	3.64	1.19	down	1.52E-01	8.95E-01	-	-
1385119_at	---	---	---	Rn.165984	AI043832	3.01	2.78	2.51	3.72	2.79	2.54	1.19	up	5.56E-01	8.95E-01	-	-
1398345_at	---	---	---	Rn.1664	BM389225	3.20	2.46	2.47	2.47	2.49	2.43	1.19	down	3.66E-01	8.95E-01	-	-
1375707_at	---	---	---	---	AA817993	7.56	8.29	8.06	8.39	6.89	7.89	1.19	down	6.39E-01	8.95E-01	-	-
1377677_a_at	---	---	---	Rn.12094	AA900692	4.60	4.58	4.62	4.56	4.16	4.33	1.19	down	9.94E-02	8.95E-01	-	-
1383060_at	Gkap1	G kinase anchoring protein 1	361202	Rn.2003	BE112067	6.59	7.08	6.73	6.50	6.95	7.69	1.19	up	5.45E-01	8.95E-01	-	-
1398494_at	Rev1	REV1 homolog (S. cerevisiae)	316344	Rn.94641	BF404279	2.45	2.42	3.13	2.41	2.42	2.41	1.19	down	3.45E-01	8.95E-01	-	-
1382299_at	---	---	---	Rn.166119	AW914657	3.34	2.58	2.56	2.62	2.59	2.54	1.19	down	3.91E-01	8.95E-01	-	-
1374210_at	Nsmce1	non-SMC element 1 homolog (S. cerevisiae)	361645	Rn.17063	BM383870	7.37	7.90	6.36	7.19	7.53	7.67	1.19	up	6.28E-01	8.95E-01	-	-
1388073_a_at	Nupl1	nucleoporin like 1	245922	Rn.11099	AF000901	5.85	6.64	7.27	6.97	7.20	6.33	1.19	up	6.36E-01	8.95E-01	-	-
1375536_at	Numb	numb homolog (Drosophila)	29419	Rn.102078	BI287975	8.92	8.21	7.88	8.18	7.78	8.30	1.19	down	5.12E-01	8.95E-01	-	-
1383376_at	ajc30 /// LOC8805	DnaJ (Hsp40) homolog, subfamily C, member 30 /// similar to Williams-Beure	368190 /// 680976	Rn.29127	AI717529	5.85	6.14	6.57	5.74	5.58	6.49	1.19	down	5.17E-01	8.95E-01	-	-
1398993_at	Rbm39	RNA binding motif protein 39	362251	Rn.8555	AI045458	7.65	8.08	7.75	7.88	7.95	8.39	1.19	up	2.93E-01	8.95E-01	-	-
1371483_at	Nnt	nicotinamide nucleotide transhydrogenase	310378	Rn.3128	AA891872	7.38	7.83	7.17	7.25	7.98	7.89	1.19	up	4.56E-01	8.95E-01	-	-
1370119_at	Lat1	leukocyte specific transcript 1	84569	Rn.91085	NM_022634	2.49	2.52	2.49	2.62	3.13	2.48	1.19	up	2.81E-01	8.95E-01	-	-
1390857_at	Xylb	xylulokinase homolog (H. influenzae)	316067	Rn.8732	BI279844	9.98	10.17	9.12	10.28	9.68	10.05	1.19	up	5.35E-01	8.95E-01	-	-
1367925_at	Mvp	major vault protein	64681	Rn.10028	NM_022715	7.76	6.71	6.87	6.73	7.04	6.82	1.19	down	5.04E-01	8.95E-01	-	-
1368924_at	Ghr	growth hormone receptor	25235	Rn.2178	NM_017094	9.53	9.55	10.03	9.09	9.41	9.88	1.19	down	4.30E-01	8.95E-01	-	-
1374441_at	Spryd4	SPRY domain containing 4	288772	Rn.144447	AI180035	3.10	3.10	2.96	3.17	3.77	2.96	1.19	up	3.69E-01	8.95E-01	-	-
1371732_at	Dpt	dermatopontin	289178	Rn.8396	BI285485	7.84	7.50	7.47	7.52	7.69	6.86	1.19	down	4.23E-01	8.95E-01	-	-
1378057_at	Flrt3	fibronectin leucine rich transmembrane protein 3	366205	Rn.220263	BE103354	3.48	3.70	3.44	3.67	4.32	3.37	1.19	up	4.41E-01	8.95E-01	-	-
1379188_at	Arid2	AT rich interactive domain 2 (Arid-rfk like)	366980	Rn.42849	BI289741	5.39	4.71	4.42	4.86	4.32	4.61	1.19	down	4.89E-01	8.95E-01	-	-
1397458_at	Pmm2	phosphomannomutase 2	302915	Rn.58278	AW533978	4.55	5.15	5.75	5.51	5.23	5.46	1.19	up	5.26E-01	8.95E-01	-	-
1371481_at	Reep5	receptor accessory protein 5	364838	Rn.40477	BI274372	10.52	10.38	10.66	10.86	10.57	10.88	1.19	up	1.29E-01	8.95E-01	-	-
1378581_at	Ccdc62	coiled-coil domain containing 62	689909	Rn.208219	BI295536	3.11	2.51	2.50	2.32	2.60	2.45	1.19	down	3.19E-01	8.95E-01	-	-
1383047_at	Gas6	growth arrest specific 6	58935	Rn.52228	AA957335	9.16	7.74	8.17	8.21	8.97	7.15	1.19	down	7.32E-01	9.14E-01	-	-
1393329_at	---	---	---	---	BE099038	2.28	2.27	2.29	2.29	3.02	2.27	1.19	up	3.74E-01	8.95E-01	-	-
1376856_at	RGD1310414	similar to hypothetical protein FLJ23263	290811	Rn.12987	AI111579	2.35	2.35	2.36	3.10	2.36	2.34	1.19	up	3.76E-01	8.95E-01	-	-
1382452_at	Sdpr	serum deprivation response	316384	Rn.203035	AI630408	5.44	5.50	4.85	6.00	4.34	4.34	1.19	up	7.12E-01	9.10E-01	-	-
1384987_at	---	---	---	---	BM386877	2.49	2.46	2.50	3.17	2.56	2.47	1.19	up	3.21E-01	8.95E-01	-	-
1393857_at	---	---	---	Rn.199601	AW253255	2.68	2.68	2.57	3.23	2.76	2.68	1.19	up	2.34E-01	8.95E-01	-	-
1389704_at	---	---	---	Rn.7013	AA850490	7.29	7.92	7.07	6.96	7.27	8.79	1.19	up	7.10E-01	9.09E-01	-	-
1375569_at	Ccdc92	coiled-coil domain containing 92	100036765	Rn.32270	BM386267	3.93	3.15	3.76	3.60	3.33	3.16	1.19	down	4.09E-01	8.95E-01	-	-
1380344_at	---	---	---	Rn.203813	BM387968	3.28	2.60	2.77	2.64	2.67	2.60	1.19	down	2.97E-01	8.95E-01	-	-
1373386_at	Gjb2	gap junction protein, beta 2	394266	Rn.219269	AI179953	10.20	10.47	9.99	10.46	10.29	10.66	1.19	up	2.33E-01	8.95E-01	-	-
1385407_at	Tiparp	TCDD-inducible poly(ADP-ribose) polymerase	310467	Rn.24217	AI511405	2.95	2.90	3.07	2.84	2.90	2.44	1.19	down	1.84E-01	8.95E-01	-	-
1374443_at	Ict1	immature colon carcinoma transcript 1	303673	Rn.22728	AW915478	7.03	8.00	7.56	7.86	7.67	7.81	1.19	up	4.33E-01	8.95E-01	-	-
1395433_at	---	---	---	Rn.92837	BI298143	3.72	4.41	5.13	5.39	3.60	5.01	1.19	up	7.34E-01	9.15E-01	-	-
1380775_at	Kif20b	kinesin family member 20B	309523	Rn.208134	BE110723	2.98	2.95	3.04	3.75	2.99	2.97	1.19	up	3.92E-01	8.95E-01	-	-
1393859_at	---	---	---	Rn.206882	AW531315	2.49	2.48	3.20	2.48	2.50	2.44	1.19	down	3.60E-01	8.95E-01	-	-
1378332_at	Klf3	Kruppel-like factor 3 (basic)	114845	Rn.218431	AA956804	7.34	7.10	5.40	6.39	6.96	7.23	1.19	up	7.27E-01	9.13E-01	-	-
1371300_at	Rpl3	ribosomal protein L3	300079	Rn.107726	AA892367	11.10	11.16	12.69	11.43	11.19	11.58	1.19	down	6.66E-01	8.96E-01	-	-
1372264_at	Pck1	phosphoenolpyruvate carboxykinase 1 (soluble)	362282	Rn.104376	BI277460	13.21	12.88	13.38	12.95	12.84	12.94	1.19	down	1.74E-01	8.95E-01	-	-
1388984_at	Polr3b	polymerase (RNA) III (DNA directed) polypeptide B	362858	Rn.37546	BF397989	4.14	4.89	4.18	4.12	4.17	4.18	1.19	down	3.71E-01	8.95E-01	-	-
1373715_at	LOC304396	similar to hypothetical protein DKFZp434K1815	304396	Rn.144942	BI274516	4.62	4.72	3.82	4.59	4.66	4.66	1.19	up	4.35E-01	8.95E-01	-	-
1383719_at	Map7	microtubule-associated protein 7	293016	Rn.23807	AW531489	7.83	7.16	7.52	7.33	6.53	7.90	1.19	down	6.04E-01	8.95E-01	-	-
1367623_at	Rpl18	ribosomal protein L18	81766	Rn.484	NM_031102	10.59	11.36	10.57	10.93	10.97	11.35	1.19	up	4.47E-01	8.95E-01	-	-
1372310_at	Isoc1	isochorismatase domain containing 1	364879	Rn.1166	AI227941	8.24	8.78	8.51	7.82	8.57	8.40	1.19	down	4.18E-01	8.95E-01	-	-
1388475_at	Prnpip1	Prion protein interacting protein 1	313535	Rn.3222	AA896150	3.19	3.08	3.19	3.18	3.84	3.18	1.19	up	3.28E-01	8.95E-01	-	-
1385108_at	---	---	---	Rn.206236	AW524173	6.25	5.87	6.48	6.00	5.46	6.39	1.19	down	4.87E-01	8.95E-01	-	-
1379581_at	Mapk1ip1l	mitogen-activated protein kinase 1 interacting protein 1-like	361028	Rn.22587	BI288586	4.99	4.59	2.92	3.54	4.24	3.98	1.19	down	7.30E-01	9.14E-01	-	-
1380389_at	---	---	--

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1370927_at	Col12a1	collagen, type XII, alpha 1	25683	Rn.11218	BE108345	3.87	3.11	3.14	3.13	3.15	3.11	1.19	down	3.79E-01	8.95E-01	-	-
1393550_at	Crem	cAMP responsive element modulator	25620	Rn.10251	BF564195	4.13	3.97	4.43	4.06	5.12	4.09	1.19	up	5.47E-01	8.95E-01	-	-
1369344_at	Wdr7	WD repeat domain 7	66031	Rn.211985	NM_023975	5.45	3.49	3.06	6.18	3.06	3.49	1.19	up	8.50E-01	9.53E-01	-	-
1376945_at	---	---	---	Rn.47139	BI296435	2.35	2.66	2.76	2.67	2.66	3.17	1.19	up	3.04E-01	8.95E-01	-	-
1374213_at	Arfgef2	ADP-ribosylation factor guanine nucleotide-exchange factor 2 (brefeldin A-inh	296380	Rn.161866	BM384718	4.35	5.49	4.98	4.19	4.74	5.15	1.19	down	5.99E-01	8.95E-01	-	-
1377903_at	---	---	---	Rn.203118	AI408914	7.62	7.70	8.10	7.56	7.78	7.36	1.19	down	2.70E-01	8.95E-01	-	-
1372178_at	---	---	---	Rn.220402	BM385981	4.34	3.32	3.94	4.34	4.20	3.80	1.19	up	5.06E-01	8.95E-01	-	-
1390242_at	---	---	---	Rn.170579	AA891123	2.28	2.27	2.28	2.30	2.99	2.26	1.19	up	3.60E-01	8.95E-01	-	-
1392576_at	RGD1359508	similar to protein C33A12.3	361941	Rn.7605	AI175445	3.00	3.07	2.78	2.88	3.63	3.07	1.19	up	3.67E-01	8.95E-01	-	-
1397078_at	Itfg2	integrin alpha FG-GAP repeat containing 2	362441	Rn.148803	AI111920	2.84	3.30	2.83	3.15	3.56	2.99	1.19	up	3.46E-01	8.95E-01	-	-
1371805_at	Ankrd46	ankyrin repeat domain 46	299982	Rn.11978	AI406508	7.24	6.49	6.72	6.79	6.66	6.27	1.19	down	4.20E-01	8.95E-01	-	-
1384368_at	Slc25a16	solute carrier family 25 (mitochondrial carrier, Graves disease autoantigen), m	361836	Rn.21448	AA900084	3.92	4.33	3.39	3.92	4.20	4.25	1.19	up	4.44E-01	8.95E-01	-	-
1389166_at	Cib2	calcium and integrin binding family member 2	300719	Rn.46320	BF403998	3.85	4.84	5.78	4.58	4.58	4.58	1.19	down	6.82E-01	9.03E-01	-	-
1384089_at	Rabgef1	RAB guanine nucleotide exchange factor (GEF) 1	360797	Rn.21688	AI575052	5.41	4.06	3.21	4.07	3.55	4.33	1.19	down	7.37E-01	9.15E-01	-	-
1382101_at	Hs2st1	heparan sulfate 2-O-sulfotransferase 1	292155	Rn.98872	AI714262	4.24	3.62	4.33	3.58	3.53	4.35	1.19	down	5.19E-01	8.95E-01	-	-
1388623_at	Ehd1	EH-domain containing 1	293692	Rn.8141	BI277003	3.14	3.50	4.58	3.43	3.33	3.72	1.19	down	6.13E-01	8.95E-01	-	-
1395265_at	Gns	glucosamine (N-acetyl)-6-sulfatase	299825	Rn.65392	BF419323	8.03	8.57	7.94	7.95	8.14	7.71	1.19	down	3.53E-01	8.95E-01	-	-
1374109_at	---	---	---	---	AI230466	6.87	6.97	6.85	7.32	7.10	7.00	1.19	up	7.38E-02	8.95E-01	-	-
1393050_at	LOC302495	hypothetical LOC302495	302495	Rn.204468	BG664069	6.26	6.45	6.42	6.10	5.79	6.50	1.19	down	3.16E-01	8.95E-01	-	-
1391585_at	Harbi1	harbinger transposase derived 1	690164	Rn.198635	AW253379	3.53	4.20	3.78	4.23	3.48	3.07	1.19	down	5.68E-01	8.95E-01	-	-
1372557_at	Arl6	ADP-ribosylation factor-like 6	363760	Rn.101944	AI409182	6.07	5.25	6.26	5.17	5.36	6.32	1.19	down	6.30E-01	8.95E-01	-	-
1386621_at	---	---	---	Rn.164736	AW142419	4.84	4.47	4.82	4.84	5.20	4.84	1.18	up	2.22E-01	8.95E-01	-	-
1377061_at	Rics	Rho GTPase-activating protein	315530	Rn.106129	BE097238	2.33	3.08	2.34	2.33	2.36	2.32	1.18	down	3.78E-01	8.95E-01	-	-
1370531_a_at	Plcl1	phospholipase D1	25096	Rn.11130	U69552	8.72	10.28	8.18	8.97	8.89	10.08	1.18	up	7.55E-01	9.20E-01	-	-
1384182_at	Fermt2	fermitin family homolog 2 (Drosophila)	289992	Rn.7658	BE128738	6.37	6.83	6.94	6.28	6.54	6.57	1.18	down	2.81E-01	8.95E-01	-	-
1387798_a_at	Cr1l	complement component (3b/4b) receptor 1-like	54243	Rn.5825	D42115	9.97	9.90	9.89	10.02	10.40	10.07	1.18	up	1.13E-01	8.95E-01	-	-
1383650_at	---	---	---	---	BI291080	2.51	2.44	3.46	2.68	2.52	2.49	1.18	down	5.07E-01	8.95E-01	-	-
1374452_at	Pde9a	phosphodiesterase 9A	191569	Rn.20981	BF399743	3.72	3.65	4.16	3.99	3.99	4.28	1.18	up	2.64E-01	8.95E-01	-	-
1382321_at	Tmem161a	transmembrane protein 161A	364535	Rn.21915	AI071312	6.20	6.21	7.60	6.81	6.82	7.11	1.18	up	6.33E-01	8.95E-01	-	-
1394975_at	Zfml	zinc finger, matrin-like	312491	Rn.15272	BF396896	6.21	5.49	4.67	5.05	5.17	5.42	1.18	down	6.22E-01	8.95E-01	-	-
1397606_at	---	---	---	---	D88807	3.50	2.57	2.44	2.66	2.61	2.51	1.18	down	5.09E-01	8.95E-01	-	-
1381267_at	---	---	---	Rn.200331	BI292529	2.50	2.48	2.60	2.93	2.58	2.82	1.18	up	9.17E-02	8.95E-01	-	-
1375354_at	RGD1308048	Similar to HT014	298557	Rn.22682	BE098366	3.56	3.49	4.14	3.65	3.32	3.48	1.18	down	3.39E-01	8.95E-01	-	-
1369327_at	Pdzd2	PDZ domain containing 2	65034	Rn.48728	NM_022940	3.53	3.80	3.53	3.00	3.69	3.43	1.18	down	3.28E-01	8.95E-01	-	-
1371448_at	---	---	---	Rn.216456	AI599295	5.75	6.34	6.25	5.66	5.88	6.06	1.18	down	3.24E-01	8.95E-01	-	-
1367504_at	---	---	---	Rn.199095	AI411286	4.27	4.46	5.27	4.51	4.23	4.53	1.18	down	4.89E-01	8.95E-01	-	-
1390672_at	Rprm	reprimo, TP53 dependent G2 arrest mediator candidate	680110	Rn.45197	BG381258	2.36	2.35	2.41	2.37	3.13	2.36	1.18	up	3.91E-01	8.95E-01	-	-
1383650_at	---	---	---	---	AI071958	7.40	9.15	9.57	8.66	7.86	8.87	1.18	down	7.56E-01	9.20E-01	-	-
1383349_at	Rfx5	regulatory factor X, 5 (influences HLA class II expression)	310659	Rn.19941	BE115594	3.07	3.05	3.01	3.00	3.57	3.29	1.18	up	2.17E-01	8.95E-01	-	-
1394417_at	---	---	---	Rn.169122	BF396165	4.62	4.26	3.92	6.05	3.44	4.05	1.18	up	7.79E-01	9.28E-01	-	-
1367470_at	Sar1a	SAR1 homolog A (S. cerevisiae)	361842	Rn.15780	AA851321	9.55	9.51	9.66	9.67	9.56	10.22	1.18	up	3.09E-01	8.95E-01	-	-
1390651_at	RGD1309821	similar to KIAA1161 protein	366360	Rn.106115	AI236271	2.39	2.38	2.40	3.14	2.40	2.37	1.18	up	3.88E-01	8.95E-01	-	-
1368366_at	Cml1	camello-like 1	59300	Rn.205093	NM_021668	7.40	7.85	7.61	7.01	7.56	7.55	1.18	down	3.36E-01	8.95E-01	-	-
1388534_at	---	---	---	Rn.95113	AA851369	9.09	8.37	8.21	8.33	8.17	8.44	1.18	down	4.35E-01	8.95E-01	-	-
1388878_at	Nob1	NIN1/RPN12 binding protein 1 homolog (S. cerevisiae)	291996	Rn.102586	BI279756	4.70	5.72	5.62	5.82	5.31	5.64	1.18	up	5.31E-01	8.95E-01	-	-
1377169_at	---	---	---	Rn.216528	BI273710	3.65	5.66	5.54	5.25	4.58	5.75	1.18	up	7.56E-01	9.21E-01	-	-
1367695_at	Qdpr	quinoid dihydropteridine reductase	64192	Rn.241	NM_022390	8.14	8.54	8.11	8.39	8.56	8.57	1.18	up	1.79E-01	8.95E-01	-	-
1374306_at	Zdhhc18	zinc finger, DHHC domain containing 18	362613	Rn.203345	BF394933	2.36	2.81	2.83	3.03	2.88	2.82	1.18	up	2.16E-01	8.95E-01	-	-
1397709_at	Arl6ip1	ADP-ribosylation factor-like 6 interacting protein 1	293551	Rn.203188	BG672259	2.90	5.85	5.70	5.12	4.83	5.24	1.18	up	8.13E-01	9.40E-01	-	-
1371032_at	Nid1	nidogen 1	25494	Rn.105658	BG372942	8.85	9.22	9.00	9.03	8.95	9.83	1.18	up	4.61E-01	8.95E-01	-	-
1394844_s_at	Cyp4a2 /// Cyp4a3	cytochrome P450, family 4, subfamily a, polypeptide 2 /// cytochrome P450, fa	24306 /// 298423	Rn.33492	AA893326	11.92	11.99	12.29	11.87	11.85	11.75	1.18	down	1.07E-01	8.95E-01	-	-
1385214_at	Ddx3x	DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, X-linked	317335	Rn.95841	BF391513	10.03	10.44	10.43	9.99	9.80	10.39	1.18	down	3.32E-01	8.95E-01	-	-
1389838_at	Marcks	Myristoylated alanine rich protein kinase C substrate	25603	Rn.9560	AW527201	5.32	4.78	3.92	4.74	4.86	3.70	1.18	down	6.80E-01	9.03E-01	-	-
1380187_at	Plekho1	pleckstrin homology domain containing, family O member 1	310674	Rn.21037	BI286219	3.43	2.66	2.62	2.66	2.66	2.66	1.18	down	4.09E-01	8.95E-01	-	-
1391771_at	Atp2a2	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2	29693	Rn.2305	AA863859	2.45	3.14	2.44	2.44	2.42	2.43	1.18	down	3.54E-01	8.95E-01	-	-
1377109_at	Eif4g1	Eukaryotic translation initiation factor 4 gamma, 1	287986	Rn.101803	AA957450	2.55	2.51	2.62	3.35	2.59	2.48	1.18	up	4.24E-01	8.95E-01	-	-
1388938_at	Usp5	ubiquitin specific peptidase 5 (isopeptidase T)	297593	Rn.44078	AI411387	5.74	5.67	5.45	5.93	5.97	5.70	1.18	up	1.16E-01	8.95E-01	-	-
1392074_at	LOC500046	similar to hypothetical protein FLJ21986	500046	Rn.32719	AA926082	3.56	2.49	2.46	2.45	2.44	2.89	1.18	down	5.68E-01	8.95E-01	-	-
1391412_at	Xrn2	5'-3' exoribonuclease 2	362229	Rn.64021	AA996841	6.35	5.80	6.16	5.56	5.89	6.13	1.18	down	3.52E-01	8.95E-01	-	-
1367815_at	Slc5a6	solute carrier family 5 (sodium-dependent vitamin transporter), member 6	170551	Rn.11105	NM_130746	8.59	8.82	8.48	8.10	8.52	8.54	1.18	down	2.33E-01	8.95E-01	-	-
1395530_at	---	---	---	Rn.199169	AI555739	3.18	2.46	2.41	2.40	2.46	2.46	1.18	down	3.86E-01	8.95E-01	-	-
1372621_at	Fam176b	family with sequence similarity 176, member B	362597	Rn.22919	AI179588	2.31	2.63	3.48	2.64	2.66	2.66	1.18	up	5.35E-01	8.95E-01	-	-
1399107_at	RGD1305158	similar to RIKEN cDNA 1810030N24	297971	Rn.16772	BE112193	4.40	4.90	4.44	4.73	4.52	5.22	1.18	up	4.08E-01	8.95E-01	-	-
1374598_at	---	---	---	Rn.160441	AW914984	3.01	4.01	3.09	3.05	2.41	3.91	1.18	down	6.75E-01	9.01E-01	-	-
1374712_at	Psmd11	proteasome (prosome, macropain) 26S subunit, non-ATPase, 11	303353	Rn.11861	AA946509	10.36	10.18	10.33	10.08	10.03	10.02	1.18	down	1.25E-02	8.95E-01	-	-
1381399_at	186 /// RGD15613	similar to ribosomal protein L37 /// similar to ribosomal protein L37 /// similar to 44 /// 679570 /// 6		Rn.65053	BG381338	5.23	4.73	4.91	4.66	5.63	3.84	1.18	down	6.75E-01	9.01E-01	-	-
1389279_at	---	---	---	Rn.167297	BM386204	4.57	4.22	3.78	3.91	3.75	4.77	1.18	down	6.63E-01	8.99E-01	-	-
1375276_at	Timm17b	translocase of inner mitochondrial membrane 17 homolog B (yeast)	317374	Rn.17526	BI274139	5.69	5.75	5.78	5.72	5.06	5.72	1.18	down	3.33E-01	8.95E-01	-	-
1389907_at	Enc3	ensolase 3, beta, muscle	25438	Rn.3442	NM_012949	3.56	2.87	2.89	2.88	2.89	2.82	1.18	down	3.43E-01	8.95E-01	-	-
1390590_at	Pofut2	protein O-fucosyltransferase 2	309686	Rn.11702	AA965207	2.40	2.38	2.41	2.97	2.40	2.55	1.18	up	2.28E-01	8.95E-01	-	-
1368785_a_at	Pitx2	paired-like homeodomain 2	54284	Rn.17591	NM_019334	3.66	3.17	2.74	3.29	2.83	4.18	1.18	up	6.38E-01	8.95E-01	-	-
1392793_at	---	---	---	Rn.159952	AA926030	2.64	2.87	2.97	2.68	2.69	3.83	1.18	up	5.70E-01	8.95E-01	-	-
1382637_at	Elf2	E74-like factor 2	361944	Rn.107459	AI137223	2.72	5.81	3.84	3.46	3.57	4.61	1.18	down	8.15E-01	9.40E-01	-	-
1378249_x_at	---	---	---	---	BE110241	9.44	10.14	8.84	10.10	8.64	8.95	1.18	down	6.98E-01	9.07E-01	-	-
1388998_at	Epb4.9	erythrocyte protein band 4.9	361069	Rn.9618	AW522835	4.55	6.07	6.93	6.19	6.13	5.95	1.18	up	7.46E-01	9.18E-01	-	-
1375156_at	---	---	---	Rn.18973	AI599528	6.71	6.22	6.04	6.76	6.68	6.28	1.18	up	3.86E-01	8.95E-01	-	-
1393326_s_at	Gtpbp6	GTP binding protein 6 (putative)	363931	Rn.98504	BG378917	3.20	3.47	3.22	2.84	3.12	3.20	1.18	down	1.51E-01	8.95E-01	-	-
1381685_a_at	Clec16a	C-type lectin domain family 16, member A	287044	Rn.12453	BI276419	4.58	4.87	4.72	4.04	4.70	4.70	1.18	down	3.59E-01	8.95E-01	-	-
1373454_at	RGD1305823	similar to RIKEN cDNA 0610037P05	369461	Rn.3055	AI230689	7.34	7.47	7.23	7.39	6.49	7.44	1.18	down	4.88E-01	8.95E-01	-	-
1393311_at	---	---	---	Rn.204032	AI044549	7.05	7.04	6.58	7.31	6.56	6.07	1.18	down	5.69E-01	8.95E-01	-	-
1378049_at	Zfp362 /// Zscan20	zinc finger protein 362 /// zinc finger and SCAN domain containing 20	297879 /// 500549	Rn.25043	AI603565	6.21	6.72	4.96	6.54	5.78	6.29	1.18	up	6.92E-01	9.05E-01	-	-
1372607_at	Nutp2	nucleotide binding protein 2	287125	Rn.203395	BM384157	8.47	7.85	7.30	7.90	7.06	7.94	1.18	down	6.13E-01	8.95E-01	-	-
1398957_at	c21 /// RGD15663	cell division cycle 2 homolog (S.pombe)-like 1 /// similar to cell division cycle 2	252879 /// 315362	Rn.10204	AA817907	7.31	7.46	7.52	7.36	6.96	7.25	1.18	down	1.47E-01	8.95E-01	-	-
1386863_at	Ppp1ca	protein phosphatase 1, catalytic subunit, alpha isoform	24668	Rn.2024	NM_031527	7.94	8.17	8.01	8.15	8.55	8.15	1.18	up	1.83E-01	8.95E-01	-	-
1389148_at	Apool	apolipoprotein O-like	317191	Rn.106347	AW254686	6.18	5.61	5.01	5.39	4.91	5.77	1.18	down	5.95E-01	8.95E-01	-	-
1383651_a_at	Wdr45l	Wd-45like	360682	Rn.11823	AA864509	9.15	8.72	8.21	8.80	9.11	8.90	1.18	up	4.44E-01	8.95E-01	-	-
1389057_at	Arv1	ARV1 homolog (S. cerevisiae)	292097	Rn.13417	AI007774	4.66	4.67	5.12	4.68	4.72	4.32	1.18	down	2.92E-01	8.95E-01	-	-
1389054_at	LOC498368	similar to RIKEN cDNA 0610040J01	498368	Rn.29370	BE113616	6.92	8.33	8.01	7.81	8.00	8.18	1.18	up	6.09E-01	8.95E-01	-	-
1395328_at	Nsmce4a	non-SMC element 4 homolog A (S. cerevisiae)	293528	Rn.8649	AI102954	3.32	3.60	3.71	4.01	3.69	3.67	1.18	up	2.05E-01	8.95E-01	-	-
1368214_at	Smad2	SMAD family member 2	29357	Rn.2755	NM_019191	5.72	5.77	5.73	5.42	5.20	5.87	1.18	down	2.87E-01	8.95E-01	-	-
1395081_at	Ncoa7	nuclear receptor coactivator 7	498995	Rn.79194	BI290843	7.42	7.59	7.84	7.59	7.68	8.30	1.18	up	3.93E-01	8.95E-01	-	-
1369131_at	Slc18a2	solute carrier family 18 (vesicular monoamine), member 2	25549	Rn.9686	M97381	7.19	6.12	6.21	6.46	6.02	6.33	1.18	down	5.44E-01	8.95E-01	-	-
1380869_at	---	---	---	Rn.43078	AA893836	4.55	3.82	3.83	3.83	3.81	3.81	1.18	down	3.74E-01	8.95E-01	-	-
1384879_at	Trpt1	tRNA phosphotransferase 1	293704	Rn.166015	AI045958	3.37	3.60	3.15	3.70	3.27	3.87	1.18	up	3.33E-01	8.95E-01	-	-
1378492_at	---	---	---	Rn.206853	BF396209	4.53	3.93	4.14	3.49	4.30	4.08	1.18	down	4.64E-01	8.95E-01	-	-
1377020_at	Atp6v0a2 /// Tect2	ATPase, H+ transporting, lysosomal V0 subunit A2 /// tectonic 2	116455 /// 689779	Rn.204067	BF416408	3.48	3.61	3.58	3.62	3.83	3.95	1.18	up	8.10E-02	8.95E-01	-	-
1371431_at	Pex5	peroxisomal biogenesis factor 5	312703	Rn.14316	BI296577	8.76	8.08	8.32	8.08	8.15	8.20	1.18	down	2.94E-01	8.95E-01	-	-
1387654_at	Myo1c	myosin IC	65261	Rn.55135	NM_023092	3.73	4.16	3.87	4.71	3.92	3.86	1.18	up	4.68E-01	8.95E-01	-	-
1385404_at	Ankrd16	ankyrin repeat domain 16	307102	Rn.45470	AW522699	4.87	5.15	5.16	5.60	5.17	5.14	1.18	up	2.42E-01	8.95E-01	-	-
1390939_at	---	---	---	Rn.174745	AA944518	5.55	4.80	4.62	5.72	4.55	5.43	1.18	up	6.20E-01	8.95E-01	-	-
1382074_at	Rnf19b	ring finger protein 19B	313806	Rn.18272	AI113237	2.26	3.61	3.11	3.50	3.11	3.10	1.18	up	5.92E-01	8.95E-01	-	-
1383494_at	Srbd1	S1 RNA binding domain 1	301665	Rn.105705	BF414338	2.65	3.16	3.27	2.84	2.68	2.83	1.18	down	2.84E-01	8.95E-01	-	-
1392610_at	Topors	topoisomerase I binding, arginine/serine-rich	362501	Rn.55605	AI176588	7.68	7.17	7.07	7.50	7.68	7.47	1.18	up	2.92E-01	8.95E-01	-	-
1367500_at	Shfm1	split hand/foot malformation (ectrodactyly) type 1	680532	Rn.8472	AI169461	7.92	9.00	9.17	8.88	9.16	8.78	1.18	up	5.85E-01	8.95E-01	-	-
1375119_at	Nedd4	neural precursor cell expressed, developmentally down-regulated gene 4	25489	Rn.99540	BI284798	9.25	9.37	9.49	9.22	8.91	9.25	1.18	down	1.34E-01	8.95E-01	-	-
1382856_at	Xrcc6bp1	XRCC6 binding protein 1	299828	Rn.61651	BI295313	4.22	4.17	4.15	3.80	3.86	4.16	1.18	down	9.77E-02	8.95E-01	-	-
1393058_at	Eid2	EP300 interacting inhibitor of differentiation 2	685691	Rn.53893	BE101947	4.37	4.72	5.40	4.98	3.53	5.25	1.18	down	7.12E-01	9.10E-01	-	-
1374075_at	Napg	N-ethylmaleimide-sensitive factor attachment protein, gamma	307382	Rn.24090	AI175533	7.22	7.20	7.14	7.57	7.17	7.55	1.18	up	1.46E-01	8.95E-01	-	-
1380640_at	---	---	---	Rn.49823	BM389373	4.26	4.23	3.47	4.39	3.57	4.72	1.18	up	6.02E-01	8.95E-01	-	-
1390784_at	Wdr37	WD repeat domain 37	307075	Rn.163358	BG662814	2.74	4.40	4.34	3.38	3.92	4.90	1.18	up	7.48E-01	9.18E-01	-	-
1389296_at	Ttc35	tetratricopeptide repeat domain 35	362905	Rn.203197	AI104356	7.82	7.68	7.84	7.72	7.20	7.70	1.18	down	2.44E-01	8.95E-01	-	-
1392959_at	Bwk1	Bwk1 leukemia-related gene	296466	Rn.28608	AA925983	5.16	5.57	5.79	5.18	5.33	5.28	1.18	down	2.75E-01	8.95E-01	-	-
1372174_at	Pef1	penta-EF hand domain containing 1	297900	Rn.96097	AI009656	7.54	7.03	7.42	7.59	7.60	7.53	1.18	up	1.93E-01	8.95E-01	-	-
1367954_at	Gfra1	GDNF family receptor alpha 1	25454	Rn.88489	NM_012959	3.00	2.41	2.71	2.58	2.30	2.51	1.18	down	2.68E-01	8.95E-01	-	-
1377517_at	---	---	---	Rn.16212	AA945491	5.73	5.34	5.12	5.29	4.51	5.67	1.18	down	5.63E-01	8.95E-01	-	-
1378408_at	RGD1563351	RIKEN cDNA 1563351	296350	Rn.35304	BE107015	2.35	3.06	2.35	2.34	2.35	2.34	1.18	down	3.67E-01	8.95E-01	-	-
1381947_at	RGD1560210	RGD1560210	295622	Rn.43872	AI169006	8.25	5.96	7.46	6.63	8.64	7.12	1.18	up	8.62E-01	9.36E-01	-	-
1388405_at	Ckap5	cytoskeleton associated protein 5	311191	Rn.6646	BI294780	7.55	7.02	7.40	7.24	7.09	6.91	1.18	down	2.58E-01	8.95E-01	-	-
1375717_at	Aes	Amino-terminal enhancer of split	29466	Rn.11495	AI547966	2.69	3.14	2.71	2.73	2.40	2.69	1.18	down	2.51E-01	8.95E-01	-	-
1376222_at	RGD1309307	similar to HCDI protein	361044	Rn.38645	AI710677	7.27	7.36	6.28	7.42	6.05	8.16	1.18	up	7.50E-01	9.19E-01	-	-
1387458_at	Rnf4	ring finger protein 4	29274	Rn.205059	NM_019182	5.60	6.28	6.52	5.98	6.88	6.26	1.18	up	5.62E-01	8.95E-01	-	-
1383676_at	Sfrs8	splicing factor, arginine/serine-rich 8	304431	Rn.12338	AA996595	5.25	5.34	5.24	5.24	6.07	5.25	1.18	up	4.30E-01	8.95E-01	-	-
1371670_at	Exosc4	exosome component 4	300045	Rn.28481	BF407149	6.53	6.43	6.32	6.80	6.51	6.69	1.18	up	8.06E-02	8.95E-01	-	-
1389923_at	Bbs9	Bbs9 (PQ2) domain containing 9	294318	Rn.48897	BE104474	4.47	5.36	4.95	5.80	4.32	5.38	1.18	up	6.81E-01	8.98E-01	-	-
1383762_at	RGD1565545	similar to zinc finger protein ZFP	308337	Rn.198482	BI274613	4.71	3.87	4.02	3.67	4.61	5.05	1.18	up	6.43E-01	8.95E-01	-	-
1376936_at	Slc24a6	solute carrier family 24 (sodium/potassium/calcium exchanger), member 6	498185	Rn.13225	BI298215	2.51	2.62	2.85	2.41	2.42	2.42	1.18	down	7.33E-02	8.95E-01	-	-
1398780_at	Rabac1	Rab acceptor 1 (prenylated)	83583	Rn.25604	NM_031774	6.99	6.91	6.22	6.66	6.20	6.55	1.18	down	4.40E-01	8.95E-01	-	-
1387114_at	Prkcd	protein kinase C, delta	170538	Rn.98279	NM_133307	5.59	5.19	4.94	5.73	5.29	5.42	1.18	up	3.54E-01	8.95E-01	-	-
1387087_at	Cebpb	CCAAT/enhancer binding protein (C/EBP), beta	24253	Rn.6479	NM_024125	4.59	4.53	4.16	4.82	4.60	4.59	1.18	up	1.92E-01	8.95E-01	-	-
1393279_at	---	---	---	Rn.19888	AI070869	2.47	2.47	2.48	2.46	3.27	2.42	1.18	up	4.33E-01	8.95E-01	-	-
1372198_at	Mepce	methylphosphate capping enzyme	304361	Rn.198943	BG376471	4.77	4.13	4.03	4.07	4.08	4.07	1.18	down	3.57E-01	8.95E-01	-	-
1390757_at	c21 /// RGD15663	cell division cycle 2 homolog (S.pombe)-like 1 /// similar to cell division cycle 2	252879 /// 315362	Rn.10204	BE116564	4.83	5.04	4.31	4.79	5.30	4.80	1.18	up	4.27E-01	8.95E-01	-	-
1372294_at	Pxdn	peroxidasin homolog (Drosophila)	554172	Rn.40541	BI278571	2.89	2.82	3.06	2.82	3.96	2.71	1.18	up	5.85E-01	8.95E-01	-	-
1373304_at	Coasy	Coenzyme A synthase	287711	Rn.36938	BM392002	7.81	8.77	8.18	8.70	7.75	9.02	1.18	up	6.36E-01	8.95E-01	-	-
1371702_at	Tspan7	tetraspanin 7	363447	Rn.13685	AI234044	4.65	4.97	5.32	5.19	6.06	4.41	1.18	up	6.62E-01	8.98E-01	-	-
1375421_a_at	Pja2	praja 2, RING-H2 motif containing	192256	Rn.18446	AI600019	5.89	6.36	6.48	6.36	5.97	7.12	1.18	up	5.65E-01	8.95E-01	-	-
1375176_at	Mrps36	mitochondrial ribosomal protein S36	294696	Rn.3406	AW142276

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)				REG	MTC
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval		
1388212_a_at	H2-T23 /// H2-T24	histocompatibility 2, T region locus 23 /// histocompatibility 2, T region locus 22	294228 /// 414784	---	AJ243974	7.72	6.54	6.73	6.86	6.66	8.18	1.18	up	7.12E-01	9.10E-01	-	-
1390535_at	Ctdp1	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) phosphata	291414	Rn.137952	BE098745	7.84	8.52	7.48	8.16	8.37	8.03	1.18	up	5.00E-01	8.95E-01	-	-
1385163_at	Rnf20	ring finger protein 20	313218	Rn.15969	BF397033	4.49	6.53	4.49	4.49	5.60	6.12	1.18	up	7.89E-01	9.32E-01	-	-
1372295_at	Narf	nuclear prelamin A recognition factor	360681	Rn.162225	BF551356	4.64	5.22	4.72	5.06	5.18	5.06	1.18	up	2.73E-01	8.95E-01	-	-
1374625_at	Hes6	hairy and enhancer of split 6 (Drosophila)	316626	Rn.11980	AI176616	8.05	8.45	8.94	8.07	8.43	8.23	1.18	down	4.40E-01	8.95E-01	-	-
1397343_at	---	---	---	---	BE113258	2.62	2.60	2.61	2.59	3.43	2.52	1.18	up	4.61E-01	8.95E-01	-	-
1372993_at	---	---	---	Rn.206466	BI209621	2.52	2.50	3.48	2.80	2.50	2.48	1.18	down	5.19E-01	8.95E-01	-	-
1398647_at	---	---	---	Rn.200318	BI288939	6.70	6.94	7.48	7.29	7.16	7.39	1.18	up	3.77E-01	8.95E-01	-	-
1370464_at	Abcb1a	ATP-binding cassette, sub-family B (MDR/TAP), member 1A	170913	Rn.154810	AF286167	2.98	2.76	3.13	3.14	3.26	3.19	1.18	up	1.04E-01	8.95E-01	-	-
1368354_at	Gstt1	glutathione S-transferase theta 1	25260	Rn.11122	NM_012393	7.77	8.03	8.33	8.17	7.29	7.95	1.18	down	4.86E-01	8.95E-01	-	-
1369969_at	Parp1	poly (ADP-ribose) polymerase 1	25591	Rn.11327	NM_013063	4.91	4.64	4.69	4.84	5.00	5.11	1.18	up	1.07E-01	8.95E-01	-	-
1382975_at	Ceacam1	carcinoembryonic antigen-related cell adhesion molecule 1 (biliary glycoprote	81613	Rn.91235	BE097239	5.19	5.03	5.32	4.48	3.81	6.54	1.18	down	7.88E-01	9.31E-01	-	-
1377454_at	Ztrb9	zinc finger and BTB domain containing 9	294289	Rn.15118	AW524041	4.11	3.68	3.22	3.33	3.30	3.68	1.18	down	4.50E-01	8.95E-01	-	-
1391878_at	Son	Son DNA binding protein	304092	Rn.7967	AW531885	4.49	4.50	4.36	5.65	3.90	4.51	1.18	up	6.67E-01	8.99E-01	-	-
1372177_at	Mocs2	molybdenum cofactor synthesis 2	294753	Rn.13568	AI180033	8.32	7.97	8.53	7.95	8.10	8.06	1.18	down	2.37E-01	8.95E-01	-	-
1368908_at	Anxa4	annexin A4	79124	Rn.19270	NM_024155	6.33	6.97	5.59	6.53	5.60	6.04	1.18	down	6.45E-01	8.95E-01	-	-
1379977_at	Oxa3	ORAI calcium release-activated calcium modulator 3	308900	Rn.42186	AI176858	3.55	3.89	3.17	3.73	4.08	3.52	1.18	up	4.18E-01	8.95E-01	-	-
1377776_at	Wdsub1	WD repeat, sterile alpha motif and U-box domain containing 1	362137	Rn.101918	AI070369	3.15	3.93	3.63	3.89	2.91	4.64	1.18	up	6.88E-01	9.04E-01	-	-
1376645_at	RGD1307396	similar to RIKEN cDNA 6330406I15	360757	Rn.14770	AW916327	2.76	3.60	3.68	2.72	3.17	3.44	1.18	down	5.47E-01	8.95E-01	-	-
1380692_at	Rb1	retinoblastoma-like 1 (p107)	680111	Rn.208977	BM387127	2.60	3.39	2.62	2.58	2.66	2.66	1.18	down	4.12E-01	8.95E-01	-	-
1377969_at	---	---	---	Rn.155302	AI502535	2.43	2.37	2.45	2.37	3.23	2.36	1.18	up	4.55E-01	8.95E-01	-	-
1378547_at	---	---	---	Rn.202652	AI176027	4.28	4.78	4.80	4.84	4.78	4.96	1.18	up	2.53E-01	8.95E-01	-	-
1374423_at	Hiat1	hippocampus abundant gene transcript 1	100134827	Rn.128804	BE115866	6.80	7.32	6.54	7.36	6.56	7.47	1.18	up	5.52E-01	8.95E-01	-	-
1398136_at	RGD1562218	similar to RIKEN cDNA 0610039J04	292100	Rn.25199	AI716403	3.06	2.35	2.37	2.35	2.36	2.35	1.18	down	3.66E-01	8.95E-01	-	-
1372960_a_at	Xylt2	xylosyltransferase II	64134	Rn.22727	AA892497	5.24	5.38	5.62	5.73	5.39	5.84	1.18	up	2.46E-01	8.95E-01	-	-
1381525_at	---	---	---	Rn.165320	BF419130	5.54	4.79	4.82	4.77	4.80	4.87	1.18	down	3.90E-01	8.95E-01	-	-
1373352_at	LOC685385	similar to S100 calcium binding protein A14	685385	Rn.160952	BM387197	2.57	3.09	2.62	2.54	2.60	2.44	1.18	down	2.43E-01	8.95E-01	-	-
1373462_at	Eed	embryonic ectoderm development	293104	Rn.3939	AI170325	5.68	5.99	4.63	5.07	5.57	6.37	1.18	up	6.93E-01	9.05E-01	-	-
1369247_at	Sp1	Sp1 transcription factor	24790	Rn.44609	NM_012655	3.16	3.34	3.17	3.23	2.71	3.02	1.18	down	2.10E-01	8.95E-01	-	-
1372593_at	Zfp110	zinc finger protein 110	308362	Rn.204252	AI137283	6.33	7.35	5.80	6.83	4.65	7.28	1.18	down	8.11E-01	9.39E-01	-	-
1376515_at	---	---	---	Rn.7020	AI137236	2.40	2.54	2.41	3.28	2.41	2.37	1.18	up	4.71E-01	8.95E-01	-	-
1388954_at	RGD1306717	similar to hypothetical protein MGC25461	311257	Rn.40316	BI295749	2.70	2.92	2.63	3.14	2.63	3.19	1.18	up	3.02E-01	8.95E-01	-	-
1389651_at	Apln	apelin	58812	Rn.22847	AI177057	2.33	2.40	2.33	2.33	3.09	2.35	1.18	up	3.94E-01	8.95E-01	-	-
1370983_at	Pou6f1	POU class 6 homeobox 1	116545	Rn.44845	AW523687	4.01	4.86	3.74	4.62	3.93	4.77	1.18	up	6.07E-01	8.95E-01	-	-
1367496_at	Tm9sf2	transmembrane 9 superfamily member 2	306197	Rn.11839	AI179901	9.32	9.55	9.45	9.60	9.51	9.93	1.18	up	1.75E-01	8.95E-01	-	-
1372209_at	Copa5	COP9 constitutive photomorphogenic homolog subunit 5 (Arabidopsis)	312916	Rn.2243	AI105072	7.05	7.71	7.19	7.24	7.49	7.93	1.18	up	4.48E-01	8.95E-01	-	-
1386974_at	Phldb1	pleckstrin homology-like domain, family B, member 1	171434	Rn.11128	NM_134397	3.67	3.57	3.48	3.06	3.48	3.47	1.18	down	1.84E-01	8.95E-01	-	-
1396819_at	Nars	Asparaginyl-tRNA synthetase	291556	Rn.48209	AW533965	2.49	2.74	2.34	3.49	2.33	2.46	1.18	up	5.72E-01	8.95E-01	-	-
1380369_at	---	---	---	Rn.20945	AI058315	2.38	3.12	2.34	2.37	2.39	2.37	1.18	down	4.01E-01	8.95E-01	-	-
1378912_at	Anapc1	anaphase promoting complex subunit 1	311412	Rn.8	BG376091	2.56	2.52	2.57	3.24	2.58	2.53	1.18	up	3.61E-01	8.95E-01	-	-
1368550_at	Foxq1	forkhead box Q1	64826	Rn.10101	NM_022858	4.61	2.63	2.99	3.81	2.52	3.19	1.18	down	7.56E-01	9.21E-01	-	-
1384166_a_at	---	---	---	Rn.216474	AW522260	3.85	3.60	3.93	3.91	4.04	4.14	1.18	up	1.17E-01	8.95E-01	-	-
1377955_at	---	---	---	Rn.18207	AI137602	2.49	4.18	2.67	2.56	2.58	3.49	1.18	down	7.20E-01	9.11E-01	-	-
1398663_at	Zfp61	zinc finger protein 61	499094	Rn.122263	AI030120	4.66	4.45	4.11	4.62	2.76	5.13	1.18	down	7.64E-01	9.23E-01	-	-
1371795_at	---	---	---	---	AA848795	8.94	7.46	7.76	7.89	7.57	7.99	1.18	down	6.41E-01	8.95E-01	-	-
1374395_at	---	---	---	Rn.114978	AI102825	3.64	3.39	3.64	4.14	3.64	3.60	1.18	up	2.88E-01	8.95E-01	-	-
1379606_at	Rab30	RAB30, member RAS oncogene family	308821	Rn.161854	BM392291	3.14	2.45	2.45	2.43	2.45	2.44	1.18	down	3.60E-01	8.95E-01	-	-
1370663_at	Wee1	wee 1 homolog (S. pombe)	308837	Rn.208255	D31838	3.52	2.62	2.72	2.82	2.74	2.59	1.18	down	4.62E-01	8.95E-01	-	-
1380542_at	---	---	---	---	AI013758	3.21	2.52	2.55	2.53	2.54	2.49	1.18	down	3.54E-01	8.95E-01	-	-
1398364_at	RGD1359529	similar to chromosome 1 open reading frame 63	362626	Rn.3870	BF555972	10.26	10.03	9.60	9.95	9.68	9.56	1.18	down	3.50E-01	8.95E-01	-	-
1398579_at	Eea1	early endosome antigen 1	314764	Rn.23513	AA997808	5.78	5.06	4.71	5.19	4.02	5.62	1.18	down	7.01E-01	9.07E-01	-	-
1372206_at	Tmem55b	transmembrane protein 55B	364298	Rn.37250	AI412469	8.19	8.16	8.18	8.72	8.32	8.20	1.18	up	2.06E-01	8.95E-01	-	-
1369077_at	Asah1	N-acylsphingosine amidohydrolase (acid ceramidase) 1	84431	Rn.127798	NM_053407	5.16	4.63	5.58	5.62	5.08	5.39	1.18	up	4.95E-01	8.95E-01	-	-
1370035_at	Kras	v-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog	24525	Rn.24554	NM_031515	5.49	6.15	5.54	5.43	4.84	6.20	1.18	down	6.25E-01	8.95E-01	-	-
1381246_at	---	---	---	Rn.109718	BI293437	2.55	2.55	2.38	2.97	2.56	2.67	1.18	up	1.50E-01	8.95E-01	-	-
1383586_at	Arpp-19	Cyclic AMP phosphoprotein	60336	Rn.112577	BI295793	5.85	5.74	6.32	5.45	6.09	5.66	1.18	down	4.16E-01	8.95E-01	-	-
1368675_at	Chn2	chimerin (chimaerin) 2	84031	Rn.10521	NM_032084	4.94	7.06	6.92	6.42	6.28	5.51	1.18	down	7.66E-01	9.24E-01	-	-
1396344_at	---	---	---	---	AI548117	4.49	4.83	3.99	4.67	4.08	5.27	1.18	up	6.02E-01	8.95E-01	-	-
1392586_at	Mudeng	MU-2/AP1M2 domain containing, death-inducing	305861	Rn.162064	AI704512	4.96	5.35	5.71	5.47	4.85	4.99	1.18	down	4.58E-01	8.95E-01	-	-
1398360_at	LOC679532	similar to Elongation of very long chain fatty acids protein 1	679532	Rn.29724	AI009805	7.73	7.67	7.12	7.51	7.06	7.24	1.18	down	3.72E-01	8.95E-01	-	-
1385473_x_at	Tomm40b	translocase of outer mitochondrial membrane 40 homolog B (yeast)	304971	Rn.113744	AI044497	2.58	2.70	3.40	2.67	2.67	2.62	1.18	down	4.07E-01	8.95E-01	-	-
1395165_at	Paip1	PC4 and SFRS1 interacting protein 1	313323	Rn.93075	BF397386	4.12	3.23	2.99	3.49	3.50	4.05	1.18	up	5.77E-01	8.95E-01	-	-
1389984_at	LOC681740	similar to jumonji protein	681740	---	AI072294	8.86	8.23	8.11	8.50	7.70	8.30	1.18	down	5.17E-01	8.95E-01	-	-
1399055_at	Brd7	bromodomain containing 7	361374	Rn.32686	BI275924	5.13	5.33	5.72	5.92	4.74	6.23	1.18	up	6.52E-01	8.97E-01	-	-
1379249_at	Wtap	Wilms tumor 1 associated protein	499020	Rn.161764	AA900400	9.08	8.25	7.52	8.46	8.44	8.66	1.18	up	6.32E-01	8.95E-01	-	-
1373501_at	Nek7	NIMA (never in mitosis gene a)-related kinase 7	360850	Rn.3649	AA955361	4.69	6.78	6.04	5.24	5.73	7.26	1.18	up	7.97E-01	9.35E-01	-	-
1387057_at	Slc7a8	solute carrier family 7 (cationic amino acid transporter, y+ system), member 8	84551	Rn.82734	NM_053442	3.85	2.52	2.61	3.19	2.56	2.52	1.18	down	6.48E-01	8.96E-01	-	-
1382861_at	Tcea1	transcription elongation factor A (SII) 1	362479	Rn.6738	AA997486	6.45	6.57	6.89	6.53	7.08	7.01	1.18	up	3.37E-01	8.95E-01	-	-
1377635_at	Fmo2	flavin containing monooxygenase 2	246249	Rn.3928	BM389350	6.96	6.29	5.18	6.83	6.00	6.31	1.18	up	7.00E-01	9.07E-01	-	-
1397764_at	Kctd5	potassium channel tetramerisation domain containing 5	287109	Rn.161259	BG379719	7.36	7.94	7.30	7.86	7.79	7.66	1.18	up	3.29E-01	8.95E-01	-	-
1371981_at	Dscr3	Down syndrome critical region gene 3	360703	Rn.19717	BI294700	3.96	3.83	3.34	3.47	4.01	4.35	1.18	up	4.99E-01	8.95E-01	-	-
1388348_at	---	---	---	Rn.222012	BI278590	7.87	7.70	8.61	7.48	7.82	8.17	1.18	down	5.29E-01	8.95E-01	-	-
1391581_at	---	---	---	Rn.202459	BE104302	3.62	3.95	3.64	3.58	3.37	3.55	1.18	down	1.37E-01	8.95E-01	-	-
1376238_at	Hus1	HUS1 checkpoint homolog (S. pombe)	498411	Rn.12812	BI288733	6.34	6.34	5.16	6.32	5.66	6.57	1.18	up	6.47E-01	8.95E-01	-	-
1376018_at	Lmnb2	Lamin B2	299525	Rn.12408	BF398513	2.47	3.16	2.83	2.48	2.48	2.79	1.18	down	3.54E-01	8.95E-01	-	-
1374852_at	RGD1559909	RGD1559909	362592	Rn.29869	AI407613	5.04	4.97	4.86	5.26	4.80	5.51	1.18	up	3.34E-01	8.95E-01	-	-
1371389_at	LOC306766	hypothetical LOC306766	306766	Rn.162182	AI170668	11.14	11.22	11.03	10.71	11.02	10.95	1.18	down	1.03E-01	8.95E-01	-	-
1398889_at	Grin1a	glutamate receptor, ionotropic, N-methyl D-aspartate-like 1A	192147	Rn.144666	BE113383	8.70	8.74	8.47	8.73	8.88	9.01	1.18	up	1.11E-01	8.95E-01	-	-
1381966_at	Arid1b	AT rich interactive domain 1B (Swi1 like)	282546	Rn.22598	AI235085	3.31	3.45	3.55	3.12	2.93	3.55	1.18	down	2.92E-01	8.95E-01	-	-
1391363_at	---	---	---	---	BF404844	2.67	3.64	3.79	3.09	3.14	3.17	1.18	down	5.40E-01	8.95E-01	-	-
1371103_at	Rab6a	RAB6A, member RAS oncogene family	84379	Rn.1695	AA686757	6.07	5.85	6.01	5.19	5.97	6.07	1.18	down	4.57E-01	8.95E-01	-	-
1375720_at	Gabbr1	gamma-aminobutyric acid (GABA) B receptor 1	81657	Rn.30059	AI171785	3.34	2.68	2.83	2.66	2.74	2.74	1.18	down	3.07E-01	8.95E-01	-	-
1385039_at	---	---	---	Rn.219035	BF410877	2.60	2.70	2.60	2.59	2.62	3.39	1.18	up	4.19E-01	8.95E-01	-	-
1382655_at	---	---	---	Rn.165290	AA964534	6.40	6.56	6.10	6.43	6.44	6.90	1.18	up	3.12E-01	8.95E-01	-	-
1387632_at	LOC64038	sertolin	64038	Rn.25472	NM_022271	3.47	3.64	3.60	3.09	3.47	3.45	1.18	down	1.58E-01	8.95E-01	-	-
1393466_at	Cd164l2	CD164 sialomucin-like 2	689082	Rn.16127	BF411837	3.56	3.31	3.80	3.32	3.33	3.31	1.18	down	1.73E-01	8.95E-01	-	-
1371236_at	Grm6	glutamate receptor, metabotropic 6	24419	Rn.44615	AJ245718	2.40	2.39	3.10	2.39	2.41	2.38	1.18	down	3.72E-01	8.95E-01	-	-
1387183_at	Crot	carnitine O-octanoyltransferase	83842	Rn.4896	J02844	4.71	5.09	4.66	4.95	4.92	5.30	1.18	up	2.68E-01	8.95E-01	-	-
1375879_at	---	---	---	Rn.30054	BE116782	7.43	7.33	6.54	7.57	6.55	7.89	1.18	up	6.58E-01	8.98E-01	-	-
1377681_at	---	---	---	Rn.23380	AA925313	3.72	3.77	3.69	3.84	4.25	3.81	1.18	up	1.76E-01	8.95E-01	-	-
1393718_at	---	---	---	Rn.199875	BE117189	6.60	6.51	7.42	6.51	6.47	6.85	1.18	down	4.92E-01	8.95E-01	-	-
1367543_at	LOC685079	similar to Protein SYS1 homolog	685079	Rn.31818	BG377443	4.08	4.69	4.82	4.59	4.86	4.81	1.18	up	4.01E-01	8.95E-01	-	-
1369696_at	Rragb	Ras-related GTP binding B	117043	Rn.203382	NM_053972	2.41	2.42	2.41	2.40	2.42	2.42	1.18	down	3.74E-01	8.95E-01	-	-
1368026_at	Hdgfrp2	hepatoma-derived growth factor, related protein 2	171073	Rn.29462	NM_133548	7.32	6.85	7.02	7.01	6.99	6.49	1.18	down	3.47E-01	8.95E-01	-	-
1392320_s_at	Glmn	glomulin, FKBP associated protein	289437	Rn.44333	AI763657	3.17	4.62	2.96	3.25	3.18	3.61	1.18	down	6.85E-01	9.03E-01	-	-
1389797_at	---	---	---	Rn.20362	AI317854	2.27	2.26	2.27	2.27	2.97	2.27	1.18	up	3.75E-01	8.95E-01	-	-
1369982_at	Ap2a2	adaptor-related protein complex 2, alpha 2 subunit	81637	Rn.34928	NM_031008	7.02	6.96	7.41	6.85	6.67	7.17	1.18	down	3.11E-01	8.95E-01	-	-
1397964_at	Sec63	SEC63 homolog (S. cerevisiae)	309858	Rn.24233	AI406662	3.73	4.99	6.77	5.27	5.44	5.48	1.18	up	8.03E-01	9.37E-01	-	-
1374419_at	---	---	---	Rn.18792	AI044435	3.08	3.76	4.18	3.74	3.12	3.46	1.18	down	5.58E-01	8.95E-01	-	-
1396235_at	Wdr32	WD repeat domain 32	313242	Rn.199359	AI137779	3.03	2.69	3.06	2.95	3.13	3.00	1.18	up	1.45E-01	8.95E-01	-	-
1371411_at	Plxnb2	plexin B2	315217	Rn.22051	BG380275	3.69	4.71	4.63	4.09	3.69	4.54	1.18	down	5.98E-01	8.95E-01	-	-
1375995_at	RGD1304592	similar to KIAA0528 protein	362461	Rn.62095	AI180370	7.41	8.34	8.32	8.15	8.54	8.09	1.18	up	5.23E-01	8.95E-01	-	-
1391536_at	Mios	missing oocyte, meiosis regulator, homolog (Drosophila)	362324	Rn.103328	AA892645	2.63	2.72	3.13	3.26	2.71	3.22	1.18	up	3.74E-01	8.95E-01	-	-
1383286_at	Plek2	pleckstrin 2	314260	Rn.22995	AW919349	2.38	3.09	3.56	2.48	2.44	3.40	1.18	down	6.38E-01	8.95E-01	-	-
1382071_at	Nrf1	Nuclear respiratory factor 1	312195	Rn.17159	BI302916	4.26	3.58	4.98	4.62	4.53	4.38	1.18	up	5.97E-01	8.95E-01	-	-
1390648_at	Herc2	hect domain and RLD 2	308869	Rn.28217	AW523544	5.14	4.43	4.36	4.31	5.65	4.67	1.18	up	6.46E-01	8.95E-01	-	-
1379314_at	Ppp3cb	protein phosphatase 3, catalytic subunit, beta isoform	24675	Rn.11063	BF283985	5.38	6.43	6.72	5.78	6.30	5.75	1.18	down	6.24E-01	8.95E-01	-	-
1368516_at	Ptpra	protein tyrosine phosphatase, receptor type, A	25167	Rn.18043	NM_012763	4.90	5.96	5.53	5.33	5.78	5.98	1.18	up	5.51E-01	8.95E-01	-	-
1380884_at	---	---	---	Rn.147998	AW524553	2.57	2.46	2.62	3.30	2.55	2.50	1.18	up	4.22E-01	8.95E-01	-	-
1383893_at	Nedd4	neural precursor cell expressed, developmentally down-regulated gene 4	25489	Rn.99540	BI277649	7.34	7.66	7.54	6.96	7.30	7.57	1.18	down	3.04E-01	8.95E-01	-	-
1383202_at	Lsm6	LSM6 homolog, U6 small nuclear RNA associated (S. cerevisiae)	498934	Rn.139376	AA818406	5.87	5.23	5.67	5.58	5.24	5.25	1.18	down	3.48E-01	8.95E-01	-	-
1391550_at	Rad54l2	Rad54 like 2 (S. cerevisiae)	363135	Rn.21743	BE108780	5.41	4.78	5.37	5.50	3.88	5.47	1.18	down	7.02E-01	9.07E-01	-	-
1374755_at	---	---	---	Rn.164710	BG667112	3.28	2.58	2.59	2.58	2.59	2.57	1.18	down	1.69E-01	8.95E-01	-	-
1376402_a_at	Rasl10b	RAS-like, family 10, member B	303382	Rn.8804	BF557338	2.71	3.25	2.72	2.71	4.00	2.68	1.18	up	6.45E-01	8.95E-01	-	-
1378530_at	Ppp2r5e	protein phosphatase 2, regulatory subunit B', epsilon isoform	299147	Rn.24394	BF394061	2.47	2.46	2.44	2.51	2.81	2.75	1.18	up	6.09E-02	8.95E-01	-	-
1370390_at	Coro6	coronin, actin binding protein 6	245982	Rn.28432	AF140359	2.46	2.84	2.68	2.35	2.47	2.46	1.18	down	1.11E-01	8.95E-01	-	-
1389434_at	Myg1	melanocyte proliferating gene 1	300258	AA818018	6.05	5.83	5.43	5.03	6.72	6.26	1.18	up	6.85E-01	9.03E-01	-	-
1378555_at	Lrrc28	leucine rich repeat containing 28	361588	Rn.16888	BE107055	3.57	3.63	3.58	3.58	3.57	4.33	1.18	up	4.05E-01	8.95E-01	-	-
1381276_at	---	---	---	Rn.169578	AW526951	3.10	3.50	2.52	2.94	2.79	2.68	1.18	down	4.68E-01	8.95E-01	-	-
1378867_at	Hspc159	galectin-related protein	360983	Rn.17651	BE095833	3.85	4.12	3.89	3.96	3.87	4.73	1.18	up	4.62E-01	8.95E-01	-	-
1384319_at	Tlk2	Tousled-like kinase 2	303592	Rn.23125	BE098518	6.09	5.97	5.38	5.93	6.31	5.91	1.18	up	4.12E-01	8.95E-01	-	-
1392331_at	---	---	---	---	BE100256	3.24	4.31	4.64	4.67	4.02	4.19	1.18	up	6.41E-01	8.95E-01	-	-
1394572_at	---	---	---	Rn.172049	AI231560	2.52	2.51	2.53	2.56	3.21	2.49	1.18	up	3.65E-01	8.95E-01	-	-
1371399_at	Tomm6	translocase of outer mitochondrial membrane 6 homolog (yeast)	681123	Rn.1327	AA818196	9.00	8.61	8.26	8.33	8.44	8.40	1.18	down	3.44E-01	8.95E-01	-	-
1371251_at	Galt	galactose-1-phosphate uridylyltransferase	298003	Rn.102781	L05541	5.26	5.71	5.28	5.41	5.95	5.60	1.18	up	3.44E-01	8.95E-01	-	-
1381144_at	---	---	---	Rn.65720	AW524106	3.57	3.30	2.93	3.33	3.35	3.83	1.18	up	4.03E-01	8.95E-01	-	-
1388624_at	RGD1561113	similar to Hypothetical UPF0184 protein C9orf16 homolog	499780	Rn.2148	BG689670	3.04	3.11	3.24	2.73	2.72	3.24	1.18	down	2.62E-01	8.95E-01	-	-
1369709_at	Atxn1	ataxin 1	25049	Rn.207161	NM_012726	6.00	5.77	6.18	5.90	5.72	5.63	1.18	down	1.76E-01	8.95E-01	-	-
1378494_at	---	---	---	Rn.171795	BF394109	4.98	4.69	4.08	5.27	3.96	3.81	1.18	down	6.83E-01	9.03E-01	-	-
1367926_at	Phb	prohibitin	25344	Rn.29754	BI282863	6.37	7.42	7.10	7.57	6.64	7.38	1.18	up	6.09E-01	8.95E-01	-	-
1389071_at	Ehbp111	EH domain binding protein 1-like 1	309169	Rn.103357	BI287221	3.36	2.56	2.57	2.75	2.49	2.55	1.18	down	4.48E-01	8.95E-01	-	-
1367743_at	Pfkl	phosphofructokinase, liver	25741	Rn.4212	NM_013190	5.53	5.34	5.90	4.91	5.71	5.44	1.18	down	4.65E-01	8.95E-01	-	-
1391834_at	Chmp4c	Chromatin modifying protein 4C	361916	Rn.162567	BM386419	6.60	7.12	7.38	6.97	7.23	7.60	1.18	up	4.70E-01	8.95E-01	-	-
1367846_at	S100a4	S100 calcium-binding protein A4	24615	Rn.504	NM_012618	2.36	2.36	2.39	3.09	2.37	2.34	1.18	up	3.94E-01	8.95E-01	-	-
1367534_at	Rabgap1	RAB GTPase activator 1	311911	Rn.14944	BG374688	7.67	7.83	6.75	7.64	7.44	7.86	1.18	up	5.50E-01	8.95E-01	-	-
1373395_at	Trim41	tripartite motif-containing 41	303088	Rn.79871	AI044721	6.20	6.73	5.44	6.36	6.12	6.60	1.18	up	5.91E-01	8.95E-01	-	-
1375162_at	Ube2q1	ubiquitin-conjugating enzyme E2Q family member 1	295252	Rn.19034	AW805001	7.03	7.19	7.22	7.59	7.02	7.53	1.18	up	2.88E-01	8.95E-01	-	-
1390612_at	LOC682647	hypothetical protein LOC682647	682647	---	BI291259	2.57	2.99	2.88	2.57	2.58	2.59	1.18	down	1.32E-01	8.95E-01	-	-
1380371_at	NIPBL	Nipped-B homolog (Drosophila)	294787	Rn.11589	BE117361	4.55	4.35	2.94	3.15	4.66	4.73	1.18	up	7.63E-01

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1384016_at	RGD1563634	similar to R31449_3	500790	Rn.136995	AI044937	2.36	2.43	2.36	2.35	2.44	3.05	1.17	up	3.53E-01	8.95E-01	-	-
1371354_at	Tnnc1	troponin C type 1 (slow)	290561	Rn.15460	AI710682	3.20	2.60	2.63	2.60	2.62	2.51	1.17	down	3.10E-01	8.95E-01	-	-
1368933_at	Adarb1	adenosine deaminase, RNA-specific, B1	25367	Rn.89675	NM_012894	2.35	3.19	2.37	2.51	2.36	2.35	1.17	down	4.57E-01	8.95E-01	-	-
1374393_at	OC690040 /// Ptpn	similar to protein tyrosine phosphatase-like (proline instead of catalytic arginin	288058 /// 690040	Rn.108344	AI169080	6.93	6.70	6.89	5.74	6.89	7.19	1.17	down	6.32E-01	8.95E-01	-	-
1399004_at	LOC679572	similar to CG6878-PA	679572	Rn.3356	BM986309	11.89	12.09	12.02	11.99	11.63	11.69	1.17	down	1.42E-01	8.95E-01	-	-
1374215_at	Plekhj1	pleckstrin homology domain containing, family J member 1	314634	Rn.145097	AA848429	4.91	5.09	4.46	4.81	5.08	5.26	1.17	up	3.68E-01	8.95E-01	-	-
1367864_at	Pfkm	phosphofructokinase, muscle	65152	Rn.11004	BI291434	5.10	4.82	4.86	4.84	5.04	4.20	1.17	down	4.39E-01	8.95E-01	-	-
1388804_at	---	---	---	Rn.16035	BI300986	2.32	2.32	3.02	2.33	2.33	2.31	1.17	down	3.77E-01	8.95E-01	-	-
1398580_at	Wdr31	WD repeat domain 31	298096	Rn.38938	AW435480	4.79	4.39	4.56	4.53	4.73	5.17	1.17	up	3.51E-01	8.95E-01	-	-
1381124_at	---	---	---	Rn.66488	AA819672	7.26	6.84	6.42	7.12	6.96	7.13	1.17	up	4.03E-01	8.95E-01	-	-
1373301_at	Ppp1r13b	protein phosphatase 1, regulatory (inhibitor) subunit 13B	314465	Rn.30183	BE113133	3.49	3.48	3.41	4.10	3.78	3.20	1.17	up	4.30E-01	8.95E-01	-	-
1393446_at	---	---	---	Rn.146263	BI290444	3.30	2.51	2.57	2.52	2.52	2.65	1.17	down	4.17E-01	8.95E-01	-	-
1375464_at	RGD1564982	RGD1564982	308556	Rn.3332	BI290815	4.01	4.57	4.25	4.32	4.89	4.31	1.17	up	4.09E-01	8.95E-01	-	-
1387452_a_at	Nfyb	nuclear transcription factor-Y beta	25336	Rn.90077	NM_031553	2.78	4.64	2.85	4.38	2.72	3.87	1.17	up	7.81E-01	9.29E-01	-	-
1367772_at	Clns1a	chloride channel, nucleotide-sensitive, 1A	65160	Rn.4089	NM_031719	5.86	5.91	6.33	5.68	6.49	6.62	1.17	up	5.21E-01	8.95E-01	-	-
1373374_at	Lmo4	LIM domain only 4	362051	Rn.2517	BM389691	9.45	8.92	10.20	9.01	9.59	9.28	1.17	down	6.00E-01	8.95E-01	-	-
1398842_at	Cltc	clathrin, heavy chain (Hc)	54241	Rn.3589	BM386513	10.64	10.78	10.85	10.39	10.57	10.62	1.17	down	6.73E-02	8.95E-01	-	-
1388930_at	Tmem123	transmembrane protein 123	363013	Rn.12767	AI171651	5.93	5.52	5.71	5.13	5.25	6.08	1.17	down	5.10E-01	8.95E-01	-	-
1380741_at	---	---	---	Rn.166361	BF412788	3.15	2.91	3.15	3.38	2.99	3.54	1.17	up	2.73E-01	8.95E-01	-	-
1378405_at	Zfp143	zinc finger protein 143	361627	Rn.10682	AI170262	2.67	3.30	2.68	2.68	3.84	2.82	1.17	up	6.12E-01	8.95E-01	-	-
1373853_at	Zfp414	zinc finger protein 414	299647	Rn.32868	AI705797	3.59	3.74	4.43	3.60	3.74	3.73	1.17	down	4.31E-01	8.95E-01	-	-
1385498_at	Rhbdd1	rhomboid domain containing 1	316557	Rn.55926	AA848859	2.55	2.52	2.56	2.52	2.58	3.22	1.17	up	3.64E-01	8.95E-01	-	-
1399046_at	Top1	topoisomerase (DNA) I	64550	Rn.91572	BE116507	8.14	8.44	8.51	8.56	8.55	8.67	1.17	up	1.21E-01	8.95E-01	-	-
1372951_at	---	---	---	Rn.21828	BI274172	2.43	2.46	2.46	2.89	2.67	2.47	1.17	up	1.25E-01	8.95E-01	-	-
1374468_at	Myd88	myeloid differentiation primary response gene 88	301059	Rn.37341	AI236590	3.39	3.93	2.79	2.86	2.49	2.47	1.17	down	7.10E-01	9.09E-01	-	-
1382947_at	ab1b /// Rab1b-ps	RAB1B, member RAS oncogene family /// RAB1B, member RAS oncogene fa	00126191 /// 3617	Rn.105979	AI711306	5.92	5.23	5.96	4.64	7.85	5.31	1.17	up	8.29E-01	9.46E-01	-	-
1390034_at	Ralgps2	Ral GEF with PH domain and SH3 binding motif 2	304887	Rn.53983	BF393945	4.46	4.22	4.47	4.45	4.69	4.71	1.17	up	1.22E-01	8.95E-01	-	-
1385366_at	---	---	---	Rn.166478	AI071836	2.76	2.83	2.76	2.68	2.76	3.59	1.17	up	4.74E-01	8.95E-01	-	-
1373937_at	Fyco1	FYVE and coiled-coil domain containing 1	301085	Rn.17744	AA799661	7.43	7.70	6.98	7.18	6.83	7.40	1.17	down	4.36E-01	8.95E-01	-	-
1383207_at	Rrn3	RRN3 RNA polymerase I transcription factor homolog (S. cerevisiae)	304714	Rn.159763	BE103628	7.54	7.08	7.36	6.75	7.35	7.19	1.17	down	3.58E-01	8.95E-01	-	-
1376866_at	Cd3eap	CD3E antigen, epsilon polypeptide-associated protein	680493	Rn.155132	BI274923	3.68	3.74	3.74	3.74	4.16	3.95	1.17	up	1.32E-01	8.95E-01	-	-
1376198_at	Asam	adipocyte-specific adhesion molecule	286939	Rn.163013	BI303342	2.60	5.58	5.71	4.25	3.94	5.01	1.17	down	8.39E-01	9.50E-01	-	-
1369201_at	Mgat3	mannosyl (beta-1,4-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase	29582	Rn.9803	NM_019239	2.73	3.12	2.79	2.73	3.87	2.74	1.17	up	5.92E-01	8.95E-01	-	-
1394573_at	---	---	---	Rn.55604	BF288475	5.48	5.57	5.46	5.42	5.41	6.37	1.17	up	5.08E-01	8.95E-01	-	-
1373262_at	RGD1309543	similar to 2310014H01Rik protein	361790	Rn.16324	AI102745	2.28	2.29	2.28	3.00	2.27	2.28	1.17	up	3.90E-01	8.95E-01	-	-
1390202_at	---	---	---	Rn.202634	BI289584	2.27	2.32	2.91	2.27	2.28	2.27	1.17	down	3.25E-01	8.95E-01	-	-
1387392_at	Mll4	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila);	26955	Rn.58	NM_013217	6.14	6.25	6.24	5.79	6.01	6.13	1.17	down	9.73E-02	8.95E-01	-	-
1389248_at	Galk1	galactokinase 1	287835	Rn.198917	AI548699	5.22	6.53	7.17	5.70	6.99	6.92	1.17	up	7.61E-01	9.22E-01	-	-
1378437_at	---	---	---	Rn.201961	BM385012	3.11	2.43	2.44	2.43	2.44	2.42	1.17	down	3.67E-01	8.95E-01	-	-
1379268_at	---	---	---	Rn.8316	AA924312	3.21	3.20	3.20	3.20	3.91	3.19	1.17	up	3.89E-01	8.95E-01	-	-
1398635_at	---	---	---	Rn.46917	BF565662	2.23	2.22	2.23	2.92	2.23	2.22	1.17	up	3.78E-01	8.95E-01	-	-
1368519_at	Serpine1	serine (or cysteine) peptidase inhibitor, clade E, member 1	24617	Rn.29367	NM_012620	2.45	2.44	2.48	2.44	3.19	2.43	1.17	up	4.10E-01	8.95E-01	-	-
1385351_at	RGD1305090	similar to CD2-associated protein	362598	Rn.206632	AW528754	6.13	5.14	5.03	6.49	4.57	4.55	1.17	down	7.69E-01	9.24E-01	-	-
1372759_at	Cdk9	cyclin-dependent kinase 9	362110	Rn.98228	H31766	7.57	8.16	7.77	7.84	7.49	7.48	1.17	down	3.34E-01	8.95E-01	-	-
1373892_at	---	---	---	Rn.156574	AA945986	6.38	7.15	7.56	7.04	7.51	7.24	1.17	up	5.68E-01	8.95E-01	-	-
1390935_at	---	---	---	Rn.178333	AI407723	2.81	3.41	4.40	4.96	2.92	3.42	1.17	up	7.79E-01	9.28E-01	-	-
1377970_at	Parp8	poly (ADP-ribose) polymerase family, member 8	294762	Rn.59516	BE105494	3.60	3.25	2.85	3.04	3.08	2.88	1.17	down	3.62E-01	8.95E-01	-	-
1370044_at	Faim	Fas apoptotic inhibitory molecule	140930	Rn.106419	NM_080895	6.81	7.14	7.06	7.16	6.30	6.85	1.17	down	4.40E-01	8.95E-01	-	-
1382908_at	Epha4	Eph receptor A4	316539	Rn.6202	AI043909	3.03	3.00	3.12	2.98	3.01	2.47	1.17	down	2.67E-01	8.95E-01	-	-
1374515_at	RGD1306437	similar to KIAA0630 cDNA 6330409N04	290303	Rn.163304	AA848948	6.46	6.57	7.17	6.38	6.19	6.94	1.17	down	5.08E-01	8.95E-01	-	-
1392511_at	Taf2	TAF2 RNA polymerase II, TATA box binding protein (TBP)-associated factor	170844	Rn.33143	AA998513	6.13	6.15	5.81	5.81	5.81	5.78	1.17	down	1.06E-01	8.95E-01	-	-
1373166_at	RGD1563309	similar to diacylglycerol kinase, delta 130Kda isoform 1	368088	Rn.17832	BM391823	3.56	3.55	3.58	3.58	4.05	3.75	1.17	up	1.76E-01	8.95E-01	-	-
1388108_at	Elovl6	ELOVL family member 6, elongation of long chain fatty acids (yeast)	171402	Rn.46942	BE116152	2.47	2.42	2.43	3.18	2.44	2.39	1.17	up	4.18E-01	8.95E-01	-	-
1392449_at	Rad18	RAD18 homolog (S. cerevisiae)	362412	Rn.22793	BI282152	2.50	2.48	2.52	2.49	3.22	2.47	1.17	up	4.05E-01	8.95E-01	-	-
1383842_at	---	---	---	Rn.94899	BG380618	5.22	6.39	6.38	5.90	4.56	5.84	1.17	down	7.07E-01	9.08E-01	-	-
1368228_at	Zranb2	zinc finger, RAN-binding domain containing 2	58821	Rn.11361	AF013965	6.81	6.87	6.36	6.95	6.40	7.38	1.17	up	5.18E-01	8.95E-01	-	-
1378604_at	---	---	---	Rn.210137	BF396495	3.10	2.43	2.46	2.44	2.44	2.41	1.17	down	3.49E-01	8.95E-01	-	-
1369727_at	Apoa2	apolipoprotein A-II	25649	Rn.89304	NM_013112	2.44	2.46	2.44	3.18	2.45	2.39	1.17	up	4.17E-01	8.95E-01	-	-
1376768_at	---	---	---	Rn.8702	BM386807	6.24	7.47	6.22	6.97	6.49	7.16	1.17	up	6.42E-01	8.95E-01	-	-
1397892_at	Eif1a	eukaryotic translation initiation factor 1A	317163	Rn.3361	BI301150	5.65	5.11	6.56	4.80	5.66	6.18	1.17	down	7.14E-01	9.10E-01	-	-
1372156_at	Tmem97	transmembrane protein 97	303330	Rn.20057	BF414018	4.85	4.53	5.16	3.91	5.87	5.46	1.17	up	7.31E-01	9.14E-01	-	-
1368372_at	Sts	steroid sulfatase	24800	Rn.6312	NM_012861	3.69	5.21	5.18	4.56	4.55	5.67	1.17	up	7.31E-01	9.14E-01	-	-
1388307_at	Serinc1	serine incorporator 1	294421	Rn.2078	BG671458	8.48	8.48	8.57	8.75	8.48	8.99	1.17	up	2.04E-01	8.95E-01	-	-
1377834_at	Epc1	enhancer of polycomb homolog 1 (Drosophila)	307042	Rn.219240	AW434262	4.05	5.87	4.86	5.50	4.77	5.19	1.17	up	7.06E-01	9.08E-01	-	-
1370476_at	Stambp	Stam binding protein	171565	Rn.14662	AY083159	2.42	3.25	3.81	3.10	3.32	3.76	1.17	up	6.35E-01	8.95E-01	-	-
1383373_at	---	---	---	Rn.11733	AI576635	4.82	5.55	6.27	5.54	5.78	6.01	1.17	up	6.28E-01	8.95E-01	-	-
1399066_at	Tmf1	TATA element modulatory factor 1	114206	Rn.91637	AI236763	4.98	5.92	5.18	5.83	5.08	5.85	1.17	up	5.80E-01	8.95E-01	-	-
1383535_at	Asb8	ankyrin repeat and SOCS box-containing protein 8	315287	Rn.98320	BF549472	3.98	5.20	3.86	4.34	4.29	5.09	1.17	up	6.70E-01	9.00E-01	-	-
1370262_at	Mtdh	metadherin	171910	Rn.6864	AI706785	7.78	9.10	8.27	8.46	8.11	9.27	1.17	up	6.80E-01	9.03E-01	-	-
1396274_at	---	---	---	---	AI111884	3.25	4.23	4.23	3.99	4.06	4.36	1.17	up	5.43E-01	8.95E-01	-	-
1367630_at	Rps11	ribosomal protein S11	81774	Rn.2177	NM_031110	10.97	11.50	10.69	10.94	11.29	11.62	1.17	up	5.00E-01	8.95E-01	-	-
1375231_a_at	Cxxc5	CXXC finger 5	291670	Rn.105695	BI281838	5.37	5.54	4.62	6.41	4.48	5.33	1.17	up	7.33E-01	9.14E-01	-	-
1392872_at	Mtdh	Metadherin	170910	Rn.6864	BF397413	5.60	6.43	6.82	6.34	7.02	6.18	1.17	up	6.30E-01	8.95E-01	-	-
1373370_at	Hmg20a	high mobility group 20A	315689	Rn.9628	AI407467	3.77	3.77	4.58	3.77	3.78	3.88	1.17	down	4.48E-01	8.95E-01	-	-
1394829_at	---	---	---	Rn.204805	AI105271	3.33	2.62	2.76	2.63	2.81	2.58	1.17	down	3.70E-01	8.95E-01	-	-
1367760_at	Map2k1	mitogen activated protein kinase kinase 1	170851	Rn.5850	D13341	4.52	4.83	5.82	5.05	5.36	5.45	1.17	up	6.05E-01	8.95E-01	-	-
1391691_at	---	---	---	---	AA925241	2.56	2.56	3.48	2.56	2.56	2.79	1.17	down	5.09E-01	8.95E-01	-	-
1385716_at	---	---	---	Rn.206113	AW522166	5.87	5.58	5.55	5.39	4.94	6.00	1.17	down	5.18E-01	8.95E-01	-	-
1375478_at	Zfp362 /// Zscan20	zinc finger protein 362 /// zinc finger and SCAN domain containing 20	297879 /// 500549	Rn.25043	AW253376	2.64	2.61	2.86	2.62	2.68	2.13	1.17	down	2.93E-01	8.95E-01	-	-
1396088_at	---	---	---	Rn.13751	AW914780	2.45	2.43	3.78	3.09	2.46	2.41	1.17	down	6.69E-01	9.00E-01	-	-
1371499_at	Cd9	CD9 molecule	24936	Rn.2091	AI227627	4.37	3.20	3.21	4.40	3.55	3.52	1.17	up	6.59E-01	8.98E-01	-	-
1389377_at	Insig2	insulin induced gene 2	288985	Rn.16736	AA851803	4.33	4.99	5.54	4.96	5.01	5.58	1.17	up	5.99E-01	8.95E-01	-	-
1372401_at	Nans	N-acetylneuraminic acid synthase	298071	Rn.17006	AW435213	4.61	4.84	5.00	5.39	4.35	5.40	1.17	up	5.64E-01	8.95E-01	-	-
1380304_at	Foxk1	forkhead box K1	304298	Rn.211697	BI289361	3.01	2.88	4.43	2.91	3.94	2.78	1.17	down	7.29E-01	9.14E-01	-	-
1396934_at	---	---	---	---	AI410280	2.47	2.53	2.48	3.33	2.47	2.36	1.17	up	4.98E-01	8.95E-01	-	-
1388901_at	Cd36	CD36 molecule (thrombospondin receptor)	29184	Rn.102418	NM_031561	4.45	3.79	3.63	5.02	3.84	3.69	1.17	up	6.64E-01	8.96E-01	-	-
1391099_at	---	---	---	Rn.50797	BF404460	2.36	2.36	3.22	2.36	2.37	2.53	1.17	down	4.75E-01	8.95E-01	-	-
1373441_at	Dctn5	dynactin 5	308961	Rn.25812	BI296970	6.74	5.95	5.51	5.90	5.19	6.42	1.17	down	6.74E-01	9.01E-01	-	-
1370319_at	Ppif	peptidylprolyl isomerase F (cyclophilin F)	282819	Rn.2923	U68544	5.97	5.51	5.65	6.17	5.96	5.68	1.17	up	3.07E-01	8.95E-01	-	-
1388510_at	Chmp6	chromatin modifying protein 6	287873	Rn.7707	BI289511	7.13	7.90	7.04	7.64	7.02	8.10	1.17	up	6.11E-01	8.95E-01	-	-
1398214_at	Mapk8ip3	mitogen-activated protein kinase 8 interacting protein 3	302983	Rn.16158	BF399528	2.64	2.51	2.65	2.88	2.64	2.96	1.17	up	9.52E-02	8.95E-01	-	-
1381056_at	Pkp3	plakophilin 3	293619	Rn.144803	BI286045	2.73	2.79	3.17	2.80	2.42	2.78	1.17	down	2.79E-01	8.95E-01	-	-
1381887_x_at	RGD1311595	similar to KIAA2026 protein	309307	Rn.96138	AW530368	3.39	3.38	4.00	3.47	3.39	3.22	1.17	down	3.48E-01	8.95E-01	-	-
1387857_at	Stx7	syntaxin 7	60466	Rn.1993	AI406531	8.27	8.98	8.21	8.31	7.93	8.53	1.17	down	4.89E-01	8.95E-01	-	-
1388522_at	Ppfc7	PTC7 protein phosphatase homolog (S. cerevisiae)	304488	Rn.7549	AI170820	6.97	6.59	5.67	7.66	6.39	5.87	1.17	up	7.44E-01	9.17E-01	-	-
1393110_at	Mpv17l	Mpv17 transgene, kidney disease mutant-like	360463	Rn.207192	BI281552	9.03	9.45	8.64	9.63	9.60	9.58	1.17	up	2.74E-01	8.95E-01	-	-
1371798_at	---	---	---	Rn.164572	AI013011	9.63	9.52	9.97	9.38	9.57	9.48	1.17	down	1.91E-01	8.95E-01	-	-
1382631_at	---	---	---	Rn.204421	AI454735	4.63	4.21	4.64	5.01	4.64	4.52	1.17	up	3.26E-01	8.95E-01	-	-
1368251_at	Jak3	Janus kinase 3	25326	Rn.11159	NM_012855	2.93	3.91	3.03	3.04	3.14	3.01	1.17	down	5.05E-01	8.95E-01	-	-
1393077_at	---	---	---	Rn.21469	AA925179	6.12	5.31	5.60	5.40	4.57	6.38	1.17	down	7.10E-01	9.09E-01	-	-
1398761_at	Rpl5	ribosomal protein L5	81763	Rn.92980	NM_031099	11.63	11.84	11.86	11.91	11.89	12.22	1.17	up	1.57E-01	8.95E-01	-	-
1369949_at	Bcam	basal cell adhesion molecule	78958	Rn.7003	NM_031752	3.54	2.92	2.94	2.93	2.94	2.85	1.17	down	3.24E-01	8.95E-01	-	-
1376124_at	Iqub	IQ motif and ubiquitin domain containing	299836	Rn.11866	BG375480	3.24	2.73	2.83	2.71	2.53	2.88	1.17	down	2.86E-01	8.95E-01	-	-
1383177_at	---	---	---	Rn.1530	AI232085	4.97	5.50	7.13	5.74	5.73	5.43	1.17	down	7.45E-01	9.18E-01	-	-
1390607_at	Zdhhc23	zinc finger, DHHC-type containing 23	363783	Rn.43304	BG380706	4.29	4.48	4.66	4.00	4.38	4.37	1.17	down	2.34E-01	8.95E-01	-	-
1372996_at	LOC684270	similar to isochorismatase domain containing 2	684270	---	AI411245	11.22	11.69	10.72	11.44	11.35	11.52	1.17	up	4.64E-01	8.95E-01	-	-
1372727_at	---	---	---	Rn.15045	BM384088	2.36	2.34	2.37	2.36	2.58	2.81	1.17	up	1.55E-01	8.95E-01	-	-
1369023_at	Mipep	mitochondrial intermediate peptidase	81684	Rn.2266	NM_031052	6.41	6.34	6.12	6.34	6.37	6.84	1.17	up	2.81E-01	8.95E-01	-	-
1372498_at	Ciapin1	cytokine induced apoptosis inhibitor 1	307649	Rn.1274	BF285068	8.20	8.38	8.50	8.17	8.04	8.19	1.17	down	8.74E-02	8.95E-01	-	-
1376046_at	Hook3	Hook homolog 3 (Drosophila)	306548	Rn.203282	BF289012	5.87	5.49	5.38	4.77	5.39	5.90	1.17	down	5.59E-01	8.95E-01	-	-
1381930_at	Cct5	Chaperonin containing Tcp1, subunit 5 (epsilon)	294864	Rn.92645	AI030791	5.20	5.88	5.96	7.38	5.28	5.07	1.17	up	7.83E-01	9.30E-01	-	-
1372249_at	LOC362901	Ac1254	362901	Rn.214920	BE108148	9.32	9.30	10.03	9.38	9.32	9.26	1.17	down	4.00E-01	8.95E-01	-	-
1369987_at	Igbp1	immunoglobulin (CD79A) binding protein 1	58845	Rn.7079	NM_031624	6.81	7.07	7.79	7.34	7.33	7.69	1.17	up	5.07E-01	8.95E-01	-	-
1390430_at	---	---	---	---	BF284190	6.75	7.93	7.89	7.66	7.71	7.89	1.17	up	5.91E-01	8.95E-01	-	-
1370923_at	Nme6	non-metastatic cells 6, protein expressed in (nucleoside-diphosphate kinase)	58964	Rn.36170	AI014074	3.18	3.00	2.87	4.37	2.48	2.88	1.17	up	7.15E-01	9.10E-01	-	-
1374701_at	Rnf185	ring finger protein 185	360987	Rn.7234	BG378096	8.72	8.69	9.02	8.17	8.90	8.67	1.17	down	3.95E-01	8.95E-01	-	-
1379478_at	Ovol1	Ovo-like 1(Drosophila)	309164	Rn.53479	BE120195	2.51	3.00	2.64	2.50	2.47	2.49	1.17	down	1.92E-01	8.95E-01	-	-
1390768_at	Sipa1l2	Signal-induced proliferation-associated 1 like 2	361442	Rn.44190	BF399726	2.68	2.87	2.99	2.52	2.68	2.66	1.17	down	9.27E-02	8.95E-01	-	-
1377623_at	Rkhd1	ring finger (C3HC4 type) and KH domain containing 1	299613	Rn.162915	AA925355	3.38	2.97	2.95	2.85	2.93	2.84	1.17	down	1.82E-01	8.95E-01	-	-
1395852_at	Abca3	ATP-binding cassette, sub-family A (ABC1), member 3	302973	Rn.38406	BF546340	2.85	5.17	5.02	4.33	4.55	4.85	1.17	up	7.81E-01	9.29E-01	-	-
1387172_a_at	Tgfb2	transforming growth factor, beta 2	81809	Rn.24539	NM_031131	3.29	2.55	2.51	2.55	2.57	2.55	1.17	down	4.16E-01	8.95E-01	-	-
1373673_at	---	---	---	Rn.167176	BF284593	6.35	6.05	6.16	6.04	6.28	6.92	1.17	up	4.54E-01	8.95E-01	-	-
1380893_at	27 /// LOC501602	similar to peptidylprolyl isomerase D /// similar to peptidylprolyl isomerase D /// 67 /// 364127 /// 50		Rn.136915	BF416306	2.43	2.63	3.56	2.43	3.09	2.42	1.17	down	6.10E-01	8.95E-01	-	-
1370295_at	Nme1	non-metastatic cells 1, protein (NM23A) expressed in	191575	Rn.6236	D13374	7.90	7.53	7.34	7.36	7.66	7.66	1.17	down	3.96E-01	8.95E-01	-	-
1388114_at	RGD1309537	similar to Myosin regulatory light chain 2-A, smooth muscle isoform (Myosin R	501203	---	X05566	8.71	9.26	9.20	9.44	9.33	9.08	1.17	up	3.28E-01	8.95E-01	-	-
1370639_at	Prdm2	PR domain containing 2, with ZNF domain	313678	Rn.202632	U17837	4.13	4.52	5.26	4.64	3.90	4.69	1.17	down	6.16E-01	8.95E-01	-	-
1390305_at	Prkcbp1	protein kinase C binding protein 1	296374	Rn.219272	AI599263	5.35	5.83	5.31	6.03	4.74	5.03	1.17	down	6.21E-01	8.95E-01	-	-
1374142_at	RGD1311589	similar to RIKEN cDNA E130201N16	312358	Rn.37820	BE113624	8.61	9.14	9.68	8.63	8.75	9.37	1.17	down	5.85E-01	8.95E-01	-	-
1371572_at	App	amyloid beta (A4) precursor protein	54226	Rn.2104	BM986220	9.73	10.01	9.92	9.98	9.94	10.42	1.17	up	2.58E-01	8.95E-01	-	-
1374298_at	---	---	---	Rn.62411	BG373455	2.42	2.41	3.08	2.40	2.42	2.41	1.17	down	3.64E-01	8.95E-01	-	-
1382515_at	Cpsf2	cleavage and polyadenylation specific factor 2	299256	Rn.8038	AI059408	4.08	4.88	4.09	3.49	4.01	4.87	1.17	down	6.61E-01	8.98E-01	-	-
1384434_at	---	---	---	Rn.155810	BE113820	2.35	2.33	2.34	2.33	2.33	3.04	1.17	up	3.92E-01	8.95E-01	-	-
1382963_at	Abcb10	ATP-binding cassette, sub-family B (MDR/TAP), member 10	361439	Rn.22937	BF416871	3.46	2.75	2.88	2.78	3.05	2.58	1.17	down	4.26E-01	8.95E-01	-	-
1369994_at	Crcp	calcitonin gene-related peptide-receptor component protein	114205	Rn.9449	NM_053670	7.22	6.84	6.67	7.01	7.07	7.33	1.17	up	2.95E-01	8.95E-01	-	-
1381551_at	Alkbh	alkB, alkylation repair homolog (E. coli)	362766	Rn.107927	BG378461	2.99	2.62	2.50	2.49	2.51	2.43	1.17	down	2.03E-01	8.95E-01	-	-
1379023_at	---	---	---	Rn.203731	BF406975	2.42	2.40	3.12	2.42	2.44	2.39	1.17	down	3.89E-01	8.95E-01	-	-
1390833_at	LOC499602	hypothetical protein LOC499602	499602	Rn.12999	BE113228	2.93	2.86	2.95	3.63	2.88	2.93	1.17	up	4.02E-01	8.95E-01	-	-
1382639_at	LOC501406	similar to regulator of sex-limitation candidate 1	501406	---	BF290625	3.30	2.60	2.67	2.64	2.66	2.59	1.17	down	3.70E-01	8.95E-01	-	-
1397284_at	Zfp444	zinc finger protein 444	292569	Rn.43215	BF418279	2.

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicats)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1393784_at	Vezf1	vascular endothelial zinc finger 1	287615	Rn.198892	BI284190	3.44	3.15	3.24	3.14	2.67	3.35	1.17	down	3.58E-01	8.95E-01	-	-
1378677_at	---	---	---	Rn.206449	BF394318	2.59	2.55	2.59	2.56	3.31	2.54	1.17	up	4.27E-01	8.95E-01	-	-
1382076_at	Slc37a1	solute carrier family 37 (glycerol-3-phosphate transporter), member 1	294321	Rn.138019	AA955403	2.77	3.41	2.87	3.03	4.02	2.68	1.17	up	6.39E-01	8.95E-01	-	-
1374979_at	Dus3l	dihydrouridine synthase 3-like (S. cerevisiae)	301122	Rn.42187	AI102764	5.41	4.89	3.60	4.77	4.43	4.01	1.17	down	7.17E-01	9.10E-01	-	-
1397448_at	---	---	---	Rn.207955	BE108434	2.59	2.52	2.64	3.11	2.59	2.74	1.17	up	2.24E-01	8.95E-01	-	-
1376007_at	---	---	---	---	AI411772	5.41	5.89	6.15	5.41	6.96	5.77	1.17	up	6.83E-01	9.03E-01	-	-
1372205_at	Zfp278	zinc finger protein 278	305471	Rn.203833	AI713121	6.98	7.36	6.79	6.99	7.63	7.19	1.17	up	4.22E-01	8.95E-01	-	-
1394554_at	---	---	---	Rn.107310	BF564500	6.34	5.39	5.49	5.45	6.14	4.95	1.17	down	6.48E-01	8.96E-01	-	-
1388847_at	Med15	mediator complex subunit 15	360743	Rn.6342	AI177083	3.43	4.14	3.31	3.43	3.03	3.74	1.17	down	5.31E-01	8.95E-01	-	-
1394614_at	Gns	glucosamine (N-acetyl)-6-sulfatase	299825	Rn.65302	BI290687	8.49	9.36	9.32	8.91	8.80	8.78	1.17	down	4.77E-01	8.95E-01	-	-
1391510_at	Ebag9	estrogen receptor binding site associated, antigen, 9	299864	Rn.64132	BF398331	7.47	7.74	8.32	8.34	7.76	8.10	1.17	up	4.96E-01	8.95E-01	-	-
1386878_at	Lrp10	low-density lipoprotein receptor-related protein 10	305880	Rn.101349	AI104234	9.06	9.72	9.13	9.35	9.61	9.64	1.17	up	3.81E-01	8.95E-01	-	-
1387082_at	Fetub	fetuin B	83928	Rn.2464	NM_053348	3.18	2.44	2.45	3.86	2.45	2.44	1.17	up	6.93E-01	9.05E-01	-	-
1391172_at	---	---	---	Rn.148467	BE106088	2.59	2.67	2.52	2.62	2.78	3.07	1.17	up	1.76E-01	8.95E-01	-	-
1393780_at	Zfp131	zinc finger protein 131	310375	Rn.92641	AA924380	6.26	5.47	4.83	4.94	5.28	5.67	1.17	down	6.52E-01	8.97E-01	-	-
1382259_a_at	LOC474147	RBSC-skeletrophin	474147	---	BF287228	5.30	4.63	4.07	5.20	4.75	4.73	1.17	up	5.91E-01	8.95E-01	-	-
1368642_at	Cdh2	cadherin 2	83501	Rn.23200	AF097593	7.95	8.68	8.60	8.57	8.45	8.89	1.17	up	4.45E-01	8.95E-01	-	-
1378612_at	---	---	---	Rn.211006	BF404501	3.10	2.46	2.52	2.46	2.50	2.44	1.17	down	3.31E-01	8.95E-01	-	-
1373875_at	RGD1308261	similar to RIKEN cDNA 1190005P17	299818	Rn.154521	BG381541	6.17	7.17	7.06	7.04	6.69	7.35	1.17	up	5.77E-01	8.95E-01	-	-
1393211_at	---	---	---	---	AW144047	4.82	2.76	3.86	4.44	3.58	2.75	1.17	down	7.83E-01	9.30E-01	-	-
1389687_at	Dhdds	dehydrodolichyl diphosphate synthase	298541	Rn.24616	BI274088	5.76	5.00	4.93	4.93	5.44	4.93	1.17	down	5.59E-01	8.95E-01	-	-
1394518_at	Adamts9	A disintegrin-like and metalloprotease (reprolysin type) with thrombospondin t	312566	Rn.162758	BF284436	2.48	2.51	3.26	2.63	2.52	2.43	1.17	down	4.37E-01	8.95E-01	-	-
1392519_at	---	---	---	Rn.216526	AA998248	6.00	6.38	5.89	5.86	6.15	5.59	1.17	down	3.59E-01	8.95E-01	-	-
1379562_at	---	---	---	Rn.148896	AA858498	2.40	2.39	2.41	2.80	2.40	2.67	1.17	up	1.30E-01	8.95E-01	-	-
1382875_at	Fam120b	family with sequence similarity 120B	308218	Rn.2666	BF386519	6.23	6.10	7.00	6.27	6.12	6.26	1.17	down	4.71E-01	8.95E-01	-	-
1392998_at	---	---	---	Rn.48066	BI294284	2.44	2.43	3.10	2.43	2.44	2.42	1.17	down	3.70E-01	8.95E-01	-	-
1375658_at	---	---	---	Rn.22768	AI412317	7.32	7.79	6.63	6.51	7.10	7.47	1.17	down	6.33E-01	8.95E-01	-	-
1367633_at	Glul	glutamate-ammonia ligase (glutamine synthetase)	24957	Rn.2204	BI275294	11.52	11.92	11.54	12.17	11.75	11.74	1.17	up	3.06E-01	8.95E-01	-	-
1398855_at	Atp5f1	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit B1	171375	Rn.3689	AA893531	9.97	10.14	10.21	9.84	9.90	9.92	1.17	down	4.05E-02	8.95E-01	-	-
1396020_at	Tlk2	tousled-like kinase 2	303592	Rn.23125	BE097972	5.14	5.54	5.76	5.46	4.84	5.46	1.17	down	4.56E-01	8.95E-01	-	-
1398455_at	Zdhhc13	Zinc finger, DHHC-type containing 13	365252	Rn.137700	BG379973	5.92	6.69	6.01	6.05	6.98	6.25	1.17	up	5.76E-01	8.95E-01	-	-
1397725_at	---	---	---	Rn.216849	BE119393	2.30	2.29	2.31	2.99	2.30	2.29	1.17	up	3.85E-01	8.95E-01	-	-
1370357_at	Slc30a4	solute carrier family 30 (zinc transporter), member 4	64469	Rn.90036	Y16774	7.92	8.29	7.98	8.46	8.10	8.31	1.17	up	2.15E-01	8.95E-01	-	-
1387430_at	Hsf2	heat shock factor 2	64441	Rn.163428	NM_031694	3.83	4.48	3.84	3.71	2.94	4.83	1.17	down	7.21E-01	9.11E-01	-	-
1377479_at	---	---	---	Rn.6812	BI296128	3.16	2.69	2.71	2.61	2.65	2.62	1.17	down	2.15E-01	8.95E-01	-	-
1368096_at	Rab71	RAB7, member RAS oncogene family-like 1	171122	Rn.4323	NM_133590	10.40	10.87	10.32	10.75	10.37	11.15	1.17	up	4.71E-01	8.95E-01	-	-
1389087_at	Anapc2	anaphase promoting complex subunit 2	296558	Rn.20099	AI599023	3.27	5.35	6.01	4.90	5.14	5.27	1.17	up	8.00E-01	9.35E-01	-	-
1372679_at	Unc45a	unc-45 homolog A (C. elegans)	308759	Rn.136574	BI296209	3.64	3.75	3.03	3.72	3.57	3.81	1.17	up	3.93E-01	8.95E-01	-	-
1379756_at	RGD1562890	RGD1562890	294945	Rn.144827	BF283938	2.57	2.60	2.61	3.25	2.61	2.60	1.17	up	3.57E-01	8.95E-01	-	-
1379315_at	Rassf7	Ras association (RalGDS/AF-6) domain family (N-terminal) member 7	293623	Rn.24007	BM385768	5.20	6.22	7.35	6.29	6.67	6.49	1.17	up	7.39E-01	9.16E-01	-	-
1371622_at	Dph1 /// Ovca2	DPH1 homolog (S. cerevisiae) /// candidate tumor suppressor in ovarian canc	287523 /// 497954	Rn.217509	AA943541	5.22	5.22	5.50	5.25	5.87	5.50	1.17	up	3.31E-01	8.95E-01	-	-
1377633_a_at	Stt3a	STT3, subunit of the oligosaccharyltransferase complex, homolog A (S. cerev	500972	Rn.98525	AW918411	2.64	2.63	2.58	2.65	3.21	2.68	1.17	up	2.86E-01	8.95E-01	-	-
1387924_at	Ngef	neuronal guanine nucleotide exchange factor	246217	Rn.20670	AF254801	3.03	2.85	3.40	2.88	2.89	2.84	1.17	down	2.35E-01	8.95E-01	-	-
1376316_at	Orc6l	origin recognition complex, subunit 6 like (yeast)	291927	Rn.41300	AI070593	2.75	2.71	2.53	3.10	2.76	2.81	1.17	up	1.53E-01	8.95E-01	-	-
1383626_at	Zfp259	zinc finger protein 259	500989	Rn.102011	BI274049	4.58	4.75	3.90	4.56	4.54	4.81	1.17	up	4.54E-01	8.95E-01	-	-
1374943_at	RGD1311378	similar to RIKEN cDNA 2010011I20	296408	Rn.220160	AI170809	4.80	4.80	5.74	4.78	4.67	5.21	1.17	down	5.58E-01	8.95E-01	-	-
1370878_at	Urod	uroporphyrinogen decarboxylase	29421	Rn.4214	Y00350	9.16	8.93	8.68	9.24	9.22	8.98	1.17	up	2.34E-01	8.95E-01	-	-
1373362_at	Uqcrc2	ubiquinol cytochrome c reductase core protein 2	293448	Rn.2334	BI296109	11.28	10.94	10.91	10.58	10.86	11.01	1.17	down	2.67E-01	8.95E-01	-	-
1376536_at	Dlgap2	Discs, large (Drosophila) homolog-associated protein 2	116681	Rn.10705	AW533496	4.26	5.84	4.53	4.87	5.18	5.25	1.17	up	6.78E-01	9.02E-01	-	-
1373065_at	Ptpn18	protein tyrosine phosphatase, non-receptor type 18	301333	Rn.9310	AW916153	3.19	2.38	2.39	2.43	2.44	2.42	1.17	down	4.50E-01	8.95E-01	-	-
1375892_at	Elavl1	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 1 (Hu antigen R)	363854	Rn.216517	BF558912	7.97	8.27	7.45	7.56	7.60	7.86	1.17	down	4.30E-01	8.95E-01	-	-
1371323_at	Ndufa4	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4	681024	Rn.793	BG666002	12.38	12.16	12.35	12.01	12.15	12.06	1.17	down	5.24E-02	8.95E-01	-	-
1370879_at	Dlst	dihydrolipoamide S-succinyltransferase (E2 component of 2-oxo-glutarate cor	299201	Rn.99702	D90401	8.88	9.01	8.86	8.84	8.52	8.72	1.17	down	9.31E-02	8.95E-01	-	-
1378266_at	Fbxo46	F-box protein 46	292686	Rn.64160	BF564168	3.66	2.59	2.61	2.60	2.84	2.74	1.17	down	5.65E-01	8.95E-01	-	-
1380237_at	Ahcyl2	S-adenosylhomocysteine hydrolase-like 2	362199	Rn.8222	AW253745	2.42	2.38	2.43	2.85	2.71	2.34	1.17	up	2.17E-01	8.95E-01	-	-
1397846_at	Cby1	chibby homolog 1 (Drosophila)	246768	Rn.3025	BE117101	4.51	5.21	4.72	5.20	5.00	4.92	1.17	up	3.71E-01	8.95E-01	-	-
1376588_at	---	---	---	Rn.6483	BF284632	5.63	5.35	5.45	4.95	5.40	5.41	1.17	down	2.65E-01	8.95E-01	-	-
1372833_at	---	---	---	Rn.14625	AW521376	4.85	5.18	5.58	5.20	5.82	5.27	1.17	up	4.81E-01	8.95E-01	-	-
1388773_at	Tnfaip2	tumor necrosis factor, alpha-induced protein 2	299339	Rn.34387	BI278479	2.37	2.98	2.34	2.36	2.33	2.33	1.17	down	3.46E-01	8.95E-01	-	-
1368123_at	Igf1r	insulin-like growth factor 1 receptor	25718	Rn.10957	NM_052807	8.39	8.36	9.18	8.70	8.18	8.37	1.17	down	5.06E-01	8.95E-01	-	-
1378842_at	Gabarapl1	GABA(A) receptor-associated protein like 1	689161	Rn.118264	AI102520	7.46	7.39	7.03	7.56	7.59	7.41	1.17	up	1.98E-01	8.95E-01	-	-
1389689_at	Vars2	valyl-tRNA synthetase 2, mitochondrial (putative)	309596	Rn.43153	BI276974	2.46	3.49	2.45	2.62	2.43	2.68	1.17	down	5.60E-01	8.95E-01	-	-
1373439_at	---	---	---	Rn.164887	AI178491	5.49	6.39	6.69	6.31	5.56	6.03	1.17	down	6.22E-01	8.95E-01	-	-
1390803_at	Htatsf1	HIV-1 Tat specific factor 1	317612	Rn.140508	BE117639	6.20	7.31	6.61	6.68	6.47	7.64	1.17	up	6.66E-01	8.99E-01	-	-
1398211_at	---	---	---	Rn.173644	BF413560	2.85	2.93	2.89	2.95	3.30	3.09	1.17	up	1.01E-01	8.95E-01	-	-
1384812_at	---	---	---	Rn.147831	AI229409	2.53	2.50	2.58	2.75	3.06	2.47	1.17	up	2.58E-01	8.95E-01	-	-
1376435_at	---	---	---	Rn.143739	BI303340	2.53	2.83	2.73	2.65	2.38	2.38	1.17	down	1.44E-01	8.95E-01	-	-
1380547_at	Clcn3	chloride channel 3	84380	Rn.4175	BI288519	5.77	5.67	4.98	4.76	4.70	6.29	1.17	down	7.16E-01	9.10E-01	-	-
1389587_at	Umps	uridine monophosphate synthetase	288051	Rn.102010	BM384966	6.95	7.58	7.80	7.17	6.90	7.58	1.17	down	5.25E-01	8.95E-01	-	-
1376009_at	Ctage5	CTAGE family, member 5	299078	Rn.58607	BI300199	10.07	10.56	10.06	10.42	10.12	10.81	1.17	up	4.33E-01	8.95E-01	-	-
1387678_at	Nras	neuroblastoma ras oncogene	24605	Rn.217722	NM_080766	4.26	3.83	3.27	3.89	3.84	4.31	1.17	up	5.24E-01	8.95E-01	-	-
1371948_at	Pigp	phosphatidylinositol glycan anchor biosynthesis, class P	288238	Rn.53715	BF415030	7.06	6.26	7.21	6.53	6.52	6.80	1.17	down	5.06E-01	8.95E-01	-	-
1396463_at	Pnn	pinin, desmosome associated protein	368070	Rn.38987	BE127046	8.09	8.52	6.00	7.68	7.69	7.91	1.17	up	7.89E-01	9.32E-01	-	-
1371824_at	Ak3l1	adenylate kinase 3-like 1	29223	Rn.1086	AA891949	11.88	11.83	11.90	11.77	11.40	11.77	1.17	down	1.50E-01	8.95E-01	-	-
1396300_at	Afmid	aryiformamidase	688283	Rn.216742	BI277442	7.25	7.53	7.58	7.21	7.19	7.28	1.17	down	1.02E-01	8.95E-01	-	-
1367583_at	Tpt1	tumor protein, translationally-controlled 1	116646	Rn.36610	NM_053867	12.38	12.35	12.36	12.61	12.60	12.56	1.17	up	1.51E-04	8.95E-01	-	-
1369989_at	Pnpo	pyridoxine 5'-phosphate oxidase	64533	Rn.158883	NM_022601	9.72	9.51	9.19	9.86	9.62	9.62	1.17	up	2.63E-01	8.95E-01	-	-
1367556_s_at	Alb	albumin	24186	Rn.202968	NM_134326	2.60	2.46	2.97	2.45	2.48	2.43	1.17	down	2.15E-01	8.95E-01	-	-
1384678_at	---	---	---	Rn.147562	BF556356	2.69	2.69	2.69	3.35	2.68	2.70	1.17	up	3.66E-01	8.95E-01	-	-
1396325_at	Zfp819	zinc finger protein 819	308561	Rn.145000	BF413179	2.45	2.61	2.48	2.51	3.29	2.41	1.17	up	4.72E-01	8.95E-01	-	-
1368858_at	Ugt8	UDP glycosyltransferase 8	50555	Rn.9744	L21698	2.50	2.41	3.21	2.48	2.50	2.47	1.17	down	4.28E-01	8.95E-01	-	-
1384228_at	---	---	---	Rn.201845	AI501087	2.35	2.35	2.36	2.35	2.36	3.02	1.17	up	3.74E-01	8.95E-01	-	-
1389131_at	Nt5c3l	5'-nucleotidase, cytosolic III-like	360629	Rn.24114	BF412799	3.10	2.82	4.18	3.50	2.84	3.10	1.17	down	6.51E-01	8.97E-01	-	-
1396759_at	---	---	---	Rn.172725	BF393502	2.61	2.60	2.72	3.45	2.62	2.52	1.17	up	4.95E-01	8.95E-01	-	-
1384120_at	---	---	---	Rn.149983	BF386877	2.83	2.82	2.84	2.68	3.67	2.81	1.17	up	5.11E-01	8.95E-01	-	-
1391078_at	Rfc1	replication factor C (activator 1) 1	89809	Rn.103272	BM391856	4.93	5.40	4.84	4.49	6.55	4.80	1.17	up	7.52E-01	9.20E-01	-	-
1377508_at	---	---	---	Rn.211581	BI298836	2.62	2.52	2.62	3.03	2.84	2.56	1.17	up	1.92E-01	8.95E-01	-	-
1378154_at	---	---	---	Rn.15170	BG668499	3.44	2.75	2.76	2.75	2.73	2.79	1.17	down	3.88E-01	8.95E-01	-	-
1373506_at	LOC687750	similar to early estrogen-induced gene 1 protein	687750	---	AA944568	7.10	7.60	7.73	7.73	7.46	7.92	1.17	up	3.91E-01	8.95E-01	-	-
1372534_at	---	---	---	---	AW434092	9.46	9.28	9.73	9.05	9.55	9.19	1.17	down	3.26E-01	8.95E-01	-	-
1382945_at	A2ld1	AIG2-like domain 1	290500	Rn.17263	AI028809	10.37	10.51	10.53	10.20	10.21	10.33	1.17	down	2.93E-02	8.95E-01	-	-
1376357_at	Ankib1	ankyrin repeat and IBR domain containing 1	368062	Rn.2999	AA875143	8.33	8.88	8.82	8.62	7.92	8.82	1.17	down	5.31E-01	8.95E-01	-	-
1373534_at	Sfrs18	splicing factor, arginine/serine-rich 18	297942	Rn.8700	BE107209	7.45	8.66	8.49	8.36	7.86	7.72	1.17	down	6.27E-01	8.95E-01	-	-
1394724_at	Tcea1	transcription elongation factor A (SII) 1	362479	Rn.6738	BE109084	6.15	6.89	7.19	6.83	6.81	7.26	1.17	up	5.48E-01	8.95E-01	-	-
1368094_at	Secisbp2	SECIS binding protein 2	79049	Rn.25076	NM_024002	6.39	5.87	4.87	5.94	5.79	6.07	1.17	up	6.47E-01	8.95E-01	-	-
1377622_at	Rsf1	remodeling and spacing factor 1	308839	Rn.23988	AI717078	4.55	4.75	4.53	4.51	4.18	4.47	1.17	down	1.50E-01	8.95E-01	-	-
1387383_at	Gabbr2	gamma-aminobutyric acid (GABA) B receptor 2	83633	Rn.162814	NM_031802	2.36	2.35	2.38	2.37	2.38	3.00	1.17	up	3.44E-01	8.95E-01	-	-
1369959_at	Zfp36l1	zinc finger protein 36, C3H type-like 1	29344	Rn.6142	NM_017172	8.64	8.74	8.52	8.37	9.22	8.98	1.17	up	4.42E-01	8.95E-01	-	-
1388943_at	Chrac1	chromatin accessibility complex 1	315058	Rn.17653	BI279670	5.53	5.94	6.71	6.21	5.92	6.71	1.17	up	6.21E-01	8.95E-01	-	-
1392807_at	Lig3	ligase III, DNA, ATP-dependent	303369	Rn.203089	AA875471	3.44	3.51	3.43	3.94	3.12	3.99	1.17	up	4.74E-01	8.95E-01	-	-
1383664_a_at	---	---	---	---	AI172176	4.95	5.66	5.22	4.73	5.16	5.28	1.17	down	4.49E-01	8.95E-01	-	-
1393095_at	Tnks1bp1	tankyrase 1 binding protein 1	295707	Rn.139703	BI276113	2.53	3.17	2.53	2.52	2.53	2.51	1.17	down	3.59E-01	8.95E-01	-	-
1388279_at	324 /// Ly6al /// Ly6	similar to Ly6-B antigen gene /// lymphocyte antigen 6 complex, locus A-like /// 300024 /// 497935		Rn.40119	AW251927	2.64	2.84	2.94	3.20	3.08	2.81	1.17	up	1.99E-01	8.95E-01	-	-
1394682_at	Aff4	AF4/FMR2 family, member 4	303132	Rn.17594	BF290030	5.43	4.82	4.80	4.80	4.80	4.91	1.17	down	3.36E-01	8.95E-01	-	-
1380907_at	---	---	---	Rn.208059	BE109785	3.05	2.40	2.42	2.40	2.41	2.38	1.17	down	3.56E-01	8.95E-01	-	-
1381030_at	Slu7	SLU7 splicing factor homolog (S. cerevisiae)	303057	Rn.137183	AI411326	5.15	5.81	6.79	6.58	5.86	5.97	1.17	up	6.94E-01	9.05E-01	-	-
1390115_at	Sec63	SEC63 homolog (S. cerevisiae)	309858	Rn.24233	BM384667	7.79	7.73	7.84	8.29	7.36	8.39	1.17	up	5.37E-01	8.95E-01	-	-
1393080_at	Zfr	zinc finger RNA binding protein	365703	Rn.11634	BF389264	6.72	6.02	8.90	6.93	6.86	7.18	1.17	down	8.10E-01	9.39E-01	-	-
1381245_at	---	---	---	Rn.7590	AA943546	3.24	2.60	2.62	2.60	2.61	2.59	1.17	down	3.51E-01	8.95E-01	-	-
1372431_at	Mrpl12	mitochondrial ribosomal protein L12	303746	Rn.105932	AI575434	8.61	9.14	9.34	9.47	9.16	9.13	1.17	up	4.08E-01	8.95E-01	-	-
1384337_x_at	Cln3	ceroid-lipofuscinosis, neuronal 3	293485	Rn.102386	BF290224	2.99	3.43	2.83	2.78	2.79	3.01	1.17	down	3.20E-01	8.95E-01	-	-
1367529_at	Der1	Der1-like domain family, member 1	362912	Rn.110990	BE113989	6.36	7.08	7.76	6.86	7.44	7.56	1.17	up	6.51E-01	8.97E-01	-	-
1390414_at	RGD1308489	similar to hypothetical protein	313340	Rn.54339	BI296515	2.71	2.93	2.75	2.52	2.54	2.66	1.17	down	4.83E-02	8.95E-01	-	-
1370942_at	Rasa3	RAS p21 protein activator 3	29372	Rn.23055	AI170661	3.64	3.70	3.88	3.62	3.29	3.63	1.17	down	1.70E-01	8.95E-01	-	-
1376613_at	Ttc9c	tetratricopeptide repeat domain 9C	309196	Rn.162477	BI279201	5.18	6.02	5.67	4.92	5.26	6.03	1.17	down	6.14E-01	8.95E-01	-	-
1373731_at	RGD1564300	similar to phosphoseryl-tRNA kinase	361661	---	AI409901	6.66	6.01	4.94	5.97	6.07	6.24	1.17	up	6.84E-01	9.03E-01	-	-
1383495_at	Ddx1e	DNA cross-link repair 1A, PSO2 homolog (S. cerevisiae)	292127	Rn.41244	AI556858	3.23	4.22	3.95	2.88	5.35	3.84	1.17	up	7.89E-01	9.32E-01	-	-
1379765_at	Nlk	nemo like kinase	497961	Rn.113514	AI111738	3.13	3.15	3.14	3.12	3.83	3.14	1.17	up	3.98E-01	8.95E-01	-	-
1382795_at	---	---	---	Rn.122139	AI228346	2.47	3.75	2.50	2.62	2.63	2.80	1.17	down	6.28E-01	8.95E-01	-	-
1389670_at	Hoxa10	Homeo box A10	368057	Rn.852	AI008960	2.58	2.57	2.43	2.72	2.77	2.75	1.17	up	1.06E-02	8.95E-01	-	-
1392193_at	---	---	---	---	BE106074	2.49	2.49	2.47	3.16	2.45	2.51	1.17	up	3.83E-01	8.95E-01	-	-
1392851_at	Pex26	peroxisome biogenesis factor 26	297570	Rn.28713	AI146048	4.55	4.64	3.60	4.81	3.49	5.16	1.17	up	7.32E-01	9.14E-01	-	-
1374403_at	Efnb1	ephrin B1	25186	Rn.44398	BF412072	6.17	5.22	5.44	6.18	6.03	5.28	1.17	up	6.08E-01	8.95E-01	-	-
1369007_at	Nr4a2	nuclear receptor subfamily 4, group A, member 2	54278	Rn.88129	U72345	2.58	2.58	2.58	2.58	3.25	2.58	1.17	up	3.74E-01	8.95E-01	-	-
1383752_at	Nol1	nucleolar protein 1	314969	Rn.32804	BG375714	6.29	6.56	4.64	5.89	5.07	5.88	1.17	down	7.53E-01	9.20E-01	-	-
1374083_at	---	---	---	Rn.3717	AA799740	2.56	2.56	2.58	2.56	2.60	3.21	1.17	up	3.53E-01	8.95E-01	-	-
1384246_at	Smarca5	SWI/SNF related, matrix associated, actin dependent regulator of chromatin,	307766	Rn.221918	AA896404	6.26	6.76	6.69	5.65	7.73	6.99	1.17	up	7.41E-01	9.17E-01	-	-
1385325_at	Sntg2	syntrophin, gamma 2	298936	Rn.212984	BM389545	2.77	3.44	2.67	2.73	2.78	2.69	1.17	down	4.16E-01	8.95E-01	-	-
1380558_at	Cldn8	claudin 8	304124	Rn.79297	BI292090	4.15	2.90	3.85	4.46	3.74	3.38	1.17	up	6.75E-01	9.01E-01	-	-
1369743_a_at	P2rx4	purinergic receptor P2X, ligand-gated ion channel 4	29659	Rn.7176	U32497	3.35	2.97	2.98	3.12	3.67	3.18	1.17	up	3.60E-01	8.95E-01	-	-
1375516_at	Ndufc2	NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 2	293130	Rn.62471	AA891171	8.94	9.74	9.22	9.29	9.63	9.64	1.17	up	4.46E-01	8.95E-01	-	-
1368121_at	Akr7a3	aldo-keto reductase family 7, member A3 (aflatoxin aldehyde reductase)	26760	Rn.6043	NM_013215	10.93	11.37	11.59	11.14	10.97	11.11	1.17	down	3.33E-01	8.95E-01	-	-
1377135_at	---	---	---	Rn.22711	AA944958	7.49	7.85	7.06	7.22	6.80	7.72	1.17	down	5.62E-01	8.95E-01	-	-
1370609_a_at	Slc16a7	solute carrier family 16, member 7 (monocarboxylic acid transporter 2)	29735	Rn.217495	X97445	6.11	3.47	3.14	4.78	5.72	2.89	1.17	up	8.68E-01	9.59E-01	-	-
1393094_at	---	---	---	Rn.199316	AI385367	2.24	2.24	2.25	2.23	2.24	2.91	1.17	up	3.82E-01	8.95E-01	-	-
1389442_at	---	---	---	Rn.21790	AI406804	4.29	4.57	4.65	4.39	3.69	4.77	1.17	down	5.45E-01	8.95E-01	-	-
1367582_at	Rpl29	ribosomal protein L29	29283	Rn.3973	NM_017150	9.90	10.37	10.05	10.33	10.08	10.57	1.17	up	3.20E-01	8.95E-01	-	-
1368361_a_at	Ptpn2	protein tyrosine phosphatase, non-receptor type 2	117063	Rn.33497	NM_053990	6.68	7.18	7.80	7.92	6.76	7.66	1.17	up	6.67E-01	8.99E-

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1398285_at	Ak3l1	adenylate kinase 3-like 1	29223	Rn.1086	NM_017135	11.52	11.51	11.77	11.57	11.09	11.48	1.16	down	2.68E-01	8.95E-01	-	-
1381028_at	---	---	---	Rn.211406	BF417583	2.40	2.38	3.08	2.39	2.43	2.38	1.16	down	3.97E-01	8.95E-01	-	-
1383876_at	Ift74	intraflagellar transport 74 homolog (Chlamydomonas)	313365	Rn.15267	BG376705	5.87	4.33	4.10	4.93	2.94	5.77	1.16	down	8.37E-01	9.49E-01	-	-
1381611_at	Ahctf1	AT hook containing transcription factor 1	360886	Rn.48190	BF396355	4.88	5.11	5.04	4.86	4.34	5.18	1.16	down	4.35E-01	8.95E-01	-	-
1386942_at	Golga2	golgi autoantigen, golgin subfamily a, 2	64528	Rn.6165	NM_022596	5.92	6.72	5.34	5.46	6.00	5.86	1.16	down	6.38E-01	8.95E-01	-	-
1372115_at	LOC363188	similar to ubiquitin protein ligase E3 component n-recognin 2	363188	Rn.67473	AI408477	5.93	5.60	5.90	6.19	5.82	6.07	1.16	up	2.17E-01	8.95E-01	-	-
1399109_at	---	---	---	Rn.101809	BI281673	3.72	5.22	4.84	4.78	4.52	5.13	1.16	up	6.72E-01	9.01E-01	-	-
1376343_at	LOC361335	hypothetical protein LOC361335	361335	Rn.137956	BI296321	5.50	4.63	4.45	4.63	4.66	4.63	1.16	down	5.32E-01	8.95E-01	-	-
1396713_at	RGD1303066	Similar to RIKEN cDNA 2610110G12	361789	Rn.136935	BE121434	3.04	3.40	3.02	3.41	3.75	2.96	1.16	up	4.45E-01	8.95E-01	-	-
1381872_at	---	---	---	Rn.204554	AI137061	4.81	6.16	6.70	5.55	5.97	5.48	1.16	down	7.25E-01	9.13E-01	-	-
1370974_at	Vps54	vacuolar protein sorting 54 homolog (S. cerevisiae)	286932	Rn.107171	AJ010392	6.36	6.05	6.52	6.85	5.92	6.82	1.16	up	5.48E-01	8.95E-01	-	-
1383031_at	---	---	---	Rn.148402	AI030212	2.50	2.80	4.12	2.49	3.10	3.17	1.16	down	7.06E-01	9.08E-01	-	-
1373919_at	Cisd2	CDGSH iron sulfur domain 2	295457	Rn.24858	AA943801	7.74	7.81	7.54	7.84	7.73	8.19	1.16	up	2.46E-01	8.95E-01	-	-
1394056_at	Nicn1	nicolin 1	619581	Rn.19831	BF551160	4.50	4.12	3.08	4.19	4.13	4.04	1.16	up	6.32E-01	8.95E-01	-	-
1384012_at	---	---	---	Rn.24745	AW524995	2.46	3.03	2.47	2.46	2.47	2.38	1.16	down	3.12E-01	8.95E-01	-	-
1390729_x_at	Cpsf7	cleavage and polyadenylation specific factor 7, 59kDa	365407	Rn.98627	BM391768	6.20	5.36	5.03	5.64	5.82	4.47	1.16	down	7.09E-01	9.09E-01	-	-
1368129_at	Sfmbt1	Scm-like with four mbt domains 1	58967	Rn.14839	NM_031647	3.42	3.95	3.77	3.51	3.42	3.54	1.16	down	2.39E-01	8.95E-01	-	-
1390092_at	---	---	---	Rn.209307	BF410328	2.39	2.38	2.40	3.07	2.39	2.37	1.16	up	3.94E-01	8.95E-01	-	-
1372836_at	---	---	---	Rn.9547	AI170399	3.29	3.85	3.53	3.61	3.34	3.06	1.16	down	3.91E-01	8.95E-01	-	-
1395098_at	Btaf1	basic leucine zipper nuclear factor 1	498266	Rn.11987	BF390143	2.63	2.88	2.92	2.55	2.62	2.60	1.16	down	7.71E-02	8.95E-01	-	-
1377858_at	Prdm2	PR domain containing 2, with ZNF domain	313678	Rn.202632	BE120443	2.56	3.42	2.59	2.76	2.63	2.51	1.16	down	4.92E-01	8.95E-01	-	-
1398973_at	Tm9sf3	transmembrane 9 superfamily member 3	309475	Rn.17150	BI296499	7.11	7.10	7.30	7.10	7.11	7.96	1.16	up	4.96E-01	8.95E-01	-	-
1372496_at	Fdx1l	ferredoxin 1-like	313786	Rn.15041	BG371538	8.04	8.14	7.94	7.52	7.55	8.39	1.16	down	4.94E-01	8.95E-01	-	-
1374727_at	Dnajb12	DnaJ (Hsp40) homolog, subfamily B, member 12	294513	Rn.20419	AF244895	5.31	5.27	5.22	5.30	5.68	5.49	1.16	up	1.20E-01	8.95E-01	-	-
1381046_at	Asph	aspartate-beta-hydroxylase	312981	Rn.22695	BG375603	3.05	3.15	3.39	3.91	3.53	2.82	1.16	up	5.46E-01	8.95E-01	-	-
1369450_at	Ust5r	integral membrane transport protein UST5r	171398	Rn.81214	NM_134380	8.41	9.34	9.29	8.92	9.25	9.53	1.16	up	5.66E-01	8.95E-01	-	-
1377503_at	Riok2	RIO kinase 2 (yeast)	308201	Rn.137079	BG371773	4.58	5.48	4.66	4.65	4.58	4.84	1.16	down	5.04E-01	8.95E-01	-	-
1383368_at	---	---	---	Rn.165206	BF550060	6.35	6.60	7.31	7.28	7.04	6.60	1.16	up	5.64E-01	8.95E-01	-	-
1388591_at	Hs1bp3	HCLS1 binding protein 3	313950	Rn.23111	BM388471	5.29	5.28	5.32	5.06	5.10	5.07	1.16	down	2.18E-04	8.95E-01	-	-
1373814_at	R3hdm2	R3H domain containing 2	362894	Rn.203556	BI291270	6.22	5.96	6.91	5.77	6.33	6.35	1.16	down	5.55E-01	8.95E-01	-	-
1371683_at	Lsm4	LSM4 homolog, U6 small nuclear RNA associated (S. cerevisiae)	295647	Rn.27306	AI103250	7.30	6.82	7.04	7.27	6.37	6.85	1.16	down	5.00E-01	8.95E-01	-	-
1372648_at	---	---	---	Rn.203838	BI291338	3.26	2.84	3.00	2.82	2.82	2.80	1.16	down	1.47E-01	8.95E-01	-	-
1397588_at	RGD1561796	RGD1561796	360483	Rn.138657	BF406341	8.17	8.26	8.27	8.11	8.60	8.65	1.16	up	2.77E-01	8.95E-01	-	-
1375664_at	Tnrc6a	trinucleotide repeat containing 6a	308971	Rn.6839	BI294732	7.40	7.42	7.80	8.15	7.51	7.63	1.16	up	4.05E-01	8.95E-01	-	-
1390918_at	Adprhl1 /// Grtp1	ADP-ribosylhydrolase like 1 /// growth hormone regulated TBC protein 1	290880 /// 361180	Rn.144754	BE099056	7.12	7.36	7.77	7.11	7.22	7.26	1.16	down	3.25E-01	8.95E-01	-	-
1373165_at	---	---	---	Rn.8351	BF404539	4.62	4.84	5.10	4.38	5.03	4.50	1.16	down	4.20E-01	8.95E-01	-	-
1384925_at	---	---	---	Rn.204090	AI045021	5.77	3.98	2.61	3.14	3.55	5.00	1.16	down	8.48E-01	9.53E-01	-	-
1389792_at	Solh	small optic lobes homolog (Drosophila)	303000	Rn.131050	BE329471	2.71	2.49	2.59	2.58	3.38	2.49	1.16	up	4.91E-01	8.95E-01	-	-
1369813_at	Dnajc5	DnaJ (Hsp40) homolog, subfamily C, member 5	79130	Rn.100120	U39320	3.47	3.35	3.32	3.22	2.95	3.31	1.16	down	1.38E-01	8.95E-01	-	-
1374218_at	LOC685244	similar to IQ motif and Sec7 domain 2	685244	Rn.12018	BG379491	2.42	3.06	2.42	2.42	2.42	2.41	1.16	down	3.60E-01	8.95E-01	-	-
1378986_at	---	---	---	Rn.210890	BF405626	2.50	2.45	3.18	2.51	2.51	2.45	1.16	down	4.05E-01	8.95E-01	-	-
1370004_at	H2afy	H2A histone family, member Y	29384	Rn.11098	M99065	5.42	6.05	7.84	5.57	6.49	6.59	1.16	down	7.97E-01	9.34E-01	-	-
1386745_at	---	---	---	Rn.167993	BF523839	4.75	5.51	6.67	5.38	5.40	5.49	1.16	down	7.15E-01	9.10E-01	-	-
1397784_at	---	---	---	Rn.53695	BI297092	3.35	2.54	2.75	2.65	2.74	2.60	1.16	down	4.25E-01	8.95E-01	-	-
1395130_at	Zeb2	Zinc finger E-box binding homeobox 2	311071	Rn.59710	AA924745	2.45	2.44	2.47	2.45	3.13	2.44	1.16	up	3.92E-01	8.95E-01	-	-
1385066_a_at	---	---	---	Rn.95126	BM390527	2.61	2.64	2.65	2.62	3.25	2.69	1.16	up	3.33E-01	8.95E-01	-	-
1393528_at	---	---	---	Rn.164743	AI059227	2.45	2.45	2.44	2.34	2.46	3.21	1.16	up	4.66E-01	8.95E-01	-	-
1397747_at	Xpo7	exportin 7	361070	Rn.32535	BF563958	7.51	8.26	8.54	8.57	6.99	8.08	1.16	down	7.16E-01	9.10E-01	-	-
1394809_at	---	---	---	Rn.148415	AW522733	2.73	2.78	2.97	2.84	3.56	2.75	1.16	up	4.54E-01	8.95E-01	-	-
1370166_at	Sdc2	syndecan 2	25615	Rn.11127	BG668421	8.55	9.03	9.16	8.43	8.96	8.69	1.16	down	4.18E-01	8.95E-01	-	-
1367873_at	Atp6ap1	ATPase, H+ transporting, lysosomal accessory protein 1	83615	Rn.93045	NM_031785	8.85	8.91	9.30	8.71	8.89	8.79	1.16	down	2.16E-01	8.95E-01	-	-
1377806_at	Vezf1	vascular endothelial zinc finger 1	287615	Rn.198892	BF556273	4.87	5.68	6.89	5.41	5.02	6.35	1.16	down	7.72E-01	9.26E-01	-	-
1391066_at	Zfhx3	Zinc finger homeobox 3	307829	Rn.204355	AI502569	2.44	2.43	2.45	2.44	2.44	3.09	1.16	up	3.73E-01	8.95E-01	-	-
1382812_at	RGD1310429	similar to Protein Njmu-R1	303764	Rn.198882	BE096596	5.58	5.53	4.56	4.40	4.81	5.80	1.16	down	7.02E-01	9.07E-01	-	-
1377598_at	Spfa2	sperm specific antigen 2	311146	Rn.12870	AI044347	7.61	7.25	7.82	7.01	7.34	7.68	1.16	down	4.36E-01	8.95E-01	-	-
1396618_at	---	---	---	Rn.169712	BE097299	2.61	2.59	3.30	2.60	2.65	2.59	1.16	down	4.03E-01	8.95E-01	-	-
1392884_at	Rufy3	RUN and FYVE domain containing 3	360921	Rn.203111	AI172267	8.48	8.23	8.11	7.95	8.11	8.10	1.16	down	1.41E-01	8.95E-01	-	-
1387148_at	Gprasp1	G protein-coupled receptor associated sorting protein 1	171407	Rn.108184	NM_134386	3.74	3.09	3.57	3.03	3.63	4.39	1.16	up	6.45E-01	8.95E-01	-	-
1397425_at	Rabgap1	RAB GTPase activating protein 1	311911	Rn.14944	AI172341	4.84	4.41	3.60	4.42	4.69	4.40	1.16	up	5.91E-01	8.95E-01	-	-
1367586_at	Ldha	lactate dehydrogenase A	24533	Rn.107896	NM_017025	9.41	9.82	9.83	9.50	10.56	9.65	1.16	up	5.77E-01	8.95E-01	-	-
1385767_at	LOC304000	cell adhesion molecule JCAM	304000	Rn.61796	BF411017	8.69	7.81	7.03	7.95	7.51	8.72	1.16	up	7.32E-01	9.14E-01	-	-
1373213_at	Snap29	synaptosomal-associated protein 29	116500	Rn.17902	BI274180	6.88	6.37	7.49	6.54	7.08	6.46	1.16	down	5.94E-01	8.95E-01	-	-
1388892_at	Rab2b	RAB2B, member RAS oncogene family	305853	Rn.85120	BF395178	5.27	6.09	4.46	5.72	4.51	6.24	1.16	up	7.70E-01	9.25E-01	-	-
1383653_at	Snx11	sorting nexin 11	303493	Rn.13268	BG374126	8.02	7.44	7.24	7.73	7.68	7.95	1.16	up	4.24E-01	8.95E-01	-	-
1367886_at	Pcsk7	proprotein convertase subtilisin/kexin type 7	29606	Rn.10653	NM_019246	4.81	4.15	4.09	4.14	4.11	4.14	1.16	down	3.99E-01	8.95E-01	-	-
1372127_at	Ubap2	ubiquitin-associated protein 2	313169	Rn.7333	BI275824	5.59	5.69	5.41	5.27	4.85	5.91	1.16	down	5.31E-01	8.95E-01	-	-
1372250_at	Dbndd2	dysbindin (dystrobrevin binding protein 1) domain containing 2	499941	Rn.1536	BI294932	4.38	4.57	4.01	4.23	4.08	4.00	1.16	down	2.86E-01	8.95E-01	-	-
1373381_at	Herc4	hect domain and RLD 4	309758	Rn.18143	AI236889	5.11	6.61	7.41	5.14	7.16	6.17	1.16	down	8.19E-01	9.42E-01	-	-
1383632_at	---	---	---	Rn.164498	BI295105	9.54	10.39	10.48	10.56	10.03	10.48	1.16	up	5.58E-01	8.95E-01	-	-
1375659_at	Sec61a2	Sec61, alpha subunit 2 (S. cerevisiae)	361273	Rn.8078	BG381529	4.12	4.12	4.30	4.59	4.23	4.38	1.16	up	1.44E-01	8.95E-01	-	-
1384588_at	Natl1	N-acetyltransferase 11	361718	Rn.79724	BI295602	2.36	2.56	2.45	2.55	2.78	2.69	1.16	up	6.99E-02	8.95E-01	-	-
1398039_at	---	---	---	Rn.49878	BE110002	2.52	2.48	2.52	2.49	2.56	3.12	1.16	up	3.34E-01	8.95E-01	-	-
1395100_at	Pbrm1	polybromo 1	306254	Rn.19314	BI286690	6.82	7.93	7.00	8.07	6.87	7.45	1.16	up	6.78E-01	9.02E-01	-	-
1387022_at	Aldh1a1	aldehyde dehydrogenase 1 family, member A1	24188	Rn.6132	NM_022407	10.55	8.21	9.25	9.76	9.08	8.51	1.16	down	7.90E-01	9.32E-01	-	-
1385737_at	---	---	---	Rn.208839	BE121207	3.09	2.48	2.55	2.50	2.51	2.46	1.16	down	3.21E-01	8.95E-01	-	-
1396102_at	---	---	---	Rn.205613	BF406574	2.47	3.07	2.49	2.46	2.48	2.44	1.16	down	3.33E-01	8.95E-01	-	-
1396263_at	---	---	---	Rn.134999	BI301147	5.32	5.56	4.86	5.46	3.95	5.68	1.16	down	7.27E-01	9.13E-01	-	-
1392487_at	---	---	---	Rn.25888	BI303896	3.02	3.66	3.03	3.02	3.03	3.01	1.16	down	3.59E-01	8.95E-01	-	-
1376328_at	RGD1310819	similar to putative protein (5S487)	3013351	Rn.46856	BI278776	4.22	5.90	3.89	4.61	4.61	5.44	1.16	up	7.65E-01	9.23E-01	-	-
1381827_at	Wdr25 /// Wdr25l	WD repeat domain 25 /// WD repeat domain 25-like	299317 /// 314443	Rn.134984	AW527316	3.68	3.66	3.67	4.18	3.35	4.15	1.16	up	4.69E-01	8.95E-01	-	-
1387651_at	Aqp1	aquaporin 1	25240	Rn.1618	L07268	10.50	11.18	11.14	11.16	11.16	11.15	1.16	up	3.80E-01	8.95E-01	-	-
1390815_at	Cnnm1	Cyclin M1	309387	Rn.87733	BF282870	3.85	3.90	3.91	2.50	3.91	4.60	1.16	down	7.42E-01	9.17E-01	-	-
1394480_at	LOC100302372	hypothetical protein LOC100302372	100302372	---	BE109548	2.40	2.39	3.49	2.40	2.84	2.38	1.16	down	6.10E-01	8.95E-01	-	-
1386915_at	Anp32b	acidic (leucine-rich) nuclear phosphoprotein 32 family, member B	170724	Rn.20465	NM_131911	10.55	10.60	10.60	10.86	10.56	10.97	1.16	up	1.50E-01	8.95E-01	-	-
1372142_at	Asna1	arsA arsenite transporter, ATP-binding, homolog 1 (bacterial)	288919	Rn.7354	AI406558	8.94	9.54	9.55	10.00	9.65	9.04	1.16	up	5.61E-01	8.95E-01	-	-
1372746_at	RGD1566239	similar to RIKEN cDNA 2810428I15	306348	Rn.203891	BI295800	3.32	3.41	3.06	3.42	3.59	3.43	1.16	up	1.42E-01	8.95E-01	-	-
1383905_at	---	---	---	Rn.218011	BF401729	5.19	7.27	8.57	6.54	7.11	8.03	1.16	up	8.49E-01	9.53E-01	-	-
1397182_at	Trip11	thyroid hormone receptor interactor 11	314393	Rn.92005	AI169397	5.20	3.88	3.23	4.08	3.88	4.99	1.16	up	7.62E-01	9.22E-01	-	-
1379406_at	RGD1308396	similar to chromosome 14 open reading frame 21	290235	Rn.91559	AA925559	5.75	5.90	5.35	5.82	5.64	6.20	1.16	up	4.02E-01	8.95E-01	-	-
1382317_at	---	---	---	Rn.147419	AI408597	8.14	8.26	8.22	8.32	8.56	8.39	1.16	up	5.08E-02	8.95E-01	-	-
1372919_at	Agpat6	1-acylglycerol-3-phosphate O-acyltransferase 6 (lysophosphatidic acid acyltra	290843	Rn.6835	AA851904	4.58	5.07	4.60	4.37	5.07	5.47	1.16	up	5.76E-01	8.95E-01	-	-
1386953_at	Hsd11b1	hydroxysteroid 11-beta dehydrogenase 1	25116	Rn.888	NM_017080	11.92	12.16	11.99	12.12	12.07	12.54	1.16	up	2.54E-01	8.95E-01	-	-
1370218_at	Ldhb	lactate dehydrogenase B	24534	Rn.1785	AA848319	9.02	7.47	9.45	8.75	8.72	7.82	1.16	down	7.64E-01	9.23E-01	-	-
1367824_at	Fnta	farnesyltransferase, CAAX box, alpha	25318	Rn.5990	NM_012847	8.14	8.01	8.26	8.09	7.40	8.27	1.16	down	4.71E-01	8.95E-01	-	-
1390187_at	---	---	---	Rn.122681	AI060043	2.62	2.53	2.63	2.82	2.64	2.96	1.16	up	8.74E-02	8.95E-01	-	-
1385930_at	---	---	---	Rn.40398	AI229697	3.20	3.64	4.28	3.42	3.57	3.48	1.16	down	5.31E-01	8.95E-01	-	-
1394972_at	Trove2	TROVE domain family, member 2	304833	Rn.146598	BM390782	6.75	6.27	6.56	6.80	6.48	6.94	1.16	up	3.26E-01	8.95E-01	-	-
1385187_at	Glt25d1	glycosyltransferase 25 domain containing 1	290637	Rn.105830	AI555738	4.64	5.72	6.18	5.67	4.64	5.58	1.16	down	7.19E-01	9.11E-01	-	-
1393531_at	---	---	---	Rn.23234	AA964815	8.55	8.57	8.58	8.57	8.38	9.41	1.16	up	5.32E-01	8.95E-01	-	-
1387836_at	Ykt6	YKT6 v-SNARE homolog (S. cerevisiae)	64351	Rn.65234	NM_031692	3.90	3.41	3.80	3.79	3.84	4.13	1.16	up	2.98E-01	8.95E-01	-	-
1389000_at	LOC682469	similar to jumonji domain containing 1B	682469	---	AA964998	7.13	6.23	6.35	6.34	6.30	6.41	1.16	down	4.88E-01	8.95E-01	-	-
1393686_at	---	---	---	Rn.16518	AA818655	2.68	2.66	2.60	2.88	3.00	2.71	1.16	up	7.37E-02	8.95E-01	-	-
1367924_at	Pacs1	phosphofurin acidic cluster sorting protein 1	171444	Rn.154425	NM_134406	2.42	2.41	2.36	2.74	2.42	2.66	1.16	up	9.27E-02	8.95E-01	-	-
1384191_at	---	---	---	Rn.207511	BF387765	2.40	2.39	2.41	2.40	3.06	2.39	1.16	up	3.82E-01	8.95E-01	-	-
1374965_at	---	---	---	Rn.207511	BF414261	2.45	3.11	2.44	2.44	2.45	2.45	1.16	down	3.83E-01	8.95E-01	-	-
1379255_at	Atp6ap2	ATPase, H+ transporting, lysosomal accessory protein 2	302526	Rn.12944	AI012226	8.51	8.65	8.51	7.94	8.41	8.66	1.16	down	3.76E-01	8.95E-01	-	-
1376919_at	Mfsd6	major facilitator superfamily domain containing 6	301388	Rn.21418	BG665267	5.84	6.92	6.35	6.26	5.86	7.64	1.16	up	7.45E-01	9.17E-01	-	-
1395373_at	---	---	---	Rn.92969	BF561546	6.88	6.44	5.78	6.52	6.26	6.98	1.16	up	6.01E-01	8.95E-01	-	-
1383347_at	Rev1	REV1 homolog (S. cerevisiae)	316344	Rn.94641	BM384011	5.55	6.42	5.41	6.23	5.54	4.96	1.16	down	6.77E-01	9.02E-01	-	-
1374490_at	Trip12	thyroid hormone receptor interactor 12	316575	Rn.8277	AI177845	6.73	7.03	7.12	7.08	7.73	6.96	1.16	up	5.25E-01	8.95E-01	-	-
1398151_at	---	---	---	Rn.148541	BF394120	3.04	2.32	2.37	2.35	2.40	2.31	1.16	down	4.05E-01	8.95E-01	-	-
1390401_at	---	---	---	Rn.64630	BF285365	2.52	2.50	2.53	3.18	2.54	2.49	1.16	up	3.88E-01	8.95E-01	-	-
1398950_at	Unc119b	unc-119 homolog B (C. elegans)	288702	Rn.12943	BI275914	6.83	6.56	6.95	6.50	6.64	6.54	1.16	down	1.57E-01	8.95E-01	-	-
1393230_s_at	RGD1308772	Similar to KIAA0564 protein	290381	Rn.12947	AI136714	10.27	10.54	10.48	10.32	10.29	10.04	1.16	down	1.50E-01	8.95E-01	-	-
1389051_at	Rxrb	retinoid X receptor beta	361801	Rn.49295	BI274189	6.63	4.53	4.63	5.22	4.71	5.21	1.16	down	7.74E-01	9.26E-01	-	-
1381878_at	Ubn1	ubinuclein 1	302930	Rn.49741	AI578566	7.10	7.55	7.56	7.12	7.22	7.21	1.16	down	2.35E-01	8.95E-01	-	-
1390689_at	Rps6kc1	ribosomal protein S6 kinase, polypeptide 1	289342	Rn.101893	BF401605	4.72	3.71	2.55	4.18	3.82	3.62	1.16	up	7.55E-01	9.20E-01	-	-
1397287_at	RGD1565997	similar to 4931417G12Rik protein	500294	Rn.169032	BF291148	5.43	5.50	5.52	5.37	4.77	5.66	1.16	down	4.57E-01	8.95E-01	-	-
1378088_at	Zdhhc1	zinc finger, DHHC-type containing 1	291967	Rn.41274	BM386245	3.01	2.34	2.35	2.35	2.36	2.35	1.16	down	3.85E-01	8.95E-01	-	-
1390133_at	Bnip2	BCL2/adenovirus E1B interacting protein 2	300811	Rn.11823	AI178277	5.46	5.79	5.58	5.92	5.56	4.70	1.16	down	5.94E-01	8.95E-01	-	-
1372354_at	Dusp16	dual specificity phosphatase 16	297682	Rn.6369	BM389898	5.91	5.11	4.33	5.01	5.43	5.56	1.16	up	6.79E-01	9.02E-01	-	-
1372596_at	RGD1311660	similar to RIKEN cDNA 1110007L15	288518	Rn.102176	BI284774	2.96	3.49	3.69	3.55	3.40	3.84	1.16	up	4.43E-01	8.95E-01	-	-
1384017_at	Lrrk1	leucine-rich repeat kinase 1	308703	Rn.18993	AI058817	2.88	2.81	2.50	2.49	2.61	2.44	1.16	down	1.61E-01	8.95E-01	-	-
1370882_at	Hla-dmb	major histocompatibility complex, class II, DM beta	294273	Rn.5892	AI171966	5.63	3.76	4.60	5.25	5.38	4.01	1.16	up	7.71E-01	9.25E-01	-	-
1372323_at	Sardh	sarcosine dehydrogenase	114123	Rn.89832	AI103641	8.59	8.57	8.33	8.68	8.62	8.82	1.16	up	1.02E-01	8.95E-01	-	-
1377500_at	---	---	---	Rn.96235	BE119198	4.37	4.72	4.73	5.53	4.98	3.96	1.16	up	6.73E-01	9.01E-01	-	-
1381386_at	Pop5	Processing of precursor 5, ribonuclease P/MRP subunit (S. cerevisiae)	117241	Rn.41651	AI407297	6.56	7.01	7.57	6.97	6.27	7.25	1.16	down	6.27E-01	8.95E-01	-	-
1394155_at	Rbm7	RNA binding motif protein 7	315634	Rn.22366	AI010943	3.25	3.57	2.57	2.82	3.33	3.87	1.16	up	6.36E-01	8.95E-01	-	-
1370812_at	Bcl2l1	Bcl2-like 1	24888	Rn.10323	U72350	4.52	4.55	4.05	4.73	4.52	4.52	1.16	up	2.90E-01	8.95E-01	-	-
1398937_at	Dhx15	DEAH (Asp-Glu-Ala-His) box polypeptide 15	289693	Rn.55597	BI279381	7.57	7.80	7.52	7.55	7.02	7.67	1.16	down	3.74E-01	8.95E-01	-	-
1396326_at	Pdcd11	programmed cell death 11	309458	Rn.136636	BM390873	4.67	4.11	4.93	4.51	5.19	4.66	1.16	up	5.34E-01	8.95E-01	-	-
1392341_at	---	---	---	Rn.206199	AW523444	2.68	3.05	2.76	2.68	2.77	2.39	1.16	down	2.44E-01	8.95E-01	-	-
1392482_at	Grpel2	GrpE-like 2, mitochondrial	688777	Rn.103300	BF409567	5.96	5.58	6.21	6.19	4.87	6.04	1.16	down	6.59E-01	8.98E-01	-	-
1372409_at	Madd2l1bp	MADD2L1 binding protein	316237	Rn.9596	BI286562	3.74	3.10	3.10	3.09	3.11	3.10	1.16	down	3.70E-01	8.95E-01	-	-
1375307_at	Cbx6	chromobox homolog 6	315136	Rn.161995	BI275772	4.93	5.80	5.23	5.15	5.07	5.06	1.16	down	4.49E-01	8.95E-01	-	-
1394725_at	---	---	---	---	BE121209	3.27	2.57	2.61	2.60	2.61	2.59	1.16	down	3.98E-01	8.95E-01	-	-
1373606_at	Zfand2b	zinc finger, AN1 type domain 2B	363253	Rn.32162	AI411964	3.11	3.42	3.09	4.08	2.76	3.43	1.16	up	6.15E-01	8.95E-01	-	-
1389652_at	---	---	---	Rn.205626	AI171655	4.03	3.89	3.18	3.91	3.55	4.28	1.16	up	5.55E-01	8.95E-01	-	-
1379308_at	---	---	---	Rn.15257	BF283228	4.17	3.90	3.96	4.29	4.05	4.32	1.16	up	1.42E-01	8.95E-01	-	-
1395484_at	---	---	---	Rn.73

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1372267_at	Psmd5	proteasome (prosome, macropain) 26S subunit, non-ATPase, 5	296651	Rn.13415	AI233729	6.99	5.90	5.44	5.33	6.16	6.20	1.16	down	7.12E-01	9.10E-01	-	-
1385729_at	---	---	---	Rn.161430	BE108687	7.06	6.17	5.75	6.47	6.30	6.86	1.16	up	6.36E-01	8.95E-01	-	-
1380165_at	---	---	---	---	AI234713	2.48	2.46	2.98	2.40	2.48	2.40	1.16	down	2.80E-01	8.95E-01	-	-
1377244_at	Zkscan5	zinc finger with KRAB and SCAN domains 5	304275	Rn.38399	BM390979	4.08	3.14	4.41	3.92	3.95	4.40	1.16	up	6.32E-01	8.95E-01	-	-
1377142_at	---	---	---	Rn.146142	AW531487	3.89	2.57	3.87	2.61	3.54	3.54	1.16	down	7.10E-01	9.09E-01	-	-
1379545_at	---	---	---	Rn.64806	BG372752	2.36	2.35	2.36	2.36	2.36	2.99	1.16	up	3.69E-01	8.95E-01	-	-
1383932_at	---	---	---	Rn.203246	BF386167	2.73	2.65	2.60	2.72	3.29	2.62	1.16	up	3.68E-01	8.95E-01	-	-
1398769_at	Coro1b	coronin, actin-binding protein, 1B	29474	Rn.2819	NM_019222	6.41	6.43	5.75	6.12	6.64	6.48	1.16	up	4.73E-01	8.95E-01	-	-
1384196_at	Wdr41	WD repeat domain 41	361879	Rn.146022	BI288795	2.52	2.53	2.49	3.03	2.48	2.66	1.16	up	2.62E-01	8.95E-01	-	-
1392476_at	RGD1562378	histone H4 variant H4-v.1	500351	---	BE105480	2.28	2.89	2.28	2.27	2.26	2.27	1.16	down	3.51E-01	8.95E-01	-	-
1389550_at	---	---	---	Rn.203538	BM385941	3.87	4.39	2.43	3.23	3.47	3.36	1.16	down	7.36E-01	9.15E-01	-	-
1367956_at	Ncdn	neurochondrin	89791	Rn.5653	NM_053543	4.75	5.25	4.33	5.18	4.97	4.82	1.16	up	4.98E-01	8.95E-01	-	-
1385077_at	Gbf1	golgi-specific brefeldin A resistant guanine nucleotide exchange factor 1	309451	Rn.61235	BE097285	6.09	6.35	6.09	5.34	6.09	6.45	1.16	down	5.61E-01	8.95E-01	-	-
1398708_at	Mamld1	Mastermind like 3 (Drosophila)	310405	Rn.218110	BI297590	3.22	2.77	2.81	2.77	2.78	2.61	1.16	down	2.37E-01	8.95E-01	-	-
1387889_at	Folr1	folate receptor 1 (adult)	171049	Rn.6912	AI233882	8.60	9.17	9.38	8.58	8.98	8.95	1.16	down	4.66E-01	8.95E-01	-	-
1383445_at	Zfp191	zinc finger protein 191	360204	Rn.162286	BG667490	4.56	5.04	5.09	5.05	4.70	5.59	1.16	up	5.28E-01	8.95E-01	-	-
1395176_at	---	---	---	Rn.63561	BF404785	2.48	3.17	2.50	2.41	2.49	2.61	1.16	down	4.12E-01	8.95E-01	-	-
1378404_at	---	---	---	Rn.144284	AW435040	4.89	5.60	5.07	5.70	5.11	5.39	1.16	up	4.80E-01	8.95E-01	-	-
1382884_at	---	---	---	Rn.199248	AI009813	3.53	4.37	4.05	4.64	3.58	4.36	1.16	up	6.23E-01	8.95E-01	-	-
1375335_at	Hspb9ab1	heat shock protein 90kDa alpha (cytosolic), class B member 1	301252	Rn.98667	AI237389	10.15	10.79	10.26	10.16	10.21	10.19	1.16	down	3.40E-01	8.95E-01	-	-
1371822_at	Polr3d	polymerase (RNA) III (DNA directed) polypeptide D, 44kDa	306012	Rn.16896	BI275831	5.68	5.58	6.37	5.86	5.54	5.59	1.16	down	4.71E-01	8.95E-01	-	-
1370845_at	Entpd2	ectonucleoside triphosphate diphosphohydrolase 2	64467	Rn.8276	BI288690	2.44	2.34	2.35	3.09	2.35	2.33	1.16	up	4.44E-01	8.95E-01	-	-
1379854_at	Abhd5	abhydrolase domain containing 5	316122	Rn.12459	AA996933	5.80	4.47	2.92	4.48	2.80	5.28	1.16	down	8.57E-01	9.55E-01	-	-
1375147_at	Alkbh5	alkB, alkylation repair homolog 5 (E. coli)	303193	Rn.146441	AI175740	2.93	2.81	3.56	2.88	2.98	2.81	1.16	down	4.22E-01	8.95E-01	-	-
1371599_at	LOC294154	similar to chromosome 6 open reading frame 106 isoform a	294154	Rn.116613	AI228587	8.85	9.66	8.64	9.01	9.00	9.78	1.16	up	6.24E-01	8.95E-01	-	-
1368488_at	Nfil3	nuclear factor, interleukin 3 regulated	114519	Rn.54147	NM_053727	4.14	3.68	2.69	5.04	2.43	3.67	1.16	up	8.18E-01	9.42E-01	-	-
1393940_at	---	---	---	Rn.135395	AI070444	2.76	2.68	3.47	2.74	2.78	2.75	1.16	down	4.45E-01	8.95E-01	-	-
1384850_at	---	---	---	Rn.148182	AI710183	2.78	2.79	2.83	3.46	2.88	2.70	1.16	up	4.03E-01	8.95E-01	-	-
1391591_at	Zfp275	zinc finger protein 275	293849	Rn.44882	AW532531	2.85	2.72	2.75	3.03	3.03	2.89	1.16	up	2.69E-02	8.95E-01	-	-
1388782_at	Tcf21	transcription factor 21	252856	Rn.1671	BE113336	3.96	4.22	3.59	3.98	3.72	3.43	1.16	down	4.28E-01	8.95E-01	-	-
1374903_at	Gcnt2	glucosaminyl (N-acetyl) transferase 2, I-branching enzyme	306860	Rn.8807	AI234819	7.54	7.20	8.07	7.19	7.47	7.51	1.16	down	4.79E-01	8.95E-01	-	-
1389208_at	---	---	---	---	AA944562	2.50	2.45	2.49	2.48	3.11	2.48	1.16	up	3.68E-01	8.95E-01	-	-
1372799_at	Dguok	deoxyguanosine kinase	297389	Rn.6770	BF285179	9.39	8.47	8.52	8.13	8.72	8.89	1.16	down	6.03E-01	8.95E-01	-	-
1384652_at	Hfah1	Hfa1 Tip specific factor 1	317612	Rn.140508	AI555485	7.19	7.50	7.72	7.09	6.83	7.84	1.16	down	5.66E-01	8.95E-01	-	-
1396187_at	Ddx21	DEAD (Asp-Glu-Ala-Asp) box polypeptide 21	317399	Rn.162310	AI136551	2.80	2.85	2.71	2.71	2.65	3.64	1.16	up	5.45E-01	8.95E-01	-	-
1396985_at	---	---	---	Rn.171551	BE107425	3.08	2.50	2.52	2.50	2.51	2.46	1.16	down	3.27E-01	8.95E-01	-	-
1385466_at	Phgdh1	phosphoglycerate dehydrogenase like 1	361094	Rn.2539	AI146067	4.54	5.78	4.70	5.40	4.57	5.69	1.16	up	7.00E-01	9.07E-01	-	-
1383417_at	Bbs1	Bardet-Biedl syndrome 1 homolog (human)	309156	Rn.12497	BE119990	8.52	7.12	6.12	7.05	7.07	7.00	1.16	down	7.75E-01	9.27E-01	-	-
1382779_at	Hace1	HECT domain and ankyrin repeat containing, E3 ubiquitin protein ligase 1	361866	Rn.28116	BF285833	4.32	5.30	2.85	4.07	6.27	2.77	1.16	up	8.72E-01	9.61E-01	-	-
1378429_at	---	---	---	Rn.13318	BE108925	2.55	2.53	2.63	3.18	2.49	2.68	1.16	up	3.65E-01	8.95E-01	-	-
1388431_at	Ss18	synovial sarcoma translocation, Chromosome 18	361295	Rn.1014	AA851282	6.48	5.77	6.46	6.39	6.63	6.34	1.16	up	4.45E-01	8.95E-01	-	-
1384254_at	Otud1	OTU domain containing 1	498803	Rn.41363	AI717553	4.52	6.31	5.89	5.58	5.66	6.13	1.16	up	7.27E-01	9.13E-01	-	-
1378288_at	Ostalpha	organic solute transporter alpha	303879	Rn.19056	BI292167	3.95	3.79	3.84	3.96	4.63	3.63	1.16	up	5.14E-01	8.95E-01	-	-
1373862_at	Fgf	c-fos induced growth factor	360457	Rn.10796	AI170324	2.59	3.59	2.56	2.60	2.60	2.90	1.16	down	5.82E-01	8.95E-01	-	-
1388997_at	Arf3	ADP-ribosylation factor 3	140940	Rn.10644	BG380819	9.31	8.97	9.25	9.10	9.16	8.64	1.16	down	3.36E-01	8.95E-01	-	-
1388324_at	Tie1	tyrosine kinase with immunoglobulin-like and EGF-like domains 1	89806	Rn.13171	BI289129	2.46	2.43	2.47	3.10	2.46	2.44	1.16	up	3.80E-01	8.95E-01	-	-
1397822_at	---	---	---	Rn.166826	BF554794	2.35	2.34	2.36	2.35	3.00	2.33	1.16	up	3.88E-01	8.95E-01	-	-
1378014_at	LOC64038	Sertolin	64038	Rn.25472	BF405144	4.10	3.71	3.34	3.85	4.03	4.11	1.16	up	4.63E-01	8.95E-01	-	-
1372788_at	Ube2q1	ubiquitin-conjugating enzyme E2Q family member 1	295252	Rn.19034	AI144725	2.93	2.76	2.93	2.92	3.41	2.92	1.16	up	2.88E-01	8.95E-01	-	-
1392297_at	---	---	---	Rn.154195	BF410297	2.38	2.38	2.39	2.46	2.40	2.93	1.16	up	2.74E-01	8.95E-01	-	-
1392892_at	Pcgf2	polycomb group ring finger 2	287662	Rn.11826	AA855814	3.05	3.15	3.02	2.88	2.97	2.73	1.16	down	5.96E-02	8.95E-01	-	-
1376666_at	Socs6	suppressor of cytokine signaling 6	307200	---	AI170864	5.80	5.43	6.88	4.96	5.92	6.59	1.16	down	7.58E-01	9.21E-01	-	-
1368326_at	Eif2ak3	eukaryotic translation initiation factor 2 alpha kinase 3	29702	Rn.24897	NM_031599	3.80	4.18	3.58	3.62	4.03	4.54	1.16	up	5.43E-01	8.95E-01	-	-
1372682_at	Dnlz	DNL-type zinc finger	296587	Rn.22412	BG379301	5.80	6.59	5.54	6.02	5.78	6.76	1.16	up	6.49E-01	8.96E-01	-	-
1393360_at	Zfp428l	zinc finger protein 426-like	367034	Rn.165611	BE105636	7.55	7.27	7.23	7.30	6.55	7.56	1.16	down	5.41E-01	8.95E-01	-	-
1376052_at	Tmem160	transmembrane protein 160	292654	Rn.39053	AW525031	2.91	2.64	3.16	3.30	3.14	2.91	1.16	up	3.22E-01	8.95E-01	-	-
1372480_at	Zfp462	zinc finger protein 462	362522	Rn.23557	BE117893	3.50	2.71	2.70	2.61	2.80	2.86	1.16	down	4.82E-01	8.95E-01	-	-
1399065_at	Rbpms2	RNA binding protein with multiple splicing 2	502214	Rn.201337	BM389543	7.45	8.21	7.81	7.57	7.62	7.65	1.16	down	3.91E-01	8.95E-01	-	-
1398634_at	LOC686032	hypothetical protein LOC686032	686032	Rn.12393	AI030835	5.75	5.56	6.58	6.21	5.72	5.32	1.16	down	6.28E-01	8.95E-01	-	-
1375715_at	Rwdd1	RWD domain containing 1	259218	Rn.23942	BE112777	3.07	3.02	3.08	3.21	3.13	3.48	1.16	up	1.19E-01	8.95E-01	-	-
1374344_at	Prg-2	plasticity-related gene 2	314614	Rn.107771	AI711557	2.69	3.21	2.55	2.87	2.91	3.31	1.16	up	4.37E-01	8.95E-01	-	-
1382931_at	---	---	---	Rn.105782	AA924607	3.07	3.10	3.09	2.99	3.87	3.04	1.16	up	4.98E-01	8.95E-01	-	-
1374026_at	LOC296300	similar to zinc finger protein 341	296300	Rn.202389	BI288745	2.93	2.56	2.61	2.55	2.35	2.56	1.16	down	1.86E-01	8.95E-01	-	-
1385714_at	Tmc4	transmembrane channel-like 4	308310	Rn.138375	BF545988	2.23	2.85	2.23	2.22	2.23	2.22	1.16	down	3.67E-01	8.95E-01	-	-
1376996_at	---	---	---	Rn.42983	AI556018	5.84	6.07	5.93	5.99	4.53	6.68	1.16	down	7.56E-01	9.21E-01	-	-
1389440_at	---	---	---	Rn.16546	AI178476	2.37	2.36	2.97	2.36	2.37	2.35	1.16	down	3.52E-01	8.95E-01	-	-
1398315_at	Rpl15	ribosomal protein L15	245981	Rn.27505	AA800007	9.76	10.21	10.17	10.17	10.16	10.45	1.16	up	2.89E-01	8.95E-01	-	-
1395193_at	---	---	---	Rn.205524	BM384656	2.48	2.45	2.51	2.59	3.00	2.48	1.16	up	2.56E-01	8.95E-01	-	-
1396310_at	---	---	---	Rn.210362	BF545380	2.54	2.50	2.51	2.46	3.23	2.49	1.16	up	4.45E-01	8.95E-01	-	-
1392562_at	Fam128b	family with sequence similarity 128, member B	287929	Rn.205073	BM391400	2.60	3.79	3.47	3.45	3.51	3.52	1.16	up	5.85E-01	8.95E-01	-	-
1396013_at	Letm1	leucine zipper-EF-hand containing transmembrane protein 1	305457	Rn.162290	BI293141	7.47	7.42	7.28	7.94	7.31	7.55	1.16	up	3.31E-01	8.95E-01	-	-
1371620_at	Prelid1	PRELI domain containing 1	290995	Rn.6867	BI279855	9.04	9.87	9.77	9.65	9.81	9.86	1.16	up	4.79E-01	8.95E-01	-	-
1372347_at	---	---	---	Rn.116800	BI289462	5.32	6.56	6.47	5.62	6.70	6.66	1.16	up	7.13E-01	9.10E-01	-	-
1392125_at	---	---	---	Rn.172550	BF390331	2.45	2.42	2.51	2.44	2.56	3.02	1.16	up	3.05E-01	8.95E-01	-	-
1371754_at	Slc25a25	solute carrier family 25 (mitochondrial carrier, phosphate carrier), member 25	246771	Rn.17644	AI177358	9.12	8.03	9.53	9.23	8.22	9.86	1.16	up	7.63E-01	9.23E-01	-	-
1383073_at	Usp14	ubiquitin specific peptidase 14	291796	Rn.11790	BG666028	8.43	8.96	8.05	8.63	8.46	8.97	1.16	up	5.23E-01	8.95E-01	-	-
1375852_at	Hmgcr	3-hydroxy-3-methylglutaryl-Coenzyme A reductase	25675	Rn.9437	BM390399	6.47	6.24	6.48	6.17	6.13	6.26	1.16	down	7.42E-02	8.95E-01	-	-
1376108_at	---	---	---	Rn.18629	AI030915	3.74	3.72	4.76	4.16	3.72	3.72	1.16	down	6.00E-01	8.95E-01	-	-
1367843_at	Akr7a2	aflatoxin B1 aldehyde reductase member 2	171445	Rn.8548	NM_134407	10.40	10.91	10.68	10.31	10.62	10.43	1.16	down	2.85E-01	8.95E-01	-	-
1372301_at	Aebp1	AE binding protein 1	305494	Rn.37157	BI278482	6.69	5.97	6.55	6.61	6.57	6.66	1.16	up	3.98E-01	8.95E-01	-	-
1385087_at	---	---	---	Rn.173397	BF406606	7.37	7.56	6.55	7.18	7.39	7.53	1.16	up	5.51E-01	8.95E-01	-	-
1388975_at	Sucla2	succinate-CoA ligase, ADP-forming, beta subunit	361071	Rn.62159	AA923982	7.48	7.42	8.18	7.56	7.30	7.58	1.16	down	4.66E-01	8.95E-01	-	-
1373097_at	Ercc6	excision repair cross-complementing rodent repair deficiency, complementatic	306274	Rn.19370	BF282125	3.52	4.36	3.55	5.18	4.53	4.36	1.16	up	7.57E-01	9.21E-01	-	-
1373903_at	Rcsd1	RCSD domain containing 1	360872	Rn.99138	AI011920	3.73	3.80	3.11	4.18	3.41	2.41	1.16	down	7.25E-01	9.13E-01	-	-
1382007_at	Sh3glb1	SH3-domain GRB2-like endophilin B1	292156	Rn.203013	AA964563	8.30	7.89	7.72	7.90	8.75	7.90	1.16	up	5.59E-01	8.95E-01	-	-
1393290_at	Mef2a	myocyte enhancer factor 2a	309957	Rn.162435	AW142022	2.53	2.57	2.54	2.58	2.70	3.00	1.16	up	1.73E-01	8.95E-01	-	-
1383561_at	---	---	---	Rn.153937	BF550555	4.24	5.25	4.82	5.13	5.09	4.72	1.16	up	5.45E-01	8.95E-01	-	-
1367642_at	Suclg1	succinate-CoA ligase, alpha subunit	114597	Rn.3766	NM_053752	8.55	9.04	8.85	9.04	8.83	9.20	1.16	up	3.06E-01	8.95E-01	-	-
1383232_at	Rab33b	RAB33B, member of RAS oncogene family	365793	Rn.17868	AI716944	5.83	5.53	6.60	5.98	5.14	6.21	1.16	down	6.66E-01	8.96E-01	-	-
1371548_at	Mrps25	mitochondrial ribosomal protein S25	297459	Rn.3814	BI289416	8.64	9.03	8.31	8.97	8.93	8.71	1.16	up	3.95E-01	8.95E-01	-	-
1378703_at	---	---	---	---	BF396390	2.43	2.46	2.43	2.40	3.17	2.39	1.16	up	4.60E-01	8.95E-01	-	-
1373650_at	Cmas	cytidine monophosphate N-acetylneuraminic acid synthetase	312826	Rn.16352	AI172078	8.68	8.44	8.97	8.87	8.83	9.03	1.16	up	2.70E-01	8.95E-01	-	-
1371461_at	Fam54b	family with sequence similarity 54, member B	298549	Rn.3864	BF414239	7.33	6.89	6.81	7.05	7.29	7.32	1.16	up	3.14E-01	8.95E-01	-	-
1388844_at	Znf76	zinc finger protein 76 (expressed in testis)	361809	Rn.13446	AI102904	3.38	3.43	3.41	3.42	3.93	3.49	1.16	up	2.54E-01	8.95E-01	-	-
1391681_at	Ccne2	Cyclin E2	362485	Rn.98992	AI409729	3.79	3.21	3.26	3.22	3.22	3.19	1.16	down	3.20E-01	8.95E-01	-	-
1382475_at	---	---	---	Rn.79888	AI060133	4.30	3.59	4.14	3.91	3.76	3.74	1.16	down	3.93E-01	8.95E-01	-	-
1398803_at	Dync1h1	dynein cytoplasmic 1 heavy chain 1	29489	Rn.11027	NM_019226	6.85	7.35	7.60	7.77	6.93	7.72	1.16	up	5.80E-01	8.95E-01	-	-
1398358_a_at	Itgb5	integrin, beta 5	257645	Rn.16988	AW520594	5.61	3.76	3.62	3.46	4.84	4.07	1.16	down	7.94E-01	9.34E-01	-	-
1367457_at	Becn1	beclin 1, autophagy related	114558	Rn.2776	NM_053739	7.72	8.36	8.16	7.96	8.46	8.44	1.16	up	4.49E-01	8.95E-01	-	-
1395660_at	---	---	---	Rn.91142	BF284702	7.44	7.36	7.08	7.65	6.77	8.09	1.16	up	4.28E-01	8.95E-01	-	-
1384059_at	---	---	---	Rn.161035	BE115159	3.98	3.94	4.12	3.56	4.00	3.85	1.16	down	2.08E-01	8.95E-01	-	-
1372776_at	Fbxl5	F-box and leucine-rich repeat protein 5	305424	Rn.8259	BM392017	7.26	7.30	7.43	7.62	7.50	7.51	1.16	up	2.97E-02	8.95E-01	-	-
1388592_at	---	---	---	Rn.49412	BI288858	2.77	2.77	3.41	2.77	2.79	2.75	1.16	down	3.76E-01	8.95E-01	-	-
1395802_at	LOC685144	similar to SEC24 related gene family, member C	685144	Rn.122667	BF419095	4.29	5.93	4.45	5.28	4.24	5.78	1.16	up	7.76E-01	9.27E-01	-	-
1376771_at	Ppm1l	protein phosphatase 1 (formerly 2C)-like	310506	Rn.133275	BF412303	2.75	2.77	3.01	2.78	3.33	3.06	1.16	up	3.07E-01	8.95E-01	-	-
1367735_at	Acad1	acyl-Coenzyme A dehydrogenase, long-chain	25287	Rn.174	NM_012819	9.67	9.58	9.27	8.93	9.22	9.74	1.16	down	4.73E-01	8.95E-01	-	-
1387800_at	Daxx	death-domain associated protein	140926	Rn.870	NM_080891	2.79	3.21	2.79	3.00	3.00	3.42	1.16	up	3.47E-01	8.95E-01	-	-
1378254_at	LOC686547	similar to TBC1 domain family member 4 (Akt substrate of 160 kDa) (AS160)	686547	---	BM389480	2.69	2.64	2.73	3.56	2.44	2.67	1.16	up	5.72E-01	8.95E-01	-	-
1398259_at	Nup155	nucleoporin 155	117021	Rn.11328	NM_053952	4.81	5.39	5.13	4.92	5.71	5.33	1.16	up	4.99E-01	8.95E-01	-	-
1385338_at	690559 /// Vom2r	similar to reduced expression 2 /// vomeronasal 2 receptor, pseudogene 24	292498 /// 690559	Rn.137680	BM387792	3.75	4.32	3.50	4.28	3.72	4.21	1.16	up	5.20E-01	8.95E-01	-	-
1384156_at	Osbpl7	oxysterol binding protein-like 7	303497	Rn.205144	BI293851	6.44	6.56	6.10	6.25	6.17	6.06	1.16	down	2.29E-01	8.95E-01	-	-
1374649_at	Rasgrp2	RAS guanyl releasing protein 2 (calcium and DAG-regulated)	361714	Rn.38473	BG380629	2.40	2.40	2.43	3.05	2.41	2.40	1.16	up	3.80E-01	8.95E-01	-	-
1385268_at	ilk /// RGD1561464	ilk /// RGD1561464	363402 /// 497961	Rn.113514	BF404261	6.02	5.93	5.88	6.65	5.55	6.26	1.16	up	5.52E-01	8.95E-01	-	-
1393014_at	Lsm12	LSM12 homolog (S. cerevisiae)	287731	Rn.130804	AA849210	6.55	5.82	6.72	5.97	6.15	6.33	1.16	down	5.15E-01	8.95E-01	-	-
1389384_at	Ndufaf4	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, assembly factor 4	362495	Rn.106694	BE111733	9.49	9.12	9.32	8.76	9.26	9.27	1.16	down	3.51E-01	8.95E-01	-	-
1381759_at	RGD1565975	RGD1565975	291903	Rn.39276	AI555447	4.80	6.43	7.26	5.60	5.69	6.58	1.16	down	8.03E-01	9.37E-01	-	-
1388867_at	MGC112830	similar to transcription factor	361178	Rn.13772	AI227552	5.67	4.79	6.13	5.39	5.39	5.43	1.16	up	7.02E-01	9.07E-01	-	-
1371554_at	LOC688173	similar to Telethonin (Titin cap protein)	688173	---	AA799471	2.70	2.51	2.98	2.46	2.62	2.48	1.16	down	2.21E-01	8.95E-01	-	-
1371331_at	Fstl1	follistatin-like 1	79210	Rn.95652	BG665037	6.70	5.53	5.01	5.76	6.09	4.77	1.16	down	7.58E-01	9.21E-01	-	-
1392985_at	Ube2d3p	ubiquitin-conjugating enzyme E2D binding protein	316583	Rn.205206	BF415174	3.62	3.79	3.62	3.18	3.61	3.60	1.16	down	2.43E-01	8.95E-01	-	-
1399127_at	309374 /// RGD15	LOC361485 /// similar to chromosome 6 open reading frame 70	361485 /// 499055	Rn.7393	AA964600	5.55	5.28	3.80	4.96	5.41	4.88	1.16	up	7.30E-01	9.14E-01	-	-
1389481_at	RGD735065	similar to GI:13385412-like protein splice form I	294311	Rn.104274	BI282891	6.36	6.53	7.24	6.71	6.72	7.32	1.16	up	5.68E-01	8.95E-01	-	-
1389521_at	Ivns1abp	influenza virus NS1A binding protein	289089	Rn.36174	AI408553	10.17	10.00	10.31	10.33	10.36	10.42	1.16	up	9.27E-02	8.95E-01	-	-
1390678_at	---	---	---	Rn.98833	AA855527	4.93	3.85	3.74	3.73	4.13	4.04	1.16	down	6.28E-01	8.95E-01	-	-
1390448_at	Abhd13	abhydrolase domain containing 13	306630	Rn.6621	AA800699	6.57	6.57	5.44	6.39	6.60	6.22	1.16	up	6.22E-01	8.95E-01	-	-
1395835_at	Hddc2	HD domain containing 2	361462	Rn.60559	BE113326	2.33	2.40	2.35	2.33	3.09	2.30	1.16	up	4.66E-01	8.95E-01	-	-
1395714_at	---	---	---	---	AT005664	2.64	2.63	2.64	2.64	3.34	2.56	1.16	up	4.44E-01	8.95E-01	-	-
1371725_at	Myh9	Myosin, heavy chain 9, non-muscle	25745	Rn.11385	BM392410	5.70	6.51	6.15	6.54	6.24	6.21	1.16	up	4.60E-01	8.95E-01	-	-
1391513_at	Lrrc40	Leucine rich repeat containing 40	310946	Rn.106141	BE110237	2.73	2.72	2.73	3.09	2.73	2.99	1.16	up	1.25E-01	8.95E-01	-	-
1386022_at	---	---	---	Rn.156183	AW921706	4.15	4.26	4.77	3.51	5.36	4.94	1.16	up	7.41E-01	9.16E-01	-	-
1387787_at	Mylpf	myosin light chain, phosphorylatable, fast skeletal muscle	24584	Rn.6534	NM_012605	2.54	2.82	2.95	2.71	2.48	2.49	1.16	down	2.16E-01	8.95E-01	-	-
1388249_at	Rapgef1	Rap guanine nucleotide exchange factor (GEF) 1	63881	Rn.85879	AJ249986	3.42	3.60	3.28	3.92	3.06	2.70	1.16	down	6.04E-01	8.95E-01	-	-
1384083_at	B3galt1	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase-like 1	367384	Rn.48412	AW532159	3.61	3.86	3.64	3.59	3.61	3.28	1.16	down	1.93E-01	8.95E-01	-	-
1385213_at	Epsti1	epithelial stromal interaction 1 (breast)	498547	Rn.202726	AW524454	3.05	2.49	2.49	2.48	2.48	2.44	1.16	down	3.29E-01	8.95E-01	-	-
1368232_at	Mvk	mevalonate kinase	81727	Rn.6995	AW433971	2.66	2.66	3.28	2.65	2.66	2.65	1.16	down	3.67E-01	8.95E-01	-	-
1369295_at	Pgc	progastricsin (pepsinogen C)	24864	Rn.9735	NM_133284	3.09	2.82	2.55	2.76	2.55	2.53	1.16	down	2.88E-01	8.95E-01	-	-
1372778_at	Slc39a1	solute carrier family 39 (zinc transporter), member 1	361986	Rn.43952	AA799420	8.25	8.19	8.14	8.28	8.45	8.47	1.16	up	3.42E-02	8.95E-01	-	-
1379429_at	---	---	---	Rn.16505	AI045807	3.73	4.84	5.12	4.33	4.79	5.21	1.16	up	6.94E-01	9.05E-01	-	-
1397204_s_at	---	---	---

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1382458_at	---	---	---	Rn.169353	BF411815	2.68	2.74	2.55	2.63	2.69	3.27	1.15	up	3.82E-01	8.95E-01	-	-
1371775_at	---	---	---	Rn.130237	AI172057	9.21	9.21	8.80	9.18	9.24	9.43	1.15	up	2.54E-01	8.95E-01	-	-
1375580_at	Dpp9	dipeptidyl peptidase 9	301130	Rn.41201	AI547421	3.96	3.84	3.95	4.21	3.84	4.32	1.15	up	2.37E-01	8.95E-01	-	-
1383825_at	Rdx	radixin	315655	Rn.203261	AW527313	7.84	8.83	7.55	8.51	8.15	8.19	1.15	up	6.34E-01	8.95E-01	-	-
1376488_at	RGD1310027	similar to KIAA1582 protein	303774	Rn.156128	AI101689	3.52	3.52	3.50	3.52	3.87	3.77	1.15	up	1.24E-01	8.95E-01	-	-
1396726_at	Ascc3l1	Activating signal cointegrator 1 complex subunit 3-like 1	296126	Rn.76239	AI502051	3.24	3.05	5.87	6.12	2.66	4.00	1.15	up	8.86E-01	9.65E-01	-	-
1380402_at	---	---	---	Rn.1287	AA818127	4.83	5.90	5.90	5.65	4.50	5.86	1.15	down	7.26E-01	9.13E-01	-	-
1368874_a_at	Mafg	v-maf musculoaponeurotic fibrosarcoma oncogene homolog G (avian)	64188	Rn.17361	AB050011	2.67	2.58	3.33	2.75	2.68	2.53	1.15	down	4.43E-01	8.95E-01	-	-
1396766_at	Ift81	intraflagellar transport 81 homolog (Chlamydomonas)	373066	Rn.47911	BF404488	4.94	4.42	4.68	4.33	5.47	4.86	1.15	up	5.96E-01	8.95E-01	-	-
1389023_at	RGD1311563	similar to Oligosaccharyl transferase 3 CG7748-PA	363160	Rn.23748	AI599504	9.80	10.11	10.07	10.26	9.95	10.39	1.15	up	2.70E-01	8.95E-01	-	-
1398533_at	Cyfip2	cytoplasmic FMR1 interacting protein 2	303073	Rn.44008	BE105837	2.57	2.57	2.57	3.26	2.57	2.50	1.15	up	4.36E-01	8.95E-01	-	-
1389782_at	679430 /// RGD136	hypothetical protein LOC679430 /// similar to RIKEN cDNA 2010107G23	294499 /// 679430	Rn.3681	AI408993	6.30	6.26	6.46	6.47	6.49	6.68	1.15	up	8.46E-02	8.95E-01	-	-
1387370_at	Tmod1	tropomodulin 1	25568	Rn.1646	NM_013044	2.85	2.31	2.28	2.27	2.28	2.26	1.15	down	3.27E-01	8.95E-01	-	-
1376113_at	Zswim1	zinc finger, SWIM-type containing 1	311631	Rn.27453	BI279683	6.10	6.74	6.96	7.04	6.62	6.76	1.15	up	5.07E-01	8.95E-01	-	-
1389187_at	---	---	---	Rn.203866	BI286421	4.65	3.57	3.98	3.43	3.48	4.68	1.15	down	7.09E-01	9.09E-01	-	-
1388274_at	Bmyc	brain expressed myelocytomatosis oncogene	311807	Rn.11204	AA849035	4.03	3.02	3.26	2.66	3.25	3.78	1.15	down	6.65E-01	8.99E-01	-	-
1396742_at	Ipo5	importin 5	306182	Rn.79893	BI297304	2.79	2.48	2.53	2.88	2.54	3.01	1.15	up	2.92E-01	8.95E-01	-	-
1377300_at	Dusp3	dual specificity phosphatase 3	498003	Rn.8286	AW520764	2.41	2.34	2.41	2.41	2.97	2.41	1.15	up	3.30E-01	8.95E-01	-	-
1376625_at	LOC691862	hypothetical protein LOC691862	691862	Rn.198840	BI296015	5.79	6.47	6.00	7.10	5.47	6.31	1.15	up	7.07E-01	9.08E-01	-	-
1374738_at	Sdccag10	serologically defined colon cancer antigen 10	361887	Rn.153577	BF416387	9.72	9.09	8.31	9.53	9.21	9.00	1.15	up	6.59E-01	8.98E-01	-	-
1388864_at	Ddx54	DEAD (Asp-Glu-Ala-Asp) box polypeptide 54	360815	Rn.41869	BI276976	4.82	5.97	5.83	5.82	5.21	6.22	1.15	up	6.81E-01	9.03E-01	-	-
1368314_at	Ggcx	gamma-glutamyl carboxylase	81716	Rn.22410	NM_031756	3.80	3.39	3.39	3.07	4.04	4.09	1.15	up	5.94E-01	8.95E-01	-	-
1374856_at	Bcdin3d	BCDIN3 domain containing	363001	Rn.50645	BF396478	2.97	4.69	3.92	2.94	3.78	4.24	1.15	down	7.58E-01	9.21E-01	-	-
1396126_at	---	---	---	Rn.199196	BF556812	2.53	2.54	3.11	2.56	2.54	2.47	1.15	down	3.46E-01	8.95E-01	-	-
1398798_at	Metap2	methionyl aminopeptidase 2	64370	Rn.1984	NM_022539	8.75	8.29	8.46	8.62	8.85	8.66	1.15	up	2.43E-01	8.95E-01	-	-
1394440_at	Tnpo1	transportin 1	309126	Rn.56083	BI293863	5.91	5.42	5.60	6.23	5.39	5.93	1.15	up	5.06E-01	8.95E-01	-	-
1377172_at	Gpsm2	G-protein signaling modulator 2 (AGS3-like, C. elegans)	362023	Rn.144235	BE117002	2.59	3.12	3.09	2.58	4.13	2.72	1.15	up	7.13E-01	9.10E-01	-	-
1379005_at	Arl6ip6	ADP-ribosylation-like factor 6 interacting protein 6	499798	Rn.145597	AI555974	3.92	3.76	4.43	3.96	3.80	3.73	1.15	down	3.89E-01	8.95E-01	-	-
1368754_at	P2ry6	pyrimidinergic receptor P2Y, G-protein coupled, 6	117264	Rn.10671	NM_057124	2.38	2.44	2.39	2.95	2.49	2.39	1.15	up	2.95E-01	8.95E-01	-	-
1381713_at	---	---	---	Rn.199791	BE106279	6.10	5.11	5.44	5.64	5.11	5.28	1.15	down	5.65E-01	8.95E-01	-	-
1386473_at	Iqwd1	IQ motif and WD repeats 1	289181	Rn.3917	AA848540	7.75	7.77	8.50	7.84	7.82	7.74	1.15	down	4.55E-01	8.95E-01	-	-
1377652_at	---	---	---	---	BE103109	2.32	2.32	2.95	2.32	2.33	2.32	1.15	down	3.77E-01	8.95E-01	-	-
1396882_at	---	---	---	Rn.47074	AW529096	2.67	2.62	2.71	2.91	2.79	2.93	1.15	up	1.78E-02	8.95E-01	-	-
1374995_at	Elmo3	engulfment and cell motility 3	291962	Rn.151249	BI291645	4.86	4.81	3.70	4.68	4.69	4.62	1.15	up	6.16E-01	8.95E-01	-	-
1376498_at	Rilpl1	Rab interacting lysosomal protein-like 1	304469	Rn.62627	BI282766	7.04	5.64	3.78	5.64	5.65	5.79	1.15	up	8.38E-01	9.49E-01	-	-
1391813_at	Asb13	ankyrin repeat and SOCS box-containing 13	361268	Rn.69263	AA892466	6.97	7.18	6.35	6.36	7.03	6.48	1.15	down	5.57E-01	8.95E-01	-	-
1387983_at	Thrb	thyroid hormone receptor beta	24831	Rn.88692	J03933	8.83	8.31	7.87	7.89	7.86	8.63	1.15	down	6.12E-01	8.95E-01	-	-
1381617_at	---	---	---	Rn.205942	BE102030	2.48	3.31	2.51	3.21	3.27	2.44	1.15	up	6.17E-01	8.95E-01	-	-
1391195_at	Luc7l	LUC7-like (S. cerevisiae)	360503	Rn.99992	BF401728	3.59	3.82	3.50	4.13	3.45	3.95	1.15	up	4.13E-01	8.95E-01	-	-
1383960_at	Pex16	peroxisomal biogenesis factor 16	311203	Rn.98695	BG376773	4.66	4.69	4.95	4.48	4.07	5.13	1.15	down	5.54E-01	8.95E-01	-	-
1383044_at	---	---	---	Rn.81527	BM385117	4.67	5.92	4.99	4.75	5.89	5.55	1.15	up	7.04E-01	9.07E-01	-	-
1375562_at	---	---	---	Rn.34184	BF408460	5.35	5.48	5.04	5.86	5.07	5.57	1.15	up	4.79E-01	8.95E-01	-	-
1380162_at	---	---	---	Rn.206745	BI274645	2.71	2.96	2.76	2.74	3.61	2.70	1.15	up	5.34E-01	8.95E-01	-	-
1390910_at	Sesn3	Sestrin 3	315427	Rn.136987	BF408406	2.30	2.43	2.44	2.43	2.44	2.91	1.15	up	2.81E-01	8.95E-01	-	-
1391353_at	---	---	---	Rn.13277	AI044121	7.62	7.88	7.77	7.70	7.71	8.49	1.15	up	4.90E-01	8.95E-01	-	-
1373811_at	Rap1gds1	RAP1, GTP-GDP dissociation stimulator 1	310909	Rn.160647	AA942728	6.53	7.09	7.36	6.55	7.07	6.73	1.15	down	5.11E-01	8.95E-01	-	-
1385959_at	Sos1	Son of sevenless homolog 1 (Drosophila)	313845	Rn.91844	AI176851	4.56	4.36	4.79	6.00	3.88	4.45	1.15	up	7.64E-01	9.23E-01	-	-
1383900_at	Qrich2	glutamine rich 2	501747	Rn.15060	BG377183	3.58	4.73	3.61	3.54	3.55	4.20	1.15	down	6.60E-01	8.98E-01	-	-
1369999_a_at	Nnat	neuronatin	94270	Rn.5785	NM_053601	2.37	2.38	2.38	3.01	2.37	2.36	1.15	up	3.93E-01	8.95E-01	-	-
1370393_at	Ccdc5	coiled-coil domain containing 5	192228	Rn.163388	AF092207	2.38	2.40	2.41	2.78	2.41	2.63	1.15	up	1.32E-01	8.95E-01	-	-
1398768_at	Rbbp7	retinoblastoma binding protein 7	83712	Rn.3600	NM_031816	8.94	8.89	9.16	8.51	8.79	9.07	1.15	down	3.17E-01	8.95E-01	-	-
1371346_at	Ndufb6	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 6	297990	Rn.104528	AI104528	8.64	9.40	9.52	9.04	8.86	9.03	1.15	down	5.06E-01	8.95E-01	-	-
1398852_at	Rps21	ribosomal protein S21	81775	Rn.4153	BF410811	11.56	11.71	11.62	11.71	11.80	12.00	1.15	up	1.01E-01	8.95E-01	-	-
1380599_at	---	---	---	Rn.168053	AI639258	2.51	3.39	2.47	2.83	2.48	2.43	1.15	down	5.61E-01	8.95E-01	-	-
1369915_at	---	---	---	---	NM_139186	5.28	5.49	4.36	4.23	5.09	5.20	1.15	down	6.80E-01	9.03E-01	-	-
1380943_at	RGD1311648	similar to hypothetical protein FLJ21820	313949	Rn.105274	BI301460	3.98	5.13	5.68	5.13	5.30	4.98	1.15	up	7.06E-01	9.08E-01	-	-
1382356_at	Efhc2	EF-hand domain (C-terminal) containing 2	302507	Rn.39302	BI276482	6.08	6.19	6.36	5.78	6.42	7.05	1.15	up	6.11E-01	8.95E-01	-	-
1374734_at	LOC680254	Hypothetical protein LOC680254	680254	Rn.204807	BE115842	6.45	6.75	6.94	6.37	6.03	7.12	1.15	down	5.89E-01	8.95E-01	-	-
1382511_at	E2f1	E2F transcription factor 1	399489	Rn.72471	AI713319	3.00	2.41	2.42	2.41	2.39	2.41	1.15	down	3.48E-01	8.95E-01	-	-
1382823_at	---	---	---	---	AI070008	2.38	2.40	2.39	2.40	2.82	2.56	1.15	up	1.63E-01	8.95E-01	-	-
1377695_at	Smtnl2	smoothelin-like 2	679629	Rn.32487	BF281135	3.93	3.37	3.38	3.31	3.38	3.38	1.15	down	3.28E-01	8.95E-01	-	-
1371496_at	---	---	---	Rn.13458	AI178804	10.50	10.55	10.92	10.56	10.45	10.34	1.15	down	2.37E-01	8.95E-01	-	-
1390875_a_at	Ccdc41	coiled-coil domain containing 41	366872	Rn.45405	BF290046	3.42	4.85	2.48	3.01	3.38	3.75	1.15	down	7.90E-01	9.32E-01	-	-
1392316_at	---	---	---	Rn.212204	BI293349	2.70	3.34	2.74	2.70	2.73	2.73	1.15	down	3.77E-01	8.95E-01	-	-
1375903_a_at	Yaf2	YY1 associated factor 2	690262	Rn.7352	AI012344	8.71	7.15	5.71	8.18	6.71	7.30	1.15	up	8.41E-01	9.50E-01	-	-
1390383_at	Adfp	adipose differentiation related protein	298199	Rn.101967	BI285616	7.74	7.82	7.19	7.28	7.10	7.75	1.15	down	4.96E-01	8.95E-01	-	-
1378122_a_at	---	---	---	Rn.23192	BI285319	7.20	7.18	7.37	7.72	5.63	7.78	1.15	down	7.86E-01	9.31E-01	-	-
1374487_at	Fam96a	family with sequence similarity 96, member A	300797	Rn.8196	AI199579	8.08	8.61	8.62	7.99	8.29	8.41	1.15	down	4.02E-01	8.95E-01	-	-
1389420_at	LOC361100	similar to topoisomerase (DNA) II beta	361100	Rn.104539	BM389730	4.81	5.30	4.97	4.67	5.64	5.39	1.15	up	5.59E-01	8.95E-01	-	-
1383814_at	---	---	---	Rn.19747	BF556870	5.70	6.24	5.59	5.34	5.56	6.01	1.15	down	5.05E-01	8.95E-01	-	-
1375898_at	RGD1561067	similar to RNA binding protein gene with multiple splicing	498642	Rn.8565	AW252379	4.60	2.57	3.61	4.26	3.88	3.26	1.15	up	7.88E-01	9.24E-01	-	-
1389919_at	Parvb	parvin, beta	362973	Rn.16709	BI296756	3.80	4.21	3.92	3.80	3.78	3.73	1.15	down	1.76E-01	8.95E-01	-	-
1380018_at	---	---	---	Rn.146177	BF397708	2.48	3.03	2.48	2.46	2.48	2.44	1.15	down	3.24E-01	8.95E-01	-	-
1368191_a_at	Slc22a1	solute carrier family 22 (organic cation transporter), member 1	24904	Rn.11186	U76379	6.23	5.46	7.01	6.10	5.81	6.18	1.15	down	6.78E-01	9.02E-01	-	-
1395338_at	Lrpprc	leucine-rich PPR-motif containing	313867	Rn.92051	BF289725	4.71	5.98	5.57	5.69	5.17	6.03	1.15	up	6.71E-01	9.00E-01	-	-
1377991_at	Rabn1l	round spermatid basic protein 1-like	311987	Rn.139850	BG376644	4.51	4.53	4.16	4.51	4.81	4.50	1.15	up	2.58E-01	8.95E-01	-	-
1372312_at	Ltv1	LTV1 homolog (S. cerevisiae)	361452	Rn.7361	AI176212	3.88	5.76	5.17	5.17	4.76	5.49	1.15	up	7.47E-01	9.18E-01	-	-
1373833_at	RGD1305713	similar to RIKEN cDNA 3110040N11	293059	Rn.138288	BI288945	2.46	2.49	2.50	2.68	2.55	2.84	1.15	up	6.89E-02	8.95E-01	-	-
1394414_at	SD1566766 /// Yip	hypothetical gene supported by BC088468; NM_001009712 /// Yip1 domain fa	362699 /// 500622	Rn.161898	BF386706	7.59	7.85	7.74	7.63	7.90	8.27	1.15	up	3.63E-01	8.95E-01	-	-
1390704_at	Sdad1	SDA1 domain containing 1	289504	Rn.12755	BF394953	3.69	2.86	2.67	2.60	3.19	2.81	1.15	down	5.97E-01	8.95E-01	-	-
1367898_at	Bnip3l	BCL2/adenovirus E1B interacting protein 3-like	140923	Rn.827	NM_080888	9.16	8.89	8.96	8.75	8.76	8.88	1.15	down	8.58E-02	8.95E-01	-	-
1389484_at	Coq4	coenzyme Q4 homolog (S. cerevisiae)	366013	Rn.162647	BI274693	4.36	4.61	5.16	4.81	4.98	4.96	1.15	up	4.44E-01	8.95E-01	-	-
1391560_at	Hivep1	human immunodeficiency virus type I enhancer binding protein 1	117140	Rn.50740	AI237082	3.31	3.08	3.31	3.43	3.33	3.56	1.15	up	1.19E-01	8.95E-01	-	-
1380565_at	RGD1306783	similar to 2810422O20Rik protein	304928	Rn.206031	AW532670	4.36	4.32	5.02	4.22	4.37	4.50	1.15	down	4.43E-01	8.95E-01	-	-
1388529_at	Rtcd1	RNA terminal phosphate cyclase domain 1	295395	Rn.25445	AI237372	7.16	7.47	6.66	7.25	7.17	7.48	1.15	up	4.63E-01	8.95E-01	-	-
1378119_at	Zc3h8	zinc finger CCCH type containing 8	311414	Rn.137486	BG381574	3.98	4.68	4.07	4.70	4.40	4.24	1.15	up	4.70E-01	8.95E-01	-	-
1371967_at	Mrpl16	mitochondrial ribosomal protein L16	293754	Rn.101972	AI410349	9.81	9.90	9.44	9.48	9.31	9.75	1.15	down	3.45E-01	8.95E-01	-	-
1381038_at	---	---	---	Rn.43589	BE101442	2.62	2.61	2.74	2.61	3.37	2.60	1.15	up	4.68E-01	8.95E-01	-	-
1370005_at	Cyb5b	cytochrome b5 type B (outer mitochondrial membrane)	80773	Rn.10249	NM_030586	7.07	7.49	7.71	7.40	6.60	7.66	1.15	down	6.08E-01	8.95E-01	-	-
1393759_at	---	---	---	---	BM385963	2.82	2.70	2.69	2.82	3.07	2.94	1.15	up	6.56E-02	8.95E-01	-	-
1378611_at	---	---	---	Rn.15626	BE112744	2.42	3.48	2.56	2.50	2.77	2.57	1.15	down	5.83E-01	8.95E-01	-	-
1392775_at	---	---	---	Rn.166723	AI136598	5.53	5.13	3.79	5.25	4.74	5.07	1.15	up	7.27E-01	9.13E-01	-	-
1398488_at	Ncoa5	Nuclear receptor coactivator 5	296372	Rn.8482	AW254531	2.48	2.37	2.47	2.58	2.89	2.46	1.15	up	2.04E-01	8.95E-01	-	-
1390974_a_at	---	---	---	Rn.199357	BI285675	4.99	4.07	7.17	4.96	5.90	6.00	1.15	up	8.44E-01	9.51E-01	-	-
1374507_at	Ube4b	ubiquitination factor E4B	298652	Rn.19289	BE096671	7.63	7.37	7.14	7.88	6.72	8.16	1.15	up	6.80E-01	9.03E-01	-	-
1390134_at	---	---	---	Rn.46830	AI411274	6.49	5.90	7.02	6.51	6.50	7.01	1.15	up	6.05E-01	8.95E-01	-	-
1382376_at	Bag4	BCL2-associated athanogene 4	361167	Rn.163329	BI297220	2.94	2.47	2.44	2.41	2.42	2.40	1.15	down	2.72E-01	8.95E-01	-	-
1382630_at	RGD1311558	similar to 4930506M07Rik protein	292139	Rn.16095	BI302656	7.43	7.59	7.50	6.79	7.52	7.60	1.15	down	4.75E-01	8.95E-01	-	-
1373687_at	Sgsm3	small G protein signaling modulator 3	362963	Rn.66996	BI284968	2.84	2.83	2.86	2.84	3.50	2.81	1.15	up	4.13E-01	8.95E-01	-	-
1394459_at	FAM120C	family with sequence similarity 120C	317423	Rn.41046	AI715728	2.74	4.26	2.80	2.79	2.75	3.64	1.15	down	7.40E-01	9.16E-01	-	-
1383728_at	LOC686240	similar to NMDA receptor regulated 1-like	686240	---	BM387529	2.71	2.69	2.69	2.75	2.68	3.27	1.15	up	3.35E-01	8.95E-01	-	-
1391443_at	RGD1559923	similar to chromosome 14 open reading frame 35	498489	Rn.15205	BF289340	7.77	7.40	7.28	7.65	7.39	8.01	1.15	up	4.28E-01	8.95E-01	-	-
1367740_at	Ckb	creatine kinase, brain	24264	Rn.1472	M14400	4.95	4.70	5.08	5.01	4.84	4.27	1.15	down	4.59E-01	8.95E-01	-	-
1368221_at	Nr3c1	nuclear receptor subfamily 3, group C, member 1	24413	Rn.90070	AY066016	6.69	6.29	6.34	6.12	6.22	6.38	1.15	down	2.39E-01	8.95E-01	-	-
1373029_at	Cops2	COP9 constitutive photomorphogenic homolog subunit 2 (Arabidopsis)	261736	Rn.11556	AI169377	7.95	8.32	8.25	7.94	7.81	8.15	1.15	down	2.43E-01	8.95E-01	-	-
1388566_at	Laqr1	Laqr1	29278	Rn.94195	AI102215	9.56	9.68	9.89	9.48	9.51	9.53	1.15	down	1.02E-01	8.95E-01	-	-
1377669_at	Rab27a	RAB27A, member RAS oncogene family	50645	Rn.37360	BM389524	2.54	2.53	2.55	2.53	3.17	2.52	1.15	up	3.93E-01	8.95E-01	-	-
1376798_at	---	---	---	Rn.46462	AW527232	3.08	2.42	2.43	2.21	2.43	2.68	1.15	down	4.72E-01	8.95E-01	-	-
1372021_at	Nup188	nucleoporin 188	366016	Rn.11918	AI102685	2.96	2.58	2.73	2.58	2.54	2.53	1.15	down	1.43E-01	8.95E-01	-	-
1370288_a_at	Tpm1	tropomyosin 1, alpha	24851	Rn.87540	AF372216	8.90	9.80	8.85	8.93	9.64	9.59	1.15	up	6.24E-01	8.95E-01	-	-
1375730_at	Itfg2	integrin alpha FG-GAP repeat containing 2	362441	Rn.148803	BF404626	2.40	2.40	2.43	2.40	3.11	2.34	1.15	up	4.53E-01	8.95E-01	-	-
1377123_at	Slc27a4	solute carrier family 27 (fatty acid transporter), member 4	311839	Rn.145068	BI286134	2.73	3.42	2.66	2.86	3.83	2.73	1.15	up	6.54E-01	8.97E-01	-	-
1379741_at	Atp6v0a4	ATPase, H+ transporting, lysosomal V0 subunit A4	296981	Rn.154498	BG377116	9.55	9.97	9.91	9.80	9.37	9.84	1.15	down	3.27E-01	8.95E-01	-	-
1389575_at	RGD1311703	similar to sid2057p	293160	Rn.20471	BF284868	6.85	5.85	4.83	6.08	5.81	6.24	1.15	up	7.49E-01	9.19E-01	-	-
1389309_at	Sbno1	strawberry notch homolog 1 (Drosophila)	304470	Rn.12294	AW251323	7.85	7.85	7.35	8.24	7.12	8.30	1.15	up	6.51E-01	8.96E-01	-	-
1389250_at	---	---	---	Rn.65477	AW915115	3.30	3.29	3.30	3.92	3.31	3.28	1.15	up	3.79E-01	8.95E-01	-	-
1370440_at	Nek9	NIMA (never in mitosis gene a)- related kinase 9	299204	Rn.102266	BI286772	6.25	6.82	7.37	6.88	6.96	7.22	1.15	up	5.75E-01	8.95E-01	-	-
1374923_at	Nyw1	ischemia related factor NYW-1	59319	Rn.133954	BM386444	2.89	3.47	2.84	3.33	3.28	3.20	1.15	up	3.76E-01	8.95E-01	-	-
1399081_at	Peli1	pellino 1	305549	Rn.22814	AI712911	5.93	5.94	5.64	5.88	6.02	6.22	1.15	up	2.14E-01	8.95E-01	-	-
1388820_at	RGD1307526	similar to modulator of estrogen induced transcription	315792	Rn.49132	BI286365	6.87	7.10	7.06	7.23	7.03	7.38	1.15	up	1.73E-01	8.95E-01	-	-
1385614_at	Mlph	melanophilin	316620	Rn.124575	BM388138	2.51	2.50	2.51	3.19	2.51	2.43	1.15	up	4.47E-01	8.95E-01	-	-
1388685_at	Dgcr2	DiGeorge syndrome critical region gene 2	360742	Rn.198930	AI011749	8.71	8.23	7.63	8.05	8.01	7.90	1.15	down	5.51E-01	8.95E-01	-	-
1394448_at	---	---	---	Rn.40763	BG380798	2.40	2.37	2.41	2.90	2.40	2.48	1.15	up	2.62E-01	8.95E-01	-	-
1382612_at	Hoxa9l	homeobox A9-like	297099	---	BF395928	7.66	6.31	7.58	7.41	7.55	7.20	1.15	up	6.73E-01	9.01E-01	-	-
1382094_at	---	---	---	---	BI285519	8.56	8.99	8.85	9.06	9.09	8.86	1.15	up	2.33E-01	8.95E-01	-	-
1371719_at	Brd2	bromodomain containing 2	294276	Rn.98146	AA946361	3.78	3.95	3.64	4.22	3.50	4.25	1.15	up	4.77E-01	8.95E-01	-	-
1379434_at	Fgd1	FYVE, RhoGEF and PH domain containing 1	363460	Rn.204249	BE100206	7.92	7.20	7.34	7.33	7.19	7.32	1.15	down	4.12E-01	8.95E-01	-	-
1374133_at	Trit1	tRNA isopentenyltransferase 1	362586	Rn.74419	BG373110	6.73	6.58	5.97	6.65	6.53	6.70	1.15	up	4.40E-01	8.95E-01	-	-
1398592_at	---	---	---	Rn.204006	AI045966	3.31	2.74	2.77	2.78	2.76	3.90	1.15	up	6.53E-01	8.97E-01	-	-
1395065_at	Wdr41	WD repeat domain 41	361879	Rn.146022	AW521367	3.03	3.83	2.73	2.96	3.16	2.85	1.15	down	5.81E-01	8.95E-01	-	-
1388644_at	Mgll	Monoglyceride lipase	29254	Rn.40396	AI713204	10.26	10.38	10.16	9.82	10.20	10.16	1.15	down	2.04E-01	8.95E-01	-	-
1389016_at	Usp4	ubiquitin specific peptidase 4 (proto-oncogene)	290864	Rn.92126	AI029306	8.82	8.83	8.99	8.81	9.24	9.20	1.15	up	2.39E-01	8.95E-01	-	-
1390480_at	Kif13a	kinesin family member 13A	308173	Rn.41333	AI704806	8.55	7.98	7.06	8.07	8.31	7.83	1.15	up	6.77E-01	9.02E-01	-	-
1372405_at	Lrrc68	leucine rich repeat containing 68	308398	Rn.7032	BE107128	6.40	6.83	6.12	6.17	6.32	6.06	1.15	down	2.83E-01	8.95E-01	-	-
1367519_at	Osbpl2	oxysterol binding protein-like 2	296461	Rn.12390	BG373087	6.75	5.67	5.48	6.11	6.54	5.87	1.15	up	6.69E-01	9.00E-01	-	-
1373350_at	Psip1	PC4 and SFRS1 interacting protein 1	313323	Rn.93075	H31668	2.63	2.58	3.62	2.98	2.69	2.55	1.15	down	6.01E-01	8.95E-01	-	-
1382969_at	---	---	---	Rn.166868	AI029559	7.15	8.74	9.08	8.32	8.37	8.89	1.15	up	7.60E-01	9.22E-01	-	-
1392361_at	---	---	---	Rn.49221	BE105683	3.90	4.21	4.39	3.90	4.02	3.97	1.15	down	2.37E-01	8.95E-01	-	-
1374887_at	Tubgcp6	tubulin, gamma complex associated protein 6	362980	Rn.24182	AA894189	5.19	4.27	3.58	5.11	4.28	4.27	1.15	up	7.27E-01	9.13E-01	-	-
1372367_at	Grlf1-

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1374529_at	---	---	---	---	AI406660	4.77	4.60	4.10	4.31	4.44	4.11	1.15	down	4.17E-01	8.95E-01	-	-
1371191_at	Nf2	neurofibromin 2 (merlin)	25744	Rn.46695	BF566236	4.16	3.52	2.48	3.22	3.25	3.09	1.15	down	7.02E-01	9.07E-01	-	-
1381585_at	---	---	---	---	BF419665	2.69	2.72	3.25	2.70	2.74	2.82	1.15	down	3.39E-01	8.95E-01	-	-
1397815_at	Arl8b	ADP-ribosylation factor-like 8B	500282	Rn.6283	BG671292	6.25	6.91	7.08	6.52	6.36	6.76	1.15	down	5.10E-01	8.95E-01	-	-
1381394_at	Snx27	sorting nexin family member 27	260323	Rn.7581	BM388706	7.65	8.26	7.12	7.20	8.11	8.33	1.15	up	6.95E-01	9.06E-01	-	-
1395717_at	---	---	---	Rn.172669	BF394620	4.36	4.56	4.28	5.42	3.91	4.47	1.15	up	6.75E-01	9.01E-01	-	-
1389916_at	---	---	---	Rn.144416	AI574953	8.36	8.67	8.45	7.79	8.44	8.65	1.15	down	5.03E-01	8.95E-01	-	-
1397755_at	---	---	---	---	AI575649	2.44	2.98	2.45	2.42	2.44	2.40	1.15	down	3.20E-01	8.95E-01	-	-
1374001_at	---	---	---	Rn.4081	AA851818	4.20	4.14	4.29	3.78	4.59	4.87	1.15	up	5.72E-01	8.95E-01	-	-
1369594_at	Efna5	ephrin A5	116683	Rn.10714	NM_053903	3.38	3.61	3.20	3.12	3.10	3.36	1.15	down	2.35E-01	8.95E-01	-	-
1392180_at	Sp1	Sp1 transcription factor	24790	Rn.44609	AI705174	4.44	5.42	5.05	4.35	4.98	4.97	1.15	down	5.97E-01	8.95E-01	-	-
1375166_at	Mrps26	Mitochondrial ribosomal protein S26	362216	Rn.8520	AI237581	2.19	2.48	2.59	2.58	2.59	2.69	1.15	up	1.80E-01	8.95E-01	-	-
1373571_at	Rtn3	reticulon 3	140945	Rn.11652	AI170276	7.78	7.09	7.51	7.01	7.47	7.31	1.15	down	4.53E-01	8.95E-01	-	-
1396736_at	---	---	---	---	BF409344	2.61	2.49	2.62	3.11	2.61	2.60	1.15	up	3.04E-01	8.95E-01	-	-
1389629_at	Prpf6	PRP6 pre-mRNA splicing factor 6 homolog (S. cerevisiae)	366276	Rn.17062	AA819400	6.40	6.66	6.08	6.61	5.11	6.82	1.15	down	7.39E-01	9.16E-01	-	-
1387819_at	Cela1	chymotrypsin-like elastase family, member 1	24331	Rn.6044	NM_012552	8.48	9.96	8.99	9.16	9.37	9.50	1.15	up	6.75E-01	9.01E-01	-	-
1390777_at	Scd5d	stearoil-CS-desaturase (ERG3 delta-5-desaturase homolog, S. cerevisiae)-like	114100	Rn.18741	AI710051	7.41	8.04	7.44	7.68	7.82	8.00	1.15	up	4.25E-01	8.95E-01	-	-
1397541_at	Twsg1	twisted gastrulation homolog 1 (Drosophila)	363294	Rn.8466	BG671148	4.05	4.24	4.39	3.76	4.17	4.14	1.15	down	2.90E-01	8.95E-01	-	-
1391315_at	RGD1562174	similar to mKIAA1450 protein	310538	Rn.58464	BM386843	6.43	5.91	7.81	6.26	6.75	6.54	1.15	down	7.47E-01	9.18E-01	-	-
1397307_at	---	---	---	Rn.168452	BF555100	9.22	8.65	9.25	8.70	8.45	9.36	1.15	down	5.81E-01	8.95E-01	-	-
1383963_at	---	---	---	Rn.45287	AW521929	9.01	8.47	8.19	8.90	8.73	8.33	1.15	down	7.36E-01	9.15E-01	-	-
1396219_at	31271 /// RGD155	similar to nidogen 2 /// hypothetical LOC501271 /// similar to nidogen 2 protein	367653 /// 499004	Rn.201687	BF542315	2.40	2.38	2.41	2.39	3.04	2.37	1.15	up	4.12E-01	8.95E-01	-	-
1372718_at	LOC685029	similar to anaphase promoting complex subunit 13	685029	Rn.98496	AA799572	10.05	10.49	9.89	10.44	10.22	10.38	1.15	up	3.50E-01	8.95E-01	-	-
1369119_a_at	Htr7	5-hydroxytryptamine (serotonin) receptor 7	85032	Rn.87132	X68663	2.77	2.40	2.42	2.41	3.39	2.39	1.15	up	5.97E-01	8.95E-01	-	-
1395036_at	Impad1	inositol monophosphatase domain containing 1	312952	Rn.129949	BF386788	5.78	7.25	7.34	6.99	6.84	7.16	1.15	up	7.15E-01	9.10E-01	-	-
1383405_at	LOC685398	similar to 1A6/DRIM (down-regulated in metastasis) interacting protein	685398	---	AW254703	4.23	4.37	4.33	4.80	4.28	4.46	1.15	up	2.69E-01	8.95E-01	-	-
1396526_at	---	---	---	---	BF410339	2.52	2.34	2.78	2.35	2.35	2.33	1.15	down	1.91E-01	8.95E-01	-	-
1395871_at	LOC361100	similar to topoisomerase (DNA) II beta	361100	Rn.104585	H31553	5.56	6.60	6.32	6.34	6.25	6.50	1.15	up	5.62E-01	8.95E-01	-	-
1370657_at	Cdh6	cadherin 6	25409	Rn.10390	D25290	3.81	3.34	3.25	3.35	3.12	3.34	1.15	down	3.50E-01	8.95E-01	-	-
1383230_at	RGD1311078	LOC360664	360664	Rn.15123	BI282204	6.85	6.77	6.21	5.82	6.29	7.11	1.15	down	6.62E-01	8.98E-01	-	-
1383485_at	Mdm2	Mdm2 p53 binding protein homolog (mouse)	314856	Rn.91829	BF548539	6.81	6.59	6.61	6.82	6.78	7.01	1.15	up	1.13E-01	8.95E-01	-	-
1375893_a_at	---	---	---	Rn.18516	BI296175	2.57	2.38	2.76	2.77	2.98	2.56	1.15	up	2.84E-01	8.95E-01	-	-
1369198_at	Apaf1	apoptotic peptidase activating factor 1	78963	Rn.64522	AF218388	4.50	2.80	2.57	2.89	2.82	3.56	1.15	down	7.73E-01	9.26E-01	-	-
1398953_at	Teta3	beta-cell specific transplantation antigen P35B	300036	Rn.6608	BM386183	6.50	7.12	6.53	6.11	6.16	7.27	1.15	down	6.63E-01	8.99E-01	-	-
1390715_at	Igfbp1	insulin-like growth factor binding protein-like 1	366366	Rn.32120	BF396448	2.69	3.22	3.08	2.73	2.79	2.88	1.15	down	2.89E-01	8.95E-01	-	-
1399039_at	LOC689593	similar to DnaJ (Hsp40) homolog, subfamily B, member 10 isoform 2	689593	Rn.40780	BM383865	9.57	9.67	9.31	9.59	9.15	9.20	1.15	down	3.14E-01	8.95E-01	-	-
1378745_at	Per3	period homolog 3 (Drosophila)	78962	Rn.63521	BG374483	3.20	3.65	3.20	3.20	3.22	3.04	1.15	down	2.78E-01	8.95E-01	-	-
1371752_at	Rangrf	RAN guanine nucleotide release factor	287419	Rn.52091	AI105088	5.39	6.06	6.41	6.45	5.54	6.47	1.15	up	6.63E-01	8.99E-01	-	-
1378931_at	---	---	---	Rn.87751	AW523881	2.68	2.83	2.68	2.74	3.34	2.71	1.15	up	3.96E-01	8.95E-01	-	-
1373058_at	Tmem30a	transmembrane protein 30A	300857	Rn.161918	AI409051	6.93	7.10	6.85	7.02	7.20	7.26	1.15	up	1.25E-01	8.95E-01	-	-
1369998_at	Arf6	ADP-ribosylation factor 6	79121	Rn.6993	NM_024162	7.46	6.89	7.57	7.21	7.23	6.87	1.15	down	4.48E-01	8.95E-01	-	-
1381376_at	Tnfaip2	tumor necrosis factor, alpha-induced protein 2	299339	Rn.34387	AI103284	3.15	2.74	2.68	2.67	2.67	2.61	1.15	down	2.55E-01	8.95E-01	-	-
1399035_at	Polr3h	polymerase (RNA) III (DNA directed) polypeptide H (22.9kD)	300088	Rn.13037	BE097233	7.46	6.28	6.84	6.28	7.26	6.44	1.15	down	6.83E-01	9.03E-01	-	-
1374413_at	Ubl3	ubiquitin-like 3	363869	Rn.12128	BM386522	9.10	8.97	9.34	9.00	9.69	9.33	1.15	up	4.24E-01	8.95E-01	-	-
1373226_at	RGD1308019	similar to hypothetical protein FLJ20245	311795	Rn.14609	BF400995	2.49	2.46	2.52	2.49	3.15	2.44	1.15	up	4.32E-01	8.95E-01	-	-
1386881_at	Igfbp3	insulin-like growth factor binding protein 3	24484	Rn.26369	NM_012588	8.37	6.36	7.20	8.05	7.57	5.70	1.15	down	8.38E-01	9.49E-01	-	-
1389839_at	RGD1310475	Similar to RIKEN cDNA 0610010D20	293949	Rn.13905	BE112411	8.13	7.77	7.33	7.64	7.27	7.71	1.15	down	4.94E-01	8.95E-01	-	-
1390172_at	Dhtkd1	dehydrogenase E1 and transketolase domain containing 1	361272	Rn.13539	AI409946	9.51	9.59	9.29	9.46	9.74	9.79	1.15	up	2.17E-01	8.95E-01	-	-
1373055_at	---	---	---	Rn.13039	AI407547	3.95	4.98	3.66	3.94	3.97	5.28	1.15	up	7.53E-01	9.20E-01	-	-
1369362_at	Tsc1	tuberous sclerosis 1	60445	Rn.205837	NM_021854	4.57	4.49	2.60	4.61	3.87	3.79	1.15	up	7.87E-01	9.31E-01	-	-
1398308_at	Rpa3	replication protein A3	296883	Rn.94940	BM383451	5.57	5.90	5.69	5.61	6.06	6.09	1.15	up	3.26E-01	8.95E-01	-	-
1379130_at	---	---	---	Rn.206093	BF396303	3.35	2.70	2.71	2.70	2.75	2.70	1.15	down	4.04E-01	8.95E-01	-	-
1387837_at	Apc	adenomatous polyposis coli	24205	Rn.88057	NM_012499	5.95	3.41	4.09	5.13	3.30	4.40	1.15	down	8.39E-01	9.50E-01	-	-
1398261_at	Timm44	translocase of inner mitochondrial membrane 44 homolog (yeast)	29635	Rn.10801	NM_017267	7.09	6.84	6.83	7.44	7.32	6.60	1.15	up	5.08E-01	8.95E-01	-	-
1387821_at	Rab3ip	RAB3A interacting protein (rabin3)	29885	Rn.31889	NM_017313	5.83	7.17	8.00	6.90	7.16	7.54	1.15	up	7.76E-01	9.27E-01	-	-
1375363_at	---	---	---	Rn.161441	BG374402	3.36	4.22	3.75	3.63	3.32	3.77	1.15	down	5.14E-01	8.95E-01	-	-
1384160_at	Synpo2	synaptopodin 2	499702	Rn.205751	AI547837	2.34	2.87	2.43	2.34	2.34	2.35	1.15	down	2.84E-01	8.95E-01	-	-
1385427_at	Msi2	Musashi homolog 2 (Drosophila)	360596	Rn.43808	BE118330	6.56	6.73	7.39	6.33	6.60	7.15	1.15	down	5.98E-01	8.95E-01	-	-
1373341_at	Fam53a	family with sequence similarity 53, member A	305461	Rn.19744	AI231183	7.57	7.62	7.14	7.44	8.20	7.29	1.15	up	5.66E-01	8.95E-01	-	-
1389210_at	Lcp1	lymphocyte cytosolic protein 1	306071	Rn.14256	BE109711	2.53	2.52	3.16	2.53	2.56	2.52	1.15	down	3.96E-01	8.95E-01	-	-
1387630_at	Elovl5	ELOVL family member 5, elongation of long chain fatty acids (yeast)	171400	Rn.212229	NM_134382	4.74	5.01	4.46	4.52	4.52	4.56	1.15	down	2.80E-01	8.95E-01	-	-
1370134_at	Slc33a1	solute carrier family 33 (acetyl-CoA transporter), member 1	64018	Rn.95276	NM_022252	7.05	7.57	7.06	7.04	7.41	7.83	1.15	up	5.21E-01	8.95E-01	-	-
1390183_at	LOC360990	similar to ubiquitin specific protease 34	360990	Rn.16057	AI177708	4.53	4.61	5.35	4.61	4.45	6.03	1.15	up	7.41E-01	9.17E-01	-	-
1376585_at	Mrpl50	mitochondrial ribosomal protein L50	362517	Rn.1787	BF395602	8.49	8.29	8.49	8.13	7.99	8.55	1.15	down	3.29E-01	8.95E-01	-	-
1371169_at	Vcsa2	variable coding sequence A2	289526	Rn.107044	X77815	2.40	2.35	2.92	2.36	2.37	2.35	1.15	down	3.35E-01	8.95E-01	-	-
1371530_at	Krt8	keratin 8	25626	Rn.11083	BF281337	5.73	6.33	5.89	6.27	5.70	6.57	1.15	up	5.57E-01	8.95E-01	-	-
1384313_at	Trappc5	trafficking protein particle complex 5	363858	Rn.162083	BF412520	4.99	5.54	5.83	5.96	5.48	5.52	1.15	up	5.28E-01	8.95E-01	-	-
1368955_at	Cask	calcium/calmodulin-dependent serine protein kinase (MAGUK family)	29647	Rn.72627	NM_022184	3.12	3.65	3.15	3.11	3.13	3.08	1.15	down	3.11E-01	8.95E-01	-	-
1382939_at	Tpr	translocated promoter region	304862	Rn.58980	BE118630	6.05	6.97	7.40	6.81	6.14	6.88	1.15	down	6.86E-01	9.04E-01	-	-
1388352_at	Nat5	N-acetyltransferase 5 (ARD1 homolog, S. cerevisiae)	362228	Rn.30327	BI296716	7.38	7.74	8.12	8.24	6.82	7.58	1.15	down	6.89E-01	9.05E-01	-	-
1379202_at	Ddi2	DNA-damage inducible protein 2	313668	Rn.144389	AI501945	2.91	2.90	2.91	2.91	3.51	2.90	1.15	up	3.75E-01	8.95E-01	-	-
1396521_at	Stard4	StAR-related lipid transfer (START) domain containing 4	291699	Rn.163775	BF396135	4.25	3.63	3.30	3.11	4.19	3.29	1.15	down	6.70E-01	9.00E-01	-	-
1393438_at	Zfp316	zinc finger protein 316	304293	Rn.40708	AI710341	4.63	4.41	4.89	4.47	4.63	5.43	1.15	up	5.72E-01	8.95E-01	-	-
1370311_at	Eif2b1	eukaryotic translation initiation factor 2B, subunit 1 alpha	64514	Rn.9181	U05821	4.02	4.81	4.01	4.56	3.80	5.08	1.15	up	6.85E-01	9.03E-01	-	-
1380262_at	Sgk2	serum/glucocorticoid regulated kinase 2	171497	Rn.3685	AA893436	5.52	5.79	5.88	5.12	5.75	5.72	1.15	down	4.39E-01	8.95E-01	-	-
1381777_at	---	---	---	Rn.48581	BE119680	3.16	2.71	2.90	2.71	2.89	2.55	1.15	down	2.87E-01	8.95E-01	-	-
1381703_at	---	---	---	Rn.206306	AW525915	3.07	2.48	2.42	2.48	2.41	2.47	1.15	down	3.96E-01	8.95E-01	-	-
1393930_at	---	---	---	Rn.165856	AI029426	4.38	4.84	5.64	4.67	5.32	5.47	1.15	up	6.74E-01	9.01E-01	-	-
1367594_at	Bgn	biglycan	25181	Rn.783	NM_017087	3.73	3.54	3.46	2.91	3.74	3.47	1.15	down	4.81E-01	8.95E-01	-	-
1371914_at	Smarcb1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin,	361825	Rn.73954	AI406553	5.75	5.73	5.74	5.65	5.97	6.20	1.15	up	2.76E-01	8.95E-01	-	-
1372709_at	Bcap29	B-cell receptor-associated protein 29	298943	Rn.19451	AI172204	5.64	5.02	5.33	5.10	5.44	6.06	1.15	up	5.81E-01	8.95E-01	-	-
1397302_at	Zmynd11	zinc finger, MYND domain containing 11	291259	Rn.38301	BF543495	3.78	4.15	3.79	3.97	3.42	3.72	1.15	down	3.75E-01	8.95E-01	-	-
1394386_a_at	Vps52	vacuolar protein sorting 52 homolog (S. cerevisiae)	25218	Rn.51354	BE107955	5.54	5.84	4.45	5.56	5.49	5.38	1.15	up	6.64E-01	8.99E-01	-	-
1397581_at	Rhov	ras homolog gene family, member V	171581	Rn.30047	BF416022	2.66	2.66	2.66	2.89	2.82	2.86	1.15	up	8.87E-04	8.95E-01	-	-
1384024_at	Brd1	bromodomain containing 1	315210	Rn.9133	BI301225	7.44	8.02	7.98	7.82	8.11	8.11	1.15	up	3.97E-01	8.95E-01	-	-
1398767_at	Ubc	ubiquitin C	50522	Rn.3761	NM_017314	12.64	12.24	12.25	12.20	12.60	12.04	1.15	down	2.51E-01	8.95E-01	-	-
1378510_at	---	---	---	Rn.202776	BF386239	2.84	2.98	2.32	2.64	2.48	2.42	1.15	down	4.00E-01	8.95E-01	-	-
1393135_at	---	---	---	Rn.7027	BM390238	2.82	2.74	2.75	2.60	3.57	2.75	1.15	up	5.48E-01	8.95E-01	-	-
1370542_a_at	Eif1	E74-like factor 1	85424	Rn.198987	AB030216	3.26	4.01	2.99	3.54	3.48	3.83	1.15	up	5.72E-01	8.95E-01	-	-
1370506_at	Coq7	coenzyme Q7 homolog, ubiquinone (yeast)	25249	Rn.6981	U46149	6.20	6.71	6.08	6.11	6.13	6.16	1.15	down	3.58E-01	8.95E-01	-	-
1389716_at	Cep27l	centrosomal protein 27 like	292105	---	BI295883	6.06	6.36	6.21	6.11	5.64	6.28	1.15	down	3.97E-01	8.95E-01	-	-
1368646_at	Mapk9	mitogen-activated protein kinase 9	50658	Rn.9910	NM_017322	5.04	2.78	2.36	3.29	3.12	3.17	1.15	down	8.23E-01	9.43E-01	-	-
1368362_a_at	Asgr2	asialoglycoprotein receptor 2	29403	Rn.9834	M16347	3.92	4.74	3.92	3.92	4.19	3.87	1.15	down	5.29E-01	8.95E-01	-	-
1385046_at	Fam55c	family with sequence similarity 55, member C	681096	Rn.212953	BM387916	2.47	2.44	2.96	2.43	2.44	2.41	1.15	down	3.06E-01	8.95E-01	-	-
1376037_at	Aaas	achalasia, adrenocortical insufficiency, alacrimia (Allgrove, triple-A)	300259	Rn.104730	BF283385	4.58	4.37	4.10	4.43	4.14	3.89	1.15	down	3.97E-01	8.95E-01	-	-
1391679_at	LOC691083	hypothetical protein LOC691083	691083	Rn.221906	AA944639	3.22	4.65	6.45	4.63	5.30	4.99	1.15	up	8.44E-01	9.52E-01	-	-
1371761_at	Rpl34	ribosomal protein L34	362041	Rn.2028	AI013910	10.87	11.27	10.81	10.89	11.00	11.65	1.15	up	5.12E-01	8.95E-01	-	-
1387884_at	Psma5	proteasome (prosome, macropain) subunit, alpha type 5	29672	Rn.1276	AI011191	7.72	8.47	8.85	8.02	7.89	8.53	1.15	down	6.32E-01	8.95E-01	-	-
1373677_at	Slc39a10	solute carrier family 39 (zinc transporter), member 10	363229	Rn.203621	AI598315	6.68	6.23	4.64	5.19	4.71	6.05	1.15	down	7.60E-01	9.22E-01	-	-
1397207_at	Otud4	OTU domain containing 4	307774	Rn.22342	AI171260	6.25	6.41	7.62	6.40	6.83	6.46	1.15	down	6.82E-01	9.03E-01	-	-
1380190_at	F8	coagulation factor VIII, procoagulant component	302470	Rn.95452	BE119566	5.62	4.65	4.07	4.65	4.40	4.69	1.15	down	6.87E-01	9.04E-01	-	-
1392357_at	---	---	---	Rn.47153	BI280028	2.94	2.35	2.45	2.38	2.39	2.37	1.15	down	3.33E-01	8.95E-01	-	-
1391411_at	RGD1560248	similar to formin-like 2 isoform B	499797	Rn.7075	AI179941	3.28	2.54	2.57	2.48	2.77	2.54	1.15	down	4.84E-01	8.95E-01	-	-
1392757_at	---	---	---	Rn.203287	AA850587	4.08	2.92	2.99	3.49	3.06	2.84	1.15	down	6.62E-01	8.98E-01	-	-
1389678_at	---	---	---	Rn.38259	BM389496	6.00	6.34	6.27	6.65	5.65	6.90	1.15	up	6.41E-01	8.95E-01	-	-
1383928_a_at	LOC688310	similar to CG5500-PA	688310	---	AI170737	6.29	6.04	5.52	4.75	6.39	6.12	1.15	down	7.39E-01	9.16E-01	-	-
1384401_at	---	---	---	Rn.19125	AI059296	7.94	7.37	8.49	8.21	8.03	8.16	1.15	up	5.73E-01	8.95E-01	-	-
1372046_at	Gtf3c3	general transcription factor IIIC, polypeptide 3	316810	Rn.6721	BG378725	2.78	3.20	3.26	3.21	3.21	3.42	1.15	up	2.96E-01	8.95E-01	-	-
1372971_at	RGD1305178	similar to Hypothetical protein MGC11690	311855	Rn.95284	BI291301	5.57	5.40	5.82	5.31	5.32	5.56	1.15	down	2.41E-01	8.95E-01	-	-
1388479_at	---	---	---	Rn.202406	BI294841	2.33	2.33	4.33	3.74	2.33	2.32	1.15	down	8.19E-01	9.42E-01	-	-
1372676_at	Fahd1	fumarylacetoacetate hydrolase domain containing 1	302980	Rn.3918	BI275774	11.70	11.93	11.87	11.58	11.53	11.79	1.15	down	1.33E-01	8.95E-01	-	-
1387266_at	Siah1a	seven in absentia 1A	140941	Rn.73937	NM_080905	3.54	2.89	2.99	2.91	2.96	2.95	1.15	down	3.80E-01	8.95E-01	-	-
1378635_at	---	---	---	Rn.166636	BF283341	4.85	4.77	4.84	4.80	5.19	5.07	1.15	up	1.66E-01	8.95E-01	-	-
1377905_at	Lsm14a	LSM14A, SCD6 homolog A (S. cerevisiae)	361554	Rn.2370	BF417956	5.78	5.34	4.31	4.39	4.92	5.51	1.15	down	7.32E-01	9.14E-01	-	-
1379978_at	Nphp4	nephronophthisis 4 (juvenile) homolog (human)	313749	Rn.72800	AW531484	2.86	2.26	2.27	2.26	2.28	2.26	1.15	down	3.74E-01	8.95E-01	-	-
1391006_at	---	---	---	---	AI235353	2.53	2.89	2.69	2.48	2.54	2.51	1.15	down	1.28E-01	8.95E-01	-	-
1378061_at	Ift122	intraflagellar transport 122 homolog (Chlamydomonas)	312651	Rn.207472	AI043888	4.73	4.87	4.92	4.88	4.91	5.32	1.15	up	2.68E-01	8.95E-01	-	-
1383652_at	Jagn1	jagunal homolog 1 (Drosophila)	502872	Rn.203687	BF409138	9.14	8.60	9.12	9.30	8.96	9.19	1.15	up	3.79E-01	8.95E-01	-	-
1392927_at	Paqr4	progestin and adipoQ receptor family member IV	302967	Rn.11767	BG381724	2.73	2.32	2.91	2.38	2.62	2.37	1.15	down	3.62E-01	8.95E-01	-	-
1371342_at	Cyc1	cytochrome c-1	300047	Rn.1413	BI277021	9.90	10.04	10.56	9.86	9.86	10.08	1.15	down	3.96E-01	8.95E-01	-	-
1399010_at	Cops7a	COP9 constitutive photomorphogenic homolog subunit 7A (Arabidopsis)	312710	Rn.154627	BG381740	6.83	6.60	6.50	5.85	7.30	6.18	1.15	down	6.82E-01	9.03E-01	-	-
1395785_at	---	---	---	Rn.208163	BE105453	2.63	2.99	2.64	2.59	2.66	2.42	1.15	down	2.25E-01	8.95E-01	-	-
1387412_at	Pip4k2a	phosphatidylinositol-5-phosphate 4-kinase, type II, alpha	116723	Rn.24177	NM_053926	2.52	2.60	3.63	2.62	2.52	3.02	1.15	down	6.36E-01	8.95E-01	-	-
1368046_at	Slc31a1	solute carrier family 31 (copper transporters), member 1	171135	Rn.2789	AI171135	6.16	7.43	8.20	6.56	6.96	7.68	1.15	down	7.85E-01	9.30E-01	-	-
1368000_at	C3	complement component 3	24232	Rn.11378	NM_016994	2.46	2.73	2.55	2.64	2.61	3.09	1.15	up	3.19E-01	8.95E-01	-	-
1386859_at	Tkt	transketolase	64524	Rn.5950	NM_022592	8.93	9.30	8.96	9.41	9.02	9.37	1.15	up	3.13E-01	8.95E-01	-	-
1398420_at	Smurf2	SMAD specific E3 ubiquitin protein ligase 2	303614	Rn.92843	BF393807	2.68	2.67	2.57	2.59	2.59	3.33	1.15	up	4.70E-01	8.95E-01	-	-
1372467_at	Hs6st1	heparan sulfate 6-O-sulfotransferase 1	316325	Rn.163751	AA943794	6.70	7.04	7.12	7.33	5.94	7.01	1.15	down	6.74E-01	9.01E-01	-	-
1395221_at	Snx13	sorting nexin 13	362731	Rn.30138	AA892908	3.00	2.83	2.83	2.67	2.71	2.68	1.15	down	2.64E-02	8.95E-01	-	-
1384303_s_at	Slc6a17	solute carrier family 6 (neurotransmitter transporter), member 17	613226	Rn.186904	AI712791	3.29	3.57	4.31	3.51	3.55	3.52	1.15	down	5.53E-01	8.95E-01	-	-
1371160_at	Vamp2	vesicle-associated membrane protein 2	24803	Rn.12939	AJ133104	2.43	2.43	3.02	2.43	2.44	2.42	1.15	down	3.74E-01	8.95E-01	-	-
1367680_at	Acox1	acyl-Coenzyme A oxidase 1, palmitoyl	50681	Rn.31796	NM_017340	11.42	11.27	11.63	11.39	11.15	11.19	1.15	down	1.91E-01	8.95E-01	-	-
1379036_at	Trdmt1	tRNA aspartic acid methyltransferase 1	291324	Rn.115	AI170819	2.42	2.46	2.47	2.47	3.02	2.46	1.15	up	3.49E-01	8.95E-01	-	-
1384507_at	Fam105a	family with sequence similarity 105, member A	310190	Rn.162566	AA817708	2.82	3.27	2.71	2.81	2.82	2.57	1.15	down	3.54E-01	8.95E-01	-	-
1374343_at	Perld1	per1-like domain containing 1	688174	Rn.217141	BF407189	3.90	4.29	3.33	4.09	4.02	4.01	1.15	up	5.21E-01	8.95E-01	-	-
1368036_at	Ptprf	protein tyrosine phosphatase, receptor type, F	360406	Rn.11386	M60103	5.31	5.52	5.41	5.26	5.14	5.24	1.15	down	4.79E-02	8.95E-01	-	-
1397453_at	---	---	---	Rn.212729	BM390792	2.33	2.33	2.34	2.94	2.34	2.32	1.15	up	3.85E-01	8.95E-01	-	-
1399658_at	---	---	---	Rn.45828	BI275588	2.58	2.72	3.11	2.60	2.67	2.54	1.15

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1395683_at	Nat15	N-acetyltransferase 15 (GCN5-related, putative)	363545	Rn.13255	BF419574	2.57	2.57	2.58	2.58	2.59	3.14	1.15	up	3.50E-01	8.95E-01	-	-
1384273_at	Shpk	sedoheptulokinase	287479	Rn.19663	BF419310	5.31	4.91	4.83	5.20	5.01	5.43	1.15	up	3.60E-01	8.95E-01	-	-
1373419_at	Ptprg	Protein tyrosine phosphatase, receptor type, G	171357	Rn.87083	AI556884	6.02	6.28	5.73	6.27	6.05	6.31	1.15	up	3.35E-01	8.95E-01	-	-
1369678_a_at	Nfia	nuclear factor I/A	25492	Rn.10550	D78017	7.91	7.09	7.54	7.32	7.08	7.55	1.15	down	5.09E-01	8.95E-01	-	-
1372426_at	Adamtsl4	ADAMTS-like 4	310670	Rn.62115	AI411997	2.59	2.64	2.59	2.58	2.82	3.00	1.15	up	1.79E-01	8.95E-01	-	-
1376619_at	Ptprd	protein tyrosine phosphatase, receptor type, D	313278	Rn.99077	AI412803	6.59	6.18	7.38	6.90	6.66	7.18	1.15	up	6.34E-01	8.95E-01	-	-
1396027_at	---	---	---	Rn.51497	BE110554	2.43	2.43	2.45	2.43	3.05	2.42	1.15	up	3.98E-01	8.95E-01	-	-
1391387_s_at	Slbp	stem-loop binding protein	681062	Rn.198386	AI072956	6.57	6.79	7.78	6.63	7.00	6.92	1.15	down	6.38E-01	8.95E-01	-	-
1396296_at	---	---	---	---	AI709505	2.38	2.38	2.39	2.99	2.39	2.36	1.15	up	3.95E-01	8.95E-01	-	-
1380370_at	Robo3	roundabout homolog 3 (Drosophila)	315564	Rn.45295	BF390065	2.52	2.66	2.69	3.28	2.69	2.48	1.15	up	4.68E-01	8.95E-01	-	-
1393998_at	Gabpb1 /// Gabpb1	GA repeat binding protein, beta 1 /// GA binding protein transcription factor, be	364738 /// 499883	Rn.61149	BF408529	3.07	2.49	2.50	2.44	2.56	2.47	1.15	down	3.70E-01	8.95E-01	-	-
1384874_at	LOC685001	Similar to MIR-interacting saposin-like protein precursor (Transmembrane pro	685001	Rn.147475	BF558516	6.89	8.42	7.53	7.68	6.79	7.78	1.15	down	7.37E-01	9.16E-01	-	-
1373727_at	Fibin	fin bud initiation factor homolog (zebrafish)	499856	Rn.43451	BI275179	2.91	2.34	2.37	2.35	2.35	2.33	1.15	down	3.45E-01	8.95E-01	-	-
1379102_at	---	---	---	Rn.220228	BE108842	3.03	3.01	3.04	3.01	3.26	3.40	1.15	up	1.66E-01	8.95E-01	-	-
1392154_at	Zmynd11	zinc finger, MYND domain containing 11	291259	Rn.38301	AI579418	7.14	6.96	6.60	7.09	6.80	7.39	1.15	up	4.45E-01	8.95E-01	-	-
1374940_at	Usp36	ubiquitin specific peptidase 36	303700	Rn.165326	BM388945	3.17	3.34	3.26	3.22	3.72	3.42	1.15	up	2.71E-01	8.95E-01	-	-
1390673_at	---	---	---	Rn.58184	BF400603	2.52	2.52	2.52	2.52	3.12	2.51	1.15	up	3.83E-01	8.95E-01	-	-
1392294_at	---	---	---	Rn.208691	BE119402	2.47	3.01	2.50	2.46	2.50	2.43	1.15	down	3.31E-01	8.95E-01	-	-
1379759_at	Carkd	carbohydrate kinase domain containing	361185	Rn.24864	BG377329	4.40	4.28	4.86	4.40	4.01	4.54	1.15	down	4.54E-01	8.95E-01	-	-
1373182_at	Cldn12	claudin 12	500000	Rn.18416	BF281899	8.63	8.32	9.13	8.36	8.34	8.78	1.15	down	5.17E-01	8.95E-01	-	-
1383244_at	---	---	---	Rn.23651	BI281726	4.44	4.61	3.83	4.83	4.27	4.37	1.15	up	5.41E-01	8.95E-01	-	-
1383336_at	Pnn	pinin, desmosome associated protein	368070	Rn.38987	BF549763	3.80	4.72	3.49	3.73	3.55	4.16	1.15	down	6.58E-01	8.98E-01	-	-
1376791_at	Ankrd43	ankyrin repeat domain 43	497903	---	BF291192	2.48	2.45	2.47	2.69	2.46	2.83	1.15	up	1.45E-01	8.95E-01	-	-
1375909_at	Gstm4	glutathione S-transferase mu 4	499689	Rn.198607	BI285792	2.33	2.33	2.34	2.70	2.45	2.43	1.15	up	8.91E-02	8.95E-01	-	-
1390542_at	Rad51c	Rad51 homolog c (S. cerevisiae)	497976	Rn.160309	BE111757	2.40	2.19	3.44	2.39	2.40	2.64	1.15	down	6.45E-01	8.95E-01	-	-
1382753_at	---	---	---	---	AI059982	3.03	2.47	2.55	2.49	2.51	2.46	1.15	down	3.25E-01	8.95E-01	-	-
1374706_at	Gdf11	Growth differentiation factor 11	29454	Rn.51292	BF407916	2.99	2.93	3.10	2.94	3.78	2.89	1.15	up	5.39E-01	8.95E-01	-	-
1376732_at	Calr3	calreticulin 3	364529	Rn.144131	BM388733	2.47	2.46	2.47	3.16	2.37	2.45	1.15	up	4.76E-01	8.95E-01	-	-
1383231_at	Snip1	Smad nuclear interacting protein 1	313588	Rn.8811	AA955078	4.34	4.55	4.74	4.34	4.34	4.36	1.15	down	1.70E-01	8.95E-01	-	-
1377727_at	Baz1a	bromodomain adjacent to zinc finger domain, 1A	314126	Rn.1864	BE109134	4.66	3.18	3.44	3.20	3.41	4.09	1.15	down	7.30E-01	9.14E-01	-	-
1396203_at	Mios	missing oocyte, meiosis regulator, homolog (Drosophila)	362324	Rn.103328	BE112689	2.85	3.66	2.89	2.90	2.54	3.38	1.15	down	6.13E-01	8.95E-01	-	-
1390861_at	Zfp709l2	zinc finger protein 709-like 2	362845	Rn.41593	AW524684	3.03	2.42	2.46	2.44	2.45	2.44	1.15	down	3.74E-01	8.95E-01	-	-
1368037_at	Cbr1	carbonyl reductase 1	29224	Rn.3425	NM_019170	2.88	2.46	2.60	2.42	2.48	2.45	1.15	down	1.96E-01	8.95E-01	-	-
1390355_at	Ryr1	ryanodine receptor 1, skeletal muscle	114207	Rn.198152	AI574442	2.84	3.84	3.01	2.77	2.79	3.55	1.15	down	6.52E-01	8.97E-01	-	-
1379424_at	Ints7	Integrator complex subunit 7	289382	Rn.156180	BE115825	5.05	5.37	5.24	4.68	5.35	5.05	1.15	down	4.16E-01	8.95E-01	-	-
1397836_at	Sirt4	sirtuin (silent mating type information regulation 2 homolog) 4 (S. cerevisiae)	304539	Rn.92769	BF546537	3.25	2.67	2.61	2.42	2.43	3.08	1.15	down	5.47E-01	8.95E-01	-	-
1389491_at	---	---	---	Rn.22391	BE102814	5.63	5.60	5.67	5.59	6.09	5.81	1.15	up	2.50E-01	8.95E-01	-	-
1395229_at	Arhgef12	Rho guanine nucleotide exchange factor (GEF) 12	367072	Rn.129752	BG375118	7.48	7.02	7.41	7.72	6.25	7.34	1.15	down	6.94E-01	9.05E-01	-	-
1391355_at	LOC679824	hypothetical protein LOC679824	679824	Rn.160957	AW531049	2.49	2.49	2.59	3.18	2.49	2.48	1.15	up	4.46E-01	8.95E-01	-	-
1390583_at	---	---	---	Rn.167696	AI228169	2.96	2.94	2.81	2.95	2.89	3.46	1.15	up	3.59E-01	8.95E-01	-	-
1387558_at	Trpv4	transient receptor potential cation channel, subfamily V, member 4	66026	Rn.64508	NM_023970	4.41	4.20	4.47	4.95	4.81	3.92	1.15	up	5.85E-01	8.95E-01	-	-
1388634_at	Pgm1	phosphoglucomutase 1	24645	Rn.9970	BI277505	7.28	7.25	6.81	6.80	6.59	7.35	1.15	down	5.11E-01	8.95E-01	-	-
1392046_at	---	---	---	Rn.153687	BE121124	2.39	2.39	2.40	2.98	2.40	2.39	1.15	up	3.76E-01	8.95E-01	-	-
1383596_at	Isy1	ISY1 splicing factor homolog (S. cerevisiae)	362394	Rn.25170	AA956300	2.40	2.39	2.40	2.39	2.62	2.76	1.15	up	1.45E-01	8.95E-01	-	-
1383890_at	Hip1	huntingtin interacting protein 1	192154	Rn.836	AI112383	3.03	2.40	2.40	2.39	2.47	2.38	1.14	down	4.14E-01	8.95E-01	-	-
1373478_at	---	---	---	Rn.204512	AI408557	2.39	2.38	2.40	2.38	2.68	2.68	1.14	up	1.27E-01	8.95E-01	-	-
1370287_a_at	Tpm1	tropomyosin 1, alpha	24851	Rn.87540	M23764	4.84	4.96	5.58	4.97	4.84	4.98	1.14	down	4.48E-01	8.95E-01	-	-
1374849_at	Adamts7	ADAM metallopeptidase with thrombospondin type 1 motif, 7	315879	Rn.23850	BF285745	2.98	2.39	2.38	2.48	2.40	2.37	1.14	down	3.69E-01	8.95E-01	-	-
1382371_at	Tmem77	transmembrane protein 77	362011	Rn.1279	AI172475	7.38	7.33	7.62	6.68	7.42	7.64	1.14	down	5.56E-01	8.95E-01	-	-
1373718_at	Tubb2a	tubulin, beta 2a	498736	---	BM384071	10.73	10.97	10.56	10.60	10.41	10.65	1.14	down	2.38E-01	8.95E-01	-	-
1397355_at	---	---	---	---	AW916626	4.25	3.25	3.27	3.76	3.22	3.20	1.14	down	6.34E-01	8.95E-01	-	-
1382905_at	---	---	---	Rn.23909	AI102514	3.38	3.70	3.73	3.96	3.75	3.69	1.14	up	2.33E-01	8.95E-01	-	-
1375526_at	RGD1563438	similar to novel protein of unknown function (DUF423) family member	287442	Rn.144704	AI171327	9.02	9.25	9.62	9.04	9.29	8.96	1.14	down	3.86E-01	8.95E-01	-	-
1372016_at	Gadd45b	growth arrest and DNA-damage-inducible, beta	299626	Rn.35886	BI287978	2.39	2.38	2.40	2.99	2.39	2.38	1.14	up	3.86E-01	8.95E-01	-	-
1381773_at	Abhd3	alpha/beta hydrolase domain containing 3	291793	Rn.64445	BM383335	2.50	2.50	2.51	2.76	2.86	2.47	1.14	up	1.69E-01	8.95E-01	-	-
1391636_at	---	---	---	Rn.46939	BI296260	2.40	2.39	2.98	2.40	2.41	2.38	1.14	down	3.74E-01	8.95E-01	-	-
1377051_at	---	---	---	---	AA849966	6.62	5.43	6.70	6.87	6.26	6.21	1.14	up	6.93E-01	9.05E-01	-	-
1373862_at	Tmed7	transmembrane emp24 protein transport domain containing 7	252889	Rn.67055	AI009673	5.97	6.03	6.24	5.96	6.43	6.43	1.14	up	3.33E-01	8.95E-01	-	-
1379323_at	RGD1306304	similar to hypothetical protein MGC14327	311800	Rn.23564	BE109498	7.29	5.52	6.31	5.70	6.27	6.57	1.14	down	7.51E-01	9.19E-01	-	-
1381481_at	---	---	---	Rn.199258	AI028912	2.79	2.78	3.36	2.77	2.79	2.78	1.14	down	3.71E-01	8.95E-01	-	-
1370350_x_at	367 /// LOC686655	similar to Urinary protein 3 precursor (RUP-3) /// similar to Urinary protein 2 pr	60 /// 680367 /// 68	Rn.162992	AF368860	2.46	2.44	3.05	2.46	2.49	2.42	1.14	down	3.89E-01	8.95E-01	-	-
1368832_at	Akt2	v-akt murine thymoma viral oncogene homolog 2	25233	Rn.87066	AI105076	6.23	6.22	4.85	6.16	5.57	6.16	1.14	up	7.16E-01	9.10E-01	-	-
1378467_at	---	---	---	Rn.6735	AA851361	2.55	2.53	2.57	2.54	3.17	2.52	1.14	up	4.09E-01	8.95E-01	-	-
1384995_at	Jrk	jerky homolog (mouse)	315073	Rn.26833	BM389881	2.41	2.40	3.01	2.41	2.42	2.41	1.14	down	3.92E-01	8.95E-01	-	-
1392548_at	Cwc22	CWC22 spliceosome-associated protein homolog (S. cerevisiae)	362153	Rn.51454	BF394282	5.73	4.85	4.86	4.99	4.87	4.99	1.14	down	5.43E-01	8.95E-01	-	-
1389780_at	Tfpi	tissue factor pathway inhibitor (lipoprotein-associated coagulation inhibitor)	29436	Rn.15795	AI009783	3.00	3.07	3.08	3.35	3.10	3.30	1.14	up	7.46E-02	8.95E-01	-	-
1378536_at	Hook1	hook homolog 1 (Drosophila)	313370	Rn.16596	AI638960	8.80	8.90	9.31	8.93	8.93	9.73	1.14	up	5.62E-01	8.95E-01	-	-
1384224_at	---	---	---	---	BE120549	7.73	8.07	8.99	8.30	8.58	8.49	1.14	up	6.40E-01	8.95E-01	-	-
1389157_at	Cdc42ep1	CDC42 effector protein (Rho GTPase binding) 1	315121	Rn.164707	BI275583	3.15	3.02	3.09	3.16	3.55	3.14	1.14	up	2.36E-01	8.95E-01	-	-
1388790_at	Coq5	coenzyme Q5 homolog, methyltransferase (S. cerevisiae)	304542	Rn.143996	BM384998	3.23	3.32	3.18	3.23	3.73	3.36	1.14	up	2.77E-01	8.95E-01	-	-
1393454_at	Pcdh17	protocadherin 17	306055	Rn.198988	BF558981	8.25	8.87	8.37	8.48	7.33	9.09	1.14	down	7.42E-01	9.17E-01	-	-
1396472_at	---	---	---	Rn.146797	BI276554	2.53	2.50	2.57	2.91	2.57	2.71	1.14	up	1.29E-01	8.95E-01	-	-
1376084_a_at	Espl1	extra spindle poles like 1 (S. cerevisiae)	315330	Rn.135286	AI385371	3.04	2.41	2.42	2.42	2.46	2.41	1.14	down	4.02E-01	8.95E-01	-	-
1370055_at	Rab3d	RAB3D, member RAS oncogene family	140665	Rn.9822	M83681	2.33	3.47	3.18	2.98	3.17	3.41	1.14	up	6.22E-01	8.95E-01	-	-
1372355_at	---	---	---	Rn.164744	BE109242	7.77	7.51	7.61	6.97	7.77	7.56	1.14	down	4.83E-01	8.95E-01	-	-
1368566_a_at	Ndufv3	NADH dehydrogenase (ubiquinone) flavoprotein 3	64539	Rn.6452	AA964381	9.18	10.28	9.64	9.99	9.76	9.93	1.14	up	5.84E-01	8.95E-01	-	-
1386641_at	---	---	---	Rn.21134	BF546770	8.37	8.41	8.52	8.39	7.78	8.54	1.14	down	4.57E-01	8.95E-01	-	-
1371708_at	Car6	carbonic anhydrase 6	298657	Rn.220582	BI279097	2.73	3.23	3.71	3.36	2.86	2.87	1.14	down	5.84E-01	8.95E-01	-	-
1393295_at	LOC498862	similar to RIKEN cDNA 2610019F03	498862	Rn.11716	BF290301	5.38	5.79	5.73	5.72	5.31	5.29	1.14	down	3.66E-01	8.95E-01	-	-
1382384_at	Rassf6	Ras association (RalGDS/AF-6) domain family member 6	305251	Rn.18159	BM383783	2.73	3.45	3.29	3.42	3.20	3.43	1.14	up	4.47E-01	8.95E-01	-	-
1376920_at	LOC500013	similar to sterile alpha motif domain containing 9-like	500013	Rn.98211	BF408536	3.03	2.96	3.41	2.97	3.33	2.53	1.14	down	5.13E-01	8.95E-01	-	-
1371446_at	Mapkapk2	mitogen-activated protein kinase-activated protein kinase 2	289014	Rn.6276	BI283703	4.67	5.12	5.10	4.54	5.03	4.73	1.14	down	3.97E-01	8.95E-01	-	-
1370298_at	Ccdc56	coiled-coil domain containing 56	498000	Rn.32253	AF052042	7.90	8.59	8.23	8.35	8.43	8.52	1.14	up	4.02E-01	8.95E-01	-	-
1373586_at	---	---	---	Rn.15612	AI411113	5.46	5.77	5.62	5.61	5.61	6.21	1.14	up	4.23E-01	8.95E-01	-	-
1396738_at	---	---	---	Rn.209091	BF391477	2.91	2.36	2.37	2.36	2.37	2.33	1.14	down	3.50E-01	8.95E-01	-	-
1389050_at	Dusp3	Dual specificity phosphatase 3	498003	Rn.8286	AI172797	7.44	7.86	7.43	7.27	7.43	7.45	1.14	down	2.73E-01	8.95E-01	-	-
1385289_at	---	---	---	Rn.150607	AW528303	2.39	2.44	3.03	3.58	2.45	2.41	1.14	up	6.77E-01	9.02E-01	-	-
1373203_at	Sptlc1	serine palmitoyltransferase, long chain base subunit 1	361213	Rn.18996	AI236953	7.43	7.89	7.89	7.94	7.83	8.03	1.14	up	3.02E-01	8.95E-01	-	-
1382984_at	Tor1b	torsin family 1, member B	311854	Rn.6487	AI073272	2.61	2.56	3.16	2.58	2.65	2.51	1.14	down	3.82E-01	8.95E-01	-	-
1371721_at	LOC500532	hypothetical LOC500532	500532	Rn.4241	BI281103	3.94	4.10	3.89	3.88	4.64	3.99	1.14	up	4.74E-01	8.95E-01	-	-
1372874_at	---	---	---	Rn.64427	BI299261	3.49	3.48	4.06	3.54	3.44	3.47	1.14	down	3.75E-01	8.95E-01	-	-
1394936_at	Ptdss2	phosphatidylserine synthase 2	293620	Rn.104893	AW521480	2.72	2.59	2.75	3.19	2.74	2.71	1.14	up	3.03E-01	8.95E-01	-	-
1375974_at	---	---	---	Rn.22084	AI406315	7.20	6.88	7.26	6.70	6.83	7.23	1.14	down	3.83E-01	8.95E-01	-	-
1382370_at	Ccnf	cyclin F	117524	Rn.15126	BE113938	2.90	2.32	2.33	2.32	2.33	2.32	1.14	down	3.71E-01	8.95E-01	-	-
1389687_at	---	---	---	Rn.166654	BI273981	5.96	6.67	8.01	6.18	7.04	6.84	1.14	down	7.81E-01	9.29E-01	-	-
1386120_at	LOC689147	hypothetical protein LOC689147	689147	Rn.118853	BF393607	2.65	2.52	2.66	2.74	3.09	2.58	1.14	up	2.80E-01	8.95E-01	-	-
1388948_at	Stard10	StAR-related lipid transfer (START) domain containing 10	293150	Rn.143765	AI104759	8.20	8.79	8.57	8.22	8.02	8.74	1.14	down	5.20E-01	8.95E-01	-	-
1388916_at	---	---	---	Rn.17586	BE109616	3.73	4.47	3.75	3.49	3.99	5.05	1.14	up	7.27E-01	9.13E-01	-	-
1376609_at	RGD1309102	similar to TRS85 homolog	291750	Rn.6435	BG672084	6.71	6.63	6.20	7.09	6.26	6.77	1.14	up	5.40E-01	8.95E-01	-	-
1369957_at	Rgs5	regulator of G-protein signaling 5	54294	Rn.1150	NM_019341	4.41	2.90	2.43	2.95	3.98	3.40	1.14	up	7.85E-01	9.30E-01	-	-
1371833_at	Bri3	brain protein I3	304284	Rn.7700	AI230753	6.24	6.93	6.95	7.26	6.80	6.64	1.14	up	5.50E-01	8.95E-01	-	-
1376965_at	---	---	---	Rn.7521	BM389656	2.68	3.38	3.20	3.15	3.19	3.51	1.14	up	4.61E-01	8.95E-01	-	-
1381019_x_at	Asap1	ArfGAP with SH3 domain, ankyrin repeat and PH domain 1	314961	Rn.63486	BG378709	3.05	3.41	2.90	4.31	2.66	2.97	1.14	up	7.32E-01	9.14E-01	-	-
1373413_at	Tmem128	transmembrane protein 128	360952	Rn.41433	AW531093	4.90	6.73	6.46	5.55	6.02	5.93	1.14	down	7.58E-01	9.21E-01	-	-
1384582_at	---	---	---	Rn.220479	BE107130	8.31	8.87	9.04	8.91	8.78	9.11	1.14	up	4.67E-01	8.95E-01	-	-
1387606_at	Fgf2	fibroblast growth factor 2	54250	Rn.31808	NM_019305	4.31	4.12	4.39	4.52	4.53	4.34	1.14	up	1.26E-01	8.95E-01	-	-
1395071_at	Zbtb6	zinc finger and BTB domain containing 6	366029	Rn.39069	AI010512	3.76	3.74	3.78	3.09	3.85	3.77	1.14	down	4.63E-01	8.95E-01	-	-
1376087_at	Fam134c	family with sequence similarity 134, member C	360632	Rn.28889	BM386653	5.34	5.44	5.60	5.45	5.73	5.79	1.14	up	2.12E-01	8.95E-01	-	-
1385431_at	---	---	---	---	BF409456	7.34	7.94	7.83	7.18	7.23	8.11	1.14	down	6.13E-01	8.95E-01	-	-
1375131_at	Mtch2	mitochondrial carrier homolog 2 (C. elegans)	295922	Rn.4182	BF284715	10.08	9.67	10.06	9.87	9.74	9.61	1.14	down	2.73E-01	8.95E-01	-	-
1391506_at	Phf17	PHD finger protein 17	310352	Rn.90858	BF400815	2.94	3.26	2.72	2.93	3.16	3.41	1.14	up	4.08E-01	8.95E-01	-	-
1394980_at	Tmem56	transmembrane protein 56	365924	Rn.65373	BF409442	2.34	2.33	2.36	2.34	2.95	2.33	1.14	up	3.99E-01	8.95E-01	-	-
1395538_at	Pde12	phosphodiesterase 12	306231	Rn.45577	BF555228	5.40	5.54	6.95	6.60	5.45	6.26	1.14	down	7.45E-01	9.17E-01	-	-
1391255_at	Zmynd15	zinc finger, MYND domain containing 15	287457	Rn.163126	BE110035	3.30	2.80	2.80	3.03	2.81	3.64	1.14	up	5.57E-01	8.95E-01	-	-
1375948_at	Alkbh5	alkB, alkylation repair homolog 5 (E. coli)	303193	Rn.146441	AI144919	5.05	5.05	5.09	4.64	4.70	5.26	1.14	down	3.86E-01	8.95E-01	-	-
1393132_at	RGD1560271	similar to inhibitor of MyoD family-a	501097	Rn.205245	BI293325	2.60	3.02	2.87	2.60	2.66	2.65	1.14	down	1.90E-01	8.95E-01	-	-
1398851_at	Ywhae	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, e	29753	Rn.4225	AA892315	12.26	12.23	12.22	12.00	12.01	12.12	1.14	down	8.71E-03	8.95E-01	-	-
1379660_at	---	---	---	Rn.6611	AA850472	2.40	2.40	2.41	2.40	2.99	2.40	1.14	up	3.86E-01	8.95E-01	-	-
1388985_at	---	---	---	Rn.211489	AI012869	11.96	11.26	11.96	11.76	11.80	11.03	1.14	down	6.03E-01	8.95E-01	-	-
1391245_at	Ng35	ng35 pseudogene	309813	Rn.55082	BE120894	4.38	4.95	2.68	4.42	4.25	2.77	1.14	down	8.33E-01	9.47E-01	-	-
1384962_at	Med1	mediator complex subunit 1	497991	Rn.4262	BI295735	2.82	2.92	2.83	2.86	3.47	2.82	1.14	up	4.12E-01	8.95E-01	-	-
1375769_at	Trim41	tripartite motif-containing 41	303088	Rn.79871	BI283106	3.08	2.43	2.45	2.51	2.40	2.45	1.14	down	4.21E-01	8.95E-01	-	-
1374815_at	Stard3nl	STARD3 N-terminal like	291182	Rn.86009	AA997695	4.15	3.97	4.76	4.10	4.12	4.08	1.14	down	4.64E-01	8.95E-01	-	-
1371823_at	Stag2	stromal antigen 2	313304	Rn.29288	BM392158	6.80	6.68	6.61	6.28	6.64	6.61	1.14	down	2.06E-01	8.95E-01	-	-
1376307_a_at	Rbm45	RNA binding motif protein 45	266631	Rn.204106	BI289591	7.10	7.31	7.36	6.88	7.28	7.03	1.14	down	2.44E-01	8.95E-01	-	-
1394669_at	---	---	---	Rn.29262	AI178905	3.15	2.95	3.26	2.79	2.97	3.01	1.14	down	1.64E-01	8.95E-01	-	-
1372011_at	---	---	---	Rn.24783	BI292028	4.24	5.87	5.41	4.96	5.85	5.29	1.14	up	7.43E-01	9.17E-01	-	-
1373583_at	---	---	---	Rn.9556	BF396317	7.02	6.31	6.38	7.48	5.84	5.81	1.14	down	7.63E-01	9.22E-01	-	-
1395342_at	Ckap4	cytoskeleton-associated protein 4	362859	Rn.99508	AI598942	2.33	2.32	2.69	2.52	2.33	3.06	1.14	up	4.85E-01	8.95E-01	-	-
1394965_at	Enth	enthoprotin	360515	Rn.222041	BE099701	6.55	6.80	6.00	6.56	6.35	7.02	1.14	up	5.65E-01	8.95E-01	-	-
1367870_at	Glrx3	glutaredoxin 3	58815	Rn.3578	NM_032614	10.44	10.26	10.39	10.14	9.99	10.38	1.14	down	1.96E-01	8.95E-01	-	-
1380937_at	---	---	---	Rn.11637	BE106331	3.03	2.54	4.29	2.23	4.02	3.04	1.14	down	8.06E-01	9.38E-01	-	-
1379330_s_at	LOC685729	Similar to dimerization cofactor of hepatocyte nuclear factor 1 (HNF1) from m	685729	Rn.18796	AI600082	8.71	9.70	9.62	9.29	9.56	9.76	1.14	up	6.07E-01	8.95E-01	-	-
1389220_at	LOC682879	hypothetical protein LOC682879	682879	---	BE112918	5.79	4.99	5.64	4.83	6.44	5.75	1.14	up	7.33E-01	9.14E-01	-	-
1372456_at	Mrps31	mitochondrial ribosomal protein S31	290850	Rn.22173	AI171229	9.81	9.02	9.87	9.42	9.29	9.42	1.14	down	5.27E-01	8.95E-01	-	-
1376581_at	RGD1309138	similar to hypothetical protein MGC9912	366619	Rn.105589	AW433895	6.77	5.67	5.66	5.23	6.36	5.93	1.14	down	7.16E-01	9.10E-01	-	-
1397306_at	Nin	ninein (GSK3B interacting protein)	299117	Rn.23434	AI555202	3.58	2.60	2.63	2.62	2.79	2.83	1.14	down	5.90E-01	8.95E-01	-	-
1391297_at	---	---	---	---	BI281108	4.34	4.20	4.68	5.07	4.27	4.46	1.14	up	5.32E-01	8.95E-01	-	-
1388590_at	Znrd1	zinc ribbon domain containing, 1	361784	Rn.4312	AI010455	4.72	5.68	4.73	4.77	4.55	5.24	1.14	down	6.37E-01	8.95E-01	-	-
1395923_at	NIPBL	Nipped-B homolog (Drosophila)	294787	Rn.11589	BF416343	7.06	6.51	6.13	5.95

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1395640_at	Cdc23	CDC23 (cell division cycle 23, yeast, homolog)	291689	Rn.139314	AI013729	3.12	3.17	3.81	3.17	3.20	3.15	1.14	down	4.40E-01	8.95E-01	-	-
1368808_at	Cap1	CAP, adenylate cyclase-associated protein 1 (yeast)	64185	Rn.112585	BG380723	6.67	6.17	6.89	7.07	6.64	6.59	1.14	up	5.05E-01	8.95E-01	-	-
1395596_at	---	---	---	Rn.205689	BM389675	4.77	4.09	4.17	4.38	3.98	4.10	1.14	down	4.80E-01	8.95E-01	-	-
1369963_at	Pafah1b3	platelet-activating factor acetylhydrolase, isoform 1b, subunit 3	114113	Rn.17971	NM_053654	3.47	2.72	2.71	2.91	2.71	2.70	1.14	down	5.06E-01	8.95E-01	-	-
1381817_at	---	---	---	Rn.166043	AI044318	7.79	8.33	8.73	8.00	8.64	8.79	1.14	up	6.29E-01	8.95E-01	-	-
1375357_at	Dyt1	dystonia 1	266606	Rn.20041	BE112237	4.99	5.82	5.14	5.95	4.73	5.85	1.14	up	7.03E-01	9.07E-01	-	-
1373532_at	Plekhf1	pleckstrin homology domain containing, family F (with FYVE domain) member	308543	Rn.9380	BI276934	2.77	2.68	3.41	2.76	2.77	2.76	1.14	down	4.49E-01	8.95E-01	-	-
1395684_at	---	---	---	Rn.201935	AW534805	8.13	8.34	8.31	8.07	8.51	8.78	1.14	up	4.25E-01	8.95E-01	-	-
1392133_at	Mapk1ip1l	Mitogen-activated protein kinase 1 interacting protein 1-like	361028	Rn.22587	AI502069	2.41	2.93	2.41	2.41	2.40	2.37	1.14	down	3.31E-01	8.95E-01	-	-
1372845_at	Rpp21	ribonuclease P 21 subunit (human)	406230	Rn.3720	BG380782	5.42	5.72	4.43	5.69	5.06	5.40	1.14	up	6.79E-01	9.02E-01	-	-
1383124_at	---	---	---	---	BG672201	6.71	6.64	7.16	7.26	7.02	6.80	1.14	up	4.16E-01	8.95E-01	-	-
1373964_at	LOC100174910	glutaredoxin-like protein	100174910	Rn.22418	AA818815	5.32	5.69	6.26	5.86	5.47	5.36	1.14	down	5.76E-01	8.95E-01	-	-
1380566_at	Tmem24	transmembrane protein 24	300666	Rn.57410	BI279622	6.22	6.21	6.23	6.24	5.62	6.24	1.14	down	4.10E-01	8.95E-01	-	-
1373426_at	Mapk1	mitogen activated protein kinase 1	116590	Rn.34914	BI282894	5.06	5.05	4.93	5.03	4.33	5.10	1.14	down	4.86E-01	8.95E-01	-	-
1370344_at	Hspa4	heat shock protein 4	266759	Rn.163092	AF077354	5.57	5.74	5.58	5.21	5.58	5.54	1.14	down	2.16E-01	8.95E-01	-	-
1395828_at	Kif23	kinesin family member 23	315740	Rn.63734	BF407793	2.52	2.51	2.52	2.51	2.52	3.08	1.14	up	3.70E-01	8.95E-01	-	-
1376020_at	Dph2	DPH2 homolog (S. cerevisiae)	298452	Rn.49365	BM386114	2.60	2.60	3.32	2.60	2.62	2.73	1.14	down	4.75E-01	8.95E-01	-	-
1388459_at	Col18a1	collagen, type XVIII, alpha 1	85251	Rn.12030	AI101782	6.28	5.35	4.74	5.04	5.77	6.14	1.14	up	7.47E-01	9.18E-01	-	-
1375114_at	Purb	Purine rich element binding protein B	498407	Rn.156213	AI177011	3.02	3.50	3.05	2.87	3.04	3.09	1.14	down	3.26E-01	8.95E-01	-	-
1374116_at	---	---	---	Rn.176495	AA964836	2.39	2.98	2.37	2.78	2.97	2.56	1.14	up	4.57E-01	8.95E-01	-	-
1379717_at	LOC360997	similar to ATP-binding cassette, sub-family G (WHITE), member 3	360997	Rn.36147	BM385804	5.95	4.91	5.04	5.15	5.31	6.01	1.14	up	6.74E-01	9.01E-01	-	-
1388389_at	02-Sep	septin 2	117515	Rn.98570	BF282620	5.95	6.47	6.94	6.04	6.29	6.46	1.14	down	5.72E-01	8.95E-01	-	-
1390981_at	---	---	---	Rn.165836	AI028965	5.61	5.53	5.83	6.43	5.77	5.35	1.14	up	5.94E-01	8.95E-01	-	-
1379737_a_at	Rbm39	RNA binding motif protein 39	362251	Rn.8555	BG372903	6.75	8.11	7.04	7.81	7.10	7.57	1.14	up	7.01E-01	9.07E-01	-	-
1374177_at	Taf13	TAF13 RNA polymerase II, TATA box binding protein (TBP)-associated factor	310784	Rn.15054	AI230912	8.31	8.05	8.15	7.57	7.98	8.39	1.14	down	4.83E-01	8.95E-01	-	-
1378477_a_at	Fhod1	formin homology 2 domain containing 1	291964	Rn.105655	BI281796	4.17	4.61	4.89	4.90	4.48	3.72	1.14	down	6.62E-01	8.98E-01	-	-
1391039_at	---	---	---	Rn.71071	BE115243	2.63	2.61	2.63	2.60	3.32	2.53	1.14	up	4.91E-01	8.95E-01	-	-
1370317_at	Alg10b	asparagine-linked glycosylation 10, alpha-1,2-glucosyltransferase homolog B	245960	Rn.3635	U78090	5.57	6.57	6.68	5.90	5.66	6.68	1.14	down	7.05E-01	9.08E-01	-	-
1388695_at	Shmt2	serine hydroxymethyltransferase 2 (mitochondrial)	299857	Rn.9214	BF285150	7.96	6.36	8.04	7.83	7.47	7.63	1.14	up	7.50E-01	9.19E-01	-	-
1391404_at	Stag2	stromal antigen 2	313304	Rn.29288	BF402732	3.20	4.70	6.47	4.91	4.81	5.21	1.14	up	8.52E-01	9.54E-01	-	-
1375684_at	Neu1	sialidase 1 (lysosomal sialidase)	24591	Rn.128560	BE111846	3.67	3.66	3.55	3.78	4.04	3.64	1.14	up	1.99E-01	8.95E-01	-	-
1378940_at	Shq1	SHQ1 homolog (S. cerevisiae)	297483	Rn.54034	AI170278	4.55	5.12	2.88	2.46	5.22	5.44	1.14	up	8.79E-01	9.63E-01	-	-
1376983_at	LOC680200	similar to zinc finger protein 455	680200	Rn.9167	BF417687	3.45	4.00	4.10	2.28	3.76	4.94	1.14	down	8.23E-01	9.43E-01	-	-
1391231_at	Catsper2	cation channel, sperm associated 2	366174	Rn.198648	AI639127	3.96	3.94	3.96	4.00	3.98	4.46	1.14	up	2.90E-01	8.95E-01	-	-
1372287_at	Mtmr6	myotubularin related protein 6	305935	Rn.11877	AI236780	8.06	8.48	8.61	8.30	8.92	8.50	1.14	up	4.83E-01	8.95E-01	-	-
1392467_at	Impa2	inositol (myo)-1(or 4)-monophosphatase 2	282636	Rn.856	AW525609	3.49	3.48	3.50	3.49	3.26	4.29	1.14	up	5.77E-01	8.95E-01	-	-
1381586_at	Ankib1	ankyrin repeat and IBR domain containing 1	368062	Rn.2999	BI296171	2.59	3.39	2.59	2.60	2.59	2.81	1.14	down	5.31E-01	8.95E-01	-	-
1381998_at	Zfp148	Zinc finger protein 148	58820	Rn.64671	AW519820	6.79	6.59	6.61	6.13	6.88	6.41	1.14	down	4.52E-01	8.95E-01	-	-
1384387_at	---	---	---	Rn.17517	BE110061	5.14	6.77	7.48	6.90	6.10	6.96	1.14	up	8.11E-01	9.39E-01	-	-
1390039_at	Zdhhc3	zinc finger, DHHC-type containing 3	301081	Rn.8573	AA800535	5.98	6.28	6.10	6.13	6.71	6.09	1.14	up	4.35E-01	8.95E-01	-	-
1371348_at	Pxmb5	proteasome (prosome, macropain) subunit, beta type 5	29425	Rn.2	BI285627	9.24	9.60	9.41	9.49	9.63	9.70	1.14	up	1.92E-01	8.95E-01	-	-
1392738_at	Bat2d1	BAT2 domain containing 1	360865	Rn.206334	AI602954	4.22	4.38	3.66	4.07	3.65	3.97	1.14	down	4.92E-01	8.95E-01	-	-
1396932_at	---	---	---	Rn.47423	BF564328	3.90	4.49	5.19	4.46	5.36	4.34	1.14	up	7.20E-01	9.11E-01	-	-
1378016_at	Eml4	echinoderm microtubule associated protein like 4	313861	Rn.22926	BE104462	2.63	2.70	2.57	2.85	2.79	2.83	1.14	up	9.90E-03	8.95E-01	-	-
1394664_at	---	---	---	Rn.55974	BF397839	2.38	2.37	2.39	2.38	2.98	2.36	1.14	up	4.05E-01	8.95E-01	-	-
1374197_at	---	---	---	Rn.199245	AI177275	4.35	4.19	5.30	4.02	4.97	5.42	1.14	up	7.43E-01	9.17E-01	-	-
1388048_a_at	Inpp4b	inositol polyphosphate-4-phosphatase, type II	116699	Rn.10829	U96920	2.50	2.51	2.56	3.09	2.54	2.50	1.14	up	3.76E-01	8.95E-01	-	-
1382046_at	Map3k3	mitogen activated protein kinase kinase kinase 3	303604	Rn.72680	AI963495	2.63	3.41	2.59	2.60	2.50	2.96	1.14	down	5.63E-01	8.95E-01	-	-
1392277_at	Arhgef12	Rho guanine nucleotide exchange factor (GEF) 12	367072	Rn.129752	BI303053	6.38	7.82	6.52	7.39	6.77	7.13	1.14	up	7.20E-01	9.11E-01	-	-
1392257_at	Mis12	MIS12, MIND kinetochore complex component, homolog (yeast)	501706	Rn.44723	AW253359	2.60	2.54	2.94	2.41	2.57	2.52	1.14	down	2.35E-01	8.95E-01	-	-
1370282_at	Cwp2	cysteine and glycine-rich protein 2	29317	Rn.94754	U46948	9.75	10.04	9.92	9.58	9.43	10.13	1.14	down	4.55E-01	8.95E-01	-	-
1371600_at	Pkig	protein kinase inhibitor, gamma	266709	Rn.220515	AA943815	10.11	9.94	10.22	9.78	10.21	9.72	1.14	down	3.43E-01	8.95E-01	-	-
1377060_at	Mccc2	methylcrotonoyl-Coenzyme A carboxylase 2 (beta)	361884	Rn.33635	AI410674	10.08	9.89	9.56	9.91	10.15	10.03	1.14	up	3.21E-01	8.95E-01	-	-
1370063_at	Nr2f2	nuclear receptor subfamily 2, group F, member 2	113984	Rn.17815	NM_080778	6.43	6.90	5.48	6.08	6.46	5.71	1.14	down	7.07E-01	9.08E-01	-	-
1387510_at	Snx16	sorting nexin 16	64088	Rn.64585	NM_022289	2.84	2.82	3.47	2.90	2.86	2.81	1.14	down	4.30E-01	8.95E-01	-	-
1382547_at	---	---	---	---	AA859744	3.77	3.72	3.28	3.26	3.45	3.48	1.14	down	3.26E-01	8.95E-01	-	-
1390848_at	Rbm19	RNA binding motif protein 19	304512	Rn.128382	BE118552	3.08	2.63	2.68	2.55	2.64	2.63	1.14	down	2.62E-01	8.95E-01	-	-
1371408_at	Cryba1	crystallin, beta A1	25583	Rn.20328	AI576446	2.42	2.40	2.44	2.98	2.43	2.42	1.14	up	3.65E-01	8.95E-01	-	-
1389397_at	---	---	---	Rn.165737	AI234012	5.93	6.25	6.13	6.43	5.90	6.55	1.14	up	4.36E-01	8.95E-01	-	-
1379321_at	---	---	---	Rn.14721	AI180133	4.38	5.31	5.03	5.13	4.86	5.29	1.14	up	5.63E-01	8.95E-01	-	-
1370541_at	Nr1d2	nuclear receptor subfamily 1, group D, member 2	259241	Rn.10055	U20796	6.59	6.99	7.01	6.71	7.01	7.44	1.14	up	4.98E-01	8.95E-01	-	-
1379645_at	Pbrm1	polybromo 1	306254	Rn.19314	BE113614	5.14	5.26	5.62	3.68	4.32	5.46	1.14	down	8.11E-01	9.39E-01	-	-
1378654_at	---	---	---	Rn.31650	BE107231	3.05	3.69	3.09	3.04	3.05	4.30	1.14	up	7.06E-01	9.08E-01	-	-
1373861_at	Ndfip2	Nedd4 family interacting protein 2	361089	Rn.105750	AI228114	8.44	8.65	9.27	8.99	8.96	8.97	1.14	up	4.89E-01	8.95E-01	-	-
1375268_at	---	---	---	Rn.34330	AA858591	8.20	8.48	8.55	8.58	8.29	8.92	1.14	up	4.18E-01	8.95E-01	-	-
1369168_a_at	Clock	clock homolog (mouse)	60447	Rn.205839	NM_021856	3.20	4.25	3.21	4.10	3.72	3.40	1.14	up	6.62E-01	8.98E-01	-	-
1398567_at	RGD1560724	similar to FLJ42986 protein	501127	Rn.198347	BF544658	3.39	2.91	3.04	2.91	2.95	2.91	1.14	down	2.58E-01	8.95E-01	-	-
1393345_at	---	---	---	Rn.211720	BF561145	7.79	8.31	8.71	8.12	8.48	8.79	1.14	up	5.98E-01	8.95E-01	-	-
1392112_at	---	---	---	Rn.168899	BF397377	2.86	2.29	2.30	2.29	2.31	2.28	1.14	down	3.76E-01	8.95E-01	-	-
1392642_at	Senp3	SUMO1/sentrin/SMT3 specific peptidase 3	303245	Rn.24219	AI101514	2.29	2.30	2.85	2.29	2.30	2.28	1.14	down	3.66E-01	8.95E-01	-	-
1376154_at	---	---	---	Rn.199441	AI236861	2.53	2.52	2.54	2.38	3.26	2.52	1.14	up	5.25E-01	8.95E-01	-	-
1394691_at	Foxp1	forkhead box P1	297480	Rn.33321	AA924778	3.01	2.45	2.48	2.46	2.47	2.44	1.14	down	3.55E-01	8.95E-01	-	-
1372756_at	Map4k2	mitogen activated protein kinase kinase kinase kinase 2	293694	Rn.18710	BG378166	4.00	3.99	4.32	4.00	3.38	4.37	1.14	down	5.72E-01	8.95E-01	-	-
1369937_at	Calm1	calmodulin 1	24242	Rn.4166	NM_031969	10.56	11.12	11.09	10.74	10.48	10.96	1.14	down	4.55E-01	8.95E-01	-	-
1371636_at	Ankrd13c	ankyrin repeat domain 13C	685374	Rn.100818	BE104321	8.01	8.77	8.39	8.59	8.33	8.80	1.14	up	5.05E-01	8.95E-01	-	-
1381539_at	---	---	---	Rn.172608	BI294601	2.63	2.69	2.63	3.02	2.63	2.87	1.14	up	1.79E-01	8.95E-01	-	-
1387077_at	Arpp-19	cyclic AMP phosphoprotein	60336	Rn.112577	NM_031660	10.38	10.43	10.20	10.57	10.50	10.50	1.14	up	6.04E-02	8.95E-01	-	-
1389976_at	---	---	---	Rn.167324	BE109682	2.86	4.97	5.73	4.45	4.73	4.95	1.14	up	8.39E-01	9.50E-01	-	-
1388495_at	---	---	---	Rn.12118	BI303583	5.45	5.38	5.33	5.09	5.54	6.08	1.14	up	5.48E-01	8.95E-01	-	-
1383115_at	Catf2t	cleavage stimulation factor, 3' pre-RNA subunit 2, tau	309338	Rn.1661	AW522557	7.78	7.11	7.79	7.18	7.58	7.35	1.14	down	4.99E-01	8.95E-01	-	-
1368273_at	Mapk6	mitogen-activated protein kinase 6	58840	Rn.88457	NM_031622	5.65	6.05	6.34	6.24	6.32	6.06	1.14	up	4.28E-01	8.95E-01	-	-
1370447_at	Phlpb	phospholipase B	192259	Rn.91079	D63648	2.40	2.40	2.42	2.40	2.41	2.97	1.14	up	3.76E-01	8.95E-01	-	-
1388766_at	Mtx2	metaxin 2	288150	Rn.24607	AI409049	8.33	7.92	7.50	7.54	7.52	8.12	1.14	down	5.78E-01	8.95E-01	-	-
1384119_at	Mlh3	mutL homolog 3 (E. coli)	314320	Rn.119254	AI072851	7.04	6.07	5.92	6.32	6.66	6.61	1.14	up	6.33E-01	8.95E-01	-	-
1367996_a_at	Lphn1	latrophilin 1	65096	Rn.10776	AF111099	2.38	2.37	2.26	2.44	2.50	2.63	1.14	up	4.90E-02	8.95E-01	-	-
1380978_at	---	---	---	Rn.147477	AI044494	3.89	3.72	3.00	3.90	3.72	3.55	1.14	up	5.53E-01	8.95E-01	-	-
1372137_at	Bloc1s1	biogenesis of lysosomal organelles complex-1, subunit 1	288785	Rn.9623	BI279854	7.92	7.91	7.37	7.91	7.92	7.92	1.14	up	3.62E-01	8.95E-01	-	-
1383478_at	Jak1	Janus kinase 1	84598	Rn.90191	BG671504	5.72	6.21	6.53	5.75	6.50	6.76	1.14	up	6.49E-01	8.96E-01	-	-
1398922_at	---	---	---	Rn.9259	BM389018	4.72	4.78	4.50	4.73	4.72	5.11	1.14	up	2.91E-01	8.95E-01	-	-
1377407_at	Acsm5	acyl-CoA synthetase medium-chain family member 5	361637	Rn.35367	BI290154	4.90	5.94	5.45	5.21	5.61	4.90	1.14	down	6.34E-01	8.95E-01	-	-
1398255_at	Slc15a2	solute carrier family 15 (H+/peptide transporter), member 2	60577	Rn.88268	NM_031672	9.22	10.07	9.90	9.59	9.24	9.81	1.14	down	5.74E-01	8.95E-01	-	-
1389799_at	---	---	---	Rn.212102	BG378730	2.81	2.54	3.01	3.13	2.92	2.89	1.14	up	2.97E-01	8.95E-01	-	-
1376040_at	Sipa1l2	signal-induced proliferation-associated 1 like 2	361442	Rn.44190	BI290044	2.64	2.63	2.65	2.65	3.19	3.19	1.14	up	3.56E-01	8.95E-01	-	-
1378166_at	Rtf1	Rtf1, Paf1/RNA polymerase II complex component, homolog (S. cerevisiae)	366169	Rn.22569	BE096995	2.88	5.22	2.49	3.42	3.22	3.37	1.14	down	8.37E-01	9.49E-01	-	-
1380093_at	Pak1	P21 (CDKN1A)-activated kinase 1	29431	Rn.9149	BI281735	4.03	6.07	5.93	5.57	5.04	5.99	1.14	up	8.05E-01	9.37E-01	-	-
1374272_at	LOC679383	similar to DNA segment, Chr 5, ERATO Doi 135, expressed	679383	Rn.216991	BI280268	6.55	7.49	7.73	7.10	7.11	6.99	1.14	down	6.30E-01	8.95E-01	-	-
1373560_at	Mgat4b	mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase	303100	Rn.24701	AI233172	6.95	6.93	7.05	6.98	7.12	6.26	1.14	down	5.22E-01	8.95E-01	-	-
1388669_at	Sf3a3	splicing factor 3a, subunit 3	313583	Rn.16732	BM391739	5.92	5.12	4.83	4.73	5.34	6.37	1.14	up	7.61E-01	9.22E-01	-	-
1371658_at	Cox4nb	COX4 neighbor	361405	Rn.6202	BM389065	6.74	7.10	6.59	7.01	7.01	6.97	1.14	up	2.88E-01	8.95E-01	-	-
1388959_at	Tll12	tolloid tyrosine ligase-like family, member 12	300105	Rn.120058	BI297040	3.80	3.93	4.41	3.89	3.85	3.84	1.14	down	3.65E-01	8.95E-01	-	-
1379960_at	Susd3	sushi domain containing 3	306810	Rn.3005	AI406705	4.92	5.12	5.14	5.22	4.29	6.23	1.14	up	7.57E-01	9.21E-01	-	-
1373435_at	Fxr2	fragile X mental retardation, autosomal homolog 2	287433	Rn.203858	BG373419	3.18	4.13	4.69	3.96	4.68	3.93	1.14	up	7.28E-01	9.13E-01	-	-
1383359_at	Lnx2	ligand of numb-protein X 2	360761	Rn.162084	BI389176	3.63	3.98	5.01	4.56	3.85	3.66	1.14	down	7.25E-01	9.13E-01	-	-
1377224_at	---	---	---	Rn.40190	BM391851	3.71	3.25	3.26	3.22	3.21	3.22	1.14	down	2.84E-01	8.95E-01	-	-
1396936_at	---	---	---	Rn.206663	AW529113	2.62	2.62	2.73	3.30	2.63	2.60	1.14	up	4.65E-01	8.95E-01	-	-
1395585_at	---	---	---	Rn.209205	BG375111	2.92	2.37	2.40	2.38	2.39	2.36	1.14	down	3.51E-01	8.95E-01	-	-
1373472_at	Actr6	ARP6 actin-related protein 6 homolog (yeast)	314718	Rn.16356	AI177008	4.71	5.16	5.17	4.49	4.88	5.10	1.14	down	4.68E-01	8.95E-01	-	-
1390206_at	---	---	---	Rn.54341	AW434946	3.77	3.99	3.53	3.86	3.78	4.23	1.14	up	3.85E-01	8.95E-01	-	-
1390279_at	Tssc4	tumor suppressing subtransferable candidate 4	361682	Rn.18732	BI282086	4.06	4.67	5.90	4.67	4.79	4.60	1.14	down	7.47E-01	9.18E-01	-	-
1379153_at	---	---	---	Rn.209305	BF387484	3.04	2.45	2.50	2.48	2.49	2.46	1.14	down	3.81E-01	8.95E-01	-	-
1392802_at	RGD1309707	similar to RIKEN cDNA 4930431E10	690516	Rn.13503	BI274292	2.69	2.72	3.08	2.55	2.69	2.68	1.14	down	2.36E-01	8.95E-01	-	-
1383678_at	Oscp1	organic solute carrier protein 1	362595	Rn.206846	BE102294	6.26	6.81	6.97	6.90	6.79	6.91	1.14	up	4.41E-01	8.95E-01	-	-
1379439_at	Zbtb44	zinc finger and BTB domain containing 44	363035	Rn.6858	AA850609	6.45	6.33	6.30	4.24	6.69	6.60	1.14	down	8.36E-01	9.49E-01	-	-
1385598_at	---	---	---	Rn.45443	AW522647	2.58	2.57	2.56	2.76	2.94	2.58	1.14	up	1.50E-01	8.95E-01	-	-
1387176_at	Rph3al	rabphilin 3A-like (without C2 domains)	171123	Rn.10986	NM_133591	2.58	3.35	2.90	2.87	2.61	2.79	1.14	down	4.74E-01	8.95E-01	-	-
1390854_at	Tmem24	transmembrane protein 24	300666	Rn.57410	BG378195	3.00	3.98	4.97	3.75	4.11	4.66	1.14	up	7.79E-01	9.28E-01	-	-
1373183_at	---	---	---	Rn.19804	AI229780	3.10	3.04	2.43	3.42	2.87	2.85	1.14	up	5.47E-01	8.95E-01	-	-
1380894_at	Dlc1	deleted in liver cancer 1	58834	Rn.7255	BF399476	2.99	2.50	2.47	2.48	2.50	2.43	1.14	down	3.31E-01	8.95E-01	-	-
1385344_at	---	---	---	Rn.206167	AW526794	2.46	3.07	2.49	2.48	2.52	2.47	1.14	down	4.02E-01	8.95E-01	-	-
1398072_at	---	---	---	Rn.209266	BF409833	2.90	2.36	2.37	2.34	2.37	2.36	1.14	down	3.52E-01	8.95E-01	-	-
1377183_at	---	---	---	Rn.204905	BE098555	3.33	4.93	3.24	3.35	3.92	4.78	1.14	up	7.99E-01	9.35E-01	-	-
1395370_at	Gmcl1	germ cell-less homolog 1 (Drosophila)	312516	Rn.22813	AI230498	2.71	2.96	2.73	3.56	2.75	2.65	1.14	up	5.67E-01	8.95E-01	-	-
1379770_at	Chpt1	choline phosphotransferase 1	362866	Rn.203263	BF282951	10.39	10.75	10.51	10.52	10.88	10.82	1.14	up	2.87E-01	8.95E-01	-	-
1381941_at	Cobl	cordon-bleu homolog (mouse)	305497	Rn.114948	BE112718	4.39	4.31	4.38	4.12	4.31	4.08	1.14	down	6.96E-02	8.95E-01	-	-
1376727_at	Yipf4	Yip1 domain family, member 4	362699	Rn.161898	BF283348	7.42	7.09	6.26	7.14	7.03	7.17	1.14	up	6.19E-01	8.95E-01	-	-
1368935_at	Camk2a	calcium/calmodulin-dependent protein kinase II alpha	25400	Rn.107499	NM_012920	2.36	2.35	2.37	2.36	2.95	2.35	1.14	up	3.98E-01	8.95E-01	-	-
1394855_at	---	---	---	Rn.206357	AW526448	2.97	2.42	2.46	2.43	2.45	2.41	1.14	down	3.49E-01	8.95E-01	-	-
1387645_at	Ucn	urocortin	29151	Rn.10190	NM_019150	2.99	2.49	2.51	2.45	2.53	2.45	1.14	down	3.25E-01	8.95E-01	-	-
1392960_at	RGD1309906	similar to RIKEN cDNA 2310004I24 gene	287406	Rn.163104	AI713860	3.94	3.85	5.47	4.92	4.50	4.41	1.14	up	7.49E-01	9.19E-01	-	-
1383751_at	Snx8	sorting nexin 8	288506	Rn.19565	AI555007	10.55	11.02	10.15	10.91	10.78	10.60	1.14	up	5.21E-01	8.95E-01	-	-
1398999_at	Stard3	STAR-related lipid transfer (START) domain containing 3	363675	Rn.145430	BF283508	5.20	5.91	6.09	5.92	4.11	6.61	1.14	down	8.26E-01	9.45E-01	-	-
1384525_at	Dock11	dedicator of cytokinesis 11	313438	Rn.22563	AI549335	3.68	3.65	4.32	3.58	3.98	3.53	1.14	down	5.14E-01	8.95E-01	-	-
1376155_at	Fam151b	family with sequence similarity 151, member B	499507	Rn.115871	BE113295	3.98	3.69	3.67	3.41	4.26	4.23	1.14	up	5.62E-01	8.95E-01	-	-
1380261_at	LOC499806	Similar to RIKEN cDNA 4933404M02	499806	Rn.20672	BE328914	2.39	2.94	2.40	2.38	2.39	2.39	1.14	down	3.58E-01	8.95E-01	-	-
1378661_x_at	LOC679290	hypothetical protein LOC679290	679290	---	BM389983	2.76	2.76	3.06	2.76	2.76	2.50	1.14	down	2.33E-01	8.95E-01	-	-
1384116_at	Acot2	Acyl-CoA thioesterase 2	192272	Rn.37524	BF555448	10.39	10.66	10.24	10.31	10.53	11.02	1.14	up	4.81E-01	8.95E-01	-	-
1391589_at	---	---	---	Rn.6442	BM385772	2.56	2.52	2.60	2.96	2.76	2.50	1.14	up	2.38E-01	8.95E-01	-	-
1377634_at	Tmem126a	transmembrane protein 126A	293113	Rn.143768	BE107851	5.63	7.28	6.68	6.58	5.96	6.48	1.14	down	7.37E-01	9.15E-01	-	-
1398422_at	Rab20	RAB20, member RAS oncogene family	689377	Rn.140755	BF418929	3.89	4.93	4.05	5.21	3.93	4.30	1.14	up	7.27E-01	9.13E-01	-	-
1389216_at	---	---

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1374565_at	Nek6	NIMA (never in mitosis gene a)-related kinase 6	360161	Rn.18744	BF282365	6.27	6.75	6.51	6.50	6.56	7.02	1.14	up	4.36E-01	8.95E-01	-	-
1384964_at	RGD1566368	similar to Solute carrier family 6 (neurotransmitter transporter), member 20	301083	Rn.161981	BI281911	7.46	8.19	7.77	8.28	7.82	7.87	1.14	up	5.09E-01	8.95E-01	-	-
1368012_at	Tep1	telomerase associated protein 1	64523	Rn.5890	NM_022591	3.65	3.87	4.35	3.60	4.84	3.99	1.14	up	6.82E-01	9.03E-01	-	-
1389124_at	Ankrd40	ankyrin repeat domain 40	690586	Rn.17667	AI009814	5.37	5.44	4.19	4.54	4.93	4.98	1.14	down	6.89E-01	9.04E-01	-	-
1390144_at	RGD1359108	similar to RIKEN cDNA 3110043O21	313155	Rn.13725	BF411622	2.70	3.41	4.14	3.19	3.71	3.91	1.14	up	7.12E-01	9.10E-01	-	-
1383576_at	---	---	---	Rn.51134	AW917643	5.30	4.53	4.64	4.96	4.74	5.33	1.14	up	5.62E-01	8.95E-01	-	-
1376744_at	---	---	---	Rn.211835	BI285572	2.45	2.49	3.05	2.49	2.45	2.49	1.14	down	3.94E-01	8.95E-01	-	-
1369485_at	Acot12	acyl-CoA thioesterase 12	170570	Rn.212205	NM_130747	4.44	3.62	3.46	3.47	3.71	3.77	1.14	down	5.91E-01	8.95E-01	-	-
1377616_at	Fam92a1	family with sequence similarity 92, member A1	297903	Rn.92601	BE114214	5.42	5.48	5.99	5.42	5.06	5.85	1.14	down	5.57E-01	8.95E-01	-	-
1399026_at	Paip2	poly(A) binding protein interacting protein 2	361309	Rn.1073	AI178191	8.62	8.85	8.78	9.14	8.91	8.76	1.14	up	2.22E-01	8.95E-01	-	-
1371929_at	Mlx	MAX-like protein X	360631	Rn.16914	BI278563	4.97	5.63	6.51	5.58	5.81	6.27	1.14	up	7.24E-01	9.12E-01	-	-
1386980_at	Apom	apolipoprotein M	55939	Rn.262	NM_019373	9.08	9.40	8.93	8.89	9.06	8.90	1.14	down	2.86E-01	8.95E-01	-	-
1373642_at	Paqr6	progestin and adipoQ receptor family member VI	681021	Rn.204669	AI145383	3.41	3.48	3.49	4.02	4.25	2.67	1.14	up	7.26E-01	9.13E-01	-	-
1387910_at	Epb4.1l1	erythrocyte protein band 4.1-like 1	59317	Rn.20361	AB019256	8.19	8.05	4.77	5.94	6.58	5.94	1.14	down	8.65E-01	9.58E-01	-	-
1378041_at	Abcb8	ATP-binding cassette, sub-family B (MDR/TAP), member 8	362302	Rn.79339	BM388756	2.45	2.44	3.00	2.45	2.45	2.44	1.14	down	3.75E-01	8.95E-01	-	-
1375674_at	RGD1310686	similar to chromosome 16 open reading frame 5	360480	Rn.101805	BI294949	3.79	5.45	4.81	4.24	4.29	4.97	1.14	down	7.47E-01	9.18E-01	-	-
1398814_at	Rab11a	RAB11a, member RAS oncogene family	81830	Rn.1016	NM_031152	9.16	9.40	9.31	8.87	9.29	9.16	1.14	down	2.60E-01	8.95E-01	-	-
1381915_at	RGD1305938	similar to expressed sequence AW549877	310362	Rn.29775	AI111735	6.97	8.25	7.79	8.12	7.47	7.98	1.14	up	6.85E-01	9.03E-01	-	-
1378017_at	Pitrm1	pitrilysin metalloppeptidase 1	307081	Rn.27622	AI408960	3.64	4.27	3.64	3.65	3.78	4.68	1.14	up	6.55E-01	8.98E-01	-	-
1393028_at	---	---	---	Rn.203720	BM383152	4.22	4.03	4.19	4.00	3.98	3.91	1.14	down	4.91E-02	8.95E-01	-	-
1382930_at	---	---	---	Rn.19881	BE106754	3.15	3.85	3.40	4.20	3.39	3.37	1.14	up	6.15E-01	8.95E-01	-	-
1370547_at	Pzp	pregnancy-zone protein	252922	Rn.11295	M84000	9.79	9.22	7.77	8.75	8.67	8.61	1.14	down	7.74E-01	9.26E-01	-	-
1383658_at	Laptm5	lysosomal multispanning membrane protein 5	89783	Rn.24799	BF406601	3.06	3.24	3.71	3.45	3.25	2.75	1.14	down	5.51E-01	8.95E-01	-	-
1390973_at	Trim45	tripartite motif-containing 45	295323	Rn.102590	BI294747	2.91	3.27	2.95	2.75	2.93	2.90	1.14	down	2.14E-01	8.95E-01	-	-
1373600_at	Gltd1	glycosyltransferase 8 domain containing 3	300173	Rn.14826	AI412518	5.00	5.20	5.44	5.23	5.48	5.49	1.14	up	2.96E-01	8.95E-01	-	-
1377820_a_at	Ate1	arginine-tRNA-protein transferase 1	293526	Rn.40326	BI276525	4.42	4.80	5.34	4.89	4.66	4.46	1.14	down	5.63E-01	8.95E-01	-	-
1382236_at	---	---	---	Rn.165192	BI288538	7.51	7.52	7.42	7.06	7.22	7.62	1.14	down	3.33E-01	8.95E-01	-	-
1370285_at	Calcoco1	calcium binding and coiled coil domain 1	246047	Rn.162973	AY078385	4.85	4.83	5.04	4.74	5.77	4.76	1.14	up	6.24E-01	8.95E-01	-	-
1370614_s_at	Stk39	serine/threonine kinase 39, STE20/SPS1 homolog (yeast)	54348	Rn.34414	AF068261	4.67	4.38	5.28	5.06	5.67	4.16	1.14	up	7.37E-01	9.16E-01	-	-
1389556_at	Kifap3	kinesin-associated protein 3	289168	Rn.163223	BI286000	7.17	6.21	7.38	6.67	6.59	6.95	1.14	down	6.48E-01	8.96E-01	-	-
1385585_at	---	---	---	Rn.21134	AI111674	8.49	8.42	8.85	8.50	8.44	8.27	1.14	down	2.83E-01	8.95E-01	-	-
1369851_at	Mef2d	myocyte enhancer factor 2D	81518	Rn.89018	NM_030860	2.44	2.39	2.40	3.03	2.41	2.36	1.14	up	4.42E-01	8.95E-01	-	-
1369100_at	Nlrp6	NLR family, pyrin domain containing 6	171390	Rn.9669	NM_134375	8.12	8.52	7.56	8.15	7.68	8.92	1.14	up	7.06E-01	9.08E-01	-	-
1375946_at	---	---	---	Rn.19790	BF415909	2.63	2.50	2.64	2.51	2.71	3.10	1.14	up	3.60E-01	8.95E-01	-	-
1367831_at	Tp53	tumor protein p53	24842	Rn.54443	NM_030989	5.14	6.02	7.06	5.44	6.22	6.00	1.14	down	7.75E-01	9.27E-01	-	-
1374354_at	Phf19	PHD finger protein 19	296653	Rn.48468	BE349704	5.04	4.91	5.82	5.33	5.60	5.39	1.14	up	5.66E-01	8.95E-01	-	-
1378211_s_at	Mll1	myeloid/lymphoid or mixed-lineage leukemia 1	315606	Rn.62341	BE114473	5.83	6.19	5.11	4.33	7.10	6.24	1.14	up	8.44E-01	9.51E-01	-	-
1384602_at	Gpr107	G protein-coupled receptor 107	311857	Rn.168447	AA943788	2.67	2.67	2.55	2.55	2.68	3.23	1.14	up	4.31E-01	8.95E-01	-	-
1390025_at	Rp9	Retinitis pigmentosa 9 (human)	363032	Rn.6585	AI169230	2.31	2.30	2.34	2.31	2.73	2.46	1.14	up	2.08E-01	8.95E-01	-	-
1398844_at	Txn2	thioredoxin 2	79462	Rn.55043	AA800180	8.29	8.52	8.87	8.48	8.53	8.12	1.14	down	4.33E-01	8.95E-01	-	-
1388571_at	Syngr2	Synaptogyrin 2	89815	Rn.34912	BF285314	7.18	6.06	5.64	6.11	6.11	6.10	1.14	down	7.09E-01	9.09E-01	-	-
1394465_at	---	---	---	---	BG381387	2.50	3.06	2.46	2.42	2.54	2.50	1.14	down	4.04E-01	8.95E-01	-	-
1398884_at	Pfdn5	prefoldin subunit 5	300257	Rn.3401	BM384924	8.94	9.09	8.52	8.89	8.68	9.54	1.14	up	5.82E-01	8.95E-01	-	-
1371513_at	---	---	---	Rn.7217	BG378743	6.26	6.99	6.87	6.85	6.44	7.38	1.14	up	6.29E-01	8.95E-01	-	-
1389228_at	Fam136a	family with sequence similarity 136, member A	297415	Rn.198157	AI412282	5.25	6.54	5.44	6.15	5.58	6.06	1.14	up	6.97E-01	9.07E-01	-	-
1397587_at	Hdac5	Histone deacetylase 5	84580	Rn.79863	BI300820	2.63	2.72	3.38	2.97	2.74	2.47	1.14	down	5.41E-01	8.95E-01	-	-
1377921_at	Etnk2	ethanolamine kinase 2	360843	Rn.65516	AA875050	4.37	4.35	4.39	4.36	4.35	4.95	1.14	up	4.07E-01	8.95E-01	-	-
1389141_at	Orc2l	origin recognition complex, subunit 2-like (yeast)	301430	Rn.75605	BF288111	5.43	5.53	5.95	5.18	5.37	5.91	1.14	up	5.54E-01	8.95E-01	-	-
1370407_at	Pcyox1	prenylcysteine oxidase 1	246302	Rn.34505	AF332142	7.82	7.20	8.23	7.31	7.65	7.73	1.14	down	6.03E-01	8.95E-01	-	-
1397372_at	Mobkl1b	MOB1, Mps One Binder kinase activator-like 1B (yeast)	297387	Rn.74475	BI289004	3.22	3.50	3.25	3.14	3.15	3.13	1.14	down	1.02E-01	8.95E-01	-	-
1398622_at	Crim1	cysteine rich transmembrane BMP regulator 1 (chordin like)	298744	Rn.64366	AI703807	6.48	6.83	6.59	6.67	7.16	6.42	1.14	up	4.52E-01	8.95E-01	-	-
1383638_at	---	---	---	Rn.68627	AW524125	4.88	5.46	4.93	4.98	4.88	4.85	1.14	down	3.88E-01	8.95E-01	-	-
1371210_s_at	T1-Aw2 /// RT1-CE	RT1 class Ib, locus Aw2 /// RT1 class I, CE5	24737 /// 309607	Rn.40130	AJ276126	4.16	4.15	4.53	4.12	4.13	4.04	1.14	down	2.25E-01	8.95E-01	-	-
1377743_at	---	---	---	Rn.202421	BI292687	6.59	6.44	6.23	6.42	5.49	6.80	1.14	down	6.70E-01	9.00E-01	-	-
1376394_at	Clec9a	C-type lectin domain family 9, member a	502901	Rn.14822	AW915454	2.38	2.37	2.42	2.38	2.97	2.38	1.14	up	4.06E-01	8.95E-01	-	-
1381549_at	---	---	---	Rn.210133	BG376818	3.07	2.52	2.59	2.56	2.58	2.49	1.14	down	3.54E-01	8.95E-01	-	-
1394347_at	Golga4	golgi autoantigen, golgin subfamily a, 4	501069	Rn.198228	BF568007	6.82	5.87	4.58	6.15	5.83	5.85	1.14	up	7.94E-01	9.34E-01	-	-
1386102_at	---	---	---	---	AA851046	3.85	3.75	3.86	4.00	4.34	3.67	1.14	up	4.02E-01	8.95E-01	-	-
1367872_at	Ap1b1	adaptor-related protein complex 1, beta 1 subunit	29663	Rn.37383	NM_017277	5.17	5.16	4.83	5.89	4.84	4.98	1.14	up	6.25E-01	8.95E-01	-	-
1390205_at	---	---	---	---	BE108876	3.13	3.47	3.17	2.76	3.15	3.31	1.14	down	4.00E-01	8.95E-01	-	-
1373496_at	Mkrn1	makorin ring finger protein 1	296988	Rn.101798	AI137294	6.13	6.62	6.87	6.39	5.85	6.83	1.14	down	6.31E-01	8.95E-01	-	-
1391511_at	---	---	---	Rn.147945	AA897877	2.80	2.76	2.74	2.76	3.33	2.76	1.14	up	3.89E-01	8.95E-01	-	-
1367731_at	Gnb1	guanine nucleotide binding protein (G protein), beta polypeptide 1	24400	Rn.126047	U34958	6.87	7.15	6.32	6.84	7.02	7.03	1.14	up	5.10E-01	8.95E-01	-	-
1391910_at	Rftn1	Raftlin lipid raft linker 1	501095	Rn.204423	BF550405	2.66	2.66	2.66	3.13	2.66	2.73	1.14	up	2.79E-01	8.95E-01	-	-
1398400_at	Strada	STE20-related kinase adaptor alpha	303605	Rn.11563	AW433595	3.76	3.58	3.94	3.71	4.17	3.94	1.14	up	3.34E-01	8.95E-01	-	-
1373834_at	LOC688966	similar to K11B4.2	688966	Rn.27139	AI233983	4.93	5.49	5.18	5.47	5.22	5.47	1.14	up	3.75E-01	8.95E-01	-	-
1382719_at	---	---	---	Rn.166123	AA943841	2.47	2.46	2.48	2.46	3.04	2.45	1.14	up	4.01E-01	8.95E-01	-	-
1367711_at	Psmc2	proteasome (prosome, macropain) 26S subunit, ATPase 2	25581	Rn.1202	NM_033238	10.47	10.34	10.17	10.13	9.86	10.44	1.14	down	3.88E-01	8.95E-01	-	-
1372019_at	Med10	mediator complex subunit 10	290939	Rn.1773	AI231789	5.65	5.40	5.53	5.65	5.73	5.75	1.14	up	7.88E-02	8.95E-01	-	-
1372551_at	Fastk	Fas-activated serine/threonine kinase	296741	Rn.7680	AI227743	4.47	4.55	4.84	5.17	4.39	4.85	1.14	up	5.09E-01	8.95E-01	-	-
1375360_at	Rheb	Ras homolog enriched in brain	26954	Rn.859	BE099437	6.28	7.03	7.43	6.60	6.70	6.89	1.14	down	6.24E-01	8.95E-01	-	-
1388509_at	---	---	---	---	BI274303	4.43	4.36	4.38	4.76	4.45	4.49	1.14	up	1.44E-01	8.95E-01	-	-
1398507_at	---	---	---	---	BE108415	8.92	7.77	9.12	8.40	9.32	8.64	1.14	up	7.34E-01	9.15E-01	-	-
1372033_at	Isoc2b	isochorismatase domain containing 2b	361501	Rn.1804	BM385414	5.80	6.36	6.35	5.96	6.74	6.36	1.14	up	5.63E-01	8.95E-01	-	-
1382527_at	Plcxd2	phosphatidylinositol-specific phospholipase C, X domain containing 2	363780	Rn.198266	AI764706	2.56	2.53	3.67	3.43	2.73	3.15	1.14	up	6.91E-01	9.05E-01	-	-
1383760_at	Dph3	DPH3, KTI11 homolog (S. cerevisiae)	680594	Rn.3536	AI058665	3.00	2.35	2.44	2.44	2.39	2.41	1.14	down	4.15E-01	8.95E-01	-	-
1395747_at	---	---	---	---	AT003319	4.77	4.65	5.60	5.04	5.05	5.49	1.14	up	6.13E-01	8.95E-01	-	-
1367454_at	Copb2	coatomer protein complex, subunit beta 2 (beta prime)	60384	Rn.37178	NM_021765	9.31	9.30	9.39	9.38	9.44	9.74	1.14	up	1.87E-01	8.95E-01	-	-
1385606_at	Brp16	brain protein 16	315094	Rn.17102	BF569826	2.26	2.25	2.26	2.74	2.26	2.32	1.14	up	2.97E-01	8.95E-01	-	-
1390165_at	Prdm15	PR domain containing 15	304054	Rn.7986	BI288756	6.12	6.83	6.77	6.76	6.90	6.61	1.14	up	4.90E-01	8.95E-01	-	-
1370177_at	PVR	poliovirus receptor	25066	Rn.10677	AI548856	2.37	2.37	2.38	2.39	2.38	2.89	1.14	up	3.37E-01	8.95E-01	-	-
1375316_at	---	---	---	Rn.212010	BI291310	2.53	2.53	2.54	3.09	2.54	2.52	1.14	up	3.80E-01	8.95E-01	-	-
1379221_at	Rspry1	ring finger and SPRY domain containing 1	689249	Rn.205644	AI716277	4.31	5.15	7.16	6.39	4.26	5.43	1.14	down	8.69E-01	9.59E-01	-	-
1374112_at	Mapk1ip1	mitogen-activated protein kinase 1 interacting protein 1	499280	Rn.163750	BI296251	3.82	4.08	3.92	4.18	3.09	4.01	1.14	down	6.25E-01	8.95E-01	-	-
1378685_at	LOC689836	hypothetical protein LOC689836	689836	Rn.167628	AI235586	3.21	3.38	3.23	3.21	3.22	3.95	1.14	up	5.04E-01	8.95E-01	-	-
1381316_at	---	---	---	Rn.204762	BF388256	3.47	2.36	2.79	2.77	3.68	2.72	1.14	up	7.03E-01	9.07E-01	-	-
1374959_at	Nqo2	NAD(P)H dehydrogenase, quinone 2	291084	Rn.7882	AA945624	7.23	6.84	7.32	6.94	7.09	6.81	1.14	down	3.32E-01	8.95E-01	-	-
1375442_at	Mphosph10	M-phase phosphoprotein 10 (U3 small nucleolar ribonucleoprotein)	293828	Rn.103228	BG375380	5.68	5.71	5.04	5.23	5.19	5.46	1.14	down	4.78E-01	8.95E-01	-	-
1377939_at	Atg4c	ATG4 autophagy related 4 homolog C (S. cerevisiae)	313391	Rn.233778	AW527217	4.51	3.36	4.07	3.97	4.46	4.07	1.14	up	6.44E-01	8.95E-01	-	-
1370376_a_at	Csda	cold shock domain protein A	83807	Rn.3306	AA866458	7.16	6.30	5.82	6.97	5.54	7.31	1.14	up	7.98E-01	9.35E-01	-	-
1393349_x_at	Vav2	vav 2 guanine nucleotide exchange factor	296603	Rn.98555	BI288992	6.39	6.44	6.77	6.90	5.87	7.37	1.14	up	7.10E-01	9.09E-01	-	-
1384640_at	---	---	---	Rn.203757	AA897287	2.48	2.50	2.52	3.07	2.51	2.47	1.14	up	3.97E-01	8.95E-01	-	-
1397466_at	Eif3h	Eukaryotic translation initiation factor 3, subunit H	299899	Rn.129213	BI282573	7.60	7.86	7.42	7.87	7.67	7.88	1.14	up	2.68E-01	8.95E-01	-	-
1378916_at	---	---	---	Rn.140643	AI029234	2.84	2.83	2.90	3.52	2.84	2.75	1.14	up	4.92E-01	8.95E-01	-	-
1381690_at	Ank3	ankyrin 3, epithelial	361833	Rn.220009	BF409378	2.86	3.17	2.82	2.68	3.59	3.13	1.14	up	5.55E-01	8.95E-01	-	-
1396356_at	Elk4	ELK4, member of ETS oncogene family	304746	Rn.204345	BI290042	5.20	4.37	5.60	6.01	4.65	5.07	1.14	up	7.52E-01	9.20E-01	-	-
1398386_at	LOC501515	Similar to Zinc finger CCHC domain-containing protein 6	501515	Rn.16458	AW915951	3.67	3.61	3.30	3.17	3.46	3.40	1.14	down	2.77E-01	8.95E-01	-	-
1384370_at	Mthfs	5,10-methenyltetrahydrofolate synthetase (5-formyltetrahydrofolate cyclo-liga	300886	Rn.2215	BF542664	2.86	2.85	2.61	3.10	2.93	2.84	1.14	up	1.79E-01	8.95E-01	-	-
1376828_at	Zfp189	zinc finger protein 189	313219	Rn.19954	AI407872	4.95	4.62	5.01	5.57	4.79	4.77	1.14	up	5.63E-01	8.95E-01	-	-
1396262_at	Nampt	nicotinamide phosphoribosyltransferase	297508	Rn.203598	BM384271	8.24	4.81	4.35	4.40	4.89	5.56	1.14	down	7.95E-01	9.34E-01	-	-
1391218_at	Fam76b	family with sequence similarity 76, member B	367021	Rn.52995	BI294343	3.31	3.67	3.39	3.33	4.24	3.35	1.14	up	5.98E-01	8.95E-01	-	-
1396694_at	---	---	---	Rn.147374	BF400272	3.04	2.47	2.50	2.49	2.49	2.49	1.14	down	3.81E-01	8.95E-01	-	-
1384916_at	---	---	---	Rn.40898	AI717256	8.69	9.07	9.29	9.39	9.26	8.95	1.14	up	4.52E-01	8.95E-01	-	-
1397430_at	---	---	---	Rn.173262	BF403977	2.48	2.32	2.33	2.32	3.04	2.32	1.14	up	5.02E-01	8.95E-01	-	-
1378019_at	Nudt13	nudix (nucleoside diphosphate linked moiety X)-type motif 13	682978	Rn.160892	AI104278	2.79	3.24	2.82	3.62	2.99	2.80	1.14	up	5.61E-01	8.95E-01	-	-
1396489_at	---	---	---	Rn.157337	BF404442	2.86	2.64	2.75	3.03	2.98	2.79	1.14	up	1.31E-01	8.95E-01	-	-
1380773_at	---	---	---	Rn.155429	BI288767	4.89	4.23	4.20	4.06	5.12	3.59	1.14	down	7.36E-01	9.15E-01	-	-
1371868_at	Bcas2	breast carcinoma amplified sequence 2	295334	Rn.1225	AA851386	8.92	9.20	9.91	9.31	8.69	9.48	1.14	down	6.55E-01	8.97E-01	-	-
1367912_at	Ltbp1	latent transforming growth factor beta binding protein 1	59107	Rn.40942	NM_021587	3.42	3.08	2.71	3.13	2.58	2.95	1.14	down	5.23E-01	8.95E-01	-	-
1370326_at	Pctk1	PCTAIRE protein kinase 1	81741	Rn.16871	U36444	6.65	7.17	7.00	6.39	6.97	6.90	1.14	down	4.90E-01	8.95E-01	-	-
1393561_at	---	---	---	Rn.210200	BF396511	4.65	4.93	4.76	4.83	4.96	5.10	1.14	up	1.82E-01	8.95E-01	-	-
1368175_at	Zhx1	zinc fingers and homeoboxes 1	171159	Rn.16902	NM_133620	5.76	6.54	6.04	5.50	6.32	5.96	1.14	down	6.10E-01	8.95E-01	-	-
1395810_at	---	---	---	---	BM383094	8.89	7.68	7.64	8.38	8.33	8.03	1.13	up	9.05E-01	9.05E-01	-	-
1397200_at	Chd4	chromodomain helicase DNA binding protein 4	117535	Rn.63247	BF412612	6.96	7.64	6.42	5.85	7.42	7.21	1.13	down	7.78E-01	9.28E-01	-	-
1370158_at	Myh10	myosin, heavy chain 10, non-muscle	79433	Rn.98166	AA946388	3.69	4.72	4.39	4.29	4.24	4.81	1.13	up	6.34E-01	8.95E-01	-	-
1391498_at	Sin3a	SIN3 homolog A, transcription regulator (yeast)	363067	Rn.63749	AI072877	4.47	6.17	5.30	3.87	5.75	5.77	1.13	down	8.31E-01	9.47E-01	-	-
1373222_at	Hexa	hexosaminidase A	300757	Rn.92939	AI230271	10.85	11.28	10.82	10.98	11.32	11.20	1.13	up	3.60E-01	8.95E-01	-	-
1381062_at	---	---	---	Rn.169882	AW530948	2.49	3.03	2.49	2.48	2.49	2.48	1.13	down	3.67E-01	8.95E-01	-	-
1368217_at	Ralbp1	ralA binding protein 1	84014	Rn.7107	U28830	3.26	3.62	2.69	3.60	2.77	3.75	1.13	up	6.78E-01	9.02E-01	-	-
1387033_at	Ucp1	uncoupling protein 1 (mitochondrial, proton carrier)	24860	Rn.10228	NM_012682	2.74	2.41	2.62	2.40	2.41	2.40	1.13	down	1.36E-01	8.95E-01	-	-
1384207_at	Nif3l1	NIF3 NGG1 interacting factor 3-like 1 (S. pombe)	301431	Rn.18112	AI028960	2.56	3.09	2.70	2.62	2.61	2.57	1.13	down	3.20E-01	8.95E-01	-	-
1391331_at	---	---	---	Rn.45499	BE106891	3.13	2.49	2.53	2.70	2.53	2.39	1.13	down	4.64E-01	8.95E-01	-	-
1395965_at	---	---	---	Rn.206587	BI298589	6.04	6.61	6.36	5.70	6.24	6.51	1.13	down	5.63E-01	8.95E-01	-	-
1371645_at	Sdf2	stromal cell derived factor 2	287470	Rn.3965	BI284339	6.55	6.75	7.15	7.13	6.53	7.33	1.13	up	5.74E-01	8.95E-01	-	-
1371435_at	Naca	nascent-polypeptide-associated complex alpha polypeptide	288770	Rn.219226	BI279561	10.99	11.20	11.17	11.32	11.23	11.35	1.13	up	6.93E-02	8.95E-01	-	-
1374752_at	Mdfic	MyoD family inhibitor domain containing	362325	Rn.18295	AI408734	2.49	2.47	3.37	2.48	2.91	3.49	1.13	up	6.85E-01	9.03E-01	-	-
1389130_at	Elf2	E74-like factor 2	361944	Rn.107459	AW525131	3.03	3.35	3.13	3.12	2.73	3.12	1.13	down	3.25E-01	8.95E-01	-	-
1378387_at	Tinf2	TERF1 (TRF1)-interacting nuclear factor 2	290232	Rn.107132	BI275245	3.94	3.68	3.50	4.33	3.41	3.93	1.13	up	5.71E-01	8.95E-01	-	-
1381325_at	---	---	---	Rn.6829	BE097765	4.11	4.13	5.00	3.87	4.70	5.22	1.13	up	7.29E-01	9.14E-01	-	-
1391207_at	Fam19a5	family with sequence similarity 19 (chemokine (C-C motif)-like), member A5	500915	Rn.13126	BF557676	2.69	3.26	3.50	3.77	3.01	3.22	1.13	up	6.12E-01	8.95E-01	-	-
1371908_at	Nxt1	NTF2-like export factor 1	296219	Rn.8541	AA891920	3.28	4.71	6.04	5.42	4.45	4.71	1.13	up	8.41E-01	9.50E-01	-	-
1372558_at	Narg1	NMDA receptor regulated 1	310399	Rn.12587	AI177404	4.85	5.84	5.91	5.61	5.73	5.81	1.13	up	6.30E-01	8.95E-01	-	-
1390458_at	---	---	---	---	BG666849	2.58	2.57	3.19	2.57	2.57	2.65	1.13	down	4.25E-01	8.95E-01	-	-
1376180_at	---	---	---	---	AW915012	3.98	4.23	3.75	3.72	4.19	4.59	1.13	up	5.61E-01	8.95E-01	-	-
1389966_at	Col6a3	procollagen, type VI, alpha 3	367313	Rn.219672	AI176126	2.73	2.82	2.38	2.69	2.32	2.37	1.13	down	3.63E-01	8.95E-01	-	-
1382448_at	---	---	---	---	AI071189	2.57	3.15	2.55	2.62	2.54	2.57	1.13	down	4.12E-01	8.95E-01	-	-
1372192_at	---	---	---	Rn.3580	AI145385	4.79	4.90	4.94	5.46	3.35	5.27	1.13	down	8.01E-01	9.38E-01	-	-
1391409_at	Amn	amnionless homolog (mouse)	314459	Rn.7787	BI276097	8.34	8.96	8.36	8.45	8.53	8.13	1.13	down	4.87E-01	8.95E-01	-	-
1380587_at	---	---	---	Rn.208983	BF404982	2.77	2.62	2.44	2.43	2.44	2.42	1.13	down	1.24E-01	8.95E-01	-	-
1389147_at	---	---	---	Rn.16536	BE116020	7.08	6.84	7.31	7.14	7.17	7.46	1.13	up

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1371516_at	Xpo7	exportin 7	361070	Rn.219364	BM391834	6.74	7.74	8.19	7.31	7.10	7.73	1.13	down	7.19E-01	9.11E-01	-	-
1368400_at	Timm8a1	translocase of inner mitochondrial membrane 8 homolog a1 (yeast)	84383	Rn.162342	NM_053370	6.00	5.64	6.22	6.24	5.52	5.57	1.13	down	5.63E-01	8.95E-01	-	-
1381602_at	Mid1	Midline 1	54252	Rn.15169	AI502076	3.17	2.41	2.42	2.63	2.42	2.41	1.13	down	5.30E-01	8.95E-01	-	-
1385933_at	---	---	---	Rn.19220	AA875227	8.46	8.71	8.69	8.84	8.68	8.87	1.13	up	1.46E-01	8.95E-01	-	-
1378062_at	---	---	---	Rn.206272	BF398677	2.57	2.87	2.51	2.55	2.37	2.50	1.13	down	2.21E-01	8.95E-01	-	-
1396262_at	Prps2	phosphoribosyl pyrophosphate synthetase 2	24689	Rn.11320	NM_012634	2.49	3.06	2.53	2.49	2.54	2.51	1.13	down	3.82E-01	8.95E-01	-	-
1396469_at	---	---	---	Rn.35466	AI502701	2.39	2.34	2.42	2.95	2.39	2.36	1.13	up	4.00E-01	8.95E-01	-	-
1375641_at	bc5l /// RGD156034	actin related protein 2/3 complex, subunit 5-like /// similar to actin related prot	296710 /// 501132	Rn.110752	BI296526	8.98	9.46	9.82	9.05	9.16	9.51	1.13	down	5.53E-01	8.95E-01	-	-
1387489_at	Ext3	exostoses (multiple)-like 3	56819	Rn.48671	NM_020097	3.07	3.22	3.25	3.23	3.37	3.49	1.13	up	1.29E-01	8.95E-01	-	-
1369254_a_at	Ptger1	prostaglandin E receptor 1 (subtype EP1)	25637	Rn.11423	D88752	3.10	2.71	2.57	2.70	2.59	2.55	1.13	down	3.40E-01	8.95E-01	-	-
1398906_at	LOC287274	sedlin-like	287274	---	BM391354	8.50	8.23	8.03	7.73	7.95	8.53	1.13	down	5.49E-01	8.95E-01	-	-
1373115_at	Ccdc115	coiled-coil domain containing 115	363213	Rn.17453	BI281909	5.14	5.55	5.06	4.94	5.69	5.67	1.13	up	5.69E-01	8.95E-01	-	-
1393395_at	---	---	---	Rn.15108	BI275654	3.14	2.53	2.58	2.54	2.46	2.73	1.13	down	4.41E-01	8.95E-01	-	-
1377651_at	---	---	---	Rn.21406	AI577848	6.42	6.19	5.82	6.22	5.69	5.99	1.13	down	4.86E-01	8.95E-01	-	-
1381757_at	RGD1309501	hypothetical LOC305552	305552	Rn.6266	AA965058	5.23	6.08	4.39	5.10	5.32	5.83	1.13	up	7.53E-01	9.20E-01	-	-
1384985_at	---	---	---	---	BG671979	2.64	2.63	2.39	2.63	2.64	2.92	1.13	up	2.25E-01	8.95E-01	-	-
1396028_at	---	---	---	Rn.147844	BF392616	3.22	3.61	3.06	3.04	3.05	3.26	1.13	down	3.71E-01	8.95E-01	-	-
1367807_at	Plod1	procollagen-lysine 1, 2-oxoglutarate 5-dioxygenase 1	116552	Rn.4445	NM_053827	3.01	3.59	3.57	3.60	3.17	3.94	1.13	up	5.74E-01	8.95E-01	-	-
1388376_at	RGD1309710	similar to RIKEN cDNA 0610038D11	293700	Rn.2190	AI235498	9.28	9.49	9.78	9.50	9.92	9.67	1.13	up	3.99E-01	8.95E-01	-	-
1376406_at	---	---	---	Rn.169543	BI300322	2.44	2.43	2.44	2.98	2.44	2.43	1.13	up	3.76E-01	8.95E-01	-	-
1382115_at	Tctn3	tectonic family member 3	309486	Rn.22713	BE096174	4.69	4.69	5.45	5.14	4.48	4.67	1.13	down	6.05E-01	8.95E-01	-	-
1387256_at	Adam1a	a disintegrin and metalloprotease domain 1a	56777	Rn.42919	NM_020078	3.94	3.53	3.54	4.05	3.37	3.05	1.13	down	6.09E-01	8.95E-01	-	-
1374572_at	Gatsl3	GATS protein-like 3	360969	Rn.155378	BI294229	5.22	4.78	5.07	5.66	4.68	4.19	1.13	down	7.11E-01	9.10E-01	-	-
1386852_x_at	Ubb	ubiquitin B	192255	Rn.1253	D16554	12.37	12.59	12.66	12.36	12.26	12.47	1.13	down	1.70E-01	8.95E-01	-	-
1391758_at	---	---	---	---	BE109438	5.37	5.58	4.18	4.68	5.23	5.43	1.13	down	7.25E-01	9.13E-01	-	-
1398031_at	Pyroxd2	pyridine nucleotide-disulphide oxidoreductase domain 2	309381	Rn.102445	BF406285	5.91	6.26	6.03	5.88	5.92	5.88	1.13	down	1.58E-01	8.95E-01	-	-
1397525_at	---	---	---	Rn.8697	AA945370	7.38	7.79	8.31	7.52	8.13	8.38	1.13	up	6.55E-01	8.97E-01	-	-
1378575_at	---	---	---	Rn.209448	BF404457	2.41	2.40	2.41	2.95	2.41	2.40	1.13	up	3.78E-01	8.95E-01	-	-
1375434_at	F8a1	Coagulation factor VIII-associated (intronic transcript) 1	501661	Rn.41311	AI576484	3.94	3.35	3.36	3.49	3.39	3.23	1.13	down	4.42E-01	8.95E-01	-	-
1367669_a_at	Map1lc3b	microtubule-associated protein 1 light chain 3 beta	64862	Rn.41412	AI233190	8.46	8.62	8.10	8.65	8.33	8.74	1.13	up	4.21E-01	8.95E-01	-	-
1382610_at	---	---	---	Rn.165091	AA957105	9.02	8.43	8.68	8.25	8.26	9.08	1.13	down	6.09E-01	8.95E-01	-	-
1374577_at	Tbrg4	transforming growth factor beta regulator 4	360977	Rn.22830	AW254561	7.55	6.29	6.35	6.53	6.39	6.73	1.13	down	6.93E-01	9.05E-01	-	-
1372628_at	Ap4s1	adaptor-related protein complex AP-4, sigma 1	366618	Rn.6307	AA800277	9.04	9.56	9.70	9.52	9.37	9.94	1.13	up	5.33E-01	8.95E-01	-	-
1376432_at	Zfand3	zinc finger, AN1-type domain 3	361816	Rn.136939	BM383785	5.39	5.70	5.48	4.97	5.38	5.68	1.13	down	4.71E-01	8.95E-01	-	-
1372900_at	Pigt	phosphatidylinositol glycan anchor biosynthesis, class T	296360	Rn.40488	BI274156	6.23	7.07	6.25	6.56	6.82	6.71	1.13	up	5.67E-01	8.95E-01	-	-
1389364_at	Ndfip2	Nedd4 family interacting protein 2	361089	Rn.105750	BF406709	7.02	6.82	7.49	6.98	6.78	7.05	1.13	down	4.51E-01	8.95E-01	-	-
1367903_at	Hmox2	heme oxygenase (decyclizing) 2	79239	Rn.10241	J05405	6.23	6.75	6.95	6.62	6.19	6.58	1.13	down	5.20E-01	8.95E-01	-	-
1378954_at	---	---	---	Rn.212687	AI711116	7.07	6.52	5.43	4.75	7.38	6.37	1.13	down	8.52E-01	9.54E-01	-	-
1373744_at	Anapc1	anaphase promoting complex subunit 1	311412	Rn.8	BF548006	3.40	3.51	3.14	3.18	2.66	3.68	1.13	down	5.99E-01	8.95E-01	-	-
1383615_a_at	Hectd1	HECT domain containing 1	362736	Rn.36797	AI059295	10.04	10.24	10.42	10.15	10.63	10.44	1.13	up	3.72E-01	8.95E-01	-	-
1372377_at	Ddx41	DEAD (Asp-Glu-Ala-Asp) box polypeptide 41	314336	Rn.114971	BM388310	5.83	5.47	5.31	5.49	5.56	6.10	1.13	up	5.11E-01	8.95E-01	-	-
1380446_at	Mllt10	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila);	361285	Rn.3620	BF396749	5.91	6.29	5.35	6.15	5.15	5.71	1.13	down	6.76E-01	9.02E-01	-	-
1393021_at	---	---	---	Rn.48920	BE113061	3.34	3.02	3.29	3.01	3.11	3.00	1.13	down	1.63E-01	8.95E-01	-	-
1369641_at	Pafah1b2	platelet-activating factor acetylhydrolase, isoform 1b, subunit 2	64189	Rn.24751	BM392396	5.23	5.44	5.49	5.40	5.62	5.68	1.13	up	2.00E-01	8.95E-01	-	-
1387806_at	Rap1b	RAP1B, member of RAS oncogene family	171337	Rn.95071	NM_134346	10.77	10.92	10.71	10.80	10.87	11.28	1.13	up	3.15E-01	8.95E-01	-	-
1381494_at	Capzb	Capping protein (actin filament) muscle Z-line, beta	298584	Rn.105999	AA964419	2.44	2.42	2.45	2.99	2.45	2.41	1.13	up	3.90E-01	8.95E-01	-	-
1368960_at	Lgals8	lectin, galactoside-binding, soluble, 8	116641	Rn.10069	NM_053862	8.75	9.09	8.45	8.85	9.25	8.72	1.13	up	5.06E-01	8.95E-01	-	-
1395464_at	RGD1311154	similar to hypothetical protein FLJ12242	300317	Rn.198231	AI237163	2.71	2.64	3.87	3.18	2.65	2.85	1.13	down	6.98E-01	9.07E-01	-	-
1371720_at	Mrpl20	mitochondrial ribosomal protein L20	680747	Rn.2913	AI599839	7.40	7.50	8.51	7.54	8.62	7.79	1.13	up	7.31E-01	9.14E-01	-	-
1370829_at	Fntb	farnesyltransferase, CAAX box, beta	64511	Rn.8873	M69056	2.35	2.35	2.36	2.35	2.91	2.34	1.13	up	4.00E-01	8.95E-01	-	-
1397759_at	---	---	---	Rn.168731	BI296243	3.55	4.72	3.85	3.55	3.40	4.62	1.13	down	7.49E-01	9.19E-01	-	-
1388419_at	Cdk5rap2	CDK5 regulatory subunit associated protein 2	286919	Rn.13247	AW915005	3.52	2.89	2.65	2.63	3.57	3.39	1.13	up	6.69E-01	9.00E-01	-	-
1374511_at	---	---	---	Rn.17289	BI291354	2.29	2.39	2.39	2.68	2.39	2.53	1.13	up	1.19E-01	8.95E-01	-	-
1393610_at	Fam76a	family with sequence similarity 76, member A	362618	Rn.27338	AI137173	2.32	2.33	2.33	2.86	2.34	2.32	1.13	up	3.88E-01	8.95E-01	-	-
1376494_at	Pole3	polymerase (DNA directed), epsilon 3 (p17 subunit)	298098	Rn.3290	BI282908	3.09	3.18	3.12	3.04	2.73	4.16	1.13	up	7.04E-01	9.07E-01	-	-
1393654_at	Neil1	nei endonuclease VIII-like 1 (E. coli)	367090	Rn.154781	BM391891	3.12	3.20	3.24	3.69	3.20	3.19	1.13	up	3.53E-01	8.95E-01	-	-
1398797_at	Hnrnpk	heterogeneous nuclear ribonucleoprotein K	117282	Rn.11854	NM_057141	9.26	9.30	8.98	9.14	9.33	9.61	1.13	up	3.55E-01	8.95E-01	-	-
1399095_at	Sumo1	SMT3 suppressor of mif two 3 homolog 1 (S. cerevisiae)	301442	Rn.1221	AI407918	8.04	7.89	8.08	8.02	7.29	8.16	1.13	down	5.54E-01	8.95E-01	-	-
1373550_at	Trim11	tripartite motif-containing 11	360534	Rn.9308	BI280318	5.90	5.81	6.13	5.85	5.70	5.76	1.13	down	1.68E-01	8.95E-01	-	-
1372045_at	Ap1m1	adaptor-related protein complex 1, mu 1 subunit	306332	Rn.220709	BE112941	4.77	4.19	4.49	4.37	5.14	4.48	1.13	up	5.77E-01	8.95E-01	-	-
1379659_at	Bmp2k	BMP-2 inducible kinase	498333	Rn.103861	BF284068	2.91	2.93	3.53	2.94	2.91	2.99	1.13	down	4.31E-01	8.95E-01	-	-
1389088_at	Adnp	activity-dependent neuroprotector homeobox	64622	Rn.48777	AI600029	9.84	9.06	8.89	9.68	9.31	9.34	1.13	up	6.04E-01	8.95E-01	-	-
1384462_at	---	---	---	Rn.82177	AA819526	3.10	3.08	3.10	3.08	2.56	3.11	1.13	down	3.74E-01	8.95E-01	-	-
1390709_at	Trio	triple functional domain (PTPRF interacting)	310192	Rn.221920	AI102364	4.40	4.66	3.98	4.31	4.43	4.83	1.13	up	5.20E-01	8.95E-01	-	-
1381933_at	Rfc5	Replication factor C (activator 1) 5	304528	Rn.105670	AW434510	5.55	5.55	5.56	5.76	5.51	4.85	1.13	down	5.47E-01	8.95E-01	-	-
1374718_at	Dtx3l	deltex 3-like (Drosophila)	498089	Rn.1971	AA945915	4.03	3.98	3.53	3.51	3.52	3.98	1.13	down	4.70E-01	8.95E-01	-	-
1367934_at	Rpl39	ribosomal protein L39	25347	Rn.6172	NM_012875	3.03	3.26	3.33	3.40	3.49	3.28	1.13	up	1.75E-01	8.95E-01	-	-
1385901_at	Ptdss2	phosphatidylserine synthase 2	293620	Rn.104893	BE118197	2.89	2.74	2.80	3.21	2.89	2.86	1.13	up	2.14E-01	8.95E-01	-	-
1389868_at	Kctd2	potassium channel tetramerisation domain containing 2	498024	Rn.21595	BI301226	7.21	6.16	6.62	6.79	6.43	6.23	1.13	down	6.34E-01	8.95E-01	-	-
1372302_at	Fam82a2	family with sequence similarity 82, member A2	311328	Rn.18772	BF284897	6.21	7.37	7.85	7.58	6.91	7.47	1.13	up	7.54E-01	9.20E-01	-	-
1378806_at	---	---	---	Rn.209162	BF392451	3.06	2.49	2.51	2.54	2.52	2.47	1.13	down	3.96E-01	8.95E-01	-	-
1383137_at	Sox4	SRY (sex determining region Y)-box 4	364712	Rn.163667	AA956294	2.54	2.50	2.58	2.73	2.57	2.86	1.13	up	1.10E-01	8.95E-01	-	-
1389526_at	Efr3a	EFR3 homolog A (S. cerevisiae)	362923	Rn.21009	BG373853	4.05	4.33	4.04	4.79	3.66	4.51	1.13	up	6.40E-01	8.95E-01	-	-
1387503_at	Cpn1	carboxypeptidase N, polypeptide 1	365466	Rn.145303	NM_053526	6.03	5.70	5.56	6.02	5.75	6.05	1.13	up	3.54E-01	8.95E-01	-	-
1388128_at	Actr3	ARP3 actin-related protein 3 homolog (yeast)	81732	Rn.103326	BI292004	5.67	5.26	5.27	5.32	5.15	5.21	1.13	down	2.84E-01	8.95E-01	-	-
1375371_at	Ranbp2	RAN binding protein 2	294429	Rn.101115	BI296662	8.98	9.05	8.48	8.97	8.97	9.10	1.13	up	3.90E-01	8.95E-01	-	-
1387808_at	Slc7a7	solute carrier family 7 (cationic amino acid transporter, y+ system), member 7	83509	Rn.163294	AF200684	4.18	3.87	4.18	4.46	4.44	3.85	1.13	up	4.74E-01	8.95E-01	-	-
1396745_at	---	---	---	Rn.171620	BF394256	2.52	2.98	2.50	2.46	2.55	2.44	1.13	down	3.29E-01	8.95E-01	-	-
1373324_at	Dusp14	dual specificity phosphatase 14	360580	Rn.25406	AI236997	2.95	2.37	2.39	2.39	2.42	2.36	1.13	down	4.03E-01	8.95E-01	-	-
1374289_at	Polr1c	polymerase (RNA) I polypeptide C	301246	Rn.107990	AA818183	8.12	7.94	8.05	8.38	8.24	8.02	1.13	up	2.02E-01	8.95E-01	-	-
1389189_at	Actn1	actinin, alpha 1	81634	Rn.6401	BF555956	2.66	3.06	2.67	3.27	2.70	2.94	1.13	up	4.53E-01	8.95E-01	-	-
1381929_at	---	---	---	---	AI555382	2.66	2.54	2.72	2.94	2.83	2.68	1.13	up	1.20E-01	8.95E-01	-	-
1398966_at	LOC687029	similar to differentially expressed in B16F10 1	687029	---	AI169154	8.13	8.49	8.64	8.77	8.06	8.97	1.13	up	6.05E-01	8.95E-01	-	-
1375487_at	---	---	---	Rn.176438	BI296529	2.38	2.37	2.38	2.87	2.38	2.42	1.13	up	3.22E-01	8.95E-01	-	-
1395704_at	---	---	---	Rn.23284	BF561525	2.59	2.81	2.88	3.35	2.68	2.78	1.13	up	4.73E-01	8.95E-01	-	-
1370485_a_at	Bcl2l1	Bcl2-like 1	24888	Rn.10323	AF279286	6.05	6.75	6.05	5.86	5.23	6.29	1.13	up	8.48E-01	9.53E-01	-	-
1373970_at	Il33	interleukin 33	361749	Rn.106849	AI716248	7.43	7.94	7.58	7.27	7.42	7.72	1.13	down	4.32E-01	8.95E-01	-	-
1378590_at	---	---	---	Rn.89151	AW527807	5.23	5.76	5.32	5.14	5.35	5.29	1.13	down	3.70E-01	8.95E-01	-	-
1398575_at	Zbtb5	zinc finger and BTB domain containing 5	298084	Rn.23809	AI716554	2.51	2.49	2.49	3.27	2.40	2.34	1.13	up	5.88E-01	8.95E-01	-	-
1399106_at	Myeov2	myeloma overexpressed 2	681389	Rn.14866	AI176121	11.31	11.12	11.36	11.17	10.89	11.21	1.13	down	2.26E-01	8.95E-01	-	-
1380033_at	---	---	---	Rn.167968	AI408858	3.04	3.04	3.09	3.01	3.00	3.69	1.13	up	4.81E-01	8.95E-01	-	-
1371207_at	Nupl1	nucleoporin like 1	245922	Rn.11099	AF000898	5.45	5.99	6.91	6.03	6.24	5.56	1.13	down	7.26E-01	9.13E-01	-	-
1376594_at	Vezf1	vascular endothelial zinc finger 1	287615	Rn.198892	AW524517	7.08	6.64	7.19	6.86	6.29	7.24	1.13	down	6.12E-01	8.95E-01	-	-
1390806_at	RGD1309730	similar to RIKEN cDNA B230118H07	295952	Rn.19353	AW251111	5.70	5.58	4.98	5.38	5.46	5.96	1.13	up	5.71E-01	8.95E-01	-	-
1382818_at	Fam126b	family with sequence similarity 126, member B	316415	Rn.149172	AI177067	7.82	7.90	8.66	8.03	8.35	8.53	1.13	up	5.91E-01	8.95E-01	-	-
1386158_at	---	---	---	Rn.49822	AI639147	2.42	2.42	2.43	2.42	2.43	2.96	1.13	up	3.76E-01	8.95E-01	-	-
1385482_at	---	---	---	Rn.200334	BI293434	2.56	2.49	2.52	3.12	2.52	2.47	1.13	up	4.47E-01	8.95E-01	-	-
1378008_at	---	---	---	Rn.204209	AF417386	2.48	2.47	2.42	2.51	2.92	2.47	1.13	up	2.92E-01	8.95E-01	-	-
1391424_at	---	---	---	Rn.107130	AA944326	2.46	2.45	2.47	3.00	2.46	2.45	1.13	up	3.86E-01	8.95E-01	-	-
1370109_a_at	Eef1a1	eukaryotic translation elongation factor 1 alpha 1	171361	Rn.144660	NM_033539	12.11	12.16	12.20	12.29	12.33	12.38	1.13	up	9.58E-03	8.95E-01	-	-
1372339_at	Cdc26	cell division cycle 26	366381	Rn.203072	BM387151	5.10	4.61	4.96	4.64	4.91	5.66	1.13	up	6.30E-01	8.95E-01	-	-
1381825_at	RGD1303271	similar to chromosome 1 open reading frame 172	313018	Rn.106844	BM385475	3.45	3.59	3.59	3.98	3.60	3.58	1.13	up	2.68E-01	8.95E-01	-	-
1368809_at	Cap1	CAP, adenylate cyclase-associated protein 1 (yeast)	64185	Rn.112585	BG380723	7.23	7.58	6.69	7.15	6.42	7.39	1.13	down	6.74E-01	9.01E-01	-	-
1385365_at	Extl1	exostoses (multiple)-like 1	313610	Rn.50146	BI289035	2.60	2.57	2.61	2.53	2.68	3.10	1.13	up	3.53E-01	8.95E-01	-	-
1398882_at	Rps5	ribosomal protein S5	25538	Rn.203028	BI282255	9.06	9.31	9.77	9.19	9.36	10.13	1.13	up	6.47E-01	8.95E-01	-	-
1390441_at	Asap1	ArfGAP with SH3 domain, ankyrin repeat and PH domain 1	314961	Rn.63466	AW527409	2.48	2.56	2.99	2.50	2.50	2.50	1.13	down	3.24E-01	8.95E-01	-	-
1391333_at	Lrrfip2	Leucine rich repeat (in FLII) interacting protein 2	301035	Rn.20528	AI602218	3.01	3.02	3.07	3.06	3.06	3.50	1.13	up	3.00E-01	8.95E-01	-	-
1397955_at	Rtel1	regulator of telomere elongation helicase 1	362288	Rn.98315	BF409660	5.40	5.99	5.12	6.16	5.19	5.70	1.13	up	6.66E-01	8.99E-01	-	-
1389703_at	Zzef1	Zinc finger, ZZ-type with EF hand domain 1	287476	Rn.24218	BI295225	4.87	4.57	4.36	4.51	4.41	4.34	1.13	down	3.18E-01	8.95E-01	-	-
1370129_at	Mgea5	meningioma expressed antigen 5 (hyaluronidase)	154968	Rn.162539	NM_131904	5.84	5.94	4.92	4.93	5.43	5.81	1.13	down	6.92E-01	9.05E-01	-	-
1381737_at	---	---	---	Rn.208667	BF404993	3.08	2.37	2.38	2.37	2.37	2.55	1.13	down	5.08E-01	8.95E-01	-	-
1381984_at	---	---	---	Rn.24648	AI600142	6.98	7.06	7.29	6.76	7.01	7.03	1.13	down	2.37E-01	8.95E-01	-	-
1374032_at	Phf12	PHD finger protein 12	303274	Rn.101513	AA998886	4.13	4.38	4.42	4.18	3.78	4.44	1.13	down	4.51E-01	8.95E-01	-	-
1390864_at	Tmem116	transmembrane protein 116	690442	Rn.39141	AI410837	2.79	2.92	2.95	2.75	3.42	3.02	1.13	up	4.33E-01	8.95E-01	-	-
1372135_at	LOC684352	similar to twinfilin-like protein	684352	Rn.220779	AI171452	3.34	2.67	2.67	2.67	2.82	2.66	1.13	down	4.85E-01	8.95E-01	-	-
1398481_at	---	---	---	Rn.172254	BF402699	4.15	4.65	4.99	4.60	5.08	4.64	1.13	up	5.71E-01	8.95E-01	-	-
1379676_a_at	Dnase1l1	deoxyribonuclease 1-like 1	363522	Rn.163455	AW527320	3.90	4.30	3.90	3.91	3.95	4.77	1.13	up	6.03E-01	8.95E-01	-	-
1371319_at	Itm2b	integral membrane protein 2B	290364	Rn.107335	BF282337	10.21	10.77	10.14	10.45	10.45	10.75	1.13	up	4.72E-01	8.95E-01	-	-
1389042_at	LOC684035	similar to arginyl aminopeptidase (aminopeptidase B)-like 1	684035	---	AI030916	6.43	6.40	6.41	6.42	6.74	6.59	1.13	up	1.33E-01	8.95E-01	-	-
1399091_at	Capzb	capping protein (actin filament) muscle Z-line, beta	298584	Rn.105999	AI232101	7.97	8.48	8.04	7.98	7.90	8.09	1.13	down	3.55E-01	8.95E-01	-	-
1375896_at	Als2cr2	amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 2 (hu	501146	Rn.17696	BM392055	8.13	7.57	7.43	7.37	7.44	7.79	1.13	up	5.16E-01	8.95E-01	-	-
1384285_at	03-Mar	membrane-associated ring finger (C3HC4) 3	364878	Rn.203312	BI298096	2.88	4.45	5.96	4.43	4.55	4.84	1.13	up	8.54E-01	9.55E-01	-	-
1371711_at	Reep5	receptor accessory protein 5	364838	Rn.40477	AA800689	7.45	7.79	7.37	7.55	7.12	8.47	1.13	up	6.96E-01	9.06E-01	-	-
1377453_at	RGD1309108	similar to hypothetical protein FLJ23554	315578	Rn.218122	BF408616	2.39	2.37	2.90	2.38	2.39	2.36	1.13	down	3.67E-01	8.95E-01	-	-
1387023_at	Gstm7	glutathione S-transferase, mu 7	81869	Rn.6036	NM_031154	8.33	7.86	7.98	7.86	8.05	7.73	1.13	down	3.54E-01	8.95E-01	-	-
1385793_at	---	---	---	Rn.204066	AI045120	2.76	2.66	3.56	2.81	2.85	2.80	1.13	down	5.68E-01	8.95E-01	-	-
1368665_at	Ufd1l	ubiquitin fusion degradation 1 like (yeast)	84478	Rn.11946	NM_053418	6.33	7.32	7.13	7.62	6.74	6.94	1.13	up	6.85E-01	9.03E-01	-	-
1390278_at	Tra2a	transformer-2 alpha	500116	Rn.220184	BI279652	5.48	4.42	4.67	5.52	5.73	3.86	1.13	up	8.07E-01	9.38E-01	-	-
1387083_at	Clf1	cardiotrophin 1	29201	Rn.10253	NM_017129	6.41	7.03	7.15	7.04	6.75	6.29	1.13	down	6.08E-01	8.95E-01	-	-
1373626_at	---	---	---	Rn.164897	AI102507	4.89	4.54	5.12	4.69	4.25	5.07	1.13	down	5.77E-01	8.95E-01	-	-
1380024_at	---	---	---	Rn.177202	BI282175	2.51	3.06	2.54	2.51	2.55	2.52	1.13	down	3.81E-01	8.95E-01	-	-
1390913_at	---	---	---	Rn.25454	AW435463	3.37	3.40	4.07	3.13	3.55	3.62	1.13	down	5.59E-01	8.95E-01	-	-
1369938_at	Pank4	pantothenate kinase 4	171053	Rn.17321	NM_133531	4.35	4.00	4.12	4.00	4.02	3.92	1.13	down	1.76E-01	8.95E-01	-	-
1397161_a_at	Itsn1	intersectin 1 (SH3 domain protein)	29491	Rn.48657	AF132672	2.96	2.94	3.13	2.60	2.96	2.94	1.13	up	2.54E-01	8.95E-01	-	-
1398367_at	Spop	speckle-type POZ protein	287643	Rn.162165	BF283504	5.74	5.57	6.23	5.32	5.91	5.78	1.13	down	5.46E-01	8.95E-01	-	-
1388575_at	---	---	---	Rn.4180	AA943740	5.82	6.38	7.17	6.25	6.83	6.81	1.13	up	7.07E-01	9.08E-01	-	-
1372562_at	MGC94207	similar to RIKEN cDNA C030006K11	362946	Rn.140158	AI236816	7.33	7.08	7.12	7.15	6.69	7.16	1.13	down	3.67E-01	8.95E-01	-	-
1388135_at	Rpa2	replication protein A2	59102	Rn.40389	BM385924	2.76	3.16	2.76	2.74	2.88	3.58	1.13	up	5.80E-01	8.95E-01	-	-
1398905_at	Atp6v1g1	ATPase, H transporting, lysosomal V1 subunit G1	298103	Rn.82724	BI285183	9.74	9

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1387372_at	Slc6a13	solute carrier family 6 (neurotransmitter transporter, GABA), member 13	171163	Rn.10527	NM_133623	6.94	7.69	6.82	7.35	7.42	7.21	1.13	up	5.63E-01	8.95E-01	-	-
1389875_at	Znrf1	Zinc and ring finger 1	362367	Rn.32245	AI227951	5.21	4.37	4.73	4.36	4.64	4.78	1.13	down	5.54E-01	8.95E-01	-	-
1376340_a_at	Tasc4	tumor suppressing subtransferable candidate 4	361682	Rn.18732	BI282086	7.23	7.77	8.40	7.38	7.79	7.70	1.13	down	6.51E-01	8.97E-01	-	-
1391435_at	Pltp	phospholipid transfer protein	296371	Rn.117434	BI278687	2.48	2.43	2.48	2.48	3.02	2.42	1.13	up	4.09E-01	8.95E-01	-	-
1373874_at	Sgpp1	sphingosine-1-phosphate phosphatase 1	81536	Rn.8423	AI169638	9.20	9.44	9.41	9.43	9.34	9.80	1.13	up	3.33E-01	8.95E-01	-	-
1375463_at	---	---	---	Rn.164798	BG380847	3.63	5.20	3.63	4.65	3.86	4.48	1.13	up	7.78E-01	9.28E-01	-	-
1385975_at	---	---	---	Rn.21405	AA859916	2.70	2.68	2.69	2.72	3.18	2.68	1.13	up	3.42E-01	8.95E-01	-	-
1382978_at	---	---	---	Rn.217668	AA955691	4.06	4.60	3.44	4.25	3.97	3.36	1.13	down	7.05E-01	9.08E-01	-	-
1392813_at	---	---	---	Rn.76633	AI548994	9.90	10.04	9.83	10.05	9.69	10.56	1.13	up	5.36E-01	8.95E-01	-	-
1392203_at	---	---	---	---	AI029834	4.39	4.71	4.18	4.17	4.81	4.82	1.13	up	5.46E-01	8.95E-01	-	-
1378836_at	Alkbh5	AlkB, alkylation repair homolog 5 (E. coli)	303193	Rn.146441	AW533596	3.77	3.37	3.67	3.46	3.44	3.40	1.13	down	2.29E-01	8.95E-01	-	-
1375081_at	Nt5m	5',3'-nucleotidase, mitochondrial	287368	Rn.2189	AA819763	2.45	2.38	3.86	2.62	2.93	2.62	1.13	down	7.42E-01	9.17E-01	-	-
1385779_at	Chd4	chromodomain helicase DNA binding protein 4	117535	Rn.63247	BF413917	6.76	5.79	6.60	6.54	6.26	5.82	1.13	down	6.59E-01	8.98E-01	-	-
1382916_at	---	---	---	Rn.55900	AI179520	3.04	3.02	3.04	3.06	3.55	3.01	1.13	up	3.66E-01	8.95E-01	-	-
1384304_at	---	---	---	Rn.169460	AW524615	2.63	2.62	2.63	2.62	3.17	2.61	1.13	up	4.01E-01	8.95E-01	-	-
1387342_at	Gng5	guanine nucleotide binding protein (G protein), gamma 5	79218	Rn.2695	NM_024377	7.92	7.99	8.01	8.01	8.26	8.18	1.13	up	8.40E-02	8.95E-01	-	-
1392525_at	---	---	---	Rn.203034	AA859437	2.50	2.49	2.50	3.02	2.50	2.49	1.13	up	3.81E-01	8.95E-01	-	-
1377558_at	---	---	---	Rn.209116	BF393165	2.86	3.67	2.70	2.86	2.89	2.96	1.13	down	5.94E-01	8.95E-01	-	-
1395532_at	LOC688018	Similar to SH3-domain binding protein 3	688018	Rn.162688	AI137456	8.59	9.15	8.78	7.91	8.78	9.31	1.13	down	7.13E-01	9.10E-01	-	-
1377351_at	Susd3	sushi domain containing 3	306810	Rn.3005	AI407337	7.29	7.55	7.54	7.50	7.88	7.53	1.13	up	3.08E-01	8.95E-01	-	-
1371911_at	Tnfaip1	tumor necrosis factor, alpha-induced protein 1 (endothelial)	287543	Rn.18199	BM390023	8.39	8.13	7.17	8.14	8.11	7.96	1.13	up	6.68E-01	9.00E-01	-	-
1386867_at	Brp44l	brain protein 44-like	171087	Rn.3718	NM_133561	9.88	9.22	9.38	9.32	9.19	9.44	1.13	down	4.57E-01	8.95E-01	-	-
1386554_at	---	---	---	---	BF567806	2.61	2.44	2.97	2.52	2.53	2.44	1.13	down	3.41E-01	8.95E-01	-	-
1379177_at	Mmp28	matrix metallopeptidase 28 (epilysin)	303384	Rn.60472	BF404294	3.92	4.21	3.59	2.69	5.13	3.39	1.13	down	8.27E-01	9.45E-01	-	-
1372445_at	Srp9	signal recognition particle 9	690345	Rn.7477	AI171783	6.82	7.27	7.05	7.09	6.91	7.66	1.13	up	5.39E-01	8.95E-01	-	-
1388888_at	---	---	---	---	BI274615	2.96	2.38	3.59	3.05	2.56	2.80	1.13	down	6.68E-01	9.00E-01	-	-
1391213_at	/C300429 /// Ppp3	similar to Calcineurin subunit B isoform 1 (Protein phosphatase 2B regulatory	29748 /// 300429	Rn.42903	BF416151	2.85	2.34	2.36	2.34	2.35	2.34	1.13	down	3.58E-01	8.95E-01	-	-
1394678_at	Fgd2	FYVE, RhoGEF and PH domain containing 2	309653	Rn.89444	AI411563	3.05	2.51	2.52	2.51	2.54	2.50	1.13	down	3.83E-01	8.95E-01	-	-
1367967_at	Lepre1	leucine proline-enriched proteoglycan (leprecan) 1	114200	Rn.13741	NM_053687	2.46	2.76	2.62	2.73	2.80	2.83	1.13	up	1.32E-01	8.95E-01	-	-
1373941_at	Yeats2	YEATS domain containing 2	498112	Rn.7090	BE103152	6.29	6.06	6.09	5.92	5.81	6.20	1.13	down	2.88E-01	8.95E-01	-	-
1374765_at	---	---	---	Rn.169535	BI288055	4.31	4.92	5.84	4.91	4.31	5.33	1.13	down	7.62E-01	9.22E-01	-	-
1367884_at	Rab14	RAB14, member RAS oncogene family	94197	Rn.6008	NM_053589	7.12	7.92	7.39	7.47	7.76	7.73	1.13	up	5.29E-01	8.95E-01	-	-
1398883_at	hpa2b1 /// LOC685	heterogeneous nuclear ribonucleoprotein A2/B1 /// hypothetical protein LOC6	362361 /// 685548	Rn.4057	BI296284	10.84	10.59	10.61	10.51	10.70	10.32	1.13	down	2.70E-01	8.95E-01	-	-
1392856_at	Serf1	small EDRK-rich factor 1	502503	Rn.67679	AI549470	2.45	2.49	2.50	2.52	2.50	2.94	1.13	up	2.95E-01	8.95E-01	-	-
1392985_at	Arih1	ariadne ubiquitin-conjugating enzyme E2 binding protein homolog 1 (Drosoph	300756	Rn.29865	BF555731	3.78	3.88	3.63	3.50	3.63	3.65	1.13	down	1.16E-01	8.95E-01	-	-
1380939_at	---	---	---	Rn.172802	BE118701	2.92	2.39	2.41	2.40	2.41	2.40	1.13	down	3.78E-01	8.95E-01	-	-
1395145_at	Rgl1	ral guanine nucleotide dissociation stimulator,-like 1	289080	Rn.28005	BF544481	6.20	6.55	5.79	5.63	6.03	6.37	1.13	down	6.01E-01	8.95E-01	-	-
1373336_at	Gprc5b	G protein-coupled receptor, family C, group 5, member B	293546	Rn.47330	AI411074	2.66	2.65	2.68	3.25	2.66	2.59	1.13	up	4.55E-01	8.95E-01	-	-
1382242_at	Zfp451	zinc finger protein 451	316312	Rn.163059	BE105280	5.32	4.82	5.79	5.31	5.05	6.10	1.13	up	7.01E-01	9.07E-01	-	-
1390214_a_at	Ciz1	CDKN1A interacting zinc finger protein 1	296639	Rn.65696	BI284812	5.00	5.54	5.32	5.65	5.45	5.29	1.13	up	4.09E-01	8.95E-01	-	-
1381619_at	---	---	---	Rn.205246	BE116003	3.19	3.97	2.74	3.10	3.26	4.06	1.13	up	7.28E-01	9.13E-01	-	-
1375245_at	Ppp2r1a	protein phosphatase 2 (formerly 2A), regulatory subunit A, alpha isoform	117281	Rn.4108	AA800869	7.62	8.52	8.63	8.05	8.22	7.97	1.13	down	6.24E-01	8.95E-01	-	-
1372617_at	Btbd2	BTB (POZ) domain containing 2	500793	Rn.137561	BM385989	2.60	3.10	2.64	3.13	2.66	3.07	1.13	up	4.69E-01	8.95E-01	-	-
1383229_at	Abca7	ATP-binding cassette, sub-family A (ABC1), member 7	299609	Rn.25281	BE103071	5.43	6.61	6.05	5.61	5.98	5.98	1.13	down	6.59E-01	8.98E-01	-	-
1378191_at	Ndrp1	N-myc downstream regulated gene 1	298075	Rn.13482	AI549102	9.05	9.06	9.52	9.05	9.02	9.04	1.13	down	3.28E-01	8.95E-01	-	-
1387514_at	Cbwd1	COBW domain containing 1	171057	Rn.49017	NM_133535	2.70	3.02	2.70	2.67	2.54	2.69	1.13	down	2.11E-01	8.95E-01	-	-
1375390_at	RGD1305422	similar to mKIAA0226 protein	303885	Rn.198268	BI296459	2.34	2.85	2.35	2.34	2.34	2.33	1.13	down	3.62E-01	8.95E-01	-	-
1368747_at	Nup98	nucleoporin 98kDa	81738	Rn.11324	NM_031074	2.49	3.07	2.50	2.48	2.49	2.57	1.13	down	4.27E-01	8.95E-01	-	-
1372899_at	---	---	---	Rn.153853	AI704683	2.34	2.99	2.82	2.87	2.93	2.87	1.13	up	4.24E-01	8.95E-01	-	-
1385536_at	---	---	---	Rn.138175	AI454433	2.97	2.46	2.53	2.49	2.51	2.44	1.13	down	3.44E-01	8.95E-01	-	-
1383780_at	Hedd1	HECT domain containing 1	362736	Rn.36797	BF563800	3.65	4.43	5.92	4.78	4.99	4.75	1.13	up	8.08E-01	9.38E-01	-	-
1374077_at	---	---	---	---	AI172029	2.33	2.69	2.29	2.51	2.52	2.81	1.13	up	3.43E-01	8.95E-01	-	-
1382917_at	---	---	---	Rn.165986	AI043869	9.09	8.29	7.73	8.67	8.22	8.74	1.13	up	7.06E-01	9.08E-01	-	-
1388156_at	Plcb3	phospholipase C, beta 3 (phosphatidylinositol-specific)	29322	Rn.16983	AW526098	2.93	2.39	2.41	2.41	2.41	2.40	1.13	down	3.83E-01	8.95E-01	-	-
1368452_at	Abcc8	ATP-binding cassette, sub-family C (CFTR/MRP), member 8	81642	Rn.29976	NM_031013	4.56	5.57	4.30	4.91	4.44	4.56	1.13	down	6.98E-01	9.07E-01	-	-
1385260_at	---	---	---	Rn.125849	BE103057	3.85	2.94	3.00	3.54	2.97	2.76	1.13	down	6.68E-01	9.00E-01	-	-
1371543_at	Mtmr2	myotubularin related protein 2	315422	Rn.6511	AI170047	7.18	6.98	7.95	6.80	7.52	7.27	1.13	down	6.80E-01	8.98E-01	-	-
1379457_at	Nedd1	neural precursor cell expressed, developmentally down-regulated 1	299730	Rn.23035	AI013407	2.52	2.84	2.65	2.67	2.78	3.08	1.13	up	3.22E-01	8.95E-01	-	-
1372613_at	Bdh2	3-hydroxybutyrate dehydrogenase, type 2	295458	Rn.3651	AI232784	8.71	8.57	8.08	7.91	8.61	8.32	1.13	down	5.68E-01	8.95E-01	-	-
1393354_at	---	---	---	Rn.19111	BE097947	5.12	5.05	6.52	5.84	5.31	5.03	1.13	down	7.61E-01	9.22E-01	-	-
1375338_at	Rab10	RAB10, member RAS oncogene family	50993	Rn.65864	AA945841	5.74	6.39	6.77	7.03	6.17	6.22	1.13	up	6.94E-01	9.06E-01	-	-
1376094_at	Hint3	histidine triad nucleotide binding protein 3	246769	Rn.9467	AA925490	4.26	4.97	3.21	4.10	4.12	4.74	1.13	up	7.69E-01	9.25E-01	-	-
1398359_at	Rnf181	ring finger protein 181	297337	Rn.94883	AI008549	7.97	7.79	8.13	7.53	7.44	8.41	1.13	down	6.21E-01	8.95E-01	-	-
1384706_at	Peli2	pellino 2	305835	Rn.210929	BF406292	2.82	3.32	2.82	2.83	2.81	2.81	1.13	down	3.58E-01	8.95E-01	-	-
1390218_at	RGD1310440	similar to hypothetical protein	362594	Rn.13608	BI295650	3.82	3.58	2.71	3.34	3.62	3.66	1.13	up	6.47E-01	8.95E-01	-	-
1387851_at	Pter	phosphotriesterase related	63852	Rn.44484	NM_022224	9.94	10.53	10.35	10.11	9.92	10.27	1.13	down	4.43E-01	8.95E-01	-	-
1378760_at	RGD1311066	similar to RIKEN cDNA 0610011L14 gene	296312	Rn.52749	BF407639	2.72	2.46	2.68	2.47	2.33	2.54	1.13	down	1.59E-01	8.95E-01	-	-
1385098_at	---	---	---	Rn.46170	AW526343	2.58	2.55	2.76	2.59	3.18	2.64	1.13	up	4.37E-01	8.95E-01	-	-
1389405_at	LOC680231	similar to chromodomain helicase DNA binding protein 9	680231	Rn.165696	BG378880	6.02	6.95	6.89	7.08	6.00	6.27	1.13	down	7.16E-01	9.10E-01	-	-
1392937_at	Ccni	cyclin I	299310	Rn.6670	BF557327	7.91	8.39	7.75	8.11	7.74	7.68	1.13	down	5.01E-01	8.95E-01	-	-
1387294_at	Sh3bp5	SH3-domain binding protein 5 (BTK-associated)	117186	Rn.163321	NM_054011	8.56	8.45	8.08	7.73	8.42	8.43	1.13	down	5.65E-01	8.95E-01	-	-
1396049_x_at	OC499207 /// Rpl	similar to 60S ribosomal protein L3 (L4) /// ribosomal protein L3	300079 /// 499207	Rn.107726	BG057530	4.91	4.74	5.15	5.06	5.24	5.02	1.13	up	2.78E-01	8.95E-01	-	-
1371311_at	Sdhc	succinate dehydrogenase complex, subunit C, integral membrane protein	289217	Rn.1698	AI009817	10.65	10.68	10.61	10.35	10.43	10.64	1.13	down	1.28E-01	8.95E-01	-	-
1386494_at	Orai3	ORAI calcium release-activated calcium modulator 3	309000	Rn.42186	AA891139	3.83	3.10	3.36	3.23	3.43	3.11	1.13	down	5.01E-01	8.95E-01	-	-
1378501_at	LOC688616	similar to gem (nuclear organelle) associated protein 5	688616	---	BE113386	5.12	4.85	4.39	4.79	4.91	5.17	1.13	up	5.13E-01	8.95E-01	-	-
1389066_at	Rcan2	regulator of calcineurin 2	140666	Rn.24428	BI274408	8.23	8.23	8.20	8.10	7.88	8.16	1.13	down	1.17E-01	8.95E-01	-	-
1393185_at	p271 /// LOC6919	centrosomal protein 27 like /// similar to Centrosomal protein of 27 kDa (Cep2	292105 /// 691918	Rn.162678	BF283249	4.61	3.57	4.59	4.53	4.48	4.28	1.13	up	6.47E-01	8.95E-01	-	-
1389126_at	Chchd1	coiled-coil-helix-coiled-coil-helix domain containing 1	361005	Rn.2620	BG373580	9.15	8.77	9.84	8.90	8.96	9.37	1.13	down	6.43E-01	8.95E-01	-	-
1397730_at	RGD1307235	similar to RIKEN cDNA 2310035C23	309053	Rn.38292	C08959	9.03	8.06	7.52	8.37	8.15	7.58	1.13	down	7.48E-01	9.18E-01	-	-
1378302_at	---	---	---	Rn.155862	BF403965	8.47	8.88	8.63	8.50	8.44	8.52	1.13	down	2.26E-01	8.95E-01	-	-
1388895_at	---	---	---	Rn.207309	BG376886	2.54	2.51	2.54	3.06	2.53	2.51	1.13	up	3.91E-01	8.95E-01	-	-
1392710_at	---	---	---	Rn.203218	AI101727	8.99	8.59	8.51	8.62	8.12	8.84	1.13	down	5.44E-01	8.95E-01	-	-
1372497_at	Nbr1	neighbor of Brca1 gene 1	303554	Rn.94975	AI104094	9.54	9.97	10.04	9.96	9.95	10.16	1.13	up	3.70E-01	8.95E-01	-	-
1390771_at	Rarg	retinoic acid receptor, gamma	685072	Rn.198797	BI298646	2.44	2.50	2.45	3.06	2.44	2.40	1.13	up	4.65E-01	8.95E-01	-	-
1377214_a_at	RGD1303117	hypothetical protein LOC292764	292764	Rn.12517	BF405050	4.78	5.14	4.77	4.82	4.99	5.40	1.13	up	4.62E-01	8.95E-01	-	-
1372391_at	Rpl7l1	ribosomal protein L7-like 1	317275	Rn.102202	AI598937	6.80	6.81	6.09	6.53	6.74	6.94	1.13	up	5.55E-01	8.95E-01	-	-
1378303_at	Tnrc6b	trinucleotide repeat containing 6B	192178	Rn.17120	BE109416	2.50	2.60	2.66	2.76	2.84	2.68	1.13	up	6.28E-02	8.95E-01	-	-
1397350_at	LOC498029	similar to RIKEN cDNA A730011L01 gene	498029	Rn.138712	BE096697	4.22	3.84	5.29	4.39	4.18	4.26	1.13	down	7.14E-01	9.10E-01	-	-
1367638_at	Mlycd	malonyl-CoA decarboxylase	85239	Rn.13468	NM_053477	8.07	8.54	7.73	8.05	7.77	8.01	1.13	down	5.32E-01	8.95E-01	-	-
1382730_at	---	---	---	Rn.167257	AI233825	3.00	2.63	3.13	2.92	2.43	2.89	1.13	down	4.77E-01	8.95E-01	-	-
1369899_s_at	Rabggta	Rab geranylgeranyltransferase, alpha subunit	58983	Rn.29434	NM_013020	4.14	4.79	3.04	4.38	3.83	4.28	1.13	up	7.65E-01	9.23E-01	-	-
1375249_at	Eif2c1	eukaryotic translation initiation factor 2C, 1	313594	Rn.62413	BE109033	3.35	3.69	3.10	3.35	3.88	3.42	1.13	up	5.06E-01	8.95E-01	-	-
1398126_at	---	---	---	Rn.199674	AW529975	2.47	2.47	2.49	3.03	2.48	2.44	1.13	up	4.15E-01	8.95E-01	-	-
1381807_at	---	---	---	Rn.41599	BM383408	2.21	2.92	2.66	2.46	2.48	2.34	1.13	down	4.66E-01	8.95E-01	-	-
1379825_at	---	---	---	Rn.40322	AI112993	3.62	4.95	5.69	4.46	5.21	5.10	1.13	up	8.04E-01	9.37E-01	-	-
1372348_at	Aak1	AP2 associated kinase 1	500244	Rn.203307	AI104502	6.16	6.52	6.09	5.73	6.58	5.95	1.13	down	5.81E-01	8.95E-01	-	-
1389927_at	Zmiz1	zinc finger, MIZ-type containing 1	361103	Rn.1712	BI303536	3.41	3.42	3.41	3.51	3.44	3.80	1.13	up	1.95E-01	8.95E-01	-	-
1373310_at	---	---	---	Rn.33629	BF396512	7.14	7.73	6.58	7.36	7.14	7.47	1.13	up	6.45E-01	8.95E-01	-	-
1390650_at	Nup85	nucleoporin 85kDa	287830	Rn.198900	BI290593	3.30	3.53	3.38	3.57	3.72	3.45	1.13	up	1.66E-01	8.95E-01	-	-
1373265_at	Exoc6b	exocyst complex component 6B	500233	Rn.95210	BM383832	2.74	2.76	2.55	3.04	2.77	2.76	1.13	up	2.07E-01	8.95E-01	-	-
1387695_at	Cdo42bpb	CDC42 binding protein kinase beta (DMPK-like)	113960	Rn.105815	AF021936	4.79	5.26	4.81	4.76	4.83	4.75	1.13	down	3.33E-01	8.95E-01	-	-
1397075_at	---	---	---	Rn.149157	BF405312	2.33	2.78	2.31	2.30	2.31	2.29	1.13	down	3.28E-01	8.95E-01	-	-
1373794_at	Egln2	EGL nine homolog 2 (C. elegans)	308457	Rn.43384	BE329050	9.61	9.28	8.48	8.95	9.15	8.75	1.13	down	6.54E-01	8.97E-01	-	-
1397563_at	---	---	---	Rn.169331	AW522171	4.40	4.19	4.22	4.72	4.15	4.45	1.13	up	3.82E-01	8.95E-01	-	-
1395872_at	---	---	---	Rn.171693	BF395768	2.52	2.52	3.03	2.52	2.53	2.50	1.13	down	3.71E-01	8.95E-01	-	-
1373895_at	---	---	---	Rn.199403	BE118440	8.86	8.28	7.99	8.38	8.12	8.12	1.13	down	5.60E-01	8.95E-01	-	-
1378759_at	---	---	---	Rn.207547	BE102644	3.03	2.53	2.58	2.53	2.57	2.52	1.13	down	3.38E-01	8.95E-01	-	-
1376678_at	Apbb2	amyloid beta (A4) precursor protein-binding, family B, member 2	305338	Rn.24283	BF283712	4.61	4.79	3.68	4.70	3.79	4.07	1.13	down	7.15E-01	9.10E-01	-	-
1381496_x_at	---	---	---	Rn.125958	BF420742	4.74	5.50	4.78	4.77	5.21	5.57	1.13	up	6.38E-01	8.95E-01	-	-
1378588_at	---	---	---	---	AW527143	3.02	2.54	2.56	2.53	2.53	2.53	1.13	down	3.37E-01	8.95E-01	-	-
1376312_a_at	---	---	---	Rn.199128	BI284236	8.35	8.89	8.48	8.36	8.08	8.77	1.13	down	5.42E-01	8.95E-01	-	-
1388974_at	Srp19	signal recognition particle 19	291685	Rn.116072	AI101527	8.25	8.28	8.14	8.73	8.12	8.33	1.13	up	4.02E-01	8.95E-01	-	-
1390212_at	Nup82	nucleoporin like 2	499974	Rn.13647	BI287987	4.05	4.24	4.50	4.35	4.72	4.24	1.13	up	4.28E-01	8.95E-01	-	-
1367488_at	Ankrd17	ankyrin repeat domain 17	289521	Rn.8442	BM386411	5.62	5.97	5.42	5.50	5.41	5.59	1.13	down	3.64E-01	8.95E-01	-	-
1390941_at	Rbbp6	retinoblastoma binding protein 6	308968	Rn.95305	BI277540	7.32	7.46	7.11	7.13	6.50	7.75	1.13	down	6.72E-01	9.01E-01	-	-
1391710_at	---	---	---	---	AW251144	2.37	2.33	2.37	2.84	2.40	2.35	1.13	up	3.31E-01	8.95E-01	-	-
1383633_at	---	---	---	Rn.216679	BI289884	8.41	8.97	8.75	8.69	8.61	8.32	1.13	down	4.32E-01	8.95E-01	-	-
1367766_at	Nme2	non-metastatic cells 2, protein (NM23B) expressed in	83782	Rn.927	NM_031833	11.12	11.29	11.45	11.40	11.49	11.49	1.13	up	1.68E-01	8.95E-01	-	-
1373015_at	LOC683844	similar to RING finger protein 11 (NEDD4 WW domain-binding protein 2) (Sid	683844	---	BI280348	6.12	6.66	6.24	6.41	6.23	6.90	1.13	up	5.43E-01	8.95E-01	-	-
1390026_at	Bag3	Bcl2-associated athanogene 3	293524	Rn.46304	AI231752	5.80	6.14	6.04	6.26	5.57	5.64	1.13	down	5.15E-01	8.95E-01	-	-
1383969_at	---	---	---	Rn.47393	BI294901	2.90	2.41	2.44	2.41	2.43	2.40	1.13	down	3.46E-01	8.95E-01	-	-
1367716_at	Itfg1	integrin alpha FG-GAP repeat containing 1	171083	Rn.3622	NM_133557	7.08	7.50	7.28	7.15	7.20	6.99	1.13	down	2.80E-01	8.95E-01	-	-
1370217_at	Ddr1	discoidin domain receptor tyrosine kinase 1	25678	Rn.7807	L26525	5.91	6.35	6.49	6.39	6.17	6.71	1.13	up	5.06E-01	8.95E-01	-	-
1391448_at	Crim1	cysteine rich transmembrane BMP regulator 1 (chordin like)	298744	Rn.54364	BI289620	5.47	5.79	4.60	5.21	5.12	5.02	1.13	down	6.59E-01	8.98E-01	-	-
1391803_at	---	---	---	Rn.12095	BF557813	2.56	2.56	2.57	2.57	3.09	2.55	1.13	up	3.87E-01	8.95E-01	-	-
1368861_at	H2afz	H2A histone family, member Z	58940	Rn.112573	NM_022674	9.62	10.12	9.83	10.01	9.78	10.30	1.13	up	4.59E-01	8.95E-01	-	-
1389055_at	Ppie	peptidylprolyl isomerase E (cyclophilin E)	298508	Rn.16887	AI104479	8.40	7.68	7.23	7.99	7.95	7.89	1.13	up	6.44E-01	8.95E-01	-	-
1394633_at	Lima1	LIM domain and actin binding 1	300228	Rn.135294	BF288321	2.40	2.32	2.35	2.40	2.79	2.39	1.13	up	2.71E-01	8.95E-01	-	-
1369508_at	Kcnj15	potassium inwardly-rectifying channel, subfamily J, member 15	170847	Rn.81918	NM_133321	5.80	6.84	5.52	5.75	6.67	6.24	1.13	up	7.40E-01	9.16E-01	-	-
1396020_at	---	---	---	Rn.208861	BE120584	2.38	2.38	2.39	2.90	2.39	2.38	1.13	up	3.78E-01	8.95E-01	-	-
1377885_at	LOC685203	hypothetical protein LOC685203	685203	Rn.20787	BI281851	4.24	4.15	5.06	3.96	4.89	4.09	1.13	down	6.97E-01	9.07E-01	-	-
1398370_at	Adarb1	adenosine deaminase, RNA-specific, B1	25367	Rn.89675	AW522471	4.16	3.85	6.83	4.87	4.23	5.23	1.13	down	8.71E-01	9.60E-01	-	-
1372847_at	Acn9	ACN9 homolog (S. cerevisiae)	362323	Rn.101965	AW524458	7.31	6.78	6.21	7.02	6.77	7.03	1.13	up	6.29E-01	8.95E-01	-	-
1384356_at	Fam151b	family with sequence similarity 151, member B	499507	Rn.115871	AW141967	2.52	2.48	2.52	2.50	2.69	2.85	1.13	up	1.69E-01	8.95E-01	-	-
1388476_at	Tial1	Tia1 cytotoxic granule-associated RNA binding protein-like 1	361655	Rn.162475	AI101391	6.22	6.00	5.42	6.21	5.85	6.09	1.13	up	5.47E-01	8.95E-01	-	-
1367702_at	Acadm	acyl-Coenzyme A dehydrogenase, C-4 to C-12 straight chain	24158	Rn.6302	NM_016986	10.23	10.22	10.26	10.34	9.65	10.21	1.13	down	4.66E-01	8.95E-01	-	-
1374793_at	Wdr3	WD repeat domain 3	310720	Rn.12973	BE113663	4.84	4.57	4.95	4.87	5.10	4.90	1.13	up	2.78E-01	8.95E-01	-	-
1373669_at	Grpda2	glucosamine-6-phosphate deaminase 2	289608	Rn.219279	BG374650	2.86	3.42	2.51	2.98	3.53	2.80	1.13	up	6.46E-01	8.95E-01	-	-
1385497_x_at	Lnx1	ligand of numb-protein X 1	360926	Rn.25032	AW522661	2.52

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1388767_at	Pdcd6	programmed cell death 6	308061	Rn.104071	BI296393	7.13	7.48	7.73	6.67	7.53	7.63	1.12	down	6.53E-01	8.97E-01	-	-
1374809_at	---	---	---	Rn.16806	BG672598	6.25	5.96	6.76	5.89	6.87	6.71	1.12	up	6.80E-01	9.03E-01	-	-
1384663_at	---	---	---	---	AI690195	2.70	2.36	2.49	2.57	2.65	2.83	1.12	up	2.50E-01	8.95E-01	-	-
1371536_at	Carhsp1	calcium regulated heat stable protein 1	260416	Rn.14584	AI233208	5.96	6.01	5.55	6.00	6.04	5.99	1.12	up	3.11E-01	8.95E-01	-	-
1367729_at	Oat	ornithine aminotransferase (gyrate atrophy)	64313	Rn.1430	NM_022521	11.70	12.17	12.44	11.82	11.88	12.11	1.12	down	5.10E-01	8.95E-01	-	-
1376930_at	Mrpl51	mitochondrial ribosomal protein L51	297601	Rn.154504	BI294860	8.68	8.48	8.42	8.43	7.98	8.68	1.12	down	4.83E-01	8.95E-01	-	-
1373492_at	RGD1309216	similar to hypothetical protein FLJ20487	361726	Rn.102071	AA964545	10.44	10.43	10.57	10.35	10.23	10.36	1.12	down	5.13E-02	8.95E-01	-	-
1384060_at	Jak1	Janus kinase 1	84598	Rn.90191	BG663208	4.96	6.06	4.70	5.41	4.38	5.44	1.12	down	7.70E-01	9.25E-01	-	-
1392399_at	Wdsof1	WD repeats and SOF1 domain containing	362902	Rn.41457	BG377835	8.17	8.35	8.35	8.56	8.58	8.23	1.12	up	2.59E-01	8.95E-01	-	-
1367550_a_at	Tm2d1	TM2 domain containing 1	362545	Rn.198278	BI287742	7.28	7.58	8.29	7.70	7.43	7.50	1.12	down	6.15E-01	8.95E-01	-	-
1389039_at	---	---	---	Rn.7736	BM386520	2.99	2.49	2.50	2.49	2.50	2.48	1.12	down	3.66E-01	8.95E-01	-	-
1378397_at	---	---	---	---	BM385449	3.07	3.38	2.97	3.00	2.93	2.98	1.12	down	2.56E-01	8.95E-01	-	-
1392860_at	---	---	---	---	AI046717	2.40	2.38	2.40	2.39	2.94	2.37	1.12	up	4.19E-01	8.95E-01	-	-
1383085_at	Sh3bgrl	SH3 domain binding glutamic acid-rich protein like	302363	Rn.58623	BG672648	5.26	5.97	6.01	5.75	6.18	5.83	1.12	up	5.73E-01	8.95E-01	-	-
1374470_at	Dhx57	DEAH (Asp-Glu-Ala-Asp/His) box polypeptide 57	366532	Rn.15951	AI102264	2.79	2.84	2.74	3.31	3.01	2.56	1.12	up	4.81E-01	8.95E-01	-	-
1388802_at	Bex1	brain expressed gene 1	501625	Rn.9190	AI579422	2.95	2.74	2.81	2.98	3.11	2.91	1.12	up	1.20E-01	8.95E-01	-	-
1388882_at	Fkbp3	FK506 binding protein 3	299104	Rn.1464	AA891798	11.11	11.07	10.67	11.10	11.21	11.05	1.12	up	3.16E-01	8.95E-01	-	-
1373238_at	Tada1l	transcriptional adaptor 1 (HFI1 homolog, yeast) like	360874	Rn.23978	AI234844	5.58	4.67	4.54	4.56	4.35	5.37	1.12	down	7.28E-01	9.13E-01	-	-
1391296_at	---	---	---	Rn.60795	BF405597	3.15	2.57	2.67	2.63	2.74	2.51	1.12	down	4.27E-01	8.95E-01	-	-
1373624_at	Cfdp1	craniofacial development protein 1	292027	Rn.128746	AW433973	8.07	8.44	7.95	7.99	8.24	8.73	1.12	up	5.56E-01	8.95E-01	-	-
1384668_at	---	---	---	Rn.21283	AI070299	2.38	2.37	2.27	2.34	2.73	2.45	1.12	up	2.29E-01	8.95E-01	-	-
1393914_at	Ftsj1	Ftsj homolog 1 (E. coli)	363450	Rn.100745	AI709526	2.49	2.51	2.55	2.51	2.55	3.00	1.12	up	3.51E-01	8.95E-01	-	-
1381654_at	---	---	---	Rn.59129	BF398637	2.31	2.80	2.32	2.31	2.32	2.30	1.12	down	3.58E-01	8.95E-01	-	-
1372795_at	Alkbh6	alkB, alkylation repair homolog 6 (E. coli)	292780	Rn.107346	BI279648	2.77	2.27	2.28	2.28	2.27	2.27	1.12	down	3.66E-01	8.95E-01	-	-
1375749_at	Sec3l1	SEC3-like 1 (S. cerevisiae)	305287	Rn.204678	BF404853	5.35	5.54	4.74	5.11	5.36	5.68	1.12	up	5.95E-01	8.95E-01	-	-
1387580_at	Srd5a2	steroid-5-alpha-reductase, alpha polypeptide 2 (3-oxo-5 alpha-steroid delta 4-	64677	Rn.9938	NM_022711	3.10	2.50	2.53	2.51	2.61	2.50	1.12	down	4.41E-01	8.95E-01	-	-
1382144_at	Mrpl47	mitochondrial ribosomal protein L47	294993	Rn.219103	AW520527	6.79	6.70	7.43	6.87	6.15	7.39	1.12	down	7.14E-01	9.10E-01	-	-
1390462_at	Ghdc	GH3 domain containing	303542	Rn.19984	BI281732	2.46	3.12	2.57	2.38	2.80	2.46	1.12	down	5.23E-01	8.95E-01	-	-
1388662_at	---	---	---	Rn.17619	BF392884	5.27	5.44	5.69	6.00	5.07	5.83	1.12	up	6.13E-01	8.95E-01	-	-
1382536_at	Med13l	mediator complex subunit 13-like	360817	Rn.41407	BE109224	3.01	3.10	2.48	3.00	3.09	3.00	1.12	up	4.40E-01	8.95E-01	-	-
1385398_at	Zfdb7b	zinc finger and BTB domain containing 7B	295248	Rn.73830	BF408898	2.59	2.51	2.62	2.61	2.63	2.99	1.12	up	2.55E-01	8.95E-01	-	-
1397779_at	---	---	---	Rn.162437	BF562254	2.65	3.01	2.80	2.78	3.48	2.71	1.12	up	5.66E-01	8.95E-01	-	-
1368435_at	Cyp8b1	cytochrome P450, family 8, subfamily b, polypeptide 1	81924	Rn.23013	NM_031241	2.87	2.49	2.50	2.48	2.49	2.37	1.12	down	2.64E-01	8.95E-01	-	-
1372252_at	Trappc1	trafficking protein particle complex 1	287427	Rn.2918	BE112892	6.47	7.31	7.76	7.10	7.24	7.71	1.12	up	7.09E-01	9.09E-01	-	-
1386525_at	Thoc2	THO complex 2	313308	Rn.35526	AI556851	7.25	7.19	5.79	6.39	6.34	6.99	1.12	down	7.62E-01	9.22E-01	-	-
1376482_at	Znf667	zinc finger protein 667	308326	Rn.43493	BF402458	2.61	3.43	2.63	2.61	2.98	2.58	1.12	down	6.04E-01	8.95E-01	-	-
1370520_at	LOC257650	hippyragranin	257650	Rn.204574	AF260582	2.86	3.31	4.37	2.98	3.39	3.65	1.12	down	7.47E-01	9.18E-01	-	-
1382530_at	Rnnd5a	Required for meiotic nuclear division 5 homolog A (S. cerevisiae)	312439	Rn.11791	AI044286	6.86	7.30	7.07	6.99	7.25	7.49	1.12	up	4.29E-01	8.95E-01	-	-
1385621_at	Fam48a	family with sequence similarity 48, member A	361946	Rn.45268	BF567091	3.43	4.05	3.93	4.44	3.79	3.68	1.12	up	6.07E-01	8.95E-01	-	-
1375115_at	LOC290577	Hypothetical LOC290577	290577	Rn.8014	AI137275	3.12	2.69	2.88	2.76	3.83	2.61	1.12	up	6.97E-01	9.07E-01	-	-
1398951_at	RGD1308009	similar to KIAA1007 protein; adrenal gland protein AD-005	291841	Rn.56498	BE109021	6.27	7.27	6.98	6.55	6.43	7.03	1.12	down	6.54E-01	8.97E-01	-	-
1391625_at	Wasl	Wiskott-Aldrich syndrome-like	682507	---	AI706673	8.00	7.98	7.42	7.88	6.90	8.11	1.12	down	7.07E-01	9.08E-01	-	-
1387561_at	Vipr1	vasoactive intestinal peptide receptor 1	24875	Rn.9973	NM_012685	2.41	2.40	3.08	2.58	2.41	2.39	1.12	down	5.10E-01	8.95E-01	-	-
1390357_at	Znf574	zinc finger protein 574	308434	Rn.15466	AW525082	4.27	4.75	4.33	4.56	4.40	4.90	1.12	up	4.67E-01	8.95E-01	-	-
1398269_at	Ntn1	netrin 1	314523	Rn.41052	NM_053731	5.96	5.91	6.20	5.79	5.97	5.79	1.12	down	1.89E-01	8.95E-01	-	-
1396866_s_at	Pxmp3	peroxisomal membrane protein 3	29534	Rn.4065	AA850928	3.76	3.80	4.68	3.56	3.79	4.38	1.12	down	6.86E-01	9.03E-01	-	-
1388893_at	Gli8d1	glycosyltransferase 8 domain containing 1	306253	Rn.91636	AI411616	4.29	4.20	4.79	4.57	4.27	4.94	1.12	up	5.65E-01	8.95E-01	-	-
1374225_at	LOC500700	similar to chromosome 14 open reading frame 145	500700	Rn.27063	BE112921	2.28	2.27	2.28	2.27	2.28	2.78	1.12	up	3.78E-01	8.95E-01	-	-
1385916_at	LOC686240	similar to NMDA receptor regulated 1-like	686240	---	AI639015	3.13	3.29	3.44	3.24	3.02	3.10	1.12	down	1.92E-01	8.95E-01	-	-
1367473_at	Tomm22	translocase of outer mitochondrial membrane 22 homolog (yeast)	300075	Rn.3119	BI284237	7.62	7.96	8.33	7.61	7.97	7.83	1.12	down	5.07E-01	8.95E-01	-	-
1398339_at	Sf1	splicing factor 1	117855	Rn.1074	BE109605	6.62	6.42	6.69	5.86	6.47	6.88	1.12	down	6.15E-01	8.95E-01	-	-
1373763_at	Zbtb43	zinc finger and BTB domain containing 43	311872	Rn.7867	AI013512	6.98	7.04	7.06	7.22	6.52	7.84	1.12	up	6.82E-01	9.03E-01	-	-
1394567_at	Qsox2	quiescin Q6 sulfhydryl oxidase 2	681023	Rn.199433	AW535805	3.01	4.51	3.82	3.81	3.47	4.56	1.12	up	7.71E-01	9.25E-01	-	-
1367617_at	Aldoa	aldolase A, fructose-bisphosphate	24189	Rn.1774	NM_012495	9.53	9.12	9.32	9.41	9.70	9.36	1.12	up	3.49E-01	8.95E-01	-	-
1367678_at	Sdha	succinate dehydrogenase complex, subunit A, flavoprotein (Fp)	157074	Rn.101727	NM_130428	11.55	11.69	11.37	11.64	11.70	11.78	1.12	up	1.89E-01	8.95E-01	-	-
1395124_at	Wars	tryptophanyl-tRNA synthetase	314442	Rn.14939	BE101688	4.19	3.94	4.61	3.71	4.43	5.10	1.12	up	7.25E-01	9.13E-01	-	-
1371544_at	Erh	enhancer of rudimentary homolog (Drosophila)	681415	Rn.7881	BE109666	7.52	7.99	7.76	7.25	7.69	7.83	1.12	down	4.93E-01	8.95E-01	-	-
1383149_at	LOC684122	similar to development and differentiation enhancing factor-like 1	684122	---	AA964486	2.91	2.98	2.92	2.91	3.50	2.90	1.12	up	4.50E-01	8.95E-01	-	-
1379327_at	Smarca5	SWI/SNF related, matrix associated, actin dependent regulator of chromatin,	307766	Rn.221918	BI292524	7.13	7.52	7.78	6.76	7.55	7.62	1.12	down	6.42E-01	8.95E-01	-	-
1389103_at	Gins4	GINS complex subunit 4 (Sld5 homolog)	290842	Rn.103411	BM391005	2.56	2.57	2.57	3.10	2.56	2.55	1.12	up	4.13E-01	8.95E-01	-	-
1398294_at	Actn1	actinin, alpha 1	81634	Rn.6401	NM_031005	2.34	2.44	2.44	2.78	2.44	2.51	1.12	up	2.01E-01	8.95E-01	-	-
1388312_at	---	---	---	Rn.146338	BI274487	3.45	3.42	3.29	3.80	3.47	3.40	1.12	up	2.69E-01	8.95E-01	-	-
1398787_at	Rheb	Ras homolog enriched in brain	26954	Rn.859	NM_013216	8.17	8.58	9.11	8.25	8.34	8.76	1.12	down	6.22E-01	8.95E-01	-	-
1392570_at	Abcd4	ATP-binding cassette, sub-family D (ALD), member 4	299196	Rn.211008	BI295850	2.70	2.43	2.46	3.14	2.46	2.50	1.12	up	5.19E-01	8.95E-01	-	-
1376281_at	Ccdc134	coiled-coil domain containing 134	500909	Rn.19890	BM389698	2.91	2.97	2.99	2.90	2.93	3.55	1.12	up	4.71E-01	8.95E-01	-	-
1377821_at	---	---	---	Rn.164137	BI284288	8.71	8.60	9.71	8.40	8.84	9.28	1.12	down	7.21E-01	9.11E-01	-	-
1395551_at	Ankrd13c	ankyrin repeat domain 13C	685374	Rn.100818	BG671371	6.03	6.31	6.74	6.14	6.36	6.37	1.12	down	4.96E-01	8.95E-01	-	-
1367747_at	Ari3	ADP-ribosylation factor-like 3	64664	Rn.9538	NM_022700	8.54	7.75	7.93	8.01	7.90	7.81	1.12	down	5.34E-01	8.95E-01	-	-
1368009_at	Slc10a1	solute carrier family 10 (sodium/bile acid cotransporter family), member 1	24777	Rn.9913	NM_017047	2.58	2.50	2.38	2.90	2.55	2.50	1.12	up	2.96E-01	8.95E-01	-	-
1371607_at	Map4	microtubule-associated protein 4	367171	Rn.203122	AI230787	7.35	7.48	7.96	7.29	7.13	7.86	1.12	down	5.94E-01	8.95E-01	-	-
1372183_at	Kpna1	Karyopherin (importin) alpha 1	288064	Rn.6272	AI230596	7.90	7.65	7.88	6.90	8.14	7.90	1.12	down	6.88E-01	9.04E-01	-	-
1381016_at	---	---	---	Rn.73677	BI288152	4.96	3.95	3.65	4.27	4.05	4.75	1.12	up	7.27E-01	9.13E-01	-	-
1397944_at	---	---	---	Rn.66757	BE096457	3.49	2.46	2.54	3.02	2.50	2.47	1.12	down	6.80E-01	9.03E-01	-	-
1395118_at	Rg9mtd2	RNA (guanine-9-) methyltransferase domain containing 2	295496	Rn.202719	AW523661	3.40	3.38	5.15	3.85	4.49	4.11	1.12	up	7.99E-01	9.35E-01	-	-
1381607_at	Zfp407	zinc finger protein 407	307213	Rn.28602	AI145754	3.18	2.49	2.55	2.42	2.81	2.50	1.12	down	5.40E-01	8.95E-01	-	-
1372202_at	RGD1310553	similar to expressed sequence AI597479	301374	Rn.12996	BF284058	5.26	5.43	4.18	4.47	5.51	5.40	1.12	up	7.59E-01	9.21E-01	-	-
1370688_at	Gclc	glutamate-cysteine ligase, catalytic subunit	25283	Rn.8365	J05181	12.71	12.93	12.80	12.60	12.62	12.72	1.12	down	9.20E-02	8.95E-01	-	-
1377254_a_at	Cohh1	Cohen syndrome homolog 1	315036	Rn.7442	BI295640	5.89	4.62	4.87	4.45	5.38	6.05	1.12	up	7.95E-01	9.34E-01	-	-
1373605_at	RGD1307844	similar to 106 kDa O-GlcNAc transferase-interacting protein	316985	Rn.3090	AI176540	8.21	7.50	8.11	8.21	7.51	7.60	1.12	down	6.22E-01	8.95E-01	-	-
1376200_at	MGC72974	hypothetical LOC316976	316976	Rn.33980	BM385898	3.38	3.90	3.36	3.36	3.26	3.52	1.12	down	4.35E-01	8.95E-01	-	-
1386820_at	Pet112l	PET112-like (yeast)	361974	Rn.73993	AA851099	4.92	5.70	6.26	5.40	5.27	5.71	1.12	down	7.05E-01	9.08E-01	-	-
1382486_at	Haghl	hydroxyacylglutathione hydrolase-like	302995	Rn.27173	BI293827	2.38	2.37	2.39	2.89	2.40	2.36	1.12	up	3.82E-01	8.95E-01	-	-
1394713_at	---	---	---	Rn.202442	AI408200	2.92	2.47	2.57	2.49	2.50	2.47	1.12	down	2.91E-01	8.95E-01	-	-
1376274_at	Btbd10	BTB (POZ) domain containing 10	308890	Rn.2717	AI233751	4.90	4.79	4.68	4.49	4.76	4.62	1.12	down	1.74E-01	8.95E-01	-	-
1382050_at	---	---	---	Rn.7315	AI410262	7.68	7.76	8.35	7.60	7.84	7.85	1.12	down	5.06E-01	8.95E-01	-	-
1398441_at	Nck2	NCK adaptor protein 2	316369	Rn.9067	AA857410	4.66	3.17	3.06	3.95	3.38	4.05	1.12	up	7.79E-01	9.28E-01	-	-
1375829_at	Fam45a	family with sequence similarity 45, member A	308009	Rn.7621	AW525101	4.28	5.55	4.92	5.69	3.45	5.11	1.12	down	8.38E-01	9.49E-01	-	-
1395563_at	---	---	---	Rn.14791	AA875586	3.22	3.51	3.03	2.97	3.10	3.19	1.12	down	3.32E-01	8.95E-01	-	-
1384157_at	Arl8b	ADP-ribosylation factor-like 8B	500282	Rn.6283	AW916872	7.43	8.30	8.58	7.93	7.81	8.07	1.12	down	6.62E-01	8.98E-01	-	-
1389145_at	Cdc42ep2	CDC42 effector protein (Rho GTPase binding) 2	309175	Rn.17464	D86683	3.32	3.07	2.48	2.79	2.79	2.78	1.12	down	5.41E-01	8.95E-01	-	-
1375722_at	Mllt1	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila);	301119	Rn.33401	AI230745	2.71	3.90	3.84	2.53	5.20	3.22	1.12	up	8.60E-01	9.57E-01	-	-
1383677_at	Rnf168	ring finger protein 168	690043	Rn.101441	AA925701	2.78	4.04	3.72	3.50	3.24	4.29	1.12	up	7.53E-01	9.20E-01	-	-
1374436_at	Sbds	Shwachman-Bodian-Diamond syndrome homolog (human)	288615	Rn.107123	BI296660	8.96	9.58	9.15	8.85	8.86	9.46	1.12	down	5.74E-01	8.95E-01	-	-
1368687_at	Tesk1	testis-specific kinase 1	29460	Rn.7006	NM_031578	3.20	3.22	3.21	3.31	2.63	3.19	1.12	down	4.72E-01	8.95E-01	-	-
1388381_at	Eif3g	eukaryotic translation initiation factor 3, subunit G	298700	Rn.107880	AI411198	6.72	7.90	7.31	7.11	7.36	7.96	1.12	up	7.12E-01	9.10E-01	-	-
1368528_at	Cd99l2	CD99 molecule-like 2	171485	Rn.20204	AF481858	6.46	7.00	7.04	6.04	7.18	7.78	1.12	up	7.74E-01	9.28E-01	-	-
1376073_at	Sel1l	sel-1 suppressor of lin-12-like (C. elegans)	314352	Rn.20802	BI285936	6.75	6.21	5.91	6.54	5.95	6.87	1.12	up	6.72E-01	9.01E-01	-	-
1383372_at	Ptafr	platelet-activating factor receptor	58949	Rn.10137	BF407234	5.42	4.10	4.11	4.09	5.15	4.88	1.12	up	7.73E-01	9.26E-01	-	-
1374351_at	---	---	---	Rn.9068	AI044117	3.51	3.46	3.54	3.54	3.98	3.50	1.12	up	3.41E-01	8.95E-01	-	-
1398610_at	---	---	---	Rn.21256	AI704849	3.11	3.98	5.06	4.67	3.87	4.11	1.12	up	7.98E-01	9.35E-01	-	-
1371522_at	Bahd1	bromo adjacent homology domain containing 1	362194	Rn.6925	BI295010	4.74	5.00	4.72	4.82	5.11	5.03	1.12	up	2.48E-01	8.95E-01	-	-
1394779_at	---	---	---	Rn.168649	AI717218	2.57	2.63	2.65	2.84	2.58	2.95	1.12	up	2.11E-01	8.95E-01	-	-
1395014_at	---	---	---	Rn.173729	BI282088	2.41	4.70	2.39	2.46	2.39	4.16	1.12	down	8.70E-01	9.60E-01	-	-
1381683_at	Chd2	chromodomain helicase DNA binding protein 2	308738	Rn.1779	BE118824	6.85	6.48	6.48	6.12	6.80	6.38	1.12	down	5.14E-01	8.95E-01	-	-
1395625_at	---	---	---	Rn.36884	BF415216	2.55	2.63	2.48	2.34	2.35	3.46	1.12	up	6.79E-01	9.02E-01	-	-
1391564_at	Zfp426l2	zinc finger protein 426-like 2	363022	Rn.99479	AW526015	3.07	3.50	4.01	3.43	3.09	3.57	1.12	down	6.15E-01	8.95E-01	-	-
1379912_at	---	---	---	Rn.199990	BM392147	6.58	6.98	6.63	6.15	6.38	7.15	1.12	down	6.39E-01	8.95E-01	-	-
1379951_at	Shprh	SNF2 histone linker PHD RING helicase	308282	Rn.2515	BE104039	2.65	2.37	2.40	2.38	3.18	2.36	1.12	up	5.92E-01	8.95E-01	-	-
1370952_at	Gstm2	glutathione S-transferase mu 2	24424	Rn.625	AI169331	4.40	3.60	5.83	5.27	4.45	3.61	1.12	down	8.47E-01	9.52E-01	-	-
1391482_a_at	---	---	---	---	AI229413	3.82	4.08	3.66	3.60	4.84	3.62	1.12	up	7.17E-01	9.10E-01	-	-
1388448_at	2se2 /// LOC10019	CDC42 small effector 2 /// hypothetical LOC100191012	00191012 /// 69103	Rn.7470	AI235065	5.58	5.90	6.17	5.75	5.55	5.85	1.12	down	4.34E-01	8.95E-01	-	-
1398701_at	---	---	---	Rn.220678	AI228104	2.32	2.31	2.77	2.31	2.28	2.31	1.12	down	3.41E-01	8.95E-01	-	-
1376723_a_at	---	---	---	Rn.40208	AW142765	11.09	11.27	11.12	11.21	11.26	11.52	1.12	up	2.06E-01	8.95E-01	-	-
1372239_at	---	---	---	Rn.46460	AW527228	2.82	3.44	2.91	3.17	3.62	2.88	1.12	up	5.95E-01	8.95E-01	-	-
1390707_at	Rgs10	regulator of G-protein signaling 10	54290	Rn.23957	BI281632	3.94	3.43	3.48	3.53	4.15	2.66	1.12	down	7.36E-01	9.15E-01	-	-
1390506_at	Med1	mediator complex subunit 1	497991	Rn.4282	BF396678	6.95	6.74	6.59	7.31	6.42	7.05	1.12	up	5.88E-01	8.95E-01	-	-
1388738_at	Atmt1	attractin like 1	307992	Rn.12950	AI411227	8.34	8.44	8.30	7.82	8.12	8.63	1.12	down	5.28E-01	8.95E-01	-	-
1388230_at	Jub	jub, ajuba homolog (Xenopus laevis)	85265	Rn.144617	AJ306292	2.35	3.88	2.37	3.28	2.29	2.53	1.12	down	7.91E-01	9.33E-01	-	-
1384018_at	---	---	---	---	BG663446	5.79	5.40	5.68	5.34	5.54	5.49	1.12	down	2.74E-01	8.95E-01	-	-
1397610_at	---	---	---	Rn.148648	BI280825	2.55	2.53	2.55	3.04	2.55	2.54	1.12	up	3.75E-01	8.95E-01	-	-
1380497_at	Ash1l	ash1 (absent, small, or homeotic)-like (Drosophila)	310638	Rn.206058	AW521174	6.96	6.47	4.54	6.67	4.68	6.13	1.12	down	8.69E-01	9.59E-01	-	-
1396267_at	Pak2	P21 (CDKN1A)-activated kinase 2	29432	Rn.3840	N55607	7.26	7.42	7.13	6.98	7.27	7.06	1.12	down	2.38E-01	8.95E-01	-	-
1394481_at	Ube2z	ubiquitin-conjugating enzyme E2Z	303478	Rn.16992	BI273997	5.04	5.39	6.72	5.61	5.47	5.57	1.12	down	7.62E-01	9.22E-01	-	-
1389434_at	Zmynd17	zinc finger, MYND-type containing 17	289904	Rn.25565	AI236615	2.44	2.99	2.44	2.46	2.45	2.45	1.12	down	4.12E-01	8.95E-01	-	-
1379072_at	Phka2	phosphorylase kinase alpha 2	678739	Rn.33633	AA997659	3.17	2.52	2.56	2.55	2.65	2.55	1.12	down	4.80E-01	8.95E-01	-	-
1373411_at	Eif1b	eukaryotic translation initiation factor 1B	301068	Rn.65534	BE109655	8.24	8.67	8.41	8.40	7.86	8.56	1.12	down	5.34E-01	8.95E-01	-	-
1375219_a_at	73 /// RGD155595	similar to 40S ribosomal protein S2 /// similar to ribosomal protein S2 /// ribos	68 /// 689473 /// 8	Rn.2115	AA944861	10.10	10.16	10.08	10.18	10.23	10.42	1.12	up	9.59E-02	8.95E-01	-	-
1370128_at	Hand1	heart and neural crest derivatives expressed 1	59112	Rn.39340	NM_021592	2.46	2.46	2.96	2.46	2.47	2.46	1.12	down	3.76E-01	8.95E-01	-	-
1379420_at	RGD1565002	similar to Dehydrogenase/reductase SDR family member 7 precursor (Retinal	299135	Rn.27771	AI145019	3.52	3.07	3.73	3.58	3.70	3.54	1.12	up	4.54E-01	8.95E-01	-	-
1398954_at	Dnpep	aspartyl aminopeptidase	301529	Rn.65448	AI412298	7.94	7.58	7.69	7.64	7.44	7.83	1.12	down	2.50E-01	8.95E-01	-	-
1376323_at	---	---	---	Rn.171060	BM389562	3.63	3.84	4.44	3.62	3.93	3.86	1.12	down	5.59E-01	8.95E-01	-	-
1378080_at	Sco1	SCO cytochrome oxidase deficient homolog 1 (yeast)	497930	Rn.203819	BI274498	3.92	3.78	3.60	3.47	3.74	3.59	1.12	down	2.34E-01	8.95E-01	-	-
1392748_at	Tmcc1	Transmembrane and coiled-coil domain family 1	312654	Rn.198698	AI235594	3.44	3.43	3.61	3.67	3.44	3.86	1.12	up	2.82E-01	8.95E-01	-	-
1367755_at	Cdo1	cysteine dioxygenase, type I	81718	Rn.2589	NM_052809	10.69	10.69	10.48	10.35	10.94	10.07	1.12	down	5.67E-01	8.95E-01	-	-
1389314_at	Nvl	nuclear VCP-like	289323	Rn.8896	AW915489	4.85	4.17	3.29	4.11	4.14	4.56	1.12	up	7.44E-01	9.17E-01	-	-
1388656_at	---	---	---	Rn.163871	BI294968	7.25	6.81	7.01	6.89	6.73	6.95	1.12	down	3.16E-01	8.95E-01	-	-
1377933_at	Slc39a3	solute carrier family 39 (zinc transporter), member 3	314637	Rn.52192	BI282635	6.15	5.50	6.16	5.49	6.10	5.72	1.12	down	5.87E-01	8.95E-01	-	-
1372282_at	Gpx8	glutathione peroxidase 8	294744	Rn.106264	BF283238	2.98	2.93	2.93	3.54	2.93	2

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1373994_at	Aplf	aprataxin and PNKP like factor	500247	Rn.203883	BM388789	2.61	2.60	2.61	3.11	2.61	2.59	1.12	up	3.92E-01	8.95E-01	-	-
1374548_at	Aff4	AF4/FMR2 family, member 4	303132	Rn.17594	BE104797	7.88	7.44	5.91	6.78	7.44	7.49	1.12	up	8.10E-01	9.39E-01	-	-
1371708_at	Smn1 ///	Smn/Gemin5 syndrome chromosome region, candidate 7-like (human)	315141	Rn.62655	BI296302	5.94	5.91	5.98	6.28	5.74	6.31	1.12	up	4.22E-01	8.95E-01	-	-
1393315_at	Traf3ip3	TRAF3 interacting protein 3	360900	Rn.29176	AW142978	2.82	2.81	2.86	2.72	3.39	2.86	1.12	up	4.65E-01	8.95E-01	-	-
1370811_at	Mpst	mercaptopyruvate sulfurtransferase	192172	Rn.32263	D50564	7.26	7.45	7.71	7.83	7.71	7.38	1.12	up	4.23E-01	8.95E-01	-	-
1371502_at	Rbm42	RNA binding motif protein 42	361545	Rn.17083	AI103666	7.01	7.88	7.92	7.63	7.18	7.51	1.12	down	6.42E-01	8.95E-01	-	-
1386970_at	Eif2b4	eukaryotic translation initiation factor 2B, subunit 4 delta	117019	Rn.11060	NM_053950	6.22	6.96	6.74	6.78	6.96	6.67	1.12	up	5.22E-01	8.95E-01	-	-
1370724_a_at	Nfia	nuclear factor I/A	25492	Rn.10550	D78019	7.51	6.95	6.01	7.08	6.47	6.42	1.12	down	7.53E-01	9.20E-01	-	-
1378631_at	---	---	---	Rn.28568	BM388084	2.82	3.12	2.79	2.75	2.77	2.72	1.12	down	2.04E-01	8.95E-01	-	-
1372713_at	Ern1	endoplasmic reticulum to nucleus signaling 1	498013	Rn.198336	BI280353	3.54	2.68	2.39	2.68	2.61	2.82	1.12	down	6.64E-01	8.95E-01	-	-
1397726_at	Taok3	TAO kinase 3	304530	Rn.162145	AI178632	2.33	2.34	2.34	2.50	2.34	2.67	1.12	up	1.60E-01	8.95E-01	-	-
1385925_at	---	---	---	Rn.23216	BF550565	2.57	2.73	2.66	2.72	2.79	2.94	1.12	up	1.13E-01	8.95E-01	-	-
1374087_at	Slc48a1	solute carrier family 48 (heme transporter), member 1	300191	Rn.32236	AI411098	2.46	2.49	2.42	2.45	2.61	2.80	1.12	up	1.84E-01	8.95E-01	-	-
1394375_x_at	Bcl6b	B-cell CLL/lymphoma 6, member B (zinc finger protein)	360551	Rn.137148	BF554138	2.46	2.43	2.46	2.72	2.64	2.48	1.12	up	7.79E-02	8.95E-01	-	-
1391143_at	---	---	---	Rn.208076	BF405315	2.36	2.35	2.37	2.38	2.85	2.35	1.12	up	3.74E-01	8.95E-01	-	-
1394616_at	Mesdc2	mesoderm development candidate 2	308796	Rn.41045	AI013798	4.12	6.79	5.39	5.00	5.38	5.42	1.12	down	8.44E-01	9.52E-01	-	-
1388831_at	Slc9a3r2	solute carrier family 9 (sodium/hydrogen exchanger), member 3 regulator 2	116501	Rn.39351	BI277485	3.34	3.42	3.27	3.61	2.87	3.05	1.12	down	5.11E-01	8.95E-01	-	-
1390068_at	Ocel1	occludin/ELL domain containing 1	290628	Rn.98475	BM389499	7.68	9.03	7.99	7.98	7.94	8.29	1.12	down	7.17E-01	9.10E-01	-	-
1387242_at	Eif2ak2	eukaryotic translation initiation factor 2-alpha kinase 2	54287	Rn.10022	NM_019335	3.06	3.34	3.35	3.33	3.54	3.37	1.12	up	2.23E-01	8.95E-01	-	-
1393461_at	Zfp317	zinc finger protein 317	500950	Rn.159405	BM392157	6.48	4.55	4.59	4.58	6.21	5.32	1.12	up	8.46E-01	9.52E-01	-	-
1388703_at	Esam	endothelial cell adhesion molecule	300519	Rn.17089	BF285026	3.38	2.50	2.41	2.50	2.52	2.78	1.12	down	6.38E-01	8.95E-01	-	-
1379364_at	Camsap1	calmodulin regulated spectrin-associated protein 1	296580	Rn.203213	BI273752	5.41	3.49	2.83	3.74	4.30	4.19	1.12	down	8.55E-01	9.55E-01	-	-
1376705_a_at	Rab24	RAB24, member RAS oncogene family	361208	Rn.6295	BF289020	6.97	7.29	7.32	7.33	7.01	7.73	1.12	up	5.24E-01	8.95E-01	-	-
1389681_at	Pvrl2	poliovirus receptor-related 2	308417	Rn.203297	BI296388	3.95	3.00	3.34	3.14	3.33	3.33	1.12	down	5.97E-01	8.95E-01	-	-
1375728_at	---	---	---	Rn.205231	AI511102	2.46	2.92	2.46	2.47	2.43	2.43	1.12	down	3.41E-01	8.95E-01	-	-
1367722_at	Dpp7	dipeptidylpeptidase 7	83799	Rn.3363	NM_031973	5.13	4.53	4.71	4.48	4.70	4.69	1.12	down	4.43E-01	8.95E-01	-	-
1377251_at	---	---	---	Rn.168458	AW551255	2.96	2.41	2.50	2.49	2.47	2.42	1.12	down	3.93E-01	8.95E-01	-	-
1398991_at	---	---	---	Rn.7282	BM389704	5.43	5.93	6.42	5.38	6.03	5.89	1.12	down	6.61E-01	8.98E-01	-	-
1392543_at	7 /// Rbbp4 /// RG	similar to Chromatin assembly factor 1 subunit CG4236-PA /// retinoblastoma 1	11 /// 313048 /// 50	Rn.7745	BI293462	10.67	10.52	10.68	10.64	11.11	10.61	1.12	up	3.91E-01	8.95E-01	-	-
1382613_at	---	---	---	Rn.24594	AW144049	2.45	2.45	2.46	2.44	2.73	2.68	1.12	up	1.39E-01	8.95E-01	-	-
1380522_at	---	---	---	Rn.166332	AI060201	5.30	3.88	3.03	4.44	4.57	3.69	1.12	up	8.30E-01	9.47E-01	-	-
1395185_at	---	---	---	Rn.208345	BE115336	2.44	2.42	2.47	2.97	2.44	2.41	1.12	up	4.19E-01	8.95E-01	-	-
1377418_at	---	---	---	Rn.216892	AI411724	3.29	2.89	2.91	3.12	2.90	2.58	1.12	down	4.66E-01	8.95E-01	-	-
1371925_at	Atp13a1	ATPase type 13A1	290673	Rn.3697	AA893621	4.69	5.21	5.49	4.80	5.15	5.93	1.12	up	7.11E-01	9.09E-01	-	-
1378819_at	Aspdh	aspartate dehydrogenase domain containing	292875	Rn.54118	AW435096	6.70	6.96	6.70	6.76	6.43	6.68	1.12	down	2.77E-01	8.95E-01	-	-
1395935_at	---	---	---	---	BF282716	3.07	3.00	2.55	3.09	3.17	2.85	1.12	up	4.38E-01	8.95E-01	-	-
1374278_at	Fitm2	fat storage-inducing transmembrane protein 2	311617	Rn.107822	BG381647	5.13	4.57	4.39	4.39	5.25	4.95	1.12	up	6.53E-01	8.97E-01	-	-
1373277_at	Tm2d3	TM2 domain containing 3	292995	Rn.15627	BG373457	9.75	10.24	10.79	9.76	10.28	10.24	1.12	down	6.59E-01	8.98E-01	-	-
1395044_at	LOC679298	hypothetical protein LOC679298	679298	---	AI179766	2.70	2.69	2.67	2.87	3.03	2.65	1.12	up	2.23E-01	8.95E-01	-	-
1368948_at	Msn	moesin	81521	Rn.2762	NM_030863	9.18	9.78	10.07	9.74	9.51	9.29	1.12	down	6.04E-01	8.95E-01	-	-
1384562_at	---	---	---	---	AI071755	8.78	7.84	7.26	7.64	8.09	8.64	1.12	up	7.73E-01	9.26E-01	-	-
1369442_at	---	---	---	---	NM_022621	2.65	2.61	3.13	2.63	2.70	2.58	1.12	down	3.94E-01	8.95E-01	-	-
1375847_at	Nudt16	nudix (nucleoside diphosphate linked moiety X)-type motif 16	363129	Rn.16063	BF282594	3.19	3.65	3.05	3.04	3.13	4.20	1.12	up	7.13E-01	9.10E-01	-	-
1394663_at	Pols	polymerase (DNA directed) sigma	306672	Rn.22554	BI294686	3.00	2.59	2.78	2.46	2.71	2.71	1.12	down	3.17E-01	8.95E-01	-	-
1384567_at	---	---	---	---	AI045289	7.40	8.24	8.08	7.61	8.98	7.64	1.12	down	8.17E-01	9.41E-01	-	-
1379654_at	Glyd2	GIY-YIG domain containing 2	293489	Rn.30339	AA946433	3.64	3.29	3.29	3.16	3.29	3.28	1.12	down	2.60E-01	8.95E-01	-	-
1377257_at	---	---	---	Rn.128700	BI290077	9.27	8.53	8.57	8.82	8.37	8.69	1.12	down	5.84E-01	8.95E-01	-	-
1386287_at	Slain2	SLAIN motif family, member 2	305310	Rn.23030	AI407974	5.02	5.23	5.61	4.97	5.18	5.12	1.12	up	4.58E-01	8.95E-01	-	-
1380870_at	---	---	---	Rn.206481	AW527523	2.83	2.81	2.84	2.82	3.54	2.61	1.12	up	5.95E-01	8.95E-01	-	-
1398665_at	---	---	---	Rn.136071	BF389200	2.61	2.58	3.03	2.59	2.59	2.56	1.12	down	3.19E-01	8.95E-01	-	-
1390932_at	---	---	---	Rn.2849	AA875255	2.87	2.88	3.57	2.88	2.90	3.05	1.12	down	5.29E-01	8.95E-01	-	-
1395666_at	---	---	---	Rn.209785	BF390830	2.90	2.35	2.37	2.36	2.42	2.35	1.12	down	4.19E-01	8.95E-01	-	-
1369834_at	Foxa1	forkhead box A1	25098	Rn.10470	NM_012742	2.46	2.45	2.47	2.46	2.96	2.45	1.12	up	3.94E-01	8.95E-01	-	-
1374558_at	---	---	---	Rn.203823	AI010316	7.55	9.58	9.59	8.25	8.94	9.04	1.12	down	8.32E-01	9.47E-01	-	-
1385168_at	RGD1306520	similar to receptor-interacting factor 1	310775	Rn.82110	BM387883	2.89	2.78	3.81	2.78	3.06	3.17	1.12	down	6.62E-01	8.98E-01	-	-
1392723_at	---	---	---	Rn.209406	BF388065	2.42	2.36	2.38	2.91	2.38	2.37	1.12	up	4.15E-01	8.95E-01	-	-
1385309_at	Ccl24	chemokine (C-C motif) ligand 24	288593	Rn.138822	BI294084	3.04	2.62	2.64	2.63	2.65	2.54	1.12	down	3.12E-01	8.95E-01	-	-
1397189_at	---	---	---	Rn.17115	BE108217	2.48	2.83	2.45	2.42	2.44	2.42	1.12	down	2.56E-01	8.95E-01	-	-
1371301_at	Rpl9	ribosomal protein L9	29257	Rn.107914	BG666892	12.54	12.39	12.52	12.60	12.63	12.71	1.12	up	4.29E-02	8.95E-01	-	-
1396311_at	---	---	---	Rn.149084	BF390394	2.34	2.34	2.35	2.86	2.35	2.31	1.12	up	4.13E-01	8.95E-01	-	-
1390563_at	Abca3	ATP-binding cassette, sub-family A (ABC1), member 3	302973	Rn.38406	BE096678	6.59	7.27	6.73	7.36	6.26	7.45	1.12	up	7.28E-01	9.13E-01	-	-
1382345_at	Pctk2	PCTAIRE protein kinase 2	314743	Rn.17706	AA852299	4.50	4.27	4.24	3.18	5.20	4.15	1.12	down	7.96E-01	9.34E-01	-	-
1391551_at	---	---	---	Rn.213059	BM391857	5.45	5.44	4.53	5.61	5.94	4.37	1.12	up	7.88E-01	9.31E-01	-	-
1383973_at	RGD1559841	similar to expressed sequence AW413431	307816	Rn.20470	AI071216	4.64	3.93	3.65	4.57	3.81	4.33	1.12	up	6.82E-01	9.03E-01	-	-
1377618_at	Klf7	Kruppel-like factor 7 (ubiquitous)	363243	Rn.219339	AW534908	2.28	2.28	2.33	2.29	2.82	2.28	1.12	up	4.13E-01	8.95E-01	-	-
1388211_s_at	Acot1 /// Acot2	acyl-CoA thioesterase 1 /// acyl-CoA thioesterase 2	192272 /// 50559	Rn.37524	Y09333	4.15	4.22	4.71	3.80	4.19	4.60	1.12	down	6.06E-01	8.95E-01	-	-
1379329_at	LOC685729	Similar to dimerization cofactor of hepatocyte nuclear factor 1 (HNF1) from mo	685729	Rn.18796	AI600082	8.14	8.91	8.83	8.57	8.89	8.90	1.12	up	5.76E-01	8.95E-01	-	-
1397439_at	LOC497978	similar to diacylglycerol kinase epsilon	497978	Rn.163148	AI101639	2.47	2.42	2.49	2.94	2.47	2.46	1.12	up	3.64E-01	8.95E-01	-	-
1370824_at	Slc38a3	solute carrier family 38, member 3	252919	Rn.32047	AF273025	10.02	10.97	10.98	10.53	10.96	10.96	1.12	up	6.64E-01	8.99E-01	-	-
1375944_at	Acss2	acyl-CoA synthetase short-chain family member 2	311569	Rn.3514	AA894497	10.90	11.37	10.90	10.72	10.75	11.20	1.12	down	5.00E-01	8.95E-01	-	-
1368329_at	Slc22a6	solute carrier family 22 (organic anion transporter), member 6	29509	Rn.87849	NM_017224	11.56	11.45	11.59	11.60	11.33	11.18	1.12	down	2.76E-01	8.95E-01	-	-
1376336_at	---	---	---	Rn.204970	BM392257	5.36	6.57	5.86	6.26	6.08	5.94	1.12	up	6.76E-01	9.02E-01	-	-
1394918_at	Ccdc44	coiled-coil domain containing 44	360645	Rn.137785	BF408338	2.68	2.70	2.69	2.65	3.20	2.71	1.12	up	4.08E-01	8.95E-01	-	-
1388682_at	Cnih	cornichon homolog (Drosophila)	289994	Rn.24497	AI598397	8.84	8.86	8.77	8.93	8.84	9.18	1.12	up	2.04E-01	8.95E-01	-	-
1388802_at	Lox l1	lysyl oxidase-like 1	315714	Rn.770	AI599031	4.40	4.29	4.32	4.59	4.40	3.53	1.12	down	6.46E-01	8.95E-01	-	-
1383528_at	RGD1563945	similar to mKIAA0215 protein	299305	Rn.29348	BI276223	4.20	4.31	4.69	4.25	4.08	4.37	1.12	down	3.92E-01	8.95E-01	-	-
1381563_at	---	---	---	---	BI294761	2.20	2.19	2.20	2.18	2.70	2.20	1.12	up	3.99E-01	8.95E-01	-	-
1373678_at	---	---	---	Rn.165875	BE098848	9.16	10.68	10.18	10.15	10.18	10.18	1.12	up	7.34E-01	9.15E-01	-	-
1381509_at	OC498369 /// Nbr	similar to neighbor of Brca1 gene 1 /// neighbor of Brca1 gene 1	303554 /// 498369	Rn.94975	BF393724	10.04	9.43	8.71	9.22	9.23	9.24	1.12	down	6.94E-01	9.06E-01	-	-
1367653_a_at	Mdh1	malate dehydrogenase 1, NAD (soluble)	24551	Rn.13492	NM_033235	12.86	12.68	12.84	12.64	12.65	12.61	1.12	down	5.05E-02	8.95E-01	-	-
1380519_at	RGD1561425	similar to RIKEN cDNA 4832428D23 gene	301378	Rn.37634	AI010831	2.34	2.34	2.35	2.34	2.87	2.31	1.12	up	4.22E-01	8.95E-01	-	-
1368068_a_at	Pacsin2	protein kinase C and casein kinase substrate in neurons 2	124461	Rn.17106	NM_130740	7.02	6.74	6.75	6.74	6.38	6.90	1.12	down	4.15E-01	8.95E-01	-	-
1392639_at	---	---	---	Rn.7217	AI177281	6.93	7.55	7.11	6.89	6.99	7.21	1.12	down	4.80E-01	8.95E-01	-	-
1373556_at	RGD1561792	similar to CG14903-PA	298861	Rn.8319	AI237593	2.58	2.60	2.58	2.57	2.59	3.09	1.12	up	3.93E-01	8.95E-01	-	-
1372664_at	Traf2	Tnf receptor-associated factor 2	311786	Rn.105232	BM384229	3.03	2.54	2.55	2.55	2.55	2.54	1.12	down	3.73E-01	8.95E-01	-	-
1392887_at	---	---	---	Rn.3617	AI575082	3.83	3.83	3.84	3.83	3.59	4.57	1.12	up	6.13E-01	8.95E-01	-	-
1398828_at	Fkbp1a	FK506 binding protein 1a	25639	Rn.80611	AI598372	8.33	8.38	9.52	8.60	9.47	8.65	1.12	up	7.52E-01	9.20E-01	-	-
1374554_at	RGD1308048	similar to HT014	298557	Rn.22682	BF281325	7.41	7.36	6.69	7.56	7.03	7.36	1.12	up	5.93E-01	8.95E-01	-	-
1372428_at	Dnajc4	DnaJ (Hsp40) homolog, subfamily C, member 4	361717	Rn.91398	BG380252	6.48	5.04	5.83	5.37	5.09	6.40	1.12	down	7.92E-01	9.33E-01	-	-
1374065_at	---	---	---	Rn.205417	BG378920	8.92	9.14	8.63	9.01	8.51	9.64	1.12	up	6.74E-01	9.01E-01	-	-
1384701_at	---	---	---	Rn.207790	BE108175	3.40	2.89	2.87	3.42	3.12	3.11	1.12	up	4.65E-01	8.95E-01	-	-
1378669_at	Incenp	inner centromere protein	293733	Rn.92193	AI706871	2.80	2.76	2.99	3.04	2.53	2.49	1.12	down	4.39E-01	8.95E-01	-	-
1396513_at	---	---	---	Rn.26589	AI716081	2.45	2.43	2.92	2.44	2.46	2.41	1.12	down	3.74E-01	8.95E-01	-	-
1389523_at	Znf598	zinc finger protein 598	287119	Rn.8462	BM386127	2.92	2.92	2.58	2.93	3.06	2.91	1.12	up	2.59E-01	8.95E-01	-	-
1398976_at	Ncor1	nuclear receptor co-repressor 1	54299	Rn.24948	AA848674	7.53	7.09	5.91	7.12	5.85	7.07	1.12	down	8.12E-01	9.39E-01	-	-
1398894_at	Commd3	COMM domain containing 3	291339	Rn.3471	AI178763	10.07	10.48	10.68	10.09	10.14	10.52	1.12	down	5.08E-01	8.95E-01	-	-
1388846_at	Bcl2l12	BCL2-like 12 (proline rich)	361567	Rn.106127	AI227978	2.69	2.32	2.44	2.32	2.32	2.32	1.12	down	2.16E-01	8.95E-01	-	-
1398972_at	Cops3	COP9 constitutive photomorphogenic homolog subunit 3 (Arabidopsis)	287367	Rn.3963	AW916366	6.77	7.54	7.17	7.01	7.50	7.45	1.12	up	5.85E-01	8.95E-01	-	-
1368540_at	Tpbg	trophoblast glycoprotein	83684	Rn.43122	NM_031807	3.11	3.63	3.27	3.18	3.27	4.06	1.12	up	6.38E-01	8.95E-01	-	-
1388347_at	Ly6e	lymphocyte antigen 6 complex, locus E	362934	Rn.3321	AI233270	7.16	6.47	6.35	7.08	7.05	6.35	1.12	up	8.70E-01	9.40E-01	-	-
1383240_at	---	---	---	Rn.22382	BE110753	9.03	9.02	9.08	8.83	8.72	9.09	1.12	down	2.18E-01	8.95E-01	-	-
1389650_at	---	---	---	Rn.168669	BI295153	3.14	2.33	2.37	2.39	3.55	2.38	1.12	up	7.48E-01	9.19E-01	-	-
1374878_at	Thoc5	THO complex 5	360972	Rn.14671	H35236	6.19	6.38	6.20	6.19	6.68	6.38	1.12	up	3.55E-01	8.95E-01	-	-
1388829_at	Edc4	enhancer of mRNA decapping 4	361399	Rn.145173	AA946348	7.87	7.22	7.44	7.55	7.52	6.96	1.12	down	5.82E-01	8.95E-01	-	-
1376692_at	Hipk2	homeodomain interacting protein kinase 2	362342	Rn.8042	BM392321	3.69	6.31	4.53	5.06	4.80	5.16	1.12	up	8.45E-01	9.52E-01	-	-
1387169_at	Tle3	transducin-like enhancer of split 3 (E(sp1) homolog, Drosophila)	84424	Rn.24106	NM_053400	5.85	5.61	4.40	5.34	4.91	6.10	1.12	up	7.89E-01	9.32E-01	-	-
1383764_at	Chic2	cysteine-rich hydrophobic domain 2	83835	Rn.106037	BF567482	3.02	3.52	3.02	3.01	2.71	3.35	1.12	down	5.50E-01	8.95E-01	-	-
1371890_at	Rere	arginine-glutamic acid dipeptide (RE) repeats	116665	Rn.10277	AI172033	5.76	5.76	5.14	5.43	4.55	6.20	1.12	down	7.71E-01	9.25E-01	-	-
1378395_at	---	---	---	Rn.16997	BF411826	5.54	4.89	4.71	4.83	4.97	4.85	1.12	down	5.59E-01	8.95E-01	-	-
1389445_at	Znf688	zinc finger protein 688	293511	Rn.29826	AI406571	4.06	4.71	4.78	5.08	4.28	4.67	1.12	up	6.46E-01	8.95E-01	-	-
1371778_at	Rnf146	ring finger protein 146	308051	Rn.16849	BI296773	8.11	8.66	8.14	7.61	8.42	8.39	1.12	down	6.38E-01	8.95E-01	-	-
1384375_at	---	---	---	Rn.204030	BE100151	2.36	2.35	2.42	2.34	2.93	2.34	1.12	up	4.61E-01	8.95E-01	-	-
1368977_at	Fxc1	Fractured callus expressed transcript 1	84384	Rn.13451	AF061242	6.01	5.77	5.72	5.70	5.62	5.69	1.12	down	1.53E-01	8.95E-01	-	-
1374455_at	---	---	---	---	AI599343	4.66	3.65	4.11	4.89	3.31	4.71	1.12	up	7.94E-01	9.34E-01	-	-
1383748_at	Necap2	NECAP endocytosis associated 2	298598	Rn.56102	H31483	2.78	2.55	2.58	3.21	2.61	2.58	1.12	up	5.03E-01	8.95E-01	-	-
1388800_at	Rab5a	RAB5A, member RAS oncogene family	64633	Rn.44477	AI406667	6.52	6.18	6.72	6.46	6.48	6.97	1.12	up	5.20E-01	8.95E-01	-	-
1379530_at	---	---	---	Rn.9158	AA894658	2.45	2.90	2.50	2.45	2.49	2.43	1.12	down	3.24E-01	8.95E-01	-	-
1387272_at	Eif2ak1	eukaryotic translation initiation factor 2 alpha kinase 1	27137	Rn.3333	NM_013223	5.45	5.37	5.02	5.51	5.43	5.39	1.12	up	2.97E-01	8.95E-01	-	-
1383824_at	Ldb2	LIM domain binding 2	289664	Rn.94720	AI029445	2.56	2.55	2.75	2.57	3.26	2.52	1.12	up	5.49E-01	8.95E-01	-	-
1374247_at	---	---	---	---	BI279869	2.42	2.41	2.43	2.93	2.43	2.39	1.12	up	4.08E-01	8.95E-01	-	-
1393204_at	Sfxn4	sideroflexin 4	361778	Rn.13517	AI711190	3.02	3.11	3.36	3.00	3.01	2.99	1.12	down	1.96E-01	8.95E-01	-	-
1371593_at	---	---	---	Rn.203374	BI296121	2.96	3.05	2.50	2.95	2.86	3.18	1.12	up	4.51E-01	8.95E-01	-	-
1377357_at	---	---	---	Rn.23597	BE106428	4.52	5.53	4.97	4.41	4.49	5.64	1.12	down	7.60E-01	9.22E-01	-	-
1389661_at	Ptcd1	pentatricopeptide repeat domain 1	304278	Rn.105071	AI599413	6.57	6.01	6.47	6.36	6.81	6.36	1.12	up	5.15E-01	8.95E-01	-	-
1388564_at	Lpp	LIM domain containing preferred translocation partner in lipoma	288010	Rn.206503	AW527799	4.87	4.84	4.61	4.55	4.65	4.63	1.12	down	1.44E-01	8.95E-01	-	-
1391035_at	---	---	---	Rn.23192	BE096618	3.33	3.41	4.01	3.66	3.83	3.73	1.12	up	5.07E-01	8.95E-01	-	-
1377160_at	---	---	---	Rn.172520	BF401689	2.51	2.51	2.51	3.01	2.53	2.48	1.12	up	3.94E-01	8.95E-01	-	-
1375380_at	Gmcl1	germ cell-less homolog 1 (Drosophila)	312516	Rn.22813	AI548252	2.93	2.69	2.82	2.70	2.69	2.58	1.12	down	1.12E-01	8.95E-01	-	-
1373237_at	---	---	---	---	BI281233	2.28	3.25	2.86	2.87	3.17	2.84	1.12	up	6.22E-01	8.95E-01	-	-
1387650_at	Prok1	prokineticin 1	192205	Rn.82757	NM_138851	2.51	2.69	2.55	2.49	2.51	2.26	1.12	down	1.76E-01	8.95E-01	-	-
1374956_at	Pcm1	pericentriolar material 1	81740	Rn.98622	BE101520	8.35	7.75	7.75	7.86	7.77	7.74	1.12	down	4.75E-01	8.95E-01	-	-
1371723_at	Rragc	Ras-related GTP binding C	298514	Rn.6455	BE110635	7.43	7.56	7.66	7.63	7.46	7.08	1.12	down	4.12E-01	8.95E-01	-	-
1385854_at	LOC683655	similar to ADAM 22 precursor (A disintegrin and metalloproteinase domain 22	683655	---	AI029994	2.93	2.36	2.38	2.45	2.38	2.36	1.12	down	4.40E-01	8.95E-01	-	-
1387201_at	Rnf138	ring finger protein 138	94196	Rn.6814	NM_053588	4.02	3.53	3.52	3.51	3.72	3.36	1.12	down	4.57E-01	8.95E-01	-	-
1379544_at	---	---	---	Rn.147930	AI146108	6.59	6.44	5.99	5.33	6.41	6.79	1.12	down	7.51E-01	9.19E-01	-	-
1374617_at	Dhrs7b	dehydrogenase/reductase (SDR family) member 7B	287380	Rn.203124	AI408791	5.15	5.05	4.24	5.09	4.68	5.15	1.12	up	6.46E-01	8.95E-01	-	-
1371145_at	---	---	---	---	Z11995	6.74	3.91	3.82	4.93	5.87	3.19	1.12	down	9.03E-01	9.70E-01	-	-
1398837_at	Tceb2	transcription elongation factor B (SIII), polypeptide 2	81807	Rn.108140	NM_031129	8.02	8.59	8.33	8.60	8.22	8.59	1.12	up	4.81E-01	8.95E-01	-	-
1387974_a_at	Slc21a4	kidney specific organic anion transporter	80899	Rn.202967	AF445995	8.69	9.42	9.67	9.06	9.59	9.60	1.12	up	6.66E-01	8.99E-01	-	-
1388439_at	Fkbp10	FK506 binding protein 10	360627	Rn.62446	BI282959	2.82	2.41	2.53	2.53	3.17	2.53	1.12	up	5.46E-01	8.95E-01	-	-
1383296_a_at	Xpo4	exportin 4	299280	Rn.204363	BF397646	3.20	2.76	2.78	2.74	2.76	2.76	1.12

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1377268_at	RGD1310597	similar to RIKEN cDNA 1200014M14	294667	Rn.205704	BM390418	3.65	3.70	3.45	3.43	3.45	3.43	1.12	down	1.04E-01	8.95E-01	-	-
1375599_at	---	---	---	---	BF414469	2.92	2.51	2.56	2.46	2.57	2.48	1.12	down	2.94E-01	8.95E-01	-	-
1385837_at	Hoxd3	homeo box D3	288152	Rn.100101	AA956624	2.78	2.56	2.75	2.74	3.20	2.84	1.12	up	4.44E-01	8.95E-01	-	-
1395054_at	Usp29	ubiquitin specific peptidase 29	361495	Rn.162413	BF416262	5.02	3.80	3.75	4.17	3.84	4.09	1.12	down	7.29E-01	9.14E-01	-	-
1383131_at	Itgb2	integrin beta 2	309684	Rn.42962	AI177292	2.60	3.16	2.62	2.58	2.74	2.59	1.12	down	4.51E-01	8.95E-01	-	-
1388562_at	Stard7	StAR-related lipid transfer (START) domain containing 7	296128	Rn.20506	BI282011	8.61	8.86	8.67	8.15	8.75	8.76	1.12	down	5.05E-01	8.95E-01	-	-
1385204_at	RGD1565551	similar to RIKEN cDNA 4833418A01	499807	Rn.21777	AI639503	2.66	2.67	3.16	2.70	2.68	2.64	1.12	down	3.89E-01	8.95E-01	-	-
1392975_at	LOC686393	similar to Protease-associated domain-containing protein of 21 kDa precursor	686393	---	AI058938	6.76	7.03	6.85	7.23	6.44	7.45	1.12	up	6.43E-01	8.95E-01	-	-
1370382_at	RT1-Db1	RT1 class II, locus Db1	294270	Rn.33311	BI279526	6.17	3.38	3.82	5.80	3.07	4.02	1.12	down	8.99E-01	9.69E-01	-	-
1385353_at	Fam168a	family with sequence similarity 168, member A	361614	Rn.137163	BE116881	2.39	2.39	2.88	2.39	2.40	2.40	1.12	down	3.82E-01	8.95E-01	-	-
1379353_at	Aasdhppt	aminoadipate-semialdehyde dehydrogenase-phosphopantetheinyl transferase	300328	Rn.17217	AI233726	9.89	9.72	9.85	9.87	9.92	10.14	1.12	up	1.74E-01	8.95E-01	-	-
1390541_at	Ush1c	Usher syndrome 1C homolog (human)	308596	Rn.24615	BI291932	7.43	8.03	7.64	7.30	7.57	7.76	1.12	down	5.13E-01	8.95E-01	-	-
1392607_at	---	---	---	Rn.22751	BF391141	2.34	2.33	2.34	2.81	2.34	2.33	1.12	up	3.74E-01	8.95E-01	-	-
1394508_at	Zhx3	Zinc fingers and homeoboxes 3	311604	Rn.8221	AW523707	5.15	5.42	4.73	5.91	4.20	5.67	1.12	up	7.95E-01	9.34E-01	-	-
1372485_at	Pcbd1	pterin-4 alpha-carbinolamine dehydratase/dimerization cofactor of hepatocyte	29700	Rn.81180	BF281220	8.78	8.87	8.98	8.75	8.49	8.91	1.12	down	3.02E-01	8.95E-01	-	-
1397576_at	Rad54l2	Rad54 like 2 (S. cerevisiae)	363135	Rn.21743	AI576144	2.68	2.72	3.23	2.74	2.68	2.72	1.12	down	4.22E-01	8.95E-01	-	-
1385893_at	---	---	---	Rn.32193	AA874903	6.80	7.58	6.50	6.47	6.60	7.33	1.12	down	7.24E-01	9.12E-01	-	-
1391768_at	OC888865 /// Psm	similar to 26S protease regulatory subunit 6B (TAT-binding protein 7) (TBP-7) 117262 /// 688865		Rn.11341	AA849680	2.47	2.46	2.94	2.46	2.47	2.46	1.12	down	3.71E-01	8.95E-01	-	-
1388466_at	Psmd3	proteasome (prosome, macropain) 26S subunit, non-ATPase, 3	287670	Rn.101332	BI285842	7.63	7.75	7.77	7.99	7.85	7.79	1.12	up	9.74E-02	8.95E-01	-	-
1371811_at	Bscl2	Bemardinelli-Seip congenital lipodystrophy 2 homolog (human)	361722	Rn.105761	BI278232	8.25	8.73	8.19	8.56	8.48	8.61	1.12	up	4.16E-01	8.95E-01	-	-
1379280_at	---	---	---	Rn.24155	BF523849	2.79	2.78	3.40	2.78	2.80	2.91	1.12	down	4.87E-01	8.95E-01	-	-
1382177_at	---	---	---	Rn.15386	BF415064	2.54	3.20	2.52	2.66	2.60	2.52	1.12	down	5.20E-01	8.95E-01	-	-
1367877_at	Slc11a2	solute carrier family 11 (proton-coupled divalent metal ion transporters), memb	25715	Rn.11418	NM_013173	6.84	7.39	7.05	6.99	7.10	6.73	1.12	down	4.61E-01	8.95E-01	-	-
1385378_at	Dcxr	dicitocarbonyl L-xylulose reductase	259237	Rn.10431	BI286269	2.65	2.48	3.43	2.80	2.91	3.33	1.12	up	6.60E-01	8.98E-01	-	-
1382540_at	---	---	---	Rn.219331	BI296328	6.41	5.73	6.14	6.09	6.43	6.23	1.12	up	5.15E-01	8.95E-01	-	-
1375279_at	Sertad2	SERTA domain containing 2	498423	Rn.160886	BI295862	2.67	2.66	2.42	2.67	2.90	2.66	1.12	up	2.36E-01	8.95E-01	-	-
1395129_at	---	---	---	Rn.216500	BE107340	2.72	2.68	2.67	2.68	3.25	2.61	1.12	up	4.74E-01	8.95E-01	-	-
1384857_at	Akap9	A kinase (PRKA) anchor protein (yotiao) 9	246150	Rn.202416	AI145240	8.73	7.87	8.26	7.80	8.03	8.54	1.12	down	6.57E-01	8.98E-01	-	-
1393656_at	---	---	---	---	AA892817	2.33	2.76	2.34	2.33	2.34	2.29	1.12	down	3.27E-01	8.95E-01	-	-
1388268_at	Tpm3	tropomyosin 3, gamma	117557	Rn.37575	AF053361	4.01	4.41	4.53	4.60	4.46	4.37	1.12	up	4.06E-01	8.95E-01	-	-
1371758_at	Ufc1	ubiquitin-fold modifier conjugating enzyme 1	446268	Rn.8050	BM986259	9.82	9.95	9.95	10.14	9.85	10.21	1.12	up	2.50E-01	8.95E-01	-	-
1372715_at	Sfxn1	sideroflexin 1	364678	Rn.115752	AA819349	9.47	9.71	9.68	9.51	9.45	9.42	1.12	down	1.12E-01	8.95E-01	-	-
1395535_at	Fam98a	family with sequence similarity 98, member A	313873	Rn.12770	BF548555	5.76	6.16	6.60	6.03	5.21	6.81	1.12	down	7.77E-01	9.28E-01	-	-
1372001_at	Fam98b	family with sequence similarity 98, member B	680987	Rn.2631	BF554893	5.66	6.08	6.07	5.53	5.74	6.06	1.12	down	4.88E-01	8.95E-01	-	-
1386075_at	Mina	Myc induced nuclear antigen	266670	Rn.77753	AI710379	3.33	3.31	3.39	3.36	3.39	3.76	1.12	up	2.88E-01	8.95E-01	-	-
1368661_at	Slc13a2	solute carrier family 13 (sodium-dependent dicarboxylate transporter), membe	65202	Rn.10821	U51153	9.04	9.03	8.88	8.99	8.59	8.90	1.12	down	2.90E-01	8.95E-01	-	-
1375214_at	Galnt2	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltran	292090	Rn.144772	BE111638	6.95	5.95	5.15	6.24	6.12	6.16	1.12	up	7.77E-01	9.28E-01	-	-
1377384_at	Plekhh3	pleckstrin homology domain containing, family H (with MyTH4 domain) membr	360634	Rn.92054	AI410989	3.28	3.04	3.19	3.21	3.55	3.23	1.12	up	2.90E-01	8.95E-01	-	-
1398804_at	Mak10	MAK10 homolog, amino-acid N-acetyltransferase subunit, (S. cerevisiae)	64472	Rn.73698	NM_133324	5.07	5.15	5.14	5.05	5.23	5.54	1.12	up	3.42E-01	8.95E-01	-	-
1374602_at	Tspyl1	TSPY-like 1	29544	Rn.99721	BF407207	6.44	6.78	7.40	7.01	6.80	7.27	1.12	up	6.38E-01	8.95E-01	-	-
1397486_x_at	---	---	---	Rn.209534	BF404567	2.39	2.35	2.43	2.36	2.39	2.89	1.12	up	4.11E-01	8.95E-01	-	-
1398346_at	Mapk1	Mitogen activated protein kinase 1	116590	Rn.34914	BI275581	7.70	7.21	7.01	6.96	7.39	7.09	1.12	down	5.46E-01	8.95E-01	-	-
1397152_at	---	---	---	Rn.207991	BE108638	3.23	2.55	2.26	2.56	2.50	2.50	1.12	down	6.14E-01	8.95E-01	-	-
1396446_at	Cant1	calcium activated nucleotidase 1	246272	Rn.7241	BF522502	2.82	2.65	2.66	3.37	2.72	2.53	1.12	up	5.75E-01	8.95E-01	-	-
1395980_at	---	---	---	Rn.202402	BF393243	3.24	3.23	3.26	3.25	3.20	3.75	1.12	up	4.14E-01	8.95E-01	-	-
1385165_at	Cyp39a1	cytochrome P450, family 39, subfamily a, polypeptide 1	301264	Rn.153360	BE115944	2.92	2.33	2.34	2.45	2.34	2.32	1.12	down	4.73E-01	8.95E-01	-	-
1377963_at	---	---	---	Rn.205051	AW526938	2.67	3.42	2.50	2.49	3.65	2.91	1.12	up	7.38E-01	9.16E-01	-	-
1388783_at	Hmgb1	high mobility group box 1	25459	Rn.144565	BE107162	9.01	8.99	9.41	8.80	9.09	9.05	1.12	down	3.89E-01	8.95E-01	-	-
1381612_at	---	---	---	Rn.18944	BF407802	2.48	2.47	2.55	2.49	2.50	2.99	1.12	up	3.96E-01	8.95E-01	-	-
1384607_at	---	---	---	Rn.60050	BE120546	2.46	2.92	2.49	2.48	2.48	2.44	1.12	down	3.42E-01	8.95E-01	-	-
1392573_at	Ube2a	ubiquitin-conjugating enzyme E2A, RAD6 homolog (S. cerevisiae)	298317	Rn.8585	BF284538	6.21	6.28	5.95	5.80	5.75	6.41	1.12	down	5.38E-01	8.95E-01	-	-
1384058_at	---	---	---	Rn.21035	AI059089	2.45	2.41	2.43	2.94	2.43	2.40	1.12	up	4.22E-01	8.95E-01	-	-
1391162_at	Dcdc2	doublecortin domain containing 2	291130	Rn.45430	AW522589	2.47	2.46	2.49	2.56	2.88	2.45	1.12	up	2.87E-01	8.95E-01	-	-
1373051_at	Lmbrd1	LMBR1 domain containing 1	246046	Rn.201860	BM383988	6.99	7.63	7.27	7.42	7.35	7.59	1.12	up	4.74E-01	8.95E-01	-	-
1388925_at	Sirt5	sirtuin (silent mating type information regulation 2 homolog) 5 (S. cerevisiae)	306840	Rn.137920	AI171547	6.63	7.09	7.34	6.75	7.16	6.68	1.12	down	5.70E-01	8.95E-01	-	-
1380695_at	---	---	---	Rn.177666	BM386352	8.86	9.32	8.72	9.04	9.09	9.23	1.12	up	4.51E-01	8.95E-01	-	-
1368630_at	Fabp9	fatty acid binding protein 9, testis	64822	Rn.10078	NM_022854	2.95	2.58	2.68	2.57	2.60	2.55	1.12	down	2.36E-01	8.95E-01	-	-
1380265_at	Snapc1	small nuclear RNA activating complex, polypeptide 1	314228	Rn.18361	BI294596	5.88	5.91	5.97	5.45	5.96	5.88	1.12	down	3.84E-01	8.95E-01	-	-
1398700_at	---	---	---	Rn.170626	BE097460	2.45	2.42	2.45	2.52	2.87	2.42	1.12	up	3.15E-01	8.95E-01	-	-
1371539_at	Nola2	nucleolar protein family A, member 2	287273	Rn.4216	AW921151	6.44	7.10	7.41	7.26	6.91	7.24	1.12	up	6.35E-01	8.95E-01	-	-
1386610_at	Rcbtb2	regulator of chromosome condensation (RCC1) and BTB (POZ) domain conta	290363	Rn.125257	BG865272	2.44	2.44	2.53	2.44	2.44	2.99	1.12	up	4.44E-01	8.95E-01	-	-
1382255_at	---	---	---	---	BE110785	3.62	3.68	3.53	3.70	3.92	3.68	1.12	up	1.55E-01	8.95E-01	-	-
1372655_at	---	---	---	Rn.164183	BG380323	8.11	7.16	6.68	7.34	7.06	7.08	1.12	down	7.33E-01	9.14E-01	-	-
1383365_at	Col17a1	collagen, type XVII, alpha 1	294027	Rn.40392	AI715235	3.13	2.51	2.68	2.56	2.81	2.47	1.12	down	4.95E-01	8.95E-01	-	-
1389483_at	Clt2	coflin 2, muscle	366624	Rn.101880	BI296011	7.78	8.91	8.89	8.80	8.23	9.03	1.12	up	7.40E-01	9.16E-01	-	-
1394891_at	RGD1564541	Similar to hypothetical protein FLJ22965	313433	Rn.198467	BF548290	3.57	4.15	3.43	2.88	4.52	4.23	1.12	up	7.89E-01	9.32E-01	-	-
1369002_at	Soat1	sterol O-acyltransferase 1	81782	Rn.59	NM_031118	2.83	2.60	2.95	2.30	2.82	2.79	1.12	down	4.72E-01	8.95E-01	-	-
1398049_at	Nit1	nitrilase 1	289222	Rn.64425	BF405475	4.12	3.84	3.29	4.17	3.23	3.37	1.12	down	7.01E-01	9.07E-01	-	-
1379404_at	---	---	---	Rn.15097	AI598327	2.67	2.48	2.79	2.49	2.50	2.48	1.12	down	1.60E-01	8.95E-01	-	-
1389952_at	---	---	---	Rn.73049	BG374668	2.45	2.42	2.47	2.44	2.95	2.42	1.12	up	4.18E-01	8.95E-01	-	-
1395633_at	---	---	---	Rn.206419	BF391829	2.45	2.52	2.62	2.59	2.80	2.67	1.12	up	1.16E-01	8.95E-01	-	-
1372241_at	Oaz1	ornithine decarboxylase antizyme 1	25502	Rn.266	AI411388	9.94	10.61	10.00	10.36	10.22	10.43	1.12	up	5.19E-01	8.95E-01	-	-
1384818_at	Mylk	myosin light chain kinase	288057	Rn.203004	BM383873	6.47	6.67	6.69	7.07	6.89	6.34	1.12	up	5.29E-01	8.95E-01	-	-
1393017_at	Rhpn1	rhophilin, Rho GTPase binding protein 1	300030	Rn.17241	BG378261	7.86	8.55	7.86	8.25	7.44	8.10	1.12	down	6.67E-01	8.99E-01	-	-
1382946_a_at	/// Rab1b-ps	Rab1b, member RAS oncogene family /// RAB1B, member RAS oncogene fa	0126191 /// 36176	Rn.105979	AI711306	3.67	3.61	3.93	3.12	3.94	3.67	1.12	down	5.78E-01	8.95E-01	-	-
1376661_at	LOC313672	kazrin	313672	Rn.3753	AI556122	2.83	2.33	2.35	2.37	2.35	2.33	1.12	down	3.94E-01	8.95E-01	-	-
1377987_at	Trappc5	trafficking protein particle complex 5	363858	Rn.162083	BI281852	7.27	7.24	7.20	7.43	6.94	6.87	1.12	down	4.28E-01	8.95E-01	-	-
1371314_at	Nedd4	neural precursor cell expressed, developmentally down-regulated gene 4	25489	Rn.99540	BM389736	7.45	6.84	7.58	6.64	6.93	7.83	1.12	down	7.30E-01	9.14E-01	-	-
1395577_at	---	---	---	Rn.148550	AA800508	2.37	2.51	3.35	3.49	2.61	2.60	1.12	up	7.32E-01	9.14E-01	-	-
1383074_at	Man2a1	mannosidase, alpha, class 2A, member 1	25478	Rn.163804	H32368	7.91	8.84	8.31	8.63	8.07	8.84	1.12	up	6.81E-01	9.03E-01	-	-
1389565_at	---	---	---	Rn.22478	BE113491	2.60	2.48	2.52	2.79	2.78	2.51	1.12	up	1.88E-01	8.95E-01	-	-
1371871_at	Rab12	RAB12, member RAS oncogene family	25530	Rn.11021	AI409731	5.27	4.67	4.94	5.34	5.29	4.73	1.12	up	5.79E-01	8.95E-01	-	-
1371457_at	---	---	---	Rn.212000	BI291468	2.35	2.35	2.36	2.84	2.35	2.33	1.11	up	3.98E-01	8.95E-01	-	-
1367721_at	Sdc4	syndecan 4	24771	Rn.2029	NM_012649	8.90	8.53	8.15	8.47	8.67	8.92	1.11	up	5.67E-01	8.95E-01	-	-
1391264_at	---	---	---	Rn.163715	AA875301	8.93	9.35	9.33	9.26	9.19	9.64	1.11	up	4.68E-01	8.95E-01	-	-
1372469_at	LOC688310	similar to Ephrin type-B receptor 4 precursor (Tyrosine-protein kinase recepto	686310	---	AI178901	9.12	9.60	9.54	9.19	10.12	9.43	1.11	up	6.47E-01	8.95E-01	-	-
1377907_at	Snrnp48	small nuclear ribonucleoprotein 48k (U11/U12)	291060	Rn.39699	BF287924	2.60	2.59	2.84	2.48	2.62	2.46	1.11	down	1.80E-01	8.95E-01	-	-
1399157_at	RGD1310358	similar to NNX3	308537	Rn.106288	AA849312	4.79	5.97	6.55	5.93	4.95	6.91	1.11	up	8.48E-01	9.53E-01	-	-
1388568_at	Mtvr2	mammary tumor virus receptor 2	309170	Rn.160645	AI236101	2.91	3.08	2.44	3.28	2.77	2.87	1.11	up	5.60E-01	8.95E-01	-	-
1389258_at	Rnf138	ring finger protein 138	94196	Rn.6814	AI317840	2.92	2.49	2.50	2.45	2.50	2.49	1.11	down	3.30E-01	8.95E-01	-	-
1387262_at	Ssb	Sjogren syndrome antigen B	81783	Rn.24494	NM_031119	9.14	9.49	9.10	9.16	9.64	9.39	1.11	up	4.46E-01	8.95E-01	-	-
1372700_at	---	---	---	Rn.211999	BI297236	2.53	2.56	2.53	2.66	2.52	2.90	1.11	up	2.29E-01	8.95E-01	-	-
1372721_at	---	---	---	---	AI175447	7.35	6.48	6.92	6.85	6.90	7.47	1.11	up	6.52E-01	8.97E-01	-	-
1378785_at	---	---	---	---	BI288719	3.83	3.73	3.71	2.86	3.53	4.41	1.11	down	7.46E-01	9.18E-01	-	-
1367771_at	Tsc22d3	TSC22 domain family, member 3	83514	Rn.21970	NM_031345	6.43	5.87	5.96	6.28	5.81	6.62	1.11	up	6.20E-01	8.95E-01	-	-
1373921_at	Echdc3	enoyl Coenzyme A hydratase domain containing 3	684538	Rn.202613	AI169007	8.36	8.31	7.99	7.68	7.92	8.59	1.11	down	6.26E-01	8.95E-01	-	-
1395856_at	---	---	---	---	BF289112	3.20	3.20	3.50	2.99	3.22	3.22	1.11	down	2.85E-01	8.95E-01	-	-
1383099_at	Gpbp1	GC-rich promoter binding protein 1	294734	Rn.33325	BG670905	6.79	7.89	7.95	6.99	7.56	7.60	1.11	down	7.32E-01	9.14E-01	-	-
1393965_at	---	---	---	Rn.26605	BE113438	5.66	6.35	4.51	3.87	5.53	6.65	1.11	down	8.80E-01	9.63E-01	-	-
1394899_at	Gse1	genetic suppressor element 1	307913	Rn.44725	BF543992	2.74	2.61	2.67	2.78	2.90	2.81	1.11	up	3.80E-02	8.95E-01	-	-
1382844_at	---	---	---	Rn.148910	AA819037	3.65	3.15	3.20	3.15	3.26	3.12	1.11	down	3.91E-01	8.95E-01	-	-
1394555_at	---	---	---	Rn.167854	AI501080	2.91	3.40	2.90	3.76	3.04	2.88	1.11	up	6.47E-01	8.95E-01	-	-
1371934_at	Usp21	ubiquitin specific peptidase 21	688466	Rn.136743	AI406487	5.81	5.82	5.41	6.40	5.91	5.21	1.11	up	6.95E-01	9.06E-01	-	-
1397268_at	Slc17a4	solute carrier family 17 (sodium phosphate), member 4	679784	Rn.79713	BI295515	2.49	2.48	2.48	2.48	2.95	2.49	1.11	up	3.70E-01	8.95E-01	-	-
1393170_at	RGD1561431	similar to homeobox-containing transcription factor	500125	---	BF555514	3.74	2.83	2.84	2.85	2.99	3.10	1.11	down	6.42E-01	8.95E-01	-	-
1367562_at	Sparc	secreted protein, acidic, cysteine-rich (osteonectin)	24791	Rn.98989	D28875	8.15	7.79	7.45	8.16	8.51	7.18	1.11	up	7.43E-01	9.17E-01	-	-
1382480_at	---	---	---	Rn.166331	AI060139	8.25	8.80	7.98	8.88	7.97	8.65	1.11	up	6.90E-01	9.05E-01	-	-
1374053_at	Mcm3ap	minichromosome maintenance deficient 3 (S. cerevisiae) associated protein	294339	Rn.55967	AI235774	5.25	6.79	6.93	6.41	6.36	6.67	1.11	up	7.90E-01	9.32E-01	-	-
1371946_at	RGD1303130	kidney predominant protein NCU-G1	295231	Rn.203164	BG373288	4.98	4.81	4.74	4.86	4.65	5.49	1.11	up	5.85E-01	8.95E-01	-	-
1374736_at	---	---	---	Rn.48726	AI172004	3.63	4.43	4.25	4.53	4.22	4.05	1.11	up	6.06E-01	8.95E-01	-	-
1374505_at	---	---	---	---	AI411031	5.91	5.98	5.63	6.20	5.85	5.94	1.11	up	3.55E-01	8.95E-01	-	-
1392921_at	Ppm1k	Protein phosphatase 1K (PP2C domain containing)	312381	Rn.164392	BI294990	5.52	5.77	5.95	5.77	5.78	6.15	1.11	up	4.22E-01	8.95E-01	-	-
1396329_at	---	---	---	Rn.172892	BF403992	2.51	2.47	2.53	2.98	2.52	2.48	1.11	up	3.88E-01	8.95E-01	-	-
1378075_at	Tm9sf4	transmembrane 9 superfamily protein member 4	296279	Rn.98601	BI275978	5.61	5.27	5.55	5.21	5.40	6.29	1.11	up	6.78E-01	9.02E-01	-	-
1388472_at	---	---	---	Rn.164786	AI177860	9.24	9.30	9.67	9.20	9.12	9.42	1.11	down	3.87E-01	8.95E-01	-	-
1367839_at	Fdft1	farnesyl diphosphate farnesyl transferase 1	29580	Rn.154404	NM_019238	7.22	7.78	8.16	7.31	7.54	7.85	1.11	down	6.46E-01	8.95E-01	-	-
1390406_at	Arhgap18	Rho GTPase activating protein 18	293947	Rn.106138	AI220265	9.38	9.42	9.18	9.21	8.55	9.76	1.11	down	6.84E-01	9.03E-01	-	-
1386705_at	---	---	---	---	AW921938	2.69	2.55	2.45	2.54	3.10	2.52	1.11	up	4.83E-01	8.95E-01	-	-
1376665_at	---	---	---	Rn.216664	BG670208	5.17	5.19	5.24	5.53	5.18	5.36	1.11	up	2.12E-01	8.95E-01	-	-
1390793_at	Ttc33	tetratricopeptide repeat domain 33	294774	Rn.22216	BI295759	5.33	6.38	6.76	5.31	6.47	6.23	1.11	down	7.93E-01	9.34E-01	-	-
1397174_at	Foxk1	forkhead box K1	304298	Rn.211697	AW520453	6.00	6.05	5.43	5.94	5.74	6.28	1.11	up	5.75E-01	8.95E-01	-	-
1369655_at	Pik3c3	phosphoinositide-3-kinase, class 3	65052	Rn.30010	NM_022958	3.01	3.89	3.05	2.35	4.31	3.76	1.11	up	8.23E-01	9.43E-01	-	-
1389726_at	---	---	---	Rn.106829	AW531735	2.32	2.32	2.33	2.40	2.71	2.33	1.11	up	2.50E-01	8.95E-01	-	-
1390791_at	Gas2l1	growth arrest-specific 2 like 1	360973	Rn.22169	AI172537	2.94	2.91	2.58	2.56	3.94	2.55	1.11	down	8.20E-01	9.42E-01	-	-
1379971_at	Zc3h6	zinc finger CCCH type containing 6	311415	Rn.46791	BE102241	2.61	2.58	2.68	2.82	2.60	2.92	1.11	up	1.93E-01	8.95E-01	-	-
1367538_at	---	---	---	---	BF284303	7.16	6.35	5.46	6.23	6.86	6.35	1.11	up	7.83E-01	9.30E-01	-	-
1377470_at	Ero1lb	ERO1-like beta (S. cerevisiae)	364755	Rn.22313	AI007863	2.76	2.68	2.55	2.94	2.56	2.95	1.11	up	3.34E-01	8.95E-01	-	-
1377167_at	---	---	---	Rn.165176	AA964494	5.95	6.71	6.33	6.08	6.55	6.82	1.11	up	6.40E-01	8.95E-01	-	-
1371782_at	Nipsnap3a	nipsnap homolog 3A (C. elegans)	313211	Rn.8287	BF283798	2.65	4.15	3.59	3.52	3.10	4.24	1.11	up	7.92E-01	9.33E-01	-	-
1377944_at	---	---	---	Rn.129768	AW532214	2.90	2.83	2.91	2.90	3.27	2.94	1.11	up	2.61E-01	8.95E-01	-	-
1390579_at	RGD1305222	similar to RIKEN cDNA 1810029B16	290686	Rn.27406	BI294760	3.72	3.82	4.49	5.17	2.50	3.89	1.11	down	8.57E-01	9.55E-01	-	-
1381050_at	---	---	---	---	AW251939	2.64	2.60	2.64	2.63	3.04	2.69	1.11	up	2.95E-01	8.95E-01	-	-
1373948_at	Mare	alpha globin regulatory element containing gene	360505	Rn.22962	BG376678	4.50	3.93	3.98	3.97	4.00	3.97	1.11	down	4.47E-01	8.95E-01	-	-
1382150_at	Slc25a46	solute carrier family 25, member 46	291709	Rn.12583	BG377042	9.53	8.94	9.21	8.91	9.02	9.29	1.11	down	4.85E-01	8.95E-01	-	-
1388903_at	Dynll3	dynein light chain Tctex-type 3	363448	Rn.106023	AI179335	7.81	8.59	9.43	8.72	7.78	8.86	1.11	down	8.00E-01	9.35E-01	-	-
1398527_at	Aak1	AP2 associated kinase 1	500244	Rn.203307	BE108292	2.30	2.31	2.31	2.77	2.32	2.30	1.11	up	3.69E-01	8.95E-01	-	-
1390802_at	RGD1308839	similar to RIKEN cDNA 5033414D02	293888	Rn.106153	AI170769	4.27	5.74	5.37	5.16	5.30	5.39	1.11	up	7.45E-01	9.17E-01	-	-
1398432_at	Ankrd28	ankyrin repeat domain 28	306264	Rn.11536	AI236704	3.50	3.39	3.56	3.38	4.68	3.93	1.11	up	8.56E-01	9.55E-01	-	-
1383289_at	Nif3l1	NIF3 NGG1 interacting factor 3-like 1 (S. pombe)	301431	Rn.18112	BG373214	2.57	2.48	2.60	2.53	3.09	2.50	1.11	up	4.72E-01	8.95E-01	-	-
1383850_at	LOC690000	Similar to CG3740-PA	690000	Rn.

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1384432_at	---	---	---	Rn.44961	AW531684	6.18	6.48	6.59	5.61	6.50	6.68	1.11	down	6.85E-01	9.03E-01	-	-
1381719_at	---	---	---	Rn.208368	BE115752	2.94	2.88	2.61	2.56	2.62	2.79	1.11	down	2.84E-01	8.95E-01	-	-
1370080_at	Hmox1	heme oxygenase (decycling) 1	24451	Rn.3160	NM_012580	2.87	2.87	3.33	2.87	2.87	2.86	1.11	down	3.74E-01	8.95E-01	-	-
1374687_at	---	---	---	---	BF283386	5.25	5.52	5.21	5.22	5.24	5.06	1.11	down	2.45E-01	8.95E-01	-	-
1373692_at	Ankhd1-Eif4ebp3	Ankhd1-Eif4ebp3 fusion transcript	679725	Rn.11853	BM391907	5.50	6.08	5.61	6.50	4.33	5.90	1.11	down	8.30E-01	9.47E-01	-	-
1375817_at	---	---	---	Rn.176524	BI299780	2.34	2.33	2.80	2.34	2.35	2.33	1.11	down	3.76E-01	8.95E-01	-	-
1390719_at	---	---	---	Rn.21735	BI294889	8.38	8.36	8.80	8.20	8.44	8.44	1.11	down	4.00E-01	8.95E-01	-	-
1395997_at	Klf5c	Kinesin family member 5C	311024	Rn.50843	BF392893	2.59	2.52	3.04	2.57	2.59	2.53	1.11	down	4.02E-01	8.95E-01	-	-
1388502_at	Inpp5b	inositol polyphosphate-5-phosphatase B	362590	Rn.2252	AI412624	6.65	6.01	5.18	6.02	6.05	6.24	1.11	up	7.40E-01	9.16E-01	-	-
1371419_at	Sptbn1	spectrin, beta, non-erythrocytic 1	303614	Rn.93208	AW918614	10.09	10.08	10.27	9.82	9.83	10.32	1.11	down	4.37E-01	8.95E-01	-	-
1375355_at	Mgll	Monoglyceride lipase	29254	Rn.40396	AI763565	2.28	2.28	2.74	2.28	2.28	2.27	1.11	down	3.73E-01	8.95E-01	-	-
1376001_at	Polr1e	polymerase (RNA) I polypeptide E	313245	Rn.11499	BG380440	4.66	4.78	4.66	4.10	4.66	4.88	1.11	down	5.52E-01	8.95E-01	-	-
1372819_at	Cog4	component of oligomeric golgi complex 4	361407	Rn.107734	BM382870	3.15	3.19	4.15	3.20	3.62	3.21	1.11	down	6.86E-01	9.04E-01	-	-
1387290_at	Galnt10	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltran	170501	Rn.60224	NM_130742	3.24	2.94	2.94	3.02	2.77	2.87	1.11	down	2.76E-01	8.95E-01	-	-
1380324_at	---	---	---	Rn.147783	AW435332	2.29	2.27	2.29	2.31	2.29	2.71	1.11	up	3.17E-01	8.95E-01	-	-
1390264_at	RGD1308139	similar to RIKEN cDNA 1200014J11	360563	Rn.13279	BF413854	5.42	5.70	5.42	5.32	5.11	5.64	1.11	down	4.39E-01	8.95E-01	-	-
1374671_at	Traf3ip2	Traf3 interacting protein 2	361857	Rn.9031	BI290057	3.80	4.43	3.95	3.89	3.75	4.09	1.11	down	5.13E-01	8.95E-01	-	-
1391986_at	---	---	---	---	BF398428	2.55	2.54	2.55	2.98	2.59	2.54	1.11	up	3.37E-01	8.95E-01	-	-
1373592_at	Serpinb9	serine (or cysteine) peptidase inhibitor, clade B, member 9	361241	Rn.95177	AI407094	2.66	2.65	2.66	2.65	3.13	2.64	1.11	up	3.96E-01	8.95E-01	-	-
1372243_at	Cab39	calcium binding protein 39	301574	Rn.103055	BI285336	5.97	5.92	5.69	5.79	5.52	5.81	1.11	down	2.97E-01	8.95E-01	-	-
1391476_at	---	---	---	Rn.44028	BE113113	9.12	8.56	8.85	8.59	8.32	9.15	1.11	down	6.26E-01	8.95E-01	-	-
1390827_at	---	---	---	Rn.203196	AA997679	7.52	7.53	7.18	6.26	7.55	7.96	1.11	down	7.84E-01	9.30E-01	-	-
1378434_at	---	---	---	Rn.204439	BF400808	2.72	2.72	3.21	2.73	2.74	2.73	1.11	down	4.00E-01	8.95E-01	-	-
1372481_at	---	---	---	Rn.2721	AI102873	3.14	3.16	3.14	3.19	3.14	2.66	1.11	down	4.16E-01	8.95E-01	-	-
1382268_at	Akap13	A kinase (PRKA) anchor protein 13	293024	Rn.2027	AW526712	7.04	7.54	7.95	7.65	7.19	7.23	1.11	down	6.36E-01	8.95E-01	-	-
1394549_at	---	---	---	Rn.205173	AI501695	2.82	2.36	2.38	2.36	2.38	2.37	1.11	down	3.71E-01	8.95E-01	-	-
1385324_x_at	RGD1561413	similar to BC021442 protein	500585	Rn.162129	AI548974	3.35	4.17	4.94	4.37	4.38	4.17	1.11	up	7.58E-01	9.21E-01	-	-
1383087_at	---	---	---	---	BF409251	3.70	3.45	3.15	3.92	3.25	3.59	1.11	up	5.74E-01	8.95E-01	-	-
1372839_at	Mrps35	mitochondrial ribosomal protein S35	297727	Rn.8870	BG379352	7.84	8.75	8.50	8.42	8.33	8.80	1.11	up	6.43E-01	8.95E-01	-	-
1391023_at	---	---	---	Rn.146327	AI548713	7.28	7.89	8.84	7.50	8.02	8.04	1.11	down	7.68E-01	9.24E-01	-	-
1370316_at	Hspbp1	HSPA (heat shock 70kDa) binding protein, cytoplasmic cochaperone 1	246146	Rn.4297	AF187880	3.81	3.35	3.41	3.76	3.10	3.25	1.11	down	5.67E-01	8.95E-01	-	-
1392819_at	Ms4a11	membrane-spanning 4-domains, subfamily A, member 11	361735	Rn.101878	AW921478	2.34	2.33	2.80	2.34	2.35	2.33	1.11	down	3.77E-01	8.95E-01	-	-
1371977_at	Arpc3	actin related protein 2/3 complex, subunit 3	288669	Rn.4233	BG381477	10.08	10.35	9.90	10.20	10.27	10.32	1.11	up	3.23E-01	8.95E-01	-	-
1385169_at	---	---	---	Rn.222051	AI230598	4.76	3.64	3.80	3.68	4.24	3.82	1.11	down	7.14E-01	9.10E-01	-	-
1397600_at	Vezt	vezatin, adherens junctions transmembrane protein	299738	Rn.16786	AI717400	2.58	2.55	2.96	2.55	2.56	2.51	1.11	down	3.11E-01	8.95E-01	-	-
1384019_a_at	---	---	---	Rn.187064	BM383449	7.00	6.88	6.57	6.18	6.55	7.25	1.11	down	6.74E-01	9.01E-01	-	-
1375551_at	Ccdc86	coiled-coil domain containing 86	293738	Rn.40466	BG379782	4.51	4.53	4.71	4.89	4.52	4.78	1.11	up	2.94E-01	8.95E-01	-	-
1388805_at	Ppp2ca	Protein phosphatase 2 (formerly 2A), catalytic subunit, alpha isoform	24672	Rn.1271	AF408792	8.59	9.34	9.43	8.74	8.90	9.25	1.11	down	6.46E-01	8.95E-01	-	-
1390962_at	---	---	---	Rn.167071	BM385344	8.00	7.13	7.52	6.99	7.17	8.02	1.11	down	7.25E-01	9.13E-01	-	-
1391957_at	Katnal1	katanin p60 subunit A-like 1	288449	Rn.208215	BE113374	2.52	2.53	2.49	2.46	2.81	2.72	1.11	up	2.26E-01	8.95E-01	-	-
1382022_at	---	---	---	---	BF285121	4.55	4.65	5.07	4.04	4.55	5.22	1.11	down	7.06E-01	9.08E-01	-	-
1384367_at	RGD1563516	similar to histone protein Hist2h3c1	690148	Rn.72468	AI715140	2.63	2.63	2.76	2.62	2.63	3.22	1.11	up	4.92E-01	8.95E-01	-	-
1384343_at	---	---	---	Rn.107931	BE112536	3.54	3.06	3.11	3.09	3.07	3.08	1.11	down	3.72E-01	8.95E-01	-	-
1389352_at	---	---	---	Rn.14154	BF281980	6.88	6.87	6.81	6.45	6.78	6.88	1.11	down	3.14E-01	8.95E-01	-	-
1367463_at	Phb2	prohibitin 2	114766	Rn.64535	AI235510	9.78	10.13	9.53	10.28	9.47	10.15	1.11	up	6.43E-01	8.95E-01	-	-
1396810_at	---	---	---	Rn.123234	AI578423	2.72	3.08	2.78	2.70	2.74	2.69	1.11	down	2.45E-01	8.95E-01	-	-
1370800_at	Slc9a1	Solute carrier family 9 (sodium/hydrogen exchanger), member 1	24782	Rn.5025	AF462063	2.76	2.73	2.50	2.91	2.80	2.74	1.11	up	1.89E-01	8.95E-01	-	-
1391466_at	---	---	---	---	AI170347	5.91	6.46	6.51	6.35	6.27	5.80	1.11	down	5.85E-01	8.95E-01	-	-
1380539_at	---	---	---	Rn.40467	AA956424	4.44	3.43	3.76	3.71	3.41	4.06	1.11	down	6.87E-01	9.04E-01	-	-
1392425_x_at	Luc7l	LUC7-like (S. cerevisiae)	360503	Rn.99992	BI275713	8.15	6.92	4.29	7.23	5.89	5.78	1.11	down	9.07E-01	9.72E-01	-	-
1389480_at	Rwdd4a	RWD domain containing 4A	502084	Rn.15503	AI598462	7.69	8.40	8.70	8.10	7.76	8.46	1.11	down	6.94E-01	9.05E-01	-	-
1369087_at	Flt1	fms-related tyrosine kinase 1	54251	Rn.10239	NM_019306	2.81	2.48	2.46	2.44	2.45	2.41	1.11	down	2.45E-01	8.95E-01	-	-
1398974_at	Cse1l	chromosome segregation 1-like (S. cerevisiae)	362273	Rn.36664	AI171615	4.07	5.51	4.42	4.42	4.16	4.97	1.11	down	7.73E-01	9.26E-01	-	-
1377053_at	RGD1310810	similar to RIKEN cDNA 4930444A02	306549	Rn.39247	BE117757	5.99	6.23	5.64	5.98	5.81	6.53	1.11	up	6.13E-01	8.95E-01	-	-
1383603_at	---	---	---	Rn.165750	BM385552	5.54	6.83	6.20	6.61	6.97	7.45	1.11	up	8.59E-01	9.56E-01	-	-
1398893_at	Ndfip1	Nedd4 family interacting protein 1	291609	Rn.59254	BG671512	9.24	9.47	9.64	9.67	9.33	9.81	1.11	up	4.56E-01	8.95E-01	-	-
1399008_at	Ankrd17	ankyrin repeat domain 17	289521	Rn.8442	AW434064	4.76	4.45	4.24	4.18	4.14	4.68	1.11	down	5.50E-01	8.95E-01	-	-
1368541_at	Emb	embigin	114511	Rn.16224	NM_053719	2.73	2.41	2.48	2.40	2.40	2.36	1.11	down	1.92E-01	8.95E-01	-	-
1384530_at	LOC690208	hypothetical protein LOC690208	690208	Rn.219533	BF418775	4.80	3.79	3.12	4.41	3.67	4.09	1.11	up	7.89E-01	9.32E-01	-	-
1390624_at	RGD1559885	similar to hypothetical gene supported by BC063892	500059	Rn.20360	BM382843	2.49	2.45	2.87	2.44	2.48	2.43	1.11	down	3.23E-01	8.95E-01	-	-
1377823_at	---	---	---	Rn.165028	AW531363	6.62	7.42	7.35	7.17	7.34	7.34	1.11	up	5.91E-01	8.95E-01	-	-
1380132_at	---	---	---	Rn.166263	BI291804	2.52	2.48	2.55	2.98	2.50	2.53	1.11	up	3.84E-01	8.95E-01	-	-
1383325_at	689145 /// LOC69	hypothetical protein LOC689145 /// hypothetical protein LOC690806	689145 /// 690806	Rn.23454	AI712781	2.85	3.72	2.74	4.22	2.32	3.22	1.11	up	8.21E-01	9.43E-01	-	-
1398331_at	---	---	---	Rn.63610	BF414554	2.61	2.72	2.61	2.72	2.47	3.20	1.11	up	5.22E-01	8.95E-01	-	-
1382167_at	Sit1	signaling threshold regulating transmembrane adaptor 1	500449	Rn.47894	AW532179	2.49	5.20	3.94	3.73	3.00	5.36	1.11	up	8.92E-01	9.66E-01	-	-
1378291_at	Prpf39	PRP39 pre-mRNA processing factor 39 homolog (S. cerevisiae)	314171	Rn.12521	BF549558	2.83	3.71	3.67	3.30	3.33	3.13	1.11	down	6.34E-01	8.95E-01	-	-
1367761_at	Ndel1	nuclear distribution gene E-like homolog 1 (A. nidulans)	170845	Rn.2947	NM_133320	10.91	10.51	11.00	11.15	10.55	10.26	1.11	down	6.40E-01	8.95E-01	-	-
1377977_at	Dusp13	dual specificity phosphatase 13	361002	Rn.137327	AW534423	2.33	2.32	2.79	2.32	2.34	2.31	1.11	down	3.81E-01	8.95E-01	-	-
1398286_at	Csad	cysteine sulfinic acid decarboxylase	60356	Rn.43232	M64755	7.96	8.61	8.70	8.35	8.02	8.45	1.11	down	5.97E-01	8.95E-01	-	-
1385978_at	---	---	---	Rn.20262	AI072788	9.13	8.99	8.69	8.61	8.31	9.44	1.11	down	6.99E-01	9.07E-01	-	-
1372157_at	Bola1	bolA homolog 1 (E. coli)	365875	Rn.13864	AI232807	8.67	7.84	6.81	7.79	7.91	8.08	1.11	up	7.94E-01	9.34E-01	-	-
1396647_at	---	---	---	---	BE106767	2.30	2.31	2.31	2.29	2.30	2.78	1.11	up	3.98E-01	8.95E-01	-	-
1390856_at	---	---	---	Rn.11631	BF289100	4.23	4.73	5.08	4.22	4.09	5.28	1.11	down	7.53E-01	9.20E-01	-	-
1377893_at	LOC690000	similar to CG3740-PA	690000	Rn.2361	BM390475	5.98	5.35	6.65	5.39	5.86	6.27	1.11	down	7.55E-01	9.20E-01	-	-
1391682_at	---	---	---	---	AI698812	4.78	5.49	5.62	6.49	4.93	4.93	1.11	up	8.07E-01	9.38E-01	-	-
1391478_at	Znf532	zinc finger protein 532	307362	Rn.55564	BI281649	2.34	2.78	2.35	2.33	2.34	2.34	1.11	down	3.51E-01	8.95E-01	-	-
1382440_at	Daglb	diacylglycerol lipase, beta	304289	Rn.44074	AI410813	3.46	3.43	3.44	3.88	3.45	3.45	1.11	up	3.53E-01	8.95E-01	-	-
1387299_at	Pias2	protein inhibitor of activated STAT, 2	83422	Rn.25546	NM_053337	7.43	6.63	6.55	7.47	6.28	7.32	1.11	up	7.62E-01	9.22E-01	-	-
1373427_at	Rragd	Ras-related GTP binding D	297980	Rn.23439	BI288816	2.47	2.45	2.48	2.88	2.50	2.47	1.11	up	3.19E-01	8.95E-01	-	-
1375888_at	LOC691036	similar to SET binding factor 2	691036	Rn.37595	BE100456	4.43	3.39	2.82	3.39	3.41	3.38	1.11	down	7.63E-01	9.23E-01	-	-
1392910_at	Bop1	block of proliferation 1	300050	Rn.101388	AA859968	4.63	5.31	4.86	4.60	5.46	5.19	1.11	up	6.64E-01	8.99E-01	-	-
1396912_at	Med20	mediator complex subunit 20	316209	Rn.222033	BE102712	2.68	2.73	2.85	3.02	2.88	2.82	1.11	up	1.22E-01	8.95E-01	-	-
1368060_at	Hrsp12	heat-responsive protein 12	65151	Rn.6987	NM_031714	12.24	12.02	12.03	11.97	11.87	12.00	1.11	down	1.38E-01	8.95E-01	-	-
1379325_at	Mkrn1	makorin ring finger protein 1	296988	Rn.101798	BI274837	5.05	5.63	5.56	6.10	4.17	5.50	1.11	down	8.13E-01	9.40E-01	-	-
1381682_at	Fgd6	FYVE, RhoGEF and PH domain containing 6	500824	Rn.162933	AI072357	2.99	2.57	2.66	2.59	2.64	2.53	1.11	down	3.09E-01	8.95E-01	-	-
1393576_at	---	---	---	Rn.32972	AA863889	4.18	5.10	4.65	4.87	3.91	5.61	1.11	up	8.00E-01	9.35E-01	-	-
1391427_at	Dimt1l	DIM1 dimethyladenosine transferase 1-like (S. cerevisiae)	294718	Rn.25178	AW254563	4.78	4.69	4.81	5.14	4.64	4.96	1.11	up	3.73E-01	8.95E-01	-	-
1398845_at	Eif5	eukaryotic translation initiation factor 5	56783	Rn.40123	BE107346	8.93	8.83	8.53	8.81	8.94	8.99	1.11	up	3.07E-01	8.95E-01	-	-
1386875_a_at	Clta	clathrin, light chain (Lca)	83800	Rn.112599	M19261	9.13	10.03	9.94	9.97	9.51	10.08	1.11	up	6.74E-01	9.01E-01	-	-
1369682_at	Hnf1b	HNF1 homeobox B	25640	Rn.11342	NM_013103	7.53	7.93	6.81	7.75	7.45	7.52	1.11	up	6.78E-01	9.02E-01	-	-
1369082_at	Dffa	DNA fragmentation factor, alpha subunit	114214	Rn.6514	NM_053679	2.56	2.56	2.89	2.46	2.55	2.54	1.11	down	2.56E-01	8.95E-01	-	-
1367748_at	Arl5	ADP-ribosylation factor 5	79117	Rn.28244	NM_024149	4.59	4.57	4.71	4.02	5.74	4.57	1.11	up	7.82E-01	9.29E-01	-	-
1385248_a_at	Ogn	osteoglycin	291015	Rn.103114	AA997590	5.62	4.75	4.17	4.27	5.49	4.32	1.11	down	8.07E-01	9.38E-01	-	-
1368426_at	Crot	carnitine O-octanoyltransferase	83842	Rn.4896	J02844	5.99	6.45	6.60	6.43	6.31	6.76	1.11	up	5.42E-01	8.95E-01	-	-
1388465_at	RGD1359600	LEA_4 domain containing protein RGD1359600	307343	Rn.8288	AA891733	9.31	8.97	8.87	8.94	9.36	9.30	1.11	up	4.64E-01	8.95E-01	-	-
1382218_at	RGD1305807	Ras-related GTP binding D	297860	Rn.18576	AI012175	5.03	5.00	5.05	4.93	4.67	5.93	1.11	up	7.14E-01	9.10E-01	-	-
1385974_at	Pard6g	par-6 partitioning defective 6 homolog gamma (C. elegans)	307237	Rn.203310	BM384723	2.48	2.64	2.74	2.50	2.41	2.49	1.11	down	1.37E-01	8.95E-01	-	-
1391956_at	---	---	---	Rn.210103	BF393928	2.35	2.34	2.81	2.36	2.35	2.33	1.11	down	3.90E-01	8.95E-01	-	-
1399134_at	LOC500054	similar to POT1-like telomere end-binding protein	500054	Rn.13804	AW144008	2.52	2.56	2.54	2.56	2.74	2.78	1.11	up	9.02E-02	8.95E-01	-	-
1383690_at	LOC366473	similar to ornithine decarboxylase-like protein	366473	Rn.50921	BE121288	2.59	3.04	2.60	2.59	2.59	2.59	1.11	down	3.65E-01	8.95E-01	-	-
1375296_at	LOC684097	similar to sorting nexin 3	684097	Rn.873	AI407178	8.78	8.83	9.01	8.65	8.72	8.79	1.11	down	1.34E-01	8.95E-01	-	-
1378464_at	---	---	---	Rn.212827	BM385973	2.94	2.37	2.39	2.49	2.39	2.37	1.11	down	4.70E-01	8.95E-01	-	-
1367595_s_at	B2m	beta-2 microglobulin	24223	Rn.1868	NM_012512	10.26	10.93	11.11	10.72	10.97	11.07	1.11	up	6.15E-01	8.95E-01	-	-
1392574_at	Znf287	zinc finger protein 287	303212	Rn.13149	AI013120	2.35	2.72	2.32	2.31	2.32	2.30	1.11	down	3.03E-01	8.95E-01	-	-
1384177_at	Gramd3	GRAM domain containing 3	307288	Rn.53932	BI281497	2.51	2.58	2.61	3.00	2.62	2.54	1.11	up	3.54E-01	8.95E-01	-	-
1374535_at	Afap1l2	actin filament associated protein 1-like 2	292130	Rn.161912	BI283881	2.57	2.56	2.71	2.65	2.71	2.79	1.11	up	1.78E-02	8.95E-01	-	-
1381620_at	---	---	---	Rn.209602	BF389656	2.63	3.18	2.67	2.70	2.68	2.65	1.11	down	4.41E-01	8.95E-01	-	-
1378696_at	---	---	---	Rn.156015	BF409584	2.30	2.36	3.33	2.96	2.74	2.74	1.11	up	6.82E-01	9.03E-01	-	-
1377228_at	---	---	---	Rn.154036	BF411981	3.05	2.83	2.88	2.87	2.89	2.56	1.11	down	2.94E-01	8.95E-01	-	-
1376935_at	---	---	---	Rn.19631	BE113667	5.00	4.99	5.15	4.99	4.35	5.34	1.11	down	6.34E-01	8.95E-01	-	-
1386566_at	---	---	---	Rn.199248	BF558962	6.34	7.08	7.92	7.61	6.71	7.48	1.11	up	7.93E-01	9.33E-01	-	-
1376722_at	Nup205	nucleoporin 205	362335	Rn.23694	AI409108	3.96	2.97	2.71	2.97	2.61	3.61	1.11	down	7.69E-01	9.25E-01	-	-
1378939_at	Ccr10	chemokine (C-C motif) receptor 10	363682	Rn.49807	BG377737	2.99	2.56	2.57	2.72	2.57	2.38	1.11	down	4.31E-01	8.95E-01	-	-
1387942_at	Slc35e4	solute carrier family 35, member E4	266687	Rn.15189	AF182714	2.53	2.53	2.54	3.01	2.53	2.51	1.11	up	4.06E-01	8.95E-01	-	-
1392477_at	Etv1	ets variant 1	362733	Rn.76536	AI059914	6.87	5.78	7.89	6.96	6.83	6.30	1.11	down	8.25E-01	9.45E-01	-	-
1385969_at	Adamts16	ADAM metallopeptidase with thrombospondin type 1 motif, 16	306664	Rn.24707	AI233226	2.53	2.47	2.51	2.50	3.02	2.45	1.11	up	4.59E-01	8.95E-01	-	-
1379874_at	Mrpl51	mitochondrial ribosomal protein L51	297601	Rn.154004	BE107929	5.29	5.56	5.78	5.91	6.13	4.15	1.11	down	8.26E-01	9.45E-01	-	-
1380836_at	RGD1562726	similar to Putative protein C21orf62 homolog	498060	Rn.165531	BG380809	3.35	2.56	2.57	2.55	2.58	2.91	1.11	down	6.24E-01	8.95E-01	-	-
1398904_at	Nono	non-POU domain containing, octamer-binding	317259	Rn.8381	AI599066	9.44	9.70	9.59	9.21	9.61	9.47	1.11	down	3.35E-01	8.95E-01	-	-
1387185_at	Apbb3	amyloid beta (A4) precursor protein-binding, family B, member 3	117026	Rn.30067	NM_053957	2.69	2.72	3.06	2.73	2.58	2.72	1.11	down	2.99E-01	8.95E-01	-	-
1394078_at	---	---	---	---	AW921158	7.12	7.12	6.64	6.76	7.10	7.48	1.11	up	5.99E-01	8.95E-01	-	-
1395122_s_at	Cdk10	cyclin-dependent kinase 10	361434	Rn.20472	BF291194	3.07	3.46	2.92	3.05	2.91	3.04	1.11	down	4.20E-01	8.95E-01	-	-
1390953_at	Zbtb11	zinc finger and BTB domain containing 11	304010	Rn.162011	BE111052	2.76	2.32	2.33	2.33	2.32	2.32	1.11	down	3.57E-01	8.95E-01	-	-
1370400_at	RT1-N3	RT1 class Ib gene, H2-TL-like, grc region (N3)	24750	Rn.202956	L23128	2.80	2.47	2.43	2.43	2.42	2.40	1.11	down	2.79E-01	8.95E-01	-	-
1371794_at	LOC688018	Similar to SH3-domain binding protein 3	688018	Rn.162688	BM391449	8.76	8.97	8.85	8.91	8.92	9.19	1.11	up	2.49E-01	8.95E-01	-	-
1390399_at	Crebl2	cAMP responsive element binding protein-like 2	362453	Rn.107553	BE102391	6.27	6.42	6.57	6.26	6.13	6.43	1.11	down	2.88E-01	8.95E-01	-	-
1373264_at	Zbed3	zinc finger, BED-type containing 3	361881	Rn.103511	BE110658	2.56	2.50	3.37	2.54	2.57	2.87	1.11	down	6.42E-01	8.95E-01	-	-
1380690_at	---	---	---	Rn.168007	AW534142	3.46	3.53	3.47	3.42	3.47	4.03	1.11	up	4.89E-01	8.95E-01	-	-
1393228_at	Hpdl	4-hydroxyphenylpyruvate dioxygenase-like	313521	Rn.9366	AA957707	8.44	7.01	5.04	7.62	5.42	7.89	1.11	up	9.11E-01	9.73E-01	-	-
1378004_at	---	---	---	Rn.166203	BF287788	3.54	3.79	3.77	3.89	3.70	3.95	1.11	up	2.48E-01	8.95E-01	-	-
1370770_s_at	Kitlg	KIT ligand	60427	Rn.44216	AF071205	2.43	2.43	2.87	2.43	2.44	2.41	1.11	down	3.68E-01	8.95E-01	-	-
1373781_a_at	Sbsn	suprabasin	292793	Rn.8878	AI555257	2.49	2.48	2.96	2.48	2.96	2.47	1.11	up	4.05E-01	8.95E-01	-	-
1383427_at	Man1b1	mannosidase, alpha, class 1B, member 1	499751	Rn.86273	AI229831	2.65	2.18	2.19	2.18	3.11	2.18	1.11	up	6.88E-01	9.04E-01	-	-
1397441_at	Ttc13	tetratricopeptide repeat domain 13	292095	Rn.98912	BM390838	2.54	2.54	2.54	2.54	2.55	2.98	1.11	up	3.64E-01	8.95E-01	-	-
1371873_at	Anp32e	Acidic (leucine-rich) nuclear phosphoprotein 32 family, member E	361999	Rn.4268	AA850735	7.09	7.46	7.05	7.26	7.30	7.49	1.11	up	3.66E-01	8.95E-01	-	-
1372254_at	Serping1	serine (or cysteine) peptidase inhibitor, clade G, member 1	295703	Rn.100285	AW915763	7.65	9.23	8.75	8.40	8.11	8.66	1.11	down	7.76E-01	9.27E-01	-	-
1374008_at	---	---	---	---	BI296700	2.38	2.37	2.40	2.83	2.38	2.40	1.11	up	3.62E-01	8.95E-01	-	-
1383505_at	---	---	---	Rn.25271	BI277767	3.01	3.02	3.78	3.12	3.12	3.12	1.11	down	5.88E-01	8.95E-01	-	-
1390598_at	---	---	---	Rn.127872	BI294871	4.33	5.05	3.73	4.05	5.18	4.34	1.11	up	7.83E-01	9.30E-01	-	-
1377042_at	Pcgf5	polycomb group ring finger 5	681178	Rn.31865	BI288196	4.00	4.12	3.62	3.89	3.66	4.64	1.11	up	6.76E-01	9.02E-01	-	-
1369063_at	Anp32a	acidic (leucine-rich) nuclear phosphoprotein 32 family, member A	25379	Rn.10123	NM_012903	8.79	9.52	9.18	8.91	10.12	8.

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1388640_at	Sumo3	SMT3 suppressor of mif two 3 homolog 3 (S. cerevisiae)	499417	Rn.154914	BI279654	10.05	10.38	9.92	9.75	9.98	10.16	1.11	down	4.56E-01	8.95E-01	-	-
1391326_at	Hoxb5	homeo box B5	497987	Rn.206925	BE095733	5.92	5.14	4.71	4.15	6.21	4.96	1.11	down	8.40E-01	9.50E-01	-	-
1392653_at	---	---	---	Rn.165287	BE118116	8.30	7.72	7.48	7.53	7.68	7.85	1.11	down	5.98E-01	8.95E-01	-	-
1384123_at	---	---	---	Rn.155723	BF559782	2.73	2.79	2.66	2.65	2.64	3.33	1.11	up	5.56E-01	8.95E-01	-	-
1377261_at	---	---	---	Rn.50824	BE105858	2.96	2.52	2.56	2.53	2.55	2.51	1.11	down	3.42E-01	8.95E-01	-	-
1372351_at	Brd4	bromodomain containing 4	362844	Rn.12110	AI229448	6.67	6.68	7.03	6.43	6.84	6.66	1.11	down	4.24E-01	8.95E-01	-	-
1369227_at	Chm	choroideremia (Rab escort protein 1)	24942	Rn.10191	NM_017067	3.50	3.46	4.61	3.93	4.16	3.93	1.11	up	7.19E-01	9.11E-01	-	-
1395110_at	---	---	---	Rn.50434	BE110272	2.59	2.59	2.59	3.13	2.50	2.59	1.11	up	4.96E-01	8.95E-01	-	-
1382857_at	---	---	---	Rn.148437	BE108794	8.34	8.13	8.18	7.62	8.37	8.21	1.11	down	5.62E-01	8.95E-01	-	-
1397167_at	Senp8	SUMO/sentrin specific peptidase family member 8	315723	Rn.145873	BF283259	2.47	2.47	2.48	2.46	2.47	2.93	1.11	up	3.91E-01	8.95E-01	-	-
1373216_at	LOC691849	hypothetical protein LOC691849	691849	Rn.160156	AI236521	6.38	6.82	5.91	6.47	6.24	6.85	1.11	up	6.65E-01	8.99E-01	-	-
1367687_a_at	Pam	peptidylglycine alpha-amidating monooxygenase	25508	Rn.1121	AW534339	7.84	7.13	7.00	7.93	6.85	7.65	1.11	up	7.38E-01	9.16E-01	-	-
1380395_at	---	---	---	Rn.3287	AI230394	4.98	5.03	4.67	5.51	4.61	4.99	1.11	up	6.29E-01	8.95E-01	-	-
1373535_at	Enah	enabled homolog (Drosophila)	360891	Rn.163240	BF397848	3.75	3.73	4.56	4.38	4.14	3.97	1.11	up	6.44E-01	8.95E-01	-	-
1381912_at	---	---	---	Rn.169966	AW532251	2.61	3.02	2.62	2.60	2.61	2.59	1.11	down	3.36E-01	8.95E-01	-	-
1398042_at	---	---	---	Rn.210682	BF400265	2.39	2.54	2.41	2.99	2.40	2.39	1.11	up	5.07E-01	8.95E-01	-	-
1372330_at	LOC652955	goliath	652955	Rn.186211	BM391371	6.47	6.23	6.64	6.41	6.47	6.90	1.11	up	4.91E-01	8.95E-01	-	-
1395542_at	---	---	---	Rn.187061	BF549929	5.88	6.61	6.50	6.04	6.70	6.69	1.11	up	6.63E-01	8.98E-01	-	-
1382721_at	Ggnbp2	gametogenetin binding protein 2	360584	Rn.48466	BI280928	7.58	7.64	7.95	7.90	7.64	8.08	1.11	up	4.36E-01	8.95E-01	-	-
1389488_at	---	---	---	---	AA800750	10.38	10.63	9.73	10.36	10.42	10.40	1.11	up	6.10E-01	8.95E-01	-	-
1393542_at	---	---	---	Rn.200126	BF403870	2.72	2.47	2.75	2.46	2.56	2.47	1.11	down	1.84E-01	8.95E-01	-	-
1385004_at	---	---	---	Rn.207826	BE107527	2.50	2.87	2.50	2.49	2.49	2.44	1.11	down	2.94E-01	8.95E-01	-	-
1382326_at	Dedd	Death effector domain-containing	83631	Rn.203286	AI555347	7.89	7.89	6.58	7.24	7.62	7.94	1.11	up	7.73E-01	9.26E-01	-	-
1382296_at	---	---	---	Rn.16839	BF291041	2.89	2.42	2.46	2.43	2.46	2.43	1.11	down	3.75E-01	8.95E-01	-	-
1382780_at	---	---	---	Rn.21060	AI059229	5.78	4.69	3.66	4.86	4.67	5.04	1.11	up	8.23E-01	9.43E-01	-	-
1396082_at	Kbtbd3	kelch repeat and BTB (POZ) domain containing 3	315394	Rn.98988	BG668869	5.20	3.74	2.72	3.68	4.20	4.24	1.11	up	8.51E-01	9.54E-01	-	-
1369632_a_at	Abcc8	ATP-binding cassette, sub-family C (CFTR/MRP), member 8	25559	Rn.11187	AB052294	4.16	3.41	3.57	3.56	3.63	3.51	1.11	down	5.52E-01	8.95E-01	-	-
1380763_at	---	---	---	Rn.199908	AI101194	4.04	3.74	2.79	2.99	3.37	3.75	1.11	down	7.50E-01	9.19E-01	-	-
1380398_at	---	---	---	Rn.149024	AI168970	2.65	2.64	2.64	3.23	2.65	2.49	1.11	up	5.46E-01	8.95E-01	-	-
1384742_at	Atrx	Alpha thalassemia/mental retardation syndrome X-linked (RAD54 homolog, S	246284	Rn.107838	BF389776	3.16	2.65	2.71	2.78	2.67	2.62	1.11	down	4.27E-01	8.95E-01	-	-
1378442_at	---	---	---	Rn.210335	BF400763	2.40	2.37	2.41	2.38	2.73	2.52	1.11	up	2.22E-01	8.95E-01	-	-
1385409_at	Myo10	myosin X	310178	Rn.20775	AI045505	7.25	7.93	8.42	8.07	7.31	7.78	1.11	down	7.32E-01	9.14E-01	-	-
1389168_at	Mkks	McKusick-Kaufman syndrome	311456	Rn.8839	AI412239	7.87	8.16	8.21	7.58	8.17	8.04	1.11	down	5.17E-01	8.95E-01	-	-
1380730_at	Atp6v0a2 /// Tect2	Atp6v0a2 /// Tect2	116455 /// 679779	Rn.204067	BE110564	3.26	3.31	3.26	3.35	3.30	3.62	1.11	up	2.11E-01	8.95E-01	-	-
1390687_at	Plek	pleckstrin	364206	Rn.6178	AI556803	2.85	2.84	2.33	2.86	2.81	2.81	1.11	up	4.41E-01	8.95E-01	-	-
1396018_at	---	---	---	Rn.165856	BF416830	2.97	3.23	3.43	3.19	3.26	3.62	1.11	up	4.75E-01	8.95E-01	-	-
1387971_a_at	Mapk8ip1	mitogen-activated protein kinase 8 interacting protein 1	116457	Rn.44266	AF092450	3.96	3.96	3.96	4.86	3.51	3.96	1.11	up	7.27E-01	9.13E-01	-	-
1396437_at	---	---	---	Rn.217117	BM390854	2.46	2.44	2.49	2.43	3.00	2.41	1.11	up	4.84E-01	8.95E-01	-	-
1379369_at	Prickle1	prickle homolog 1 (Drosophila)	315259	Rn.141040	AI171526	2.88	3.57	3.15	2.73	2.74	3.69	1.11	down	7.12E-01	9.10E-01	-	-
1393760_at	Wars2	tryptophanyl tRNA synthetase 2 (mitochondrial)	690654	Rn.204847	BE116401	2.96	4.61	2.97	3.00	3.69	4.30	1.11	up	8.35E-01	9.48E-01	-	-
1381075_at	---	---	---	Rn.32887	AA956937	7.50	7.91	7.27	8.10	6.30	7.84	1.11	down	8.14E-01	9.40E-01	-	-
1380387_at	Foxp2	forkhead box P2	500037	Rn.134464	BE105492	2.70	4.47	4.15	2.94	4.63	4.20	1.11	up	8.52E-01	9.54E-01	-	-
1382313_at	---	---	---	Rn.220047	AI511408	2.83	3.67	2.56	2.83	3.16	3.51	1.11	up	7.21E-01	9.11E-01	-	-
1385845_at	RGD1564854	similar to divalent cation tolerant protein CUTA	502617	Rn.139718	BM391000	2.79	2.78	2.79	2.51	2.79	3.50	1.11	up	6.43E-01	8.95E-01	-	-
1375723_at	---	---	---	Rn.167755	AI385171	3.39	3.34	3.77	3.39	3.40	3.26	1.11	down	3.63E-01	8.95E-01	-	-
1384467_at	Nadk	NAD kinase	100125370	Rn.28371	BF420276	4.06	4.27	4.05	4.05	4.00	3.90	1.11	down	1.55E-01	8.95E-01	-	-
1382005_at	---	---	---	Rn.51103	BI280285	7.22	7.09	7.72	7.16	7.68	7.62	1.11	up	5.88E-01	8.95E-01	-	-
1369734_at	Acox3	acyl-Coenzyme A oxidase 3, pristanoyl	83522	Rn.10546	NM_053339	3.78	3.88	3.69	3.61	3.69	3.62	1.11	down	6.94E-02	8.95E-01	-	-
1374151_at	---	---	---	Rn.162432	BI289940	2.63	2.72	2.56	2.63	2.98	2.74	1.11	up	2.56E-01	8.95E-01	-	-
1372014_at	Med27	mediator complex subunit 27	296612	Rn.105472	BM392138	2.58	2.40	2.55	2.54	2.55	2.88	1.11	up	3.11E-01	8.95E-01	-	-
1370838_s_at	Spna2	alpha-spectrin 2	64159	Rn.5812	BM387423	9.35	9.56	9.14	9.45	8.99	9.15	1.11	down	4.60E-01	8.95E-01	-	-
1390070_at	---	---	---	Rn.48990	BI296990	2.90	2.44	2.45	3.36	2.45	2.42	1.11	up	6.90E-01	9.05E-01	-	-
1383571_at	Rapgef1	Rap guanine nucleotide exchange factor (GEF)-like 1	303515	Rn.17949	AF411217	2.39	2.38	2.40	2.85	2.40	2.37	1.11	up	3.92E-01	8.95E-01	-	-
1384531_at	Crb3	crumbs homolog 3 (Drosophila)	301112	Rn.14560	BF553130	5.64	3.14	2.93	3.13	4.49	3.65	1.11	down	8.85E-01	9.64E-01	-	-
1385455_at	Prpf38b	PRP38 pre-mRNA processing factor 38 (yeast) domain containing B	499691	Rn.72151	BF397866	3.67	4.70	3.05	4.07	4.04	3.75	1.11	up	7.78E-01	9.28E-01	-	-
1386671_at	Lrrc19	leucine rich repeat containing 19	680478	Rn.178166	AW921309	3.68	3.23	3.43	3.29	3.35	3.26	1.11	down	3.32E-01	8.95E-01	-	-
1374642_at	Zfp64	zinc finger protein 64	311661	Rn.6243	BI296003	2.37	2.39	2.37	2.38	2.53	2.68	1.11	up	1.70E-01	8.95E-01	-	-
1383502_at	Topbp1	topoisomerase (DNA) II binding protein 1	315969	Rn.204161	BE113753	3.35	3.68	3.36	3.30	3.33	3.32	1.11	down	2.48E-01	8.95E-01	-	-
1378808_at	---	---	---	Rn.18925	AA925542	2.56	2.67	2.54	2.97	2.76	2.48	1.11	up	3.77E-01	8.95E-01	-	-
1381335_at	---	---	---	---	BE349658	2.99	2.98	2.97	3.45	3.07	2.86	1.11	up	4.45E-01	8.95E-01	-	-
1375340_at	---	---	---	Rn.203235	AI104151	11.83	11.61	11.87	11.90	12.01	11.84	1.11	up	2.01E-01	8.95E-01	-	-
1397731_at	---	---	---	Rn.165471	AA980690	6.62	6.74	6.81	6.27	6.73	6.73	1.11	down	4.12E-01	8.95E-01	-	-
1388603_a_at	Isca1	iron-sulfur cluster assembly 1 homolog (S. cerevisiae)	290985	Rn.1180	BM384289	9.17	9.16	9.58	9.52	9.03	9.81	1.11	up	6.11E-01	8.95E-01	-	-
1372564_at	Ets2	v-ets erythroblastosis virus E26 oncogene homolog 2 (avian)	304063	Rn.164554	AI411375	6.65	7.54	7.50	7.00	7.64	7.49	1.11	up	6.95E-01	9.06E-01	-	-
1376501_at	Arhgap8	Rho GTPase activating protein 8	300115	Rn.7830	AA945062	3.47	4.07	4.30	4.50	3.65	5.25	1.11	down	8.88E-01	9.65E-01	-	-
1387019_at	Atp5i	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit E	140608	Rn.66347	NM_080481	8.38	8.04	8.36	8.14	8.10	8.09	1.11	down	2.57E-01	8.95E-01	-	-
1388769_at	Traf7	Tnf receptor-associated factor 7	360491	Rn.163128	BI287266	2.35	3.19	2.55	2.55	2.54	2.54	1.11	down	5.95E-01	8.95E-01	-	-
1388145_at	Tnxa /// Tnxb	tenascin XA /// tenascin XB	25602 /// 415089	Rn.36545	BM390128	3.75	3.64	3.65	4.10	3.56	3.82	1.11	up	4.06E-01	8.95E-01	-	-
1397255_at	Ccdc86	coiled-coil domain containing 86	293738	Rn.40486	AW533685	2.37	2.32	2.73	2.33	2.34	2.32	1.11	down	3.18E-01	8.95E-01	-	-
1384908_at	Ttbk2	tau tubulin kinase 2	311349	Rn.140880	AI715762	2.75	3.05	2.81	2.73	2.73	2.70	1.11	down	1.88E-01	8.95E-01	-	-
1394526_at	---	---	---	Rn.34271	AI236935	2.54	2.67	2.51	3.14	2.55	2.47	1.11	up	5.33E-01	8.95E-01	-	-
1380804_at	---	---	---	Rn.147550	BM391896	2.81	2.40	2.43	2.40	2.41	2.39	1.11	down	3.27E-01	8.95E-01	-	-
1384876_at	Rad9b	RAD9 homolog B (S. cerevisiae)	363924	Rn.216814	AW529993	2.31	2.35	2.36	2.35	2.36	2.75	1.11	up	3.28E-01	8.95E-01	-	-
1391880_at	---	---	---	Rn.22753	AA893670	8.72	8.55	8.91	8.53	8.22	9.00	1.11	down	5.85E-01	8.95E-01	-	-
1382340_at	Dmxl1	Dmx-like 1	307429	Rn.216799	AA924048	3.29	2.46	2.86	2.46	2.46	2.45	1.11	down	6.56E-01	8.98E-01	-	-
1396900_at	---	---	---	Rn.202732	BE106436	2.50	2.87	2.51	2.47	2.46	2.52	1.11	down	2.98E-01	8.95E-01	-	-
1369329_at	Notch3	Notch homolog 3 (Drosophila)	56761	Rn.53876	NM_020087	2.25	2.24	2.73	2.24	2.29	2.24	1.11	down	4.18E-01	8.95E-01	-	-
1387770_at	Ifi27l1	interferon, alpha-inducible protein 27 like 1	170512	Rn.3867	NM_130743	4.99	6.45	5.18	5.75	5.57	5.73	1.11	up	7.65E-01	9.23E-01	-	-
1369446_at	Cyp2	cryptochrome 2 (photolyase-like)	170917	Rn.21150	NM_133405	4.06	6.79	7.00	6.42	5.66	6.22	1.11	up	8.87E-01	9.65E-01	-	-
1388122_at	Gstp1	glutathione-S-transferase, pi 1	24426	---	X02904	10.89	11.44	11.37	11.08	11.02	11.16	1.11	up	4.55E-01	8.95E-01	-	-
1395344_at	Mtmr1	myotubularin related protein 1	317296	Rn.18311	AI574919	2.93	2.95	3.15	3.07	2.94	3.46	1.11	up	4.40E-01	8.95E-01	-	-
1394550_at	LOC691221	similar to CG1998-PA	691221	Rn.55929	AA964902	2.57	2.57	2.51	2.57	3.01	2.52	1.11	up	4.06E-01	8.95E-01	-	-
1384199_at	---	---	---	Rn.169123	BF395951	3.52	2.51	2.58	2.98	2.73	2.46	1.11	down	7.04E-01	9.07E-01	-	-
1372108_at	Ptcd3	Pentatricopeptide repeat domain 3	500199	Rn.3598	BE098359	6.90	6.35	6.67	5.95	6.62	6.92	1.11	down	6.78E-01	9.02E-01	-	-
1396080_at	RGD1305534	similar to dJ202D23.2 (novel protein similar to C21ORF5 (KIAA0933))	315864	Rn.218993	BF386701	4.22	3.84	4.61	4.70	3.43	4.11	1.11	down	7.49E-01	9.19E-01	-	-
1394826_at	---	---	---	Rn.199420	BF417759	2.98	2.41	2.35	2.34	2.38	2.57	1.11	down	5.27E-01	8.95E-01	-	-
1372764_at	LOC689601	similar to density-regulated protein	689601	Rn.101864	BI276261	6.72	6.58	6.49	6.52	6.88	6.83	1.11	up	3.27E-01	8.95E-01	-	-
1376125_at	---	---	---	Rn.34270	BI289112	4.20	3.69	3.69	3.58	3.69	3.87	1.11	down	4.85E-01	8.95E-01	-	-
1397895_at	---	---	---	---	BI290793	4.41	6.12	4.33	5.04	4.70	4.68	1.11	down	8.17E-01	9.42E-01	-	-
1388504_at	Rad21	RAD21 homolog (S. pombe)	314949	Rn.3991	AI231313	8.17	8.99	9.06	8.38	8.40	9.00	1.11	down	6.97E-01	9.07E-01	-	-
1389750_at	Cc2d1a	coiled-coil and C2 domain containing 1A	288908	Rn.21651	AW251641	3.01	3.48	3.11	3.04	3.07	3.05	1.11	down	3.68E-01	8.95E-01	-	-
1391798_at	---	---	---	Rn.207107	BF564518	2.60	3.17	2.58	2.50	2.49	2.93	1.11	down	5.76E-01	8.95E-01	-	-
1368723_at	Lat	linker for activation of T cells	81511	Rn.9773	NM_030853	2.73	2.56	2.46	2.45	2.41	2.45	1.11	down	1.40E-01	8.95E-01	-	-
1367826_at	Nfe2l2	nuclear factor, erythroid derived 2, like 2	83619	Rn.10867	NM_031789	7.91	7.78	8.05	7.44	7.93	7.92	1.11	down	4.57E-01	8.95E-01	-	-
1387847_at	Plk3cb	phosphoinositide-3-kinase, catalytic, beta polypeptide	85243	Rn.44268	NM_053481	2.80	2.87	2.81	3.36	2.42	3.15	1.11	up	6.36E-01	8.95E-01	-	-
1388723_at	Bre	brain and reproductive organ-expressed protein	362704	Rn.1432	AI171289	5.72	5.94	5.76	6.16	5.57	6.13	1.11	up	5.09E-01	8.95E-01	-	-
1371332_at	LOC684681	similar to Histone H1.2 (H1 VAR.1) (H1c)	684681	---	AA848821	8.99	8.72	9.03	9.10	8.92	9.16	1.11	up	2.92E-01	8.95E-01	-	-
1375816_at	---	---	---	Rn.200256	BI296706	2.59	2.50	2.59	2.52	2.75	2.84	1.11	up	2.15E-01	8.95E-01	-	-
1386495_x_at	Orai3	ORAI calcium release-activated calcium modulator 3	309000	Rn.42186	AA891139	4.85	3.90	4.20	4.20	4.40	3.90	1.11	down	6.66E-01	8.99E-01	-	-
1369137_at	Chrne	cholinergic receptor, nicotinic, epsilon	29422	Rn.10301	NM_017194	2.35	2.77	2.35	2.35	2.33	2.33	1.11	down	3.48E-01	8.95E-01	-	-
1370172_at	Sod2	superoxide dismutase 2, mitochondrial	24787	Rn.10488	BG671549	8.83	8.97	9.39	8.96	8.86	8.93	1.11	down	4.45E-01	8.95E-01	-	-
1395472_at	Lrrc17	leucine rich repeat containing 17	502715	Rn.207235	BF419170	2.38	2.37	2.82	2.38	2.39	2.36	1.11	down	3.82E-01	8.95E-01	-	-
1394491_at	---	---	---	Rn.210376	BI301512	2.47	2.46	2.46	2.46	2.92	2.44	1.11	up	3.99E-01	8.95E-01	-	-
1390411_at	Cldn19	claudin 19	298487	Rn.106342	BG378563	2.43	2.37	2.39	2.38	2.89	2.36	1.11	up	4.47E-01	8.95E-01	-	-
1387775_at	Gtf2a2	general transcription factor IIA, 2	83828	Rn.4053	NM_053345	7.40	7.31	7.67	7.37	7.10	7.48	1.11	down	4.02E-01	8.95E-01	-	-
1391666_at	Ask1	ASPP2 associated kinase 1	500244	Rn.203307	AI228398	2.69	2.26	2.27	2.26	2.27	2.25	1.11	down	3.66E-01	8.95E-01	-	-
1386755_at	Ccdc91	coiled-coil domain containing 91	312863	Rn.42180	BF552559	5.13	6.22	6.74	5.57	6.74	6.21	1.11	up	8.14E-01	9.40E-01	-	-
1382571_at	---	---	---	Rn.54842	AA925335	2.58	2.70	3.40	2.46	3.18	2.61	1.11	down	6.86E-01	9.04E-01	-	-
1372661_at	Tbl3	transducin (beta)-like 3	287120	Rn.32013	AI406314	4.36	3.80	3.15	3.66	4.87	3.21	1.11	up	8.21E-01	9.43E-01	-	-
1388551_at	Ube2m	ubiquitin-conjugating enzyme E2M (UBC12 homolog, yeast)	361509	Rn.15135	BG378098	5.04	5.33	5.55	5.41	5.44	5.50	1.11	up	3.84E-01	8.95E-01	-	-
1382427_at	Cggbp1	CGG triplet repeat binding protein 1	288353	Rn.101743	BG373237	5.75	5.18	5.89	5.73	4.91	5.74	1.11	down	6.99E-01	9.07E-01	-	-
1370203_at	Frag1	FGF receptor activating protein 1	116675	Rn.94200	BG373817	5.80	6.00	6.46	6.56	5.59	6.55	1.11	up	7.19E-01	9.11E-01	-	-
1374834_at	Sf3b4	splicing factor 3b, subunit 4	295270	Rn.116275	AA943520	4.68	4.77	4.70	4.68	5.53	3.50	1.11	down	8.16E-01	9.41E-01	-	-
1376127_at	---	---	---	Rn.165276	BE117201	6.15	6.29	6.41	6.29	5.81	6.31	1.11	down	4.62E-01	8.95E-01	-	-
1389060_at	---	---	---	Rn.12965	BI297313	3.77	4.25	4.06	4.13	4.14	4.25	1.11	up	3.77E-01	8.95E-01	-	-
1380915_at	---	---	---	Rn.66480	AI547937	2.58	2.92	2.60	2.53	2.65	2.48	1.11	down	3.05E-01	8.95E-01	-	-
1374273_at	---	---	---	Rn.206214	BG665433	6.14	6.45	6.96	5.96	7.39	6.64	1.11	up	7.74E-01	9.26E-01	-	-
1389026_at	Ankrd42	ankyrin repeat domain 42	293117	Rn.51262	BF399429	5.13	5.63	5.27	4.99	5.91	5.58	1.11	up	6.57E-01	8.98E-01	-	-
1373617_at	Emp2	epithelial membrane protein 2	360468	Rn.21730	AA818807	2.44	2.44	2.46	2.45	2.91	2.43	1.11	up	4.07E-01	8.95E-01	-	-
1398923_at	Rnasek	ribonuclease, RNase K	287453	---	AI101122	10.18	10.11	9.90	10.21	10.23	10.18	1.11	up	1.62E-01	8.95E-01	-	-
1389888_at	RGD1305211	similar to RIKEN cDNA 2610209A20	365314	Rn.22440	AA964142	2.66	2.65	2.98	2.49	2.74	2.63	1.11	down	3.21E-01	8.95E-01	-	-
1377794_at	---	---	---	Rn.164669	BF288862	4.09	3.92	4.12	3.93	3.69	4.07	1.11	down	3.17E-01	8.95E-01	-	-
1382385_at	Psmc6	proteasome (prosome, macropain) 26S subunit, ATPase, 6	289990	Rn.103233	BE116344	6.56	6.71	7.12	6.72	6.43	6.80	1.11	down	5.05E-01	8.95E-01	-	-
1373612_at	---	---	---	---	BM391810	3.52	4.02	2.34	3.26	2.45	3.74	1.11	down	8.27E-01	9.45E-01	-	-
1372863_at	Mycbp2	MYC binding protein 2	290447	Rn.13538	BF409872	4.03	4.78	4.88	4.21	5.12	4.80	1.11	up	7.20E-01	9.11E-01	-	-
1378093_at	---	---	---	Rn.205601	BG380366	3.75	2.38	2.34	2.58	3.78	2.56	1.11	up	8.24E-01	9.44E-01	-	-
1395053_at	Tmem26	transmembrane protein 26	309724	Rn.50686	BE104822	2.82	2.29	2.30	2.36	2.32	2.29	1.11	down	4.50E-01	8.95E-01	-	-
1379089_at	---	---	---	Rn.149027	BM382838	2.38	2.35	2.37	2.67	2.50	2.36	1.11	up	1.81E-01	8.95E-01	-	-
1368047_at	Slc13a3	solute carrier family 13 (sodium-dependent dicarboxylate transporter), membe	64846	Rn.3587	NM_022866	10.09	9.74	9.71	10.12	9.31	9.67	1.11	down	6.11E-01	8.95E-01	-	-
1380281_at	Zyg11b	zyg-11 homolog B (C. elegans)	362559	Rn.84865	BF402103	3.59	4.49	4.82	4.55	2.71	5.19	1.11	down	8.69E-01	9.59E-01	-	-
1392654_at	Mtrf1l	mitochondrial translational release factor 1-like	361473	Rn.205194	BF413389	5.01	4.59	4.30	4.04	5.20	5.11	1.11	up	7.49E-01	9.19E-01	-	-
1380562_at	Rpusd3	RNA pseudouridylate synthase domain containing 3	362416	Rn.45622	AW523351	3.24	3.03	2.82	3.67	2.83	3.03	1.11	up	6.34E-01	8.95E-01	-	-
1376849_at	Usp48	ubiquitin specific protease 48	362636	Rn.100022	BM384872	4.02	4.29	4.34	4.52	3.62	4.94	1.11	up	7.35E-01	9.15E-01	-	-
1387755_s_at	Tgoln1	trans-golgi network protein	192152	Rn.11349	NM_138840	7.89	8.50	8.67	9.14	8.48	8.89	1.11	up	8.07E-01	9.38E-01	-	-
1385613_at	---	---	---	Rn.204388	AI112079	2.68	3.11	2.52	2.71	2.69	2.47	1.11	down	4.94E-01	8.95E-01	-	-
1373335_at	Zdhhc9	zinc finger, DHHC-type containing 9	302808	Rn.15254	BE349808	6.22	6.56	6.19	6.57	5.87	6.10	1.11	down	5.73E-01	8.95E-01	-	-
1399050_at	Adss	adenylosuccinate synthase	289276	Rn.9047	AI232106	10.13	10.42	10.50	10.21	10.16	10.25	1.11	down	2.73E-01	8.95E-01	-	-
1372074_at	Nudt3	nudix (nucleoside diphosphate linked moiety X)-type motif 3	294292	Rn.195252	BI276000	6.91	7.35	7.31	7.53	7.19	7.30	1.11	up	4.50E-01	8.95E-01	-	-
1391031_at	---	---	---	Rn.163702	BF389889	6.38	5.65	5.43	6.45	4.87	5.70	1.11	down	8.00E-01	9.35E-01	-	-
1377466_a_at	RGD1565584	Similar to tyrosine kinase-associated leucine zipper protein LAZIpII	293112	Rn.35776	AA949974	4.03	5.32	6.42	6.50	5.03	4.69	1.11	up	8.77E-01	9.62E-01	-	-
1391779_at	---	---	---	Rn.146712	AA997862	2.85	2.49	2.56	2.49	2.49	2.47	1.11	down	2.53E-01	8.95E-01	-	-
1379574_at	Lemd3	LEM domain containing 3	680066	Rn.22132	AI575248	5.08	5.21	4.22	4.93	4

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1386668_a_at	---	---	---	Rn.216740	BF565188	3.27	2.84	2.82	2.95	2.77	3.63	1.11	up	6.56E-01	8.98E-01	-	-
1371935_at	Tmem9	transmembrane protein 9	289046	Rn.2747	AA943122	4.56	5.23	6.01	4.94	4.85	5.57	1.11	down	7.78E-01	9.28E-01	-	-
1398874_at	Abin10	ataxin 10	170821	Rn.6524	BI274345	7.99	8.94	8.35	7.95	8.96	8.81	1.11	up	7.48E-01	9.18E-01	-	-
1387768_at	Mb	myoglobin	59108	Rn.40511	NM_021588	2.46	2.43	2.85	2.43	2.45	2.43	1.11	down	3.54E-01	8.95E-01	-	-
1397265_at	---	---	---	Rn.169796	AW529600	2.40	2.82	2.42	2.41	2.41	2.40	1.11	down	3.52E-01	8.95E-01	-	-
1396063_at	Dek	DEK oncogene	306817	Rn.26099	AI073244	11.02	11.32	10.74	11.28	11.07	11.17	1.11	up	4.63E-01	8.95E-01	-	-
1381885_at	---	---	---	Rn.177302	BE102910	3.29	2.72	2.74	2.76	2.77	2.80	1.11	down	4.84E-01	8.95E-01	-	-
1372672_at	Qprt	quinolinate phosphoribosyltransferase	293504	Rn.9220	AI407095	8.60	8.77	8.68	8.47	8.53	8.62	1.11	down	9.89E-02	8.95E-01	-	-
1393281_at	Cav1	caveolin 1, caveolae protein	25404	Rn.22518	AW915173	2.74	2.38	2.48	2.39	2.39	2.38	1.11	down	2.58E-01	8.95E-01	-	-
1395583_at	---	---	---	Rn.92906	BG664001	2.59	2.71	2.50	2.46	2.47	2.43	1.10	down	7.81E-02	8.95E-01	-	-
1368183_at	Plcg1	phospholipase C, gamma 1	25738	Rn.11243	NM_013187	8.50	7.89	8.06	8.33	8.20	8.36	1.10	up	4.85E-01	8.95E-01	-	-
1377021_at	Trmt6	tRNA methyltransferase 6 homolog (S. cerevisiae)	311441	Rn.8742	BI303908	6.47	6.40	6.27	6.16	6.25	6.30	1.10	down	1.14E-01	8.95E-01	-	-
1394530_at	---	---	---	Rn.149084	AW535733	2.59	2.57	2.29	2.71	2.60	2.57	1.10	up	2.48E-01	8.95E-01	-	-
1381589_at	---	---	---	Rn.170585	BE096466	2.54	2.49	2.54	2.53	2.52	2.95	1.10	up	3.71E-01	8.95E-01	-	-
1373399_at	Wdr6	WD repeat domain 6	301007	Rn.164872	BI291997	8.01	7.67	7.67	7.40	7.85	7.68	1.10	down	4.54E-01	8.95E-01	-	-
1375366_at	Znf503	Zinc finger protein 503	305687	Rn.37928	AI599428	2.38	2.37	2.38	2.70	2.50	2.35	1.10	up	2.34E-01	8.95E-01	-	-
1382886_at	---	---	---	Rn.121156	BE100329	4.08	4.93	5.47	4.46	3.98	5.61	1.10	down	8.31E-01	9.47E-01	-	-
1383598_at	Wdr91	WD repeat domain 91	312225	Rn.158722	AI136294	2.63	2.53	2.38	2.37	2.38	2.37	1.10	down	1.12E-01	8.95E-01	-	-
1371642_at	Eif4a2	eukaryotic translation initiation factor 4A2	303831	Rn.143972	AI169170	10.26	10.56	10.51	10.23	10.37	10.30	1.10	down	2.24E-01	8.95E-01	-	-
1381922_at	Slc5a11	solute carrier family 5 (sodium/glucose cotransporter), member 11	252854	Rn.112669	BG374720	7.15	8.20	8.74	7.46	8.29	7.90	1.10	down	7.97E-01	9.34E-01	-	-
1372493_at	Ccdc23	coiled-coil domain containing 23	362578	Rn.2954	AI102862	3.63	3.62	3.64	3.62	4.08	3.61	1.10	up	4.04E-01	8.95E-01	-	-
1371278_at	Cdc34	cell division cycle 34 homolog (S. cerevisiae)	299602	Rn.2427	L38482	2.62	2.64	2.34	2.58	2.50	2.96	1.10	up	4.44E-01	8.95E-01	-	-
1381548_at	Golim4	golgi integral membrane protein 4	310526	Rn.24186	BF397673	8.14	7.58	6.89	8.02	7.62	7.40	1.10	up	7.41E-01	9.16E-01	-	-
1399145_at	Gpr107	G protein-coupled receptor 107	311857	Rn.168447	BF410891	4.82	5.28	4.74	5.33	4.72	5.23	1.10	up	6.00E-01	8.95E-01	-	-
1374074_at	Cdc37l1	cell division cycle 37 homolog (S. cerevisiae)-like 1	293886	Rn.60570	BF285292	4.80	4.20	4.82	4.43	4.46	4.51	1.10	down	5.20E-01	8.95E-01	-	-
1392367_at	---	---	---	---	BE112073	2.68	2.47	2.58	3.05	2.58	2.52	1.10	up	4.86E-01	8.95E-01	-	-
1382390_at	---	---	---	Rn.199412	AI177572	6.48	6.23	6.38	6.45	4.89	6.31	1.10	down	8.22E-01	9.43E-01	-	-
1392561_at	Atp5c1	ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptid	116550	Rn.63959	BF396279	9.07	6.97	5.70	8.05	7.42	6.70	1.10	up	8.98E-01	9.68E-01	-	-
1374775_at	Mki67	antigen identified by monoclonal antibody Ki-67	291234	Rn.73551	AI714002	3.02	4.29	3.19	4.34	3.48	3.11	1.10	up	8.03E-01	9.37E-01	-	-
1374394_at	Wbp2	WW domain binding protein 2	192645	Rn.198920	AI105305	7.13	7.21	6.45	7.50	6.75	6.97	1.10	up	6.83E-01	9.03E-01	-	-
1372223_at	Cpeb4	cytoplasmic polyadenylation element binding protein 4	303010	Rn.218260	BG374299	10.11	10.28	10.38	10.75	10.27	10.18	1.10	up	5.00E-01	8.95E-01	-	-
1394118_at	Ate1	Arginine-tRNA-protein transferase 1	293526	Rn.40326	AA894340	3.00	3.40	3.58	3.05	3.14	3.35	1.10	down	4.98E-01	8.95E-01	-	-
1378453_at	---	---	---	---	BM389035	2.64	3.13	4.03	3.16	3.75	3.31	1.10	up	7.82E-01	9.22E-01	-	-
1392796_at	Cnot6l	CCR4-NOT transcription complex, subunit 6-like	360917	Rn.16306	AI231609	8.59	8.52	8.11	8.32	8.59	8.74	1.10	up	5.01E-01	8.95E-01	-	-
1398378_at	Gstk1	glutathione S-transferase kappa 1	297029	Rn.109452	AI231779	8.72	8.48	7.63	7.99	8.02	8.37	1.10	down	7.04E-01	9.07E-01	-	-
1379363_at	---	---	---	Rn.89507	BF283311	9.27	9.26	9.66	9.19	9.27	9.30	1.10	down	3.49E-01	8.95E-01	-	-
1394788_at	---	---	---	---	AA800045	2.77	2.35	2.36	2.35	2.35	2.34	1.10	down	3.62E-01	8.95E-01	-	-
1371959_at	LOC690131	similar to H2A histone family, member O	690131	Rn.110508	AI235236	7.40	7.42	8.19	7.64	7.64	7.30	1.10	down	6.39E-01	8.95E-01	-	-
1369068_at	Cul5	cullin 5	64624	Rn.163001	NM_022683	5.01	5.08	4.94	4.68	5.10	5.68	1.10	up	6.49E-01	8.96E-01	-	-
1387317_at	Avp	arginine vasopressin	24221	Rn.9976	NM_016992	2.49	2.56	2.57	2.85	2.69	2.51	1.10	up	2.28E-01	8.95E-01	-	-
1383464_at	Pex19	peroxisomal biogenesis factor 19	288233	Rn.203104	AW141617	4.57	4.83	4.76	4.72	4.18	4.82	1.10	down	5.40E-01	8.95E-01	-	-
1397483_at	---	---	---	Rn.206289	BE104832	2.61	2.62	3.06	2.59	2.65	2.63	1.10	down	3.87E-01	8.95E-01	-	-
1392462_at	---	---	---	---	AA817891	8.12	8.71	8.95	8.75	8.54	8.92	1.10	up	6.23E-01	8.95E-01	-	-
1390046_at	Tubgcp2	tubulin, gamma complex associated protein 2	309098	Rn.138249	BI288110	2.42	2.42	2.43	2.54	2.42	2.74	1.10	up	1.92E-01	8.95E-01	-	-
1395503_at	Ears2	glutamyl-tRNA synthetase 2 mitochondrial (putative)	361641	Rn.79288	BF564382	4.34	4.18	3.61	3.31	5.56	4.83	1.10	down	8.67E-01	9.58E-01	-	-
1372340_at	Hat2b /// MGC94722	methionine adenosyltransferase II, beta /// similar to methionine adenosyltran	683630 /// 689330	Rn.1752	BM386355	8.68	8.43	8.75	8.29	8.86	8.27	1.10	down	5.44E-01	8.95E-01	-	-
1392465_at	Sap18	Sin3-associated polypeptide 18	290284	Rn.74373	AI228030	9.28	9.50	8.76	8.94	9.26	9.76	1.10	up	6.81E-01	9.03E-01	-	-
1388518_at	Fbxw5	F-box and WD repeat domain containing 5	362081	Rn.136952	AA799654	6.69	6.50	6.44	6.88	6.19	6.14	1.10	down	5.98E-01	8.95E-01	-	-
1376720_at	Adck2	aarF domain containing kinase 2	312258	Rn.3735	BG376414	3.18	2.92	2.99	2.94	3.14	3.45	1.10	up	4.41E-01	8.95E-01	-	-
1396971_at	---	---	---	Rn.62258	BF413140	4.13	2.85	2.49	3.95	2.98	2.96	1.10	up	8.22E-01	9.43E-01	-	-
1371836_at	Rab5c	RAB5C, member RAS oncogene family	287709	Rn.222014	H35233	5.99	6.01	6.61	5.67	6.43	6.08	1.10	down	6.59E-01	8.98E-01	-	-
1370883_at	H2-Ea	histocompatibility 2, class II antigen E alpha	294269	Rn.103146	Y00480	7.94	5.18	5.19	6.16	6.60	5.97	1.10	up	8.86E-01	9.65E-01	-	-
1387870_at	Zfp36	zinc finger protein 36	79426	Rn.82737	AB025017	9.55	9.87	10.34	10.15	9.46	9.72	1.10	down	6.62E-01	8.98E-01	-	-
1393067_at	Tek	TEK tyrosine kinase, endothelial	89804	Rn.9159	AI710931	4.20	4.20	4.20	4.63	4.20	4.19	1.10	up	3.82E-01	8.95E-01	-	-
1382658_at	LOC502710	similar to Myeloid/lymphoid or mixed-lineage leukemia protein 3 homolog (His	502710	Rn.164602	AI070638	4.50	5.33	5.51	5.48	4.48	4.98	1.10	down	7.55E-01	9.20E-01	-	-
1368389_at	Apba3	amyloid beta (A4) precursor protein-binding, family A, member 3	83611	Rn.6924	NM_031781	4.24	4.24	3.99	4.10	3.92	4.01	1.10	down	2.19E-01	8.95E-01	-	-
1369097_s_at	Gucy1b3	guanylate cyclase 1, soluble, beta 3	25202	Rn.87228	NM_012769	3.01	3.15	3.03	4.20	3.02	2.40	1.10	up	8.01E-01	9.36E-01	-	-
1379998_at	---	---	---	Rn.166690	AA944411	2.60	2.56	2.98	2.57	2.29	2.84	1.10	down	5.32E-01	8.95E-01	-	-
1369057_at	Stxbp2	syntaxin binding protein 2	81804	Rn.10121	NM_031126	4.25	4.84	4.20	4.64	4.30	4.78	1.10	up	5.99E-01	8.95E-01	-	-
1374206_at	RGD1307357	similar to hypothetical protein DKFZp434A1319	291975	Rn.106111	BI280278	2.60	2.48	2.61	2.60	2.92	2.59	1.10	up	2.86E-01	8.95E-01	-	-
1369228_at	Lifr	leukemia inhibitory factor receptor alpha	81680	Rn.14529	NM_031048	8.36	9.74	8.89	8.49	8.51	9.56	1.10	down	8.04E-01	9.37E-01	-	-
1373476_at	LOC500251	hypothetical protein LOC500251	500251	Rn.154952	AI410833	3.76	3.67	3.32	3.67	3.85	3.65	1.10	up	3.95E-01	8.95E-01	-	-
1383989_at	Sox4	SRY (sex determining region Y)-box 4	364712	Rn.163667	AI030701	4.87	4.06	4.34	4.20	4.33	4.31	1.10	down	5.84E-01	8.95E-01	-	-
1380038_at	RGD1560364	similar to vacuolar protein sorting 13C protein	363087	Rn.21609	BF393567	3.69	3.11	2.70	3.65	3.15	3.12	1.10	up	6.92E-01	9.05E-01	-	-
1374724_at	---	---	---	Rn.11731	BG378232	2.76	2.31	2.35	2.34	2.32	2.33	1.10	down	3.75E-01	8.95E-01	-	-
1398714_at	Usf2	upstream transcription factor 2	81817	Rn.44637	BF403400	3.04	2.74	2.93	2.83	2.76	2.70	1.10	down	2.06E-01	8.95E-01	-	-
1388160_a_at	Idh3b	isocitrate dehydrogenase 3 (NAD+) beta	94173	Rn.1093	AI171793	9.41	8.98	9.20	8.99	9.01	9.17	1.10	down	3.53E-01	8.95E-01	-	-
1385200_at	Olfml2a	olfactomedin-like 2A	296708	Rn.144357	BI295290	2.81	2.36	2.37	2.38	2.39	2.35	1.10	down	3.93E-01	8.95E-01	-	-
1382620_at	Ankrd11	ankyrin repeat domain 11	365028	Rn.23845	BF523248	10.23	9.38	9.96	9.78	9.69	9.67	1.10	down	6.05E-01	8.95E-01	-	-
1390584_at	Rnf165	ring finger protein 165	307251	Rn.124795	BE105967	2.74	2.73	2.76	2.73	3.21	2.71	1.10	up	4.29E-01	8.95E-01	-	-
1376079_at	---	---	---	---	BI295806	7.73	7.57	7.42	7.55	7.53	8.07	1.10	up	5.12E-01	8.95E-01	-	-
1395687_at	Atf7ip	activating transcription factor 7 interacting protein	312800	Rn.98469	BE113420	8.48	7.48	6.95	7.88	7.63	6.96	1.10	down	8.00E-01	9.35E-01	-	-
1375188_at	Katnb1	katanin p80 (WD repeat containing) subunit B 1	291852	Rn.22157	BF408552	2.90	2.82	2.54	2.71	2.52	2.58	1.10	down	3.09E-01	8.95E-01	-	-
1383139_at	---	---	---	Rn.11887	BM386881	4.08	4.06	4.37	3.89	4.02	4.18	1.10	down	3.38E-01	8.95E-01	-	-
1388343_at	Ndufb7	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 7	361385	Rn.105421	AI575943	10.60	11.22	10.88	11.01	11.01	11.11	1.10	up	4.76E-01	8.95E-01	-	-
1396960_at	Ankrd60	ankyrin repeat domain 60	296417	Rn.62712	BF405039	2.36	2.35	2.79	2.36	2.37	2.35	1.10	down	3.80E-01	8.95E-01	-	-
1389413_at	Evi2a	ecotropic viral integration site 2A	685433	Rn.203744	BI279325	2.39	2.35	2.39	2.37	2.82	2.37	1.10	up	3.94E-01	8.95E-01	-	-
1373579_at	Rara	retinoic acid receptor, alpha	24705	Rn.91057	AA945758	3.80	4.24	4.14	4.67	3.54	4.39	1.10	up	7.17E-01	9.10E-01	-	-
1391402_at	Kctd18	Potassium channel tetramerisation domain containing 18	301436	Rn.12331	AW535190	2.69	2.79	2.70	2.68	2.69	3.23	1.10	up	4.89E-01	8.95E-01	-	-
1380975_at	---	---	---	Rn.218010	AW534466	9.91	9.64	9.97	9.71	9.63	9.76	1.10	down	2.68E-01	8.95E-01	-	-
1374010_at	---	---	---	Rn.2591	BI275032	2.46	3.16	2.78	2.93	2.95	2.94	1.10	up	5.18E-01	8.95E-01	-	-
1370250_at	Ube2i	ubiquitin-conjugating enzyme E2I	25573	Rn.2274	AA799453	8.37	9.34	9.40	8.70	9.11	8.86	1.10	down	7.09E-01	9.09E-01	-	-
1396543_at	Ncstn	nicastrin	289231	Rn.51975	BE099968	3.99	3.20	2.93	3.20	3.30	3.20	1.10	down	6.80E-01	9.03E-01	-	-
1370530_a_at	Pld1	phospholipase D1	25096	Rn.11130	U69550	4.91	7.37	5.23	4.97	5.15	6.97	1.10	down	8.94E-01	9.67E-01	-	-
1369269_at	Galnt1	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltran	79214	Rn.10266	NM_024373	5.47	5.51	4.59	5.19	4.69	6.12	1.10	up	7.96E-01	9.34E-01	-	-
1398627_at	---	---	---	Rn.203017	AA818889	4.42	4.46	4.55	3.94	4.41	4.66	1.10	down	5.46E-01	8.95E-01	-	-
1372211_at	Mafk	v-maf musculoaponeurotic fibrosarcoma oncogene homolog K (avian)	246760	Rn.3818	BI284461	4.53	4.16	3.91	4.22	4.53	4.27	1.10	up	5.26E-01	8.95E-01	-	-
1392995_at	Zfp322a	zinc finger protein 322a	680201	Rn.16013	BG669396	2.44	2.59	2.67	2.66	2.79	2.68	1.10	up	1.44E-01	8.95E-01	-	-
1375211_at	Rnase2	ribonuclease T2	292306	Rn.18019	BM391506	7.99	8.17	7.73	7.96	8.40	8.10	1.10	up	5.08E-01	8.95E-01	-	-
1385438_at	ND4	NADH dehydrogenase subunit 4	26201	---	AA859612	2.76	2.66	3.32	2.76	2.83	2.72	1.10	down	5.31E-01	8.95E-01	-	-
1385707_at	Lect2	leukocyte cell-derived chemotaxin 2	361205	Rn.23016	BF550221	2.43	2.81	2.46	2.42	2.44	2.41	1.10	down	3.10E-01	8.95E-01	-	-
1375457_at	Map1d	methionine aminopeptidase 1D	311748	Rn.24026	AA875011	3.52	3.39	3.35	3.29	4.05	3.34	1.10	up	6.03E-01	8.95E-01	-	-
1398107_at	Ggct	gamma-glutamyl cyclotransferase	362368	Rn.129060	AI385379	5.68	8.21	5.63	8.10	3.44	5.56	1.10	down	9.44E-01	9.84E-01	-	-
1385578_at	---	---	---	Rn.205251	AI511324	2.39	3.29	2.38	2.55	2.38	3.56	1.10	up	7.81E-01	9.29E-01	-	-
1397878_at	---	---	---	---	BG671050	3.66	3.65	3.79	3.90	4.13	3.50	1.10	up	4.96E-01	8.95E-01	-	-
1374291_at	Dnajc17	DnaJ (Hsp40) homolog, subfamily C, member 17	311329	Rn.41217	BI291937	3.64	4.32	4.68	4.36	3.58	4.28	1.10	down	7.37E-01	9.15E-01	-	-
1390947_at	Heatr5a	HEAT repeat containing 5A	362737	Rn.7269	AA891255	6.14	5.75	5.80	5.87	6.36	5.88	1.10	up	5.27E-01	8.95E-01	-	-
1374910_at	Celsr2	cadherin, EGF LAG seven-pass G-type receptor 2 (flamingo homolog, Droso	83465	Rn.2912	BE103601	6.04	5.85	5.79	6.31	5.96	5.83	1.10	up	4.30E-01	8.95E-01	-	-
1392846_at	---	---	---	Rn.203398	AA944574	3.03	2.40	3.64	3.30	2.46	2.90	1.10	down	7.60E-01	9.22E-01	-	-
1375447_at	Glpbp1	GTP binding protein 1	300077	Rn.97210	BI291231	3.87	3.82	3.89	3.82	3.75	3.58	1.10	down	1.26E-01	8.95E-01	-	-
1388970_at	Rasip1	Ras interacting protein 1	292912	Rn.23451	AA848597	3.05	2.56	2.77	2.65	2.71	2.60	1.10	down	3.79E-01	8.95E-01	-	-
1381597_at	---	---	---	Rn.154031	AW524894	2.46	2.43	2.84	2.44	2.44	2.43	1.10	down	3.42E-01	8.95E-01	-	-
1381829_at	Zfp318	zinc finger protein 318	685082	Rn.28520	AI227744	7.66	7.68	6.48	8.01	7.59	6.65	1.10	up	8.15E-01	9.40E-01	-	-
1375971_at	Cln5	ceroid-lipofuscinosis, neuronal 5	306128	Rn.55942	BM386028	3.71	3.52	3.50	3.40	3.99	3.77	1.10	up	4.87E-01	8.95E-01	-	-
1396399_at	---	---	---	Rn.169846	AW530442	3.05	3.05	3.09	3.05	3.56	3.00	1.10	up	4.71E-01	8.95E-01	-	-
1396112_at	Mtmr10	myotubularin related protein 10	306255	Rn.3510	BF408519	4.95	5.29	5.10	4.92	4.52	5.47	1.10	down	6.55E-01	8.97E-01	-	-
1383685_at	Heatr1	HEAT repeat containing 1	361262	Rn.219575	BI276972	5.82	5.56	5.50	5.98	5.45	5.88	1.10	up	4.96E-01	8.95E-01	-	-
1377967_at	Cdt1	chromatin licensing and DNA replication factor 1	292071	Rn.8884	AI112987	2.49	2.89	2.50	2.48	2.49	2.48	1.10	down	3.41E-01	8.95E-01	-	-
1376985_at	RGD1562416	similar to RIKEN cDNA 2310007F12	317418	Rn.15417	AA866482	8.17	7.69	8.42	8.08	7.58	8.19	1.10	down	6.47E-01	8.95E-01	-	-
1392896_at	LOC887016	olfactory receptor 873	887016	---	AI111675	3.27	3.06	3.03	3.65	3.06	3.07	1.10	up	5.36E-01	8.95E-01	-	-
1379664_at	Zc3h13	zinc finger CCCH type containing 13	305955	Rn.100827	BF419602	8.13	7.64	6.15	7.34	7.13	7.03	1.10	down	8.26E-01	9.45E-01	-	-
1376217_at	Casc1	cancer susceptibility candidate 1	297720	Rn.162764	BM388768	3.77	3.18	3.15	3.17	2.88	3.62	1.10	down	6.57E-01	8.98E-01	-	-
1379954_at	S100a13	S100 calcium binding protein A13	299213	Rn.918	AW141940	2.60	2.99	2.60	2.59	2.60	2.58	1.10	down	3.39E-01	8.95E-01	-	-
1379948_at	---	---	---	Rn.205555	BM392001	4.94	5.70	3.81	4.59	4.93	4.51	1.10	down	8.14E-01	9.40E-01	-	-
1378406_at	---	---	---	Rn.198596	BF394636	2.57	2.59	2.40	2.39	2.40	2.35	1.10	down	8.24E-02	8.95E-01	-	-
1380867_a_at	Plekhn1	pleckstrin homology domain containing, family M (with RUN domain) member	303584	Rn.101335	BM383086	3.00	4.58	5.86	4.19	4.18	4.65	1.10	down	8.75E-01	9.61E-01	-	-
1380903_at	LOC691170	similar to zinc finger protein 84 (HPF2)	691170	Rn.147757	BE106376	2.88	2.91	2.94	2.92	2.93	3.31	1.10	up	3.36E-01	8.95E-01	-	-
1382936_at	---	---	---	Rn.210259	BF396501	3.27	3.71	3.32	2.92	3.32	3.64	1.10	down	6.04E-01	8.95E-01	-	-
1369379_at	Epha3	Eph receptor A3	29210	Rn.10713	NM_031564	2.36	2.35	2.76	2.35	2.36	2.33	1.10	down	3.61E-01	8.95E-01	-	-
1389242_at	---	---	---	---	BG377726	4.85	5.19	5.51	4.94	5.03	5.16	1.10	down	5.21E-01	8.95E-01	-	-
1378962_at	Ccdc45	coiled-coil domain containing 45	287766	Rn.155284	BM385701	3.01	4.57	2.57	2.89	3.27	3.57	1.10	down	8.36E-01	9.49E-01	-	-
1392170_at	Rwdd3	RWD domain containing 3	65026	Rn.54470	BE121336	5.47	5.36	5.34	4.38	5.42	5.95	1.10	down	7.75E-01	9.26E-01	-	-
1380465_at	---	---	---	---	AA965023	9.56	9.08	9.61	9.37	9.43	9.87	1.10	up	5.74E-01	8.95E-01	-	-
1386983_at	Hmbs	hydroxymethylbilane synthase	25709	Rn.11080	NM_013168	5.95	7.09	5.41	6.25	5.03	6.75	1.10	down	8.61E-01	9.54E-01	-	-
1389008_at	---	---	---	---	AI409218	5.27	6.37	5.71	5.45	5.33	6.15	1.10	down	7.48E-01	9.18E-01	-	-
1377995_at	Itfg3	integrin alpha FG-GAP repeat containing 3	360502	Rn.6244	AA799854	5.71	4.40	3.93	4.27	4.86	4.48	1.10	down	8.14E-01	9.40E-01	-	-
1396248_at	Sns /// LOC688333	glucosamine (N-acetyl)-6-sulfatase /// similar to glucosamine (N-acetyl)-6-sulf	298825 /// 688338	Rn.65392	AI454124	2.50	2.50	2.93	2.51	2.61	2.49	1.10	down	3.77E-01	8.95E-01	-	-
1370112_at	Pten	phosphatase and tensin homolog	50557	Rn.22158	NM_031606	7.72	8.18	7.96	7.71	8.03	8.54	1.10	up	6.35E-01	8.95E-01	-	-
1387345_at	Psme4	proteasome (prosome, macropain) activator subunit 4	498433	Rn.163607	NM_023986	5.93	6.14	5.78	5.89	5.67	5.86	1.10	down	3.22E-01	8.95E-01	-	-
1381256_at	---	---	---	Rn.173265	BI276190	5.10	3.73	2.80	4.62	3.74	3.70	1.10	up	8.56E-01	9.55E-01	-	-
1389807_at	RGD1308065	hypothetical LOC287935	287935	Rn.23006	AA819220	2.75	2.62	2.91	2.70	2.61	2.56	1.10	down	2.09E-01	8.95E-01	-	-
1377070_at	Sf3b2	splicing factor 3b, subunit 2	293671	Rn.103341	BE098910	6.76	8.07	6.42	7.24	6.25	7.34	1.10	down	8.29E-01	9.46E-01	-	-
1371459_at	---	---	---	Rn.207975	BF409956	2.32	2.31	2.33	2.75	2.32	2.31	1.10	up	3.85E-01	8.95E-01	-	-
1372689_at	Pamg4	proteasome (prosome, macropain) assembly chaperone 4	689623	Rn.98733	BE113476	5.22	4.41	4.14	4.37	4.30	4.68	1.10	up	7.04E-01	9.07E-01	-	-
1398410_at	Acap3	ArfGAP with coiled-coil, ankyrin repeat and PH domains 3	313772	Rn.144386	AW535349	2.46	2.46	3.11	2.68	2.47	2.46	1.10	down	5.66E-01	8.95E-01	-	-
1383534_at	---	---	---	Rn.20948	AA997058	3.22	3.36	4.97	3.87	3.36	4.74	1.10	up	8.49E-01	9.53E-01	-	-
1370705_at	Znf597	zinc finger protein 597	266774	Rn.64641	AF277900	2.36	2.36	2.36	2.78	2.29	2.43	1.10	up	3.95E-01	8.95E-01	-	-
1379768_at	---	---	---	Rn.32838	AA998903	4.81	3.66	3.76	3.55	4.17	4.08	1.10	down	7.51E-01	9.19E-01	-	-
1374015_at	---	---	---	Rn.7770	BF281697	2.32	2.31	2.34	2.31	2.78	2.30	1.10	up	4.21E-01	8.95E-01	-	-
1381519_at	Arid1a	AT rich interactive domain 1A (SWI-like)	297867	Rn.61077	BF407752	2.67	2.63	3.25

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1395881_at	Dap	Death-associated protein	64322	Rn.1531	BE110708	2.33	2.29	2.36	2.75	2.33	2.31	1.10	up	3.90E-01	8.95E-01	-	-
1383059_a_at	Gkap1	G kinase anchoring protein 1	361202	Rn.2003	BE112067	2.42	3.36	2.41	3.08	2.67	2.86	1.10	up	6.99E-01	9.07E-01	-	-
1398300_at	Atp1b3	ATPase, Na+/K+ transporting, beta 3 polypeptide	25390	Rn.5041	BI635655	7.71	7.53	6.78	6.92	6.93	7.74	1.10	down	7.41E-01	9.16E-01	-	-
1382386_at	Lmbr1	limb region 1 homolog (mouse)	362295	Rn.55189	BI274268	3.83	3.84	3.86	3.48	3.82	3.81	1.10	down	2.76E-01	8.95E-01	-	-
1378506_at	Plk3c2a	phosphoinositide-3-kinase, class 2, alpha polypeptide	361632	Rn.60820	BM385647	4.52	4.71	5.04	4.58	5.07	5.03	1.10	up	5.59E-01	8.95E-01	-	-
1392289_at	Tmem87a	transmembrane protein 87A	366170	Rn.212423	BI276179	4.46	3.83	3.96	3.59	5.02	4.07	1.10	up	7.79E-01	9.28E-01	-	-
1389862_at	Nol12	nucleolar protein 12	362855	Rn.17454	AI407084	2.60	2.58	2.59	2.92	2.59	2.68	1.10	up	2.34E-01	8.95E-01	-	-
1370132_at	Fkbp1b	FK506 binding protein 1b	58950	Rn.46439	NM_022675	3.37	3.77	3.79	3.21	3.92	3.39	1.10	down	6.11E-01	8.95E-01	-	-
1368179_at	Crlf2	cytokine receptor-like factor 2	171499	Rn.177948	NM_134465	3.59	3.65	3.81	3.66	4.16	3.65	1.10	up	4.90E-01	8.95E-01	-	-
1387614_at	Sycp3	synaptonemal complex protein 3	25561	Rn.34889	NM_013041	8.64	8.93	8.87	8.57	9.12	9.16	1.10	up	5.45E-01	8.95E-01	-	-
1378239_at	Gaa	glucosidase, alpha; acid	367562	Rn.162368	BF404337	2.78	2.78	3.15	2.78	2.73	2.78	1.10	down	3.26E-01	8.95E-01	-	-
1389233_at	Reps1	RALBP1 associated Eps domain containing 1	292944	Rn.12867	BI289596	5.41	4.32	4.28	4.95	4.86	4.62	1.10	up	7.36E-01	9.15E-01	-	-
1396167_at	Acp6	acid phosphatase 6, lysophosphatidic	295305	Rn.103296	BF555852	2.50	2.51	2.94	3.09	2.53	2.74	1.10	up	5.56E-01	8.95E-01	-	-
1374103_at	---	---	---	Rn.204546	BE102100	6.10	7.20	6.22	6.07	6.24	6.79	1.10	down	7.52E-01	9.20E-01	-	-
1383911_at	---	---	---	---	AA924574	3.67	3.62	3.64	3.76	4.05	3.54	1.10	up	4.02E-01	8.95E-01	-	-
1373625_at	Shmt1	serine hydroxymethyltransferase 1 (soluble)	287379	Rn.3684	AI412012	7.79	8.04	7.20	7.82	7.46	8.16	1.10	up	6.87E-01	9.04E-01	-	-
1373367_at	Pdlim2	PDZ and LIM domain 2	290354	Rn.105730	AI411212	2.98	2.89	3.14	2.97	2.82	2.80	1.10	down	1.99E-01	8.95E-01	-	-
1384898_at	---	---	---	Rn.148411	AA925876	2.76	2.34	2.38	2.33	2.37	2.36	1.10	down	3.61E-01	8.95E-01	-	-
1383476_at	---	---	---	Rn.203279	AW528065	5.72	6.78	6.29	6.06	6.38	6.77	1.10	up	7.26E-01	9.13E-01	-	-
1389178_at	Ngrn	neugrin, neurite outgrowth associated	499191	Rn.1278	BE329043	7.00	6.53	7.75	6.82	7.46	7.42	1.10	up	7.52E-01	9.20E-01	-	-
1372454_at	RGD1311899	similar to RIKEN cDNA 2210016L21 gene	288704	Rn.143995	BG372568	7.02	7.58	6.40	7.18	7.19	7.05	1.10	up	7.07E-01	9.08E-01	-	-
1377263_at	---	---	---	---	BF399036	5.84	6.40	5.78	6.06	6.04	6.34	1.10	up	5.61E-01	8.95E-01	-	-
1377154_at	Zfp157	zinc finger protein 157	360775	Rn.45139	BI295766	2.96	2.40	2.42	2.39	2.39	2.58	1.10	down	5.12E-01	8.95E-01	-	-
1398110_at	Zbtb22	zinc finger and BTB domain containing 22	309830	Rn.17135	AW521218	3.59	2.88	2.80	3.18	3.10	3.42	1.10	up	6.34E-01	8.95E-01	-	-
1393427_s_at	Egfl7	EGF-like-domain, multiple 7	245963	Rn.144669	BF287675	2.35	2.35	2.37	2.35	2.80	2.34	1.10	up	4.12E-01	8.95E-01	-	-
1378683_at	---	---	---	Rn.49534	BF413105	3.26	3.65	3.91	3.46	3.66	4.10	1.10	up	6.30E-01	8.95E-01	-	-
1389862_at	Rab22a	RAB22A, member RAS oncogene family	366265	Rn.37799	BM391905	2.50	2.73	3.33	2.98	2.77	2.38	1.10	down	6.73E-01	9.01E-01	-	-
1391796_at	Slc12a7	solute carrier family 12 (potassium/chloride transporters), member 7	308069	Rn.64199	AW530615	2.25	2.24	2.69	2.24	2.28	2.24	1.10	down	4.13E-01	8.95E-01	-	-
1372765_a_at	eci /// RGD1310224	peroxisomal D3,D2-enoyl-CoA isomerase /// similar to RIKEN cDNA 1810022J	291075 /// 291076	Rn.108029	BM390774	11.20	11.57	11.20	11.10	10.98	11.47	1.10	down	5.15E-01	8.95E-01	-	-
1387962_at	Zfp180	zinc finger protein 180	246279	Rn.14669	U41164	2.24	2.25	2.26	2.25	2.26	2.66	1.10	up	3.59E-01	8.95E-01	-	-
1397180_at	Styx1	serine/threonine/tyrosine interacting-like 1	360792	Rn.144029	AA998484	4.18	4.10	3.91	4.05	3.56	4.17	1.10	down	5.35E-01	8.95E-01	-	-
1388488_at	Lsm3	LSM3 homolog, U6 small nuclear RNA associated (S. cerevisiae)	297455	Rn.203046	AA943742	7.60	7.86	8.00	7.70	6.90	8.45	1.10	down	7.80E-01	9.28E-01	-	-
1383350_at	Slc35c2	solute carrier family 35, member C2	311637	Rn.12123	AA963524	2.87	5.00	5.11	4.06	4.44	4.07	1.10	down	8.61E-01	9.57E-01	-	-
1391524_at	RGD1564984	similar to WD repeat domain 11 protein	315843	Rn.23174	BE107185	3.28	3.14	3.22	3.48	3.36	3.20	1.10	up	2.01E-01	8.95E-01	-	-
1379554_at	Ppp2r5e	protein phosphatase 2, regulatory subunit B', epsilon isoform	299147	Rn.24394	AW141639	2.91	2.72	2.83	2.69	2.72	2.64	1.10	down	7.86E-02	8.95E-01	-	-
1390684_at	---	---	---	Rn.14778	AA892642	7.75	7.06	7.37	6.17	8.51	7.08	1.10	down	8.55E-01	9.55E-01	-	-
1379204_at	691708 /// LOC69	similar to ubiquitin-conjugating enzyme E2R 2 /// similar to ubiquitin-conjugati	691708 /// 691764	Rn.129735	AI710096	2.42	2.79	2.44	2.41	2.43	2.39	1.10	down	3.21E-01	8.95E-01	-	-
1373927_at	Hmgxb4	HMG box domain containing 4	307667	Rn.2792	BI283480	2.80	2.90	2.92	3.13	2.80	3.10	1.10	up	2.80E-01	8.95E-01	-	-
1373104_at	Specc1l	SPECC1-like	361828	Rn.63017	BF281872	4.13	4.12	4.41	4.11	3.72	4.41	1.10	down	5.68E-01	8.95E-01	-	-
1384563_at	---	---	---	Rn.146344	AA963343	2.39	2.69	2.38	2.35	2.34	2.35	1.10	down	2.49E-01	8.95E-01	-	-
1392461_at	Prpf4	PRP4 pre-mRNA processing factor 4 homolog (yeast)	298095	Rn.162812	BI291012	5.79	6.31	6.38	6.04	5.82	6.21	1.10	down	5.57E-01	8.95E-01	-	-
1389154_at	Lias	lipoic acid synthetase	305348	Rn.25547	AW524453	8.54	7.35	7.78	8.12	7.47	7.67	1.10	down	7.45E-01	9.17E-01	-	-
1374042_at	RGD1310453	similar to hypothetical protein FLJ23451	299521	Rn.12129	BG378161	2.34	2.36	2.32	2.48	2.34	2.61	1.10	up	1.51E-01	8.95E-01	-	-
1390556_at	---	---	---	---	BF408801	7.17	5.69	6.18	6.58	6.38	6.49	1.10	up	7.68E-01	9.24E-01	-	-
1374521_at	Pcgf3	Polycomb group ring finger 3	305624	Rn.8211	AI230320	4.17	4.10	3.80	3.77	3.78	4.11	1.10	down	4.39E-01	8.95E-01	-	-
1393025_at	---	---	---	Rn.166195	BI297354	5.37	5.71	4.16	4.45	5.43	5.78	1.10	up	8.34E-01	9.47E-01	-	-
1375102_at	---	---	---	Rn.209278	BF396123	2.63	3.55	2.80	3.43	2.97	2.99	1.10	up	6.89E-01	9.04E-01	-	-
1372160_at	Bicap	bladder cancer associated protein homolog (human)	171113	Rn.127812	BM389738	9.82	10.33	10.27	9.86	9.73	10.42	1.10	down	6.28E-01	8.95E-01	-	-
1381489_at	---	---	---	Rn.124467	BE114007	3.95	3.92	3.95	4.32	3.97	3.94	1.10	up	3.29E-01	8.95E-01	-	-
1368284_at	Plvap	plasmalemma vesicle associated protein	56765	Rn.53915	NM_020086	5.07	3.29	2.83	2.81	5.79	3.01	1.10	up	9.13E-01	9.74E-01	-	-
1389572_at	Me3	malic enzyme 3, NADP(+)-dependent, mitochondrial	361602	Rn.198167	AI410864	2.70	2.70	2.35	2.76	2.71	2.69	1.10	up	3.13E-01	8.95E-01	-	-
1384049_at	Tcfap2b	transcription factor AP-2 beta	301285	Rn.12263	BE103610	2.79	2.38	2.39	2.38	2.39	2.38	1.10	down	3.67E-01	8.95E-01	-	-
1389683_at	---	---	---	Rn.23991	AI170768	7.14	7.00	5.50	6.52	6.77	6.77	1.10	up	8.08E-01	9.38E-01	-	-
1376629_at	---	---	---	---	AA946327	4.15	4.12	4.06	3.89	4.31	4.54	1.10	up	5.11E-01	8.95E-01	-	-
1372370_at	Rpusd4	RNA pseudouridylate synthase domain containing 4	315550	Rn.20060	AI233741	3.44	4.34	3.31	3.68	3.58	3.41	1.10	down	7.00E-01	9.07E-01	-	-
1377380_at	---	---	---	---	AI060045	4.76	4.76	5.24	4.75	4.60	4.99	1.10	down	5.23E-01	8.95E-01	-	-
1380909_at	Slc25a24	solute carrier family 25 (mitochondrial carrier, phosphate carrier), member 24	310791	Rn.98927	BM385894	2.59	2.54	2.61	2.65	2.64	2.87	1.10	up	1.54E-01	8.95E-01	-	-
1379218_at	Nlk	nemo like kinase	497961	Rn.113514	BE109792	5.17	6.90	8.25	7.54	6.15	7.05	1.10	up	8.95E-01	9.67E-01	-	-
1386857_at	Stmn1	stathmin 1	29332	Rn.555	NM_017166	9.29	9.60	9.61	9.37	9.34	9.37	1.10	down	2.68E-01	8.95E-01	-	-
1391221_at	Tmem67	transmembrane protein 67	313067	Rn.72665	BE100776	5.16	5.16	5.22	5.19	5.21	5.56	1.10	up	3.21E-01	8.95E-01	-	-
1387361_s_at	Pgk1	phosphoglycerate kinase 1	24644	Rn.108127	NM_053291	10.02	10.19	9.60	10.15	9.82	10.25	1.10	up	5.59E-01	8.95E-01	-	-
1380926_at	---	---	---	Rn.165136	AA957632	7.81	8.01	7.95	7.69	7.87	7.80	1.10	down	1.59E-01	8.95E-01	-	-
1387417_a_at	Sh2bpsm1	SH2-B PH domain containing signaling mediator 1	89817	Rn.11069	NM_134456	2.48	2.80	2.44	2.44	2.44	2.43	1.10	down	2.90E-01	8.95E-01	-	-
1373578_at	Trim2	tripartite motif-containing 2	361970	Rn.16973	BM386413	2.92	4.23	2.84	2.80	2.92	3.86	1.10	down	8.19E-01	9.42E-01	-	-
1385476_x_at	Stra6	stimulated by retinoic acid gene 6	363071	Rn.12735	AI030451	2.56	2.33	2.25	2.24	2.25	2.23	1.10	down	2.08E-01	8.95E-01	-	-
1398493_at	---	---	---	Rn.205590	BG377873	5.47	5.98	6.64	5.41	6.36	5.90	1.10	down	7.67E-01	9.24E-01	-	-
1386026_at	---	---	---	Rn.28221	BF287062	2.45	2.46	2.48	2.46	2.47	2.89	1.10	up	3.85E-01	8.95E-01	-	-
1392987_at	Tada2b	Transcriptional adaptor 2 (ADA2 homolog, yeast)-beta	289717	Rn.22124	AI136895	3.62	3.93	4.23	3.72	3.90	4.57	1.10	up	6.83E-01	9.03E-01	-	-
1381195_at	---	---	---	Rn.209592	BF389423	2.72	2.86	2.81	2.68	2.70	2.60	1.10	down	5.34E-02	8.95E-01	-	-
1393051_at	Armcx1	armadillo repeat containing, X-linked 1	501619	Rn.140506	BF551457	2.47	2.46	2.57	2.47	2.99	2.46	1.10	up	4.84E-01	8.95E-01	-	-
1377706_x_at	---	---	---	---	BF549971	4.37	3.29	2.72	4.23	2.88	2.86	1.10	down	8.46E-01	9.52E-01	-	-
1379963_at	Kif3b	kinesin family member 3B	296284	Rn.41581	AW523457	2.62	3.62	3.37	3.36	2.91	3.75	1.10	up	7.39E-01	9.16E-01	-	-
1377900_at	Abhd14b	abhydrolase domain containing 14b	300983	Rn.2080	BF409560	7.55	9.03	7.98	8.26	7.72	8.16	1.10	down	7.84E-01	9.30E-01	-	-
1382200_at	Prr6	proline rich 6	501702	Rn.3337	AW917547	4.86	3.74	3.54	3.80	3.97	3.96	1.10	down	7.57E-01	9.21E-01	-	-
1370875_at	Ezr	ezrin	54319	Rn.773	AA851304	9.04	9.92	9.70	9.46	9.17	9.62	1.10	down	6.66E-01	8.99E-01	-	-
1396784_at	---	---	---	Rn.154158	BF413768	2.34	2.40	2.35	2.84	2.34	2.32	1.10	up	4.62E-01	8.95E-01	-	-
1380001_at	Pnn	pinin, desmosome associated protein	368070	Rn.38987	AW526140	8.54	8.69	8.33	8.94	8.68	8.35	1.10	up	5.27E-01	8.95E-01	-	-
1396881_at	Ddb1	damage-specific DNA binding protein 1	64470	---	AJ277077	2.90	2.88	3.23	2.88	2.91	2.81	1.10	down	3.12E-01	8.95E-01	-	-
1375714_at	RGD1562952	similar to Erbb2 interacting protein isoform 2	365661	---	BI289124	8.19	8.29	8.78	8.20	8.21	8.45	1.10	down	5.31E-01	8.95E-01	-	-
1374948_at	Tmem106a	transmembrane protein 106A	287722	Rn.16484	BI275815	8.68	8.83	8.67	8.78	8.54	8.45	1.10	down	2.82E-01	8.95E-01	-	-
1387848_at	Hmgcr	3-hydroxy-3-methylglutaryl-Coenzyme A reductase	25675	Rn.9437	NM_013134	3.34	3.35	3.34	3.00	4.19	3.25	1.10	up	7.25E-01	9.13E-01	-	-
1370579_at	LOC246295	glycine-, glutamate-, thienylcyclohexylpiperidine-binding protein	246295	Rn.25735	U53613	5.94	5.75	5.87	5.72	5.61	5.82	1.10	down	1.83E-01	8.95E-01	-	-
1385085_at	Ddc8	differential display clone 8	498028	Rn.207480	BE101971	2.47	2.85	2.49	2.47	2.48	2.45	1.10	down	3.33E-01	8.95E-01	-	-
1392947_at	---	---	---	Rn.6374	AI030349	2.56	2.97	2.56	2.55	2.57	2.56	1.10	down	3.74E-01	8.95E-01	-	-
1389159_at	---	---	---	Rn.16626	BM385437	3.12	3.32	3.13	2.74	4.13	3.12	1.10	up	7.61E-01	9.22E-01	-	-
1384222_at	---	---	---	---	BG680646	4.98	5.26	5.21	5.08	4.90	5.07	1.10	down	2.66E-01	8.95E-01	-	-
1398932_at	Hint1	histidine triad nucleotide binding protein 1	690660	Rn.138667	AI227884	10.00	10.03	10.75	10.23	10.08	10.06	1.10	down	6.14E-01	8.95E-01	-	-
1382761_at	Pde7a	Phosphodiesterase 7A	81744	Rn.39142	AW535566	2.46	2.73	2.85	2.69	2.52	2.42	1.10	down	3.87E-01	8.95E-01	-	-
1379320_at	Snrpd1	Small nuclear ribonucleoprotein D1	291794	Rn.18606	AI102691	7.22	6.85	6.88	6.26	6.85	7.42	1.10	down	7.19E-01	9.11E-01	-	-
1383688_at	---	---	---	Rn.107778	BM383349	2.97	2.49	2.41	2.57	2.44	2.46	1.10	down	4.89E-01	8.95E-01	-	-
1375014_at	Arl4c	ADP-ribosylation factor-like 4C	367311	Rn.198847	BI274857	2.28	2.31	2.31	2.30	2.31	2.71	1.10	up	3.66E-01	8.95E-01	-	-
1373174_at	Nudt16l1	nudix (nucleoside diphosphate linked moiety X)-type motif 16-like 1	497867	Rn.138647	AW915592	3.63	3.23	3.46	3.28	3.36	3.28	1.10	down	3.15E-01	8.95E-01	-	-
1381978_a_at	Sumf2	sulfatase modifying factor 2	360800	Rn.98463	AI071270	3.72	3.77	3.74	3.67	3.76	4.21	1.10	up	4.59E-01	8.95E-01	-	-
1374350_at	---	---	---	Rn.165453	BM382988	7.04	7.57	7.87	7.40	7.67	7.83	1.10	up	6.41E-01	8.95E-01	-	-
1381093_at	---	---	---	Rn.162705	BF394832	2.57	2.99	2.57	2.54	3.48	2.51	1.10	up	7.13E-01	9.10E-01	-	-
1383721_at	Fzd8	frizzled homolog 8 (Drosophila)	364754	Rn.199029	AI556075	3.48	2.80	2.47	3.45	2.63	3.08	1.10	up	7.36E-01	9.15E-01	-	-
1384699_at	---	---	---	Rn.81485	BM384930	2.74	2.86	3.52	2.73	3.22	2.75	1.10	down	6.60E-01	8.98E-01	-	-
1372034_at	Parp14	Poly (ADP-ribose) polymerase family, member 14	303903	Rn.54182	BF284106	3.67	3.66	3.66	3.40	4.37	3.64	1.10	up	6.63E-01	8.99E-01	-	-
1379681_at	Ttc22	tetratricopeptide repeat domain 22	298300	Rn.39367	BM385612	2.64	2.95	2.61	2.60	2.72	2.47	1.10	down	3.55E-01	8.95E-01	-	-
1372375_at	Atg16l1	autophagy related 16-like 1 (S. cerevisiae)	363278	Rn.101734	BF395615	4.28	5.08	4.29	4.47	4.42	4.35	1.10	down	6.36E-01	8.95E-01	-	-
1372311_at	Gnpda1	glucosamine-6-phosphate deaminase 1	683570	Rn.216905	BG380795	5.91	6.12	6.05	6.48	5.99	6.03	1.10	up	4.63E-01	8.95E-01	-	-
1374513_at	07-Sep	septin 7	64551	Rn.222063	BM389104	5.74	5.34	6.75	5.67	6.22	5.52	1.10	down	7.85E-01	9.30E-01	-	-
1380138_at	Hs6st2	heparan sulfate 6-O-sulfotransferase 2	302489	Rn.174129	AI385182	2.35	2.74	2.36	2.35	2.36	2.34	1.10	down	3.45E-01	8.95E-01	-	-
1393436_at	Scgb1c1	secretoglobin, family 1C, member 1	309100	Rn.41707	AI549033	2.73	2.72	2.77	2.72	3.12	2.79	1.10	up	3.30E-01	8.95E-01	-	-
1387675_at	Plau	plasminogen activator, urokinase	25619	Rn.6064	NM_013085	12.23	12.50	12.52	12.20	12.37	12.28	1.10	down	2.62E-01	8.95E-01	-	-
1390231_at	---	---	---	Rn.23264	BI286615	2.81	2.37	2.37	2.36	2.37	2.41	1.10	down	4.02E-01	8.95E-01	-	-
1370842_at	Bckdk	branched chain ketoacid dehydrogenase kinase	29603	Rn.31976	BI277527	5.50	5.29	5.66	5.73	4.76	5.55	1.10	down	6.88E-01	9.04E-01	-	-
1398473_at	Bloc1s2	biogenesis of lysosomal organelles complex-1, subunit 2	293938	Rn.19119	BI290651	6.03	5.98	6.07	5.97	6.47	6.05	1.10	up	4.28E-01	8.95E-01	-	-
1381199_at	---	---	---	Rn.155907	BG376537	2.84	2.76	2.79	2.84	3.20	2.77	1.10	up	3.72E-01	8.95E-01	-	-
1395572_at	Dnaja4	DnaJ (Hsp40) homolog, subfamily A, member 4	300721	Rn.198815	BF565278	4.78	4.73	4.70	4.52	4.60	4.68	1.10	down	5.10E-02	8.95E-01	-	-
1373846_at	RGD1308584	similar to RIKEN cDNA 5730449L18	289083	Rn.137840	BM388575	4.88	4.29	4.57	3.60	4.48	5.25	1.10	down	8.00E-01	9.35E-01	-	-
1376617_at	---	---	---	Rn.52459	BE107482	2.44	2.39	2.84	2.42	2.42	2.41	1.10	down	3.94E-01	8.95E-01	-	-
1380507_at	---	---	---	Rn.43626	BF283420	2.77	2.62	3.41	2.80	2.73	2.85	1.10	down	6.08E-01	8.95E-01	-	-
1372434_at	Cip98	CASK-interacting protein CIP98	313255	Rn.204268	BE098114	3.38	3.19	3.34	2.99	2.89	3.63	1.10	down	5.98E-01	8.95E-01	-	-
1368178_at	Pdzk1	PDZ domain containing 1	65144	Rn.19842	NM_031712	10.69	10.95	10.75	10.73	10.81	10.44	1.10	down	3.77E-01	8.95E-01	-	-
1377141_at	---	---	---	Rn.204793	AI103397	6.79	5.66	6.01	5.50	5.98	6.56	1.10	down	7.79E-01	9.28E-01	-	-
1397803_at	---	---	---	Rn.172039	BF286911	2.44	2.40	3.46	3.02	2.44	2.43	1.10	down	7.49E-01	9.19E-01	-	-
1371375_at	Dstn	destrin	502674	Rn.102412	BI285599	9.70	9.80	9.38	9.37	9.35	9.75	1.10	down	4.94E-01	8.95E-01	-	-
1395862_at	---	---	---	Rn.161443	BF397879	2.55	4.06	2.61	2.69	2.59	3.54	1.10	down	8.25E-01	9.45E-01	-	-
1387705_at	Setd5	SET domain containing 5	297514	Rn.49964	AW254450	4.99	4.98	4.63	4.99	4.99	5.04	1.10	up	3.15E-01	8.95E-01	-	-
1383570_at	Phf3	PHD finger protein 3	363210	Rn.21075	BF547887	6.24	7.02	6.26	6.37	6.23	6.51	1.10	down	6.40E-01	8.95E-01	-	-
1367465_at	Dad1	defender against cell death 1	192275	Rn.7262	AI013627	8.10	7.62	7.02	7.43	7.39	8.33	1.10	up	7.71E-01	9.25E-01	-	-
1373871_at	Supt7l	suppressor of Ty 7 (S. cerevisiae)-like	313905	Rn.11526	AW435481	2.57	3.48	5.20	3.87	4.60	3.18	1.10	up	8.84E-01	9.64E-01	-	-
1388398_at	Rps4y2	ribosomal protein S4, Y-linked 2	690845	Rn.107176	BI282024	2.95	3.26	2.96	2.77	2.96	3.03	1.10	down	3.49E-01	8.95E-01	-	-
1396842_at	Atg9a	ATG9 autophagy related 9 homolog A (S. cerevisiae)	363254	Rn.35248	AI500903	2.46	2.46	2.86	2.46	2.47	2.44	1.10	down	3.73E-01	8.95E-01	-	-
1391414_at	LOC679811	similar to RIKEN cDNA D930015E06	679811	Rn.160937	AI409142	3.10	3.80	2.92	3.10	3.13	4.00	1.10	up	7.51E-01	9.19E-01	-	-
1393593_at	06-Mar	membrane-associated ring finger (C3HC4) 6	294862	Rn.2039	AA874856	6.98	6.43	6.62	6.61	6.41	6.61	1.10	down	4.81E-01	8.95E-01	-	-
1390697_at	Gemin8	gem (nuclear organelle) associated protein 8	363462	Rn.18700	BI278125	3.58	3.72	3.59	3.28	3.37	3.83	1.10	down	4.86E-01	8.95E-01	-	-
1398289_a_at	Crhr1	corticotropin releasing hormone receptor 1	58959	Rn.10499	NM_030999	2.33	2.33	2.33	2.74	2.34	2.32	1.10	up	3.80E-01	8.95E-01	-	-
1389877_at	rCG_44068	Forkhead box C1	364706	Rn.11816	BE105768	3.24	5.41	4.02	3.98	4.39	3.89	1.10	down	8.45E-01	9.52E-01	-	-
1370990_at	Crlf3	cytokine receptor-like factor 3	54395	Rn.203589	AI178339	3.33	2.89	3.34	3.12	2.90	3.13	1.10	down	4.61E-01	8.95E-01	-	-
1398084_at	---	---	---	Rn.161915	BF419651	2.44	2.44	2.53	2.43	2.97	2.41	1.10	up	5.01E-01	8.95E-01	-	-
1370953_at	Ccdc58	coiled-coil domain containing 58	288065	Rn.162059	BE113639	6.40	7.41	7.77	7.01	7.50	7.48	1.10	up	7.73E-01	9.26E-01	-	-
1373138_at	Nudt5	nudix (nucleoside diphosphate linked moiety X)-type motif 5	361274	Rn.55388	AA858886	3.76	3.95	3.79	3.78	3.50	3.81	1.10	down	2.98E-01	8.95E-01	-	-
1379378_at	Mrps18c	mitochondrial ribosomal protein S18C	289469	Rn.105741	AI071605	5.91	6.46	5.88	6.25	5.69	6.71	1.10	up	7.17E-01	9.10E-01	-	-
1395884_at	Angel2	angel homolog 2 (Drosophila)	305035	Rn.62	BF414572	3.50	3.28	3.04	3.07	3.86	3.30	1.10	up	6.41E-01	8.95E-01	-	-
1398143_at	Phkx	phosphorylase, X-linked	501583	Rn.16743	BF413789	3.60	2.75	2.87	2.78	2.86	3.18	1.10	down	6.65E-01	8.99E-01	-	-
1387359_at	Stx1a	syntaxin 1A (brain)	116470	Rn.9943	NM_053788	2.40	2.78	2.42	2.40	2.42	2.38	1.10	down	3.38E-01	8.95E-01	-	-
1383703_at	---	---	---	---	BE109151	7.13	6.97	6.25	6.90	6.32	6.73	1.10	down	6.95E-01	9.06E-01	-	-
1389930_at	Hspa9	Heat shock protein 9	291671	Rn.

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1369667_at	Vps52	vacuolar protein sorting 52 homolog (S. cerevisiae)	25218	Rn.51354	NM_033097	5.48	4.24	4.69	4.68	4.75	4.57	1.10	down	7.32E-01	9.14E-01	-	-
1392532_at	Klf2a	Kinesin family member 2A	84391	Rn.218992	AI145043	3.70	2.73	3.06	3.03	3.03	3.03	1.10	down	6.64E-01	8.99E-01	-	-
1376916_at	Zbtb2	zinc finger and BTB domain containing 2	308128	Rn.36118	AW529183	6.11	5.13	4.72	4.89	6.44	5.04	1.10	up	8.44E-01	9.52E-01	-	-
1394392_at	Fitm2	fat storage-inducing transmembrane protein 2	311617	Rn.107822	BI289554	6.92	7.12	7.37	7.70	6.90	7.21	1.10	up	6.42E-01	8.95E-01	-	-
1383950_at	---	---	---	Rn.41190	BF410404	2.74	2.35	2.37	2.35	2.36	2.34	1.10	down	3.47E-01	8.95E-01	-	-
1385757_at	---	---	---	Rn.202808	BF397258	2.40	2.42	3.03	2.49	2.55	2.40	1.10	down	5.58E-01	8.95E-01	-	-
1390731_at	---	---	---	Rn.156229	BI288533	6.60	6.37	4.70	6.81	5.29	5.96	1.10	up	8.66E-01	9.58E-01	-	-
1374319_at	---	---	---	Rn.123748	BF394096	2.36	2.28	2.36	2.36	2.70	2.35	1.10	up	3.15E-01	8.95E-01	-	-
1383542_at	---	---	---	Rn.32156	BI282819	2.48	2.93	2.47	2.57	2.48	2.42	1.10	down	4.41E-01	8.95E-01	-	-
1381949_at	Prkd1	Protein kinase D1	85421	Rn.144619	BE095549	2.77	2.54	2.55	2.54	2.37	2.54	1.10	down	2.22E-01	8.95E-01	-	-
1392941_at	Hip1	huntingtin interacting protein 1	192154	Rn.836	BE103748	2.44	2.44	2.45	2.44	2.45	2.84	1.10	up	3.66E-01	8.95E-01	-	-
1368659_at	Agxt2	alanine-glyoxylate aminotransferase 2	83784	Rn.1874	D38100	12.40	12.39	12.46	12.25	12.27	12.32	1.10	down	1.37E-02	8.95E-01	-	-
1385464_at	Foxq1	Forkhead box Q1	64826	Rn.10101	AI070944	3.82	4.64	6.20	4.33	5.47	5.25	1.10	up	8.72E-01	9.60E-01	-	-
1372526_at	Ftcn	folliculin	303185	Rn.12799	BI278582	7.58	7.34	6.44	7.20	7.55	7.02	1.10	up	7.43E-01	9.17E-01	-	-
1382225_at	---	---	---	Rn.25185	BF284510	2.70	2.71	2.73	3.11	2.73	2.71	1.10	up	3.56E-01	8.95E-01	-	-
1393918_at	RGD1566099	similar to novel protein	360851	Rn.44018	BF386682	3.07	2.79	2.84	2.76	2.80	2.74	1.10	down	2.05E-01	8.95E-01	-	-
1387919_at	Mtfr2	mitofusin 2	64476	Rn.8570	U41803	6.19	7.53	7.24	7.31	6.73	7.32	1.10	up	7.82E-01	9.29E-01	-	-
1372519_at	Nup93	nucleoporin 93kDa	291874	Rn.137413	AI169375	2.52	2.54	2.56	2.92	2.55	2.54	1.10	up	3.37E-01	8.95E-01	-	-
1396600_at	---	---	---	Rn.58193	BF393953	2.34	2.34	2.35	2.34	2.35	2.74	1.10	up	3.68E-01	8.95E-01	-	-
1372689_at	Tmem103	transmembrane protein 103	363150	Rn.36184	BG381479	3.09	3.41	3.11	3.08	3.09	3.03	1.10	down	2.72E-01	8.95E-01	-	-
1395502_at	Ppp2r5d	protein phosphatase 2, regulatory subunit B', delta isoform	363193	Rn.155910	BF557885	5.52	3.43	2.63	4.00	3.34	3.84	1.10	down	8.87E-01	9.65E-01	-	-
1397218_at	---	---	---	Rn.202406	BF420803	2.53	2.51	3.09	2.52	2.70	2.51	1.10	down	5.37E-01	8.95E-01	-	-
1375044_at	---	---	---	Rn.202668	AI073208	4.23	3.78	3.61	4.23	4.03	3.76	1.10	up	5.88E-01	8.95E-01	-	-
1387547_a_at	Eifd1	EGF, latrophilin and seven transmembrane domain containing 1	64124	Rn.8733	NM_022294	2.89	3.11	2.85	2.84	2.82	2.80	1.10	down	1.77E-01	8.95E-01	-	-
1371371_at	Ndufb4	NADH dehydrogenase (ubiquinone) 1 beta subcomplex 4	288088	Rn.98986	AW434041	9.89	10.00	9.80	9.85	10.07	10.17	1.10	up	2.98E-01	8.95E-01	-	-
1376850_a_at	Ccl27	chemokine (C-C motif) ligand 27	362505	Rn.78371	AI058901	3.65	3.97	3.32	3.96	3.99	3.39	1.10	up	6.50E-01	8.96E-01	-	-
1393874_at	Meox1	mesenchyme homeobox 1	363684	Rn.149759	AA946445	2.67	3.00	2.74	2.66	2.75	2.60	1.10	down	2.86E-01	8.95E-01	-	-
1397407_at	---	---	---	Rn.27457	AI137564	2.37	2.36	2.38	2.37	2.79	2.36	1.10	up	4.01E-01	8.95E-01	-	-
1396398_at	Lpin2	lipin 2	316737	Rn.203839	BF407692	3.05	2.88	3.05	2.79	2.89	2.89	1.10	down	1.09E-01	8.95E-01	-	-
1371856_at	Prrc2	proline-rich nuclear receptor coactivator 2	100125373	Rn.118788	AI408941	7.64	7.61	7.58	7.04	7.69	7.69	1.10	down	5.72E-01	8.95E-01	-	-
1372064_at	Cxcl16	chemokine (C-X-C motif) ligand 16	497942	Rn.7070	BI296385	9.06	8.27	8.76	8.35	9.17	8.17	1.10	down	7.46E-01	9.18E-01	-	-
1395584_at	RGD1308290	Similar to RIKEN cDNA 5730454B08	360845	Rn.73695	C06826	3.25	3.29	5.16	4.96	3.35	2.99	1.10	down	8.86E-01	9.65E-01	-	-
1376431_at	Sil1	SIL1 homolog, endoplasmic reticulum chaperone (S. cerevisiae)	291673	Rn.103851	BM387357	6.76	7.02	6.87	6.60	7.10	7.35	1.10	up	5.94E-01	8.95E-01	-	-
1370969_at	Hoxa5	homeo box A5	79241	Rn.8465	BE107303	5.88	6.18	4.57	5.78	5.23	6.02	1.10	up	8.19E-01	9.42E-01	-	-
1371511_at	Arpc2	actin related protein 2/3 complex, subunit 2	301511	Rn.93317	AI009775	10.03	10.09	10.19	9.71	9.87	10.32	1.10	down	5.18E-01	8.95E-01	-	-
1377603_at	Snx24	sorting nexin 24	361328	Rn.204247	BF284123	4.65	5.29	5.28	5.51	5.07	5.03	1.10	up	6.38E-01	8.95E-01	-	-
1386581_at	Itgav	integrin alpha V	296456	Rn.23339	AW141214	7.42	7.26	7.11	6.69	6.88	7.81	1.10	down	7.28E-01	9.13E-01	-	-
1373517_at	Chuk	conserved helix-loop-helix ubiquitous kinase	309361	Rn.23019	BG671801	8.70	8.47	8.64	8.31	8.28	8.81	1.10	down	5.11E-01	8.95E-01	-	-
1378934_at	---	---	---	Rn.171457	BE116059	3.12	3.14	3.43	3.38	3.10	2.82	1.10	down	5.21E-01	8.95E-01	-	-
1384284_at	---	---	---	Rn.155328	BI290838	3.17	2.40	2.47	2.32	2.86	2.46	1.10	down	6.72E-01	9.01E-01	-	-
1376088_at	Slc25a19	solute carrier family 25 (mitochondrial thiamine pyrophosphate carrier), membr	303676	Rn.198914	AA817715	3.01	3.00	3.02	3.16	2.78	3.49	1.10	up	5.53E-01	8.95E-01	-	-
1377373_at	---	---	---	---	BF403955	2.80	2.50	2.54	2.47	2.50	2.47	1.10	down	2.34E-01	8.95E-01	-	-
1374905_at	---	---	---	---	AA925303	3.95	4.24	3.83	3.81	4.76	3.85	1.10	up	7.10E-01	9.09E-01	-	-
1373842_at	Wasl	Wiskott-Aldrich syndrome-like	682507	---	BM390718	6.27	7.02	5.53	6.54	5.55	7.12	1.10	up	8.42E-01	9.51E-01	-	-
1389681_at	Sar1b	SAR1 homolog B (S. cerevisiae)	287276	Rn.36748	AI105294	9.46	8.96	9.40	9.15	8.88	9.39	1.10	down	5.69E-01	8.95E-01	-	-
1379646_at	LOC500974	Similar to CDNA sequence BC024479	500974	Rn.96035	AI229747	4.07	4.31	5.00	4.38	5.06	3.53	1.10	down	8.11E-01	9.39E-01	-	-
1371367_at	Tardbp	TAR DNA binding protein	298648	Rn.2633	BE107459	9.98	9.99	9.44	10.05	8.95	10.01	1.10	down	7.58E-01	9.21E-01	-	-
1368404_at	Dbn1	drebrin 1	81653	Rn.11247	NM_031024	2.46	2.45	2.47	2.87	2.46	2.45	1.10	up	3.94E-01	8.95E-01	-	-
1381224_at	LOC691396	similar to Zinc finger protein 551 (Zinc finger protein KOX23)	691396	Rn.38959	AI502861	3.87	4.54	4.07	4.06	4.01	4.81	1.10	up	7.05E-01	9.08E-01	-	-
1374749_at	---	---	---	Rn.45715	BM392169	5.21	6.50	6.36	5.48	5.87	6.32	1.10	down	7.92E-01	9.33E-01	-	-
1393512_at	---	---	---	Rn.199212	AA957880	2.85	2.77	2.66	2.76	2.59	2.53	1.10	down	4.08E-01	8.95E-01	-	-
1388540_at	Maz	MYC-associated zinc finger protein (purine-binding transcription factor)	691842	Rn.100537	BM390828	5.99	6.10	5.94	6.15	6.22	6.06	1.10	up	1.23E-01	8.95E-01	-	-
1385206_at	---	---	---	---	BF406798	2.74	3.06	2.74	2.68	2.78	2.68	1.10	down	3.03E-01	8.95E-01	-	-
1371618_at	Xpot	Exportin, tRNA (nuclear export receptor for tRNAs)	314879	Rn.2238	AW251204	8.72	8.81	8.97	8.43	8.57	9.10	1.10	down	5.71E-01	8.95E-01	-	-
1374472_at	Vps37a	vacuolar protein sorting 37 homolog A (S. cerevisiae)	290775	Rn.19	AI710526	6.57	7.00	6.72	6.42	6.97	6.51	1.10	down	5.66E-01	8.95E-01	-	-
1374967_at	---	---	---	Rn.199417	BI282726	3.15	3.51	2.82	3.87	2.83	3.17	1.10	up	7.34E-01	9.15E-01	-	-
1377814_at	---	---	---	---	AA926368	2.36	2.34	2.35	2.78	2.35	2.32	1.10	up	4.20E-01	8.95E-01	-	-
1394234_x_at	Iqwd1	IQ motif and WD repeats 1	289181	Rn.3917	AA848540	9.05	8.99	9.32	8.95	8.97	9.03	1.10	down	2.67E-01	8.95E-01	-	-
1390146_at	RGD1306105	similar to RIKEN cDNA 2610318G18	360916	Rn.20251	BF414998	2.45	2.55	2.49	2.53	2.70	2.66	1.10	up	8.57E-02	8.95E-01	-	-
1372240_at	Sgca	sarcoglycan, alpha (dystrophin-associated glycoprotein)	303468	Rn.136653	BG378841	2.53	2.52	2.53	2.92	2.53	2.52	1.10	up	3.73E-01	8.95E-01	-	-
1381420_at	---	---	---	Rn.204726	BF397624	2.64	2.70	3.11	2.70	2.73	2.62	1.10	down	4.36E-01	8.95E-01	-	-
1393949_at	Hyal3	hyaluronoglucosaminidase 3	300993	Rn.72927	BG672094	3.68	3.70	5.21	5.27	3.79	3.13	1.10	down	8.78E-01	9.62E-01	-	-
1394547_at	---	---	---	---	AW143604	3.04	2.59	2.60	2.68	2.70	2.44	1.10	down	4.79E-01	8.95E-01	-	-
1372719_at	---	---	---	---	BF283702	8.60	8.90	8.20	9.04	8.15	8.90	1.10	up	7.19E-01	9.11E-01	-	-
1391069_at	RGD1309748	Similar to CG4768-PA	303783	Rn.203785	AI231713	7.77	7.76	8.43	7.16	7.58	8.82	1.10	down	8.02E-01	9.36E-01	-	-
1387053_at	Fmo1	flavin containing monooxygenase 1	25256	Rn.867	NM_012792	10.36	10.35	9.96	10.17	9.86	10.24	1.10	down	4.94E-01	8.95E-01	-	-
1385919_at	---	---	---	---	BI283971	5.76	6.39	5.36	5.93	5.80	6.18	1.10	up	6.98E-01	9.07E-01	-	-
1377966_at	---	---	---	---	BI275590	9.75	8.88	9.76	9.83	9.45	9.52	1.10	up	6.93E-01	9.05E-01	-	-
1378920_at	---	---	---	Rn.205706	BE095832	3.99	4.12	3.91	3.89	3.91	3.82	1.10	down	1.13E-01	8.95E-01	-	-
1375299_at	Dullard	Dullard homolog (Xenopus laevis)	287447	Rn.4211	AI103331	5.25	5.27	5.20	5.45	5.25	5.42	1.10	up	1.08E-01	8.95E-01	-	-
1389970_at	RGD1310606	similar to RIKEN cDNA 1200009B18; EST AA408438	297728	Rn.11521	BG378319	5.35	6.11	5.69	5.72	5.55	6.29	1.10	up	6.91E-01	9.05E-01	-	-
1398325_at	Tspan3	tetraspanin 3	300733	Rn.998	AI172464	7.09	6.56	7.58	6.50	7.25	7.09	1.10	down	7.39E-01	9.16E-01	-	-
1388321_at	Imp3	IMP3, U3 small nucleolar ribonucleoprotein, homolog (yeast)	315697	Rn.3787	BG378108	7.82	8.70	9.06	8.41	8.46	8.31	1.10	down	7.39E-01	9.16E-01	-	-
1377835_at	Dock8	dedicator of cytokinesis 8	499337	Rn.164225	BM390876	5.59	6.26	5.58	6.26	5.33	6.24	1.10	up	7.45E-01	9.17E-01	-	-
1391765_at	Lrrc48	leucine rich repeat containing 48	287371	Rn.137189	BM383632	2.57	2.71	2.51	2.55	2.57	3.06	1.10	up	4.92E-01	8.95E-01	-	-
1397464_at	---	---	---	---	AA901367	2.43	2.43	2.44	2.84	2.43	2.43	1.10	up	3.88E-01	8.95E-01	-	-
1389515_at	Rfxank	regulatory factor X-associated ankyrin-containing protein	306353	Rn.201501	AW251289	7.23	7.48	5.88	7.31	6.64	7.03	1.10	up	8.17E-01	9.41E-01	-	-
1390601_at	---	---	---	Rn.146442	BM385386	2.77	2.40	2.41	2.40	2.41	2.38	1.10	down	3.38E-01	8.95E-01	-	-
1369978_at	Prpsap2	phosphoribosyl pyrophosphate synthetase-associated protein 2	117272	Rn.2681	NM_057131	5.66	6.45	7.62	6.41	6.20	6.72	1.10	down	8.32E-01	9.47E-01	-	-
1389123_at	Ccl6	chemokine (C-C motif) ligand 6	287910	Rn.7857	BE095824	3.63	3.53	4.46	4.24	3.67	4.11	1.10	up	7.17E-01	9.10E-01	-	-
1376582_at	Med1	mediator complex subunit 1	497991	Rn.4262	BE108373	6.48	5.99	5.94	5.93	5.93	6.94	1.10	up	7.44E-01	9.17E-01	-	-
1369410_at	---	---	---	---	NM_053584	13.01	12.94	13.13	12.93	12.97	12.78	1.10	down	1.73E-01	8.95E-01	-	-
1396450_at	Enah	enabled homolog (Drosophila)	360891	Rn.163240	AW918724	5.04	5.83	6.13	5.50	5.50	5.60	1.10	down	7.04E-01	9.07E-01	-	-
1371747_at	RGD1310660	similar to RIKEN cDNA 2700038C09	296470	Rn.1389	AI406304	5.82	6.46	6.38	5.87	6.42	6.77	1.10	up	7.08E-01	9.09E-01	-	-
1369416_at	Hcn3	hyperpolarization-activated cyclic nucleotide-gated potassium channel 3	114245	Rn.48801	NM_053685	2.76	2.37	2.38	2.37	2.37	2.37	1.10	down	3.58E-01	8.95E-01	-	-
1369069_at	Akap1	A kinase (PRKA) anchor protein 1	114124	Rn.163146	NM_053665	3.61	3.59	3.62	3.61	4.22	3.38	1.10	up	6.22E-01	8.95E-01	-	-
1381454_at	---	---	---	Rn.204629	AI144856	3.39	4.11	3.33	4.29	3.15	2.99	1.10	down	7.96E-01	9.34E-01	-	-
1371796_at	Trnx2	Thioredoxin-related transmembrane protein 2	295701	Rn.3027	AA799476	7.45	8.00	8.46	7.87	7.43	8.20	1.10	down	7.37E-01	9.15E-01	-	-
1390891_at	Kif11	kinesin family member 11	171304	Rn.58850	BE116384	4.49	4.57	5.14	4.32	4.24	5.23	1.10	down	7.44E-01	9.17E-01	-	-
1392742_at	---	---	---	Rn.167498	AI230806	2.97	2.62	2.69	2.69	3.36	2.63	1.10	up	6.33E-01	8.95E-01	-	-
1379573_at	---	---	---	---	AA818730	2.91	3.18	2.74	3.00	3.16	3.07	1.10	up	3.92E-01	8.95E-01	-	-
1382119_at	Dntllp2	deoxynucleotidyltransferase, terminal, interacting protein 2	295419	Rn.15094	BI303937	3.49	3.53	3.49	3.86	3.53	3.52	1.10	up	2.96E-01	8.95E-01	-	-
1372057_at	Nrbp	nuclear receptor binding protein	619579	Rn.190830	AA800232	3.32	3.47	3.52	3.71	3.54	3.45	1.10	up	2.53E-01	8.95E-01	-	-
1374002_at	LOC100192313	hypothetical protein LOC100192313	100192313	Rn.98813	AI045904	5.47	6.04	5.54	5.65	5.86	5.94	1.10	up	5.42E-01	8.95E-01	-	-
1390997_at	---	---	---	Rn.203375	BI303253	3.48	4.30	3.19	3.47	4.44	3.46	1.10	up	7.89E-01	9.32E-01	-	-
1369944_at	Marcksl1	MARCKS-like 1	81520	Rn.2486	NM_030862	2.36	2.38	2.32	2.59	2.49	2.39	1.10	up	9.55E-02	8.95E-01	-	-
1381833_at	Cdca2	cell division cycle associated 2	305984	Rn.49950	AW532628	2.32	2.32	4.51	4.12	2.33	2.31	1.10	down	8.95E-01	9.67E-01	-	-
1368575_at	Slc6a18	solute carrier family 6, member 18	29323	Rn.9998	NM_017163	10.00	10.53	10.31	10.19	9.95	10.30	1.10	down	5.17E-01	8.95E-01	-	-
1385509_at	---	---	---	Rn.152224	AI801967	2.77	3.79	5.03	4.01	4.35	3.61	1.10	up	8.57E-01	9.55E-01	-	-
1379497_at	---	---	---	---	BI275261	8.17	9.23	8.60	9.13	8.67	8.59	1.10	up	7.26E-01	9.13E-01	-	-
1372507_at	Tcta	T-cell leukemia translocation altered gene	306587	Rn.2916	AA901093	6.90	6.71	6.72	6.65	6.57	6.70	1.10	down	1.42E-01	8.95E-01	-	-
1390421_at	RGD1310475	Similar to RIKEN cDNA 0610010D20	293949	Rn.13905	AI232524	10.51	10.48	11.18	10.53	10.37	10.88	1.10	down	6.52E-01	8.97E-01	-	-
1392789_at	Slc25a36	solute carrier family 25, member 36	501039	Rn.17305	BI296353	5.12	5.30	5.88	5.35	5.15	5.41	1.10	down	6.14E-01	8.95E-01	-	-
1388365_at	Atp6v0d1	ATPase, H+ transporting, lysosomal 38kDa, V0 subunit d1	291969	Rn.94752	BI276424	10.59	10.85	10.70	10.61	10.46	10.67	1.10	down	2.45E-01	8.95E-01	-	-
1382120_at	Epc2	enhancer of polycomb homolog 2 (Drosophila)	362132	Rn.23462	AI535147	2.97	2.98	2.80	2.97	2.96	3.21	1.10	up	2.59E-01	8.95E-01	-	-
1374807_at	RGD1310877	similar to RIKEN cDNA 1810063I07 gene	305667	Rn.20023	AI230067	5.40	5.32	5.48	5.62	5.58	5.40	1.10	up	1.85E-01	8.95E-01	-	-
1375517_at	Trp53inp2	tumor protein p53 inducible nuclear protein 2	362246	Rn.86075	AI171654	8.07	8.27	7.78	8.11	7.88	7.73	1.10	down	5.03E-01	8.95E-01	-	-
1371184_x_at	Tpm3	tropomyosin 3, gamma	117557	Rn.37575	AF053359	3.64	3.74	3.90	3.61	3.68	3.59	1.10	down	1.69E-01	8.95E-01	-	-
1384163_at	---	---	---	Rn.216772	BE103875	6.75	6.44	7.05	7.16	7.08	6.40	1.10	up	6.79E-01	9.02E-01	-	-
1387441_at	Kcnk3	potassium channel, subfamily K, member 3	29553	Rn.15536	AA943476	2.43	2.43	2.44	2.43	2.85	2.42	1.10	up	4.03E-01	8.95E-01	-	-
1381081_at	---	---	---	Rn.147885	AW523873	5.23	3.31	3.12	3.86	3.11	4.30	1.10	down	8.70E-01	9.60E-01	-	-
1376730_at	Pfdn2	prefoldin subunit 2	685607	Rn.7627	BE103377	4.31	5.92	5.76	4.91	5.41	5.27	1.10	down	8.17E-01	9.41E-01	-	-
1399042_at	Atg4b	ATG4 autophagy related 4 homolog B (S. cerevisiae)	316640	Rn.163086	AI228455	7.14	5.59	4.72	4.98	6.28	5.79	1.10	down	8.77E-01	9.62E-01	-	-
1393003_at	---	---	---	Rn.2419	AA899900	2.46	2.42	2.40	2.44	2.43	2.80	1.10	up	3.47E-01	8.95E-01	-	-
1371525_at	Slc12a7	solute carrier family 12 (potassium/chloride transporters), member 7	308069	Rn.64199	BI277550	4.95	5.73	4.83	5.43	4.81	5.66	1.10	up	7.46E-01	9.18E-01	-	-
1376070_at	Fkbp8	FK506 binding protein 8, 38kDa	290652	Rn.99789	AI236623	3.53	4.37	5.07	4.77	4.64	3.96	1.10	up	8.08E-01	9.38E-01	-	-
1398630_at	Hmgb1	high mobility group box 1	25455	Rn.144255	AA801095	2.58	2.54	2.58	2.55	2.62	2.93	1.10	up	3.17E-01	8.95E-01	-	-
1384093_at	C1ql3	complement component 1, q subcomponent-like 3	680404	Rn.13498	AW523562	4.75	4.51	4.56	4.51	4.54	4.37	1.10	down	2.17E-01	8.95E-01	-	-
1370426_a_at	Atp2a2	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2	29693	Rn.2305	J04024	10.12	10.48	10.06	10.35	10.04	10.66	1.10	up	5.85E-01	8.95E-01	-	-
1368180_s_at	ipta2 /// LOC494499	glutathione A2 /// LOC494499 glutathione A2 /// LOC494499 protein	24422 /// 494499	Rn.40574	NM_017013	13.08	12.96	12.98	12.92	12.77	12.93	1.10	down	1.06E-01	8.95E-01	-	-
1393106_x_at	Gtf2f1	general transcription factor IIF, polypeptide 1	316123	Rn.98836	BF420770	7.52	7.76	7.53	7.52	6.66	8.23	1.10	down	7.89E-01	9.32E-01	-	-
1392453_at	Clcn3	chloride channel 3	84360	Rn.4175	AI763523	3.79	3.73	4.20	3.93	3.78	4.40	1.10	up	6.10E-01	8.95E-01	-	-
1396448_at	---	---	---	Rn.150720	BE119407	2.57	2.52	2.60	3.00	2.59	2.49	1.10	up	4.51E-01	8.95E-01	-	-
1381083_at	---	---	---	Rn.148607	BF419863	2.69	2.70	2.70	2.87	2.69	2.92	1.10	up	1.25E-01	8.95E-01	-	-
1371575_at	Msn	Moesin	81521	Rn.2762	BF281185	10.01	10.34	10.07	10.15	10.12	9.76	1.10	down	4.63E-01	8.95E-01	-	-
1378885_at	---	---	---	Rn.209222	BF386920	2.46	2.44	2.56	2.45	2.95	2.45	1.10	up	4.86E-01	8.95E-01	-	-
1389845_at	---	---	---	Rn.106362	BI282224	9.74	9.71	9.67	9.70	9.60	10.22	1.10	up	5.32E-01	8.95E-01	-	-
1368244_at	As3mt	arsenic (+3 oxidation state) methyltransferase	140925	Rn.95453	NM_080890	7.78	7.10	7.56	7.32	7.37	7.36	1.10	down	5.51E-01	8.95E-01	-	-
1394500_at	RGD1311612	similar to hypothetical protein FLJ12118	361184	Rn.54352	BI288738	2.49	2.46	2.49	2.49	2.51	2.82	1.10	up	2.91E-01	8.95E-01	-	-
1395973_at	---	---	---	Rn.167282	AI236099	7.68	8.07	7.34	7.45	7.48	7.76	1.10	down	6.01E-01	8.95E-01	-	-
1397164_at	---	---	---	Rn.153998	AI175779	6.57	7.66	8.38	7.57	7.48	7.16	1.10	down	8.20E-01	9.42E-01	-	-
1372681_at	---	---	---	---	BI294716	3.45	3.17	3.95	3.11	3.45	3.61	1.10	down	6.55E-01	8.98E-01	-	-
1375091_at	Cep164	centrosomal protein 164kDa	363055	Rn.106595	BE111801	5.26	4.07	4.25	5.92	2.48	4.79	1.10	down	9.09E-01	9.72E-01	-	-
1374534_at	Rhot2	ras homolog gene family, member T2	287156	Rn.8882	AI233243	5.01	4.67	4.49	5.33	4.68	4.55	1.10	up	6.70E-01	9.00E-01	-	-
1378942_at	---	---	---	Rn.160740	AI234028	3.76	3.41	3.40	3.36	3.49	3.33	1.10	down	3.66E-01	8.95E-01	-	-
1369728_at	LOC680097	similar to germinal histone H4 gene	680097	Rn.44120	NM_022686	8.15	9.21	8.65	8.56	9.11	8.74	1.10	up	7.24E-01	9.13E-01	-	-
1392505_at	Pds5a	PDS5, regulator of cohesion maintenance, homolog A (S. cerevisiae)	305344	Rn.214568	AI229232	4.05	4.31	3.77	3.99	3.76	3.98	1.10	down	4.91E-01	8.95E-01	-	-
1369259_at	Dio1	deiodinase, iodothyronine, type I	25430	Rn.87549	NM_021653	6.14	6.42	5.96	5.83	6.13	6.17	1.10	down	4.91E-01	8.95E-01	-	-
1378123_x_at	---	---	---	Rn.23192	BI285319	6.32	6.15	6.25	6.30	5.89	6.14	1.10	down	3.64E-01	8.95E-01	-	-
1389099_at	Zfp428	zinc finger protein 428	361519	Rn.102067	AI600184	2.69	3.51	2.68	3.87	2.71	2.71	1.10	up	7.96E-01	9.34E-01	-	-
1377267_at	Magee1	melanoma antigen, family E, 1	317232	Rn.38053	BF402385	2.41	2.40	2.42	2.81	2.42	2.39

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1380142_at	Hoxb8	homeo box B8	24457	Rn.14746	BF398019	7.28	9.43	8.25	7.23	8.79	8.54	1.09	down	8.77E-01	9.62E-01	-	-
1385020_at	LOC499339	hypothetical protein LOC499339	499339	Rn.127943	BM387790	2.92	3.55	2.95	2.93	3.06	3.04	1.09	down	5.69E-01	8.95E-01	-	-
1384384_at	RGD1304592	similar to KIAA0528 protein	362461	Rn.62095	BF543289	3.15	3.14	3.40	3.32	2.89	3.08	1.09	down	4.38E-01	8.95E-01	-	-
1398800_at	Ywhab	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, b	56011	Rn.8653	NM_019377	8.44	8.43	8.81	9.03	8.38	8.66	1.09	up	5.93E-01	8.95E-01	-	-
1387410_at	Nr4a2	nuclear receptor subfamily 4, group A, member 2	54278	Rn.88129	U72345	2.47	2.50	2.52	2.70	2.60	2.58	1.09	up	2.70E-02	8.95E-01	-	-
1387843_at	Fst	follistatin	24373	Rn.162557	NM_012561	2.36	2.35	2.74	2.35	2.36	2.34	1.09	down	3.64E-01	8.95E-01	-	-
1370054_at	Cdkn2c	cyclin-dependent kinase inhibitor 2C (p18, inhibits CDK4)	54238	Rn.63865	NM_131902	3.90	5.28	4.10	4.83	4.18	4.67	1.09	up	7.97E-01	9.34E-01	-	-
1382354_at	Mphosph8	M-phase phosphoprotein 8	290270	Rn.42579	BE099884	6.86	7.25	7.64	7.41	6.84	7.11	1.09	down	6.67E-01	8.99E-01	-	-
1374324_at	---	---	---	Rn.163625	AA945828	2.43	3.38	2.46	2.42	2.45	3.01	1.09	down	7.41E-01	9.16E-01	-	-
1370536_at	Prmt3	protein arginine methyltransferase 3	89820	Rn.33389	AF059530	3.38	3.30	3.47	2.82	3.48	3.46	1.09	down	5.89E-01	8.95E-01	-	-
1399137_at	Metap1	methionyl aminopeptidase 1	295500	Rn.6799	AW527547	7.09	6.99	6.67	7.49	6.40	7.24	1.09	up	7.32E-01	9.14E-01	-	-
1384383_at	Agpat6	1-acylglycerol-3-phosphate O-acyltransferase 6 (lysophosphatidic acid acyltra	290843	Rn.6835	BF557230	2.67	2.34	2.41	2.33	2.35	2.34	1.09	down	2.58E-01	8.95E-01	-	-
1390019_at	H3f3b	H3 histone, family 3B	117056	Rn.124815	BM390456	10.24	10.65	10.55	10.28	10.16	10.61	1.09	down	5.22E-01	8.95E-01	-	-
1368674_at	Pygl	phosphorylase, glycogen, liver	64035	Rn.21399	NM_022268	7.23	7.19	7.82	7.29	6.98	7.58	1.09	down	6.92E-01	8.96E-01	-	-
1392707_at	---	---	---	---	AA946455	2.65	2.63	2.99	2.64	2.64	2.60	1.09	down	3.26E-01	8.95E-01	-	-
1393142_at	Cep70	centrosomal protein 70kDa	367153	Rn.161942	BF562621	2.67	4.39	4.12	3.32	3.14	4.33	1.09	down	8.51E-01	9.54E-01	-	-
1375718_at	LOC498525	Bm403207	498525	---	BF546105	2.17	2.17	2.57	2.18	2.17	2.17	1.09	down	3.88E-01	8.95E-01	-	-
1385586_at	RGD1306074	similar to RIKEN cDNA 1110002H13	296601	Rn.162652	AA965077	2.31	2.26	2.26	2.44	2.44	2.34	1.09	up	2.70E-02	8.95E-01	-	-
1379539_at	---	---	---	Rn.23762	AI137339	3.25	3.23	3.59	3.25	3.25	3.18	1.09	down	3.40E-01	8.95E-01	-	-
1382424_at	---	---	---	Rn.204312	AI071713	2.75	2.94	2.55	2.54	2.48	2.82	1.09	down	4.51E-01	8.95E-01	-	-
1367769_at	Polr2g	polymerase (RNA) II (DNA directed) polypeptide G	117017	Rn.106248	NM_053948	7.17	7.68	8.15	7.48	7.91	8.00	1.09	up	7.11E-01	9.10E-01	-	-
1375943_at	Cp110	CP110 protein	361634	Rn.19479	BI288873	2.72	2.34	2.32	2.31	2.37	2.31	1.09	down	3.85E-01	8.95E-01	-	-
1383169_at	---	---	---	Rn.40381	BF563716	9.72	10.70	10.25	10.13	10.41	10.51	1.09	up	6.92E-01	9.05E-01	-	-
1398351_at	Usp7	Ubiquitin specific peptidase 7 (herpes virus-associated)	360471	Rn.72721	AI175593	6.19	5.98	6.12	5.97	5.70	6.22	1.09	down	4.89E-01	8.95E-01	-	-
1371918_at	Cd99	CD99 antigen	652929	Rn.195321	AI235284	7.69	8.31	8.07	8.25	8.15	8.06	1.09	up	5.27E-01	8.95E-01	-	-
1373447_at	Hn1l	hematological and neurological expressed 1-like	360492	Rn.19357	BF281350	6.19	5.67	6.43	6.11	5.33	6.47	1.09	down	7.65E-01	9.23E-01	-	-
1389100_at	Epm2aip1	EPM2A (laforin) interacting protein 1	316021	Rn.209819	BF409831	5.32	5.72	5.52	6.08	5.61	5.35	1.09	up	6.34E-01	8.95E-01	-	-
1394819_at	Sp110	SP110 nuclear body protein	301570	Rn.6459	AI177957	2.90	2.84	2.67	3.21	2.77	2.81	1.09	up	4.50E-01	8.95E-01	-	-
1369076_at	Tmem33	transmembrane protein 33	59303	Rn.203963	NM_021671	7.59	8.28	8.10	7.69	7.91	7.98	1.09	down	5.91E-01	8.95E-01	-	-
1371355_at	Ndufa8	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 8	296658	Rn.202907	BI280270	7.30	8.06	7.96	7.78	7.31	7.83	1.09	down	6.80E-01	9.03E-01	-	-
1394397_at	Ral1d1	ribosomal L1 domain containing 1	302898	Rn.154542	BF522734	6.90	6.73	7.26	7.07	6.74	7.46	1.09	up	6.47E-01	8.95E-01	-	-
1378141_at	---	---	---	Rn.39065	AI556445	3.80	3.67	3.50	3.55	4.09	3.71	1.09	up	5.17E-01	8.95E-01	-	-
1387277_at	Lyn	v-yes-1 Yamaguchi sarcoma viral related oncogene homolog	81515	Rn.4338	NM_030857	2.50	2.48	2.54	2.73	2.53	2.66	1.09	up	9.89E-02	8.95E-01	-	-
1389175_at	Whsc2	Wolf-Hirschhorn syndrome candidate 2 (human)	305455	Rn.9138	AA956953	5.34	5.06	5.29	5.51	5.39	5.19	1.09	up	3.61E-01	8.95E-01	-	-
1373075_at	RGD1560888	similar to Cell division protein kinase 8 (Protein kinase K35)	498140	Rn.1331	BM390707	6.37	6.19	5.86	6.41	4.76	6.86	1.09	down	8.53E-01	9.54E-01	-	-
1392550_at	Dact1	dapper, antagonist of beta-catenin, homolog 1 (Xenopus laevis)	500666	Rn.17371	BE111725	2.31	2.30	2.32	2.70	2.31	2.30	1.09	up	3.85E-01	8.95E-01	-	-
1371056_at	Neo1	neogenin homolog 1 (chicken)	81735	Rn.10667	U68726	2.65	2.65	2.66	2.58	2.65	3.12	1.09	up	4.86E-01	8.95E-01	-	-
1383625_a_at	Zfp259	zinc finger protein 259	500989	Rn.102611	BF288164	11.63	10.18	10.17	11.04	10.73	10.59	1.09	up	8.09E-01	9.38E-01	-	-
1371773_at	---	---	---	Rn.22153	AI179413	7.20	8.24	7.11	7.23	7.50	8.20	1.09	up	7.94E-01	9.34E-01	-	-
1392581_at	Ncald	neurocalcin delta	553106	Rn.13744	BF420172	5.52	6.67	5.44	5.52	6.23	5.50	1.09	down	7.94E-01	9.34E-01	-	-
1376852_at	Mccc1	methylcrotonoyl-Coenzyme A carboxylase 1 (alpha)	294972	Rn.15587	BI274460	9.80	10.73	10.16	10.02	9.71	10.56	1.09	down	7.43E-01	9.17E-01	-	-
1370339_at	Tpm3	tropomyosin 3, gamma	117557	Rn.37575	BI295970	5.16	6.29	6.14	5.80	5.46	5.96	1.09	down	7.53E-01	9.20E-01	-	-
1393996_at	---	---	---	---	BF549785	3.23	3.16	3.89	3.43	2.89	3.57	1.09	down	6.99E-01	9.07E-01	-	-
1375665_at	Foxn3	Forkhead box N3	314374	Rn.10640	BF410565	3.06	2.83	2.85	2.83	2.85	2.68	1.09	down	2.24E-01	8.95E-01	-	-
1388342_at	Etv3	Ets variant 3	295297	Rn.220231	BI291344	5.20	5.19	5.44	5.05	5.26	5.13	1.09	down	2.77E-01	8.95E-01	-	-
1383015_at	Tbc1d10c	TBC1 domain family, member 10C	361697	Rn.61004	BF406973	2.88	2.50	2.55	2.53	3.30	2.49	1.09	up	6.77E-01	9.02E-01	-	-
1398062_at	Smap2	small ArfGAP2	298500	Rn.203765	BF404303	3.96	4.21	3.70	5.12	2.63	3.73	1.09	down	8.69E-01	9.59E-01	-	-
1376602_a_at	Fbxo22	F-box protein 22	300724	Rn.4284	AI030899	8.01	8.05	8.43	8.24	7.71	8.16	1.09	down	5.75E-01	8.95E-01	-	-
1398283_at	Cbp	Csk binding protein	64019	Rn.127786	NM_022253	2.81	2.71	2.61	2.60	2.60	2.54	1.09	down	1.07E-01	8.95E-01	-	-
1393583_at	Etaa1	Ewing tumor-associated antigen 1	498420	Rn.121635	BE119096	2.59	2.92	2.65	2.58	2.62	2.58	1.09	down	2.78E-01	8.95E-01	-	-
1367648_at	Igfbp2	insulin-like growth factor binding protein 2	25662	Rn.6813	AI104234	2.32	2.31	2.35	2.57	2.50	2.30	1.09	up	1.90E-01	8.95E-01	-	-
1385680_at	Srp54a	signal recognition particle 54a	116650	Rn.24880	BG667707	3.59	3.75	3.75	4.01	3.60	3.87	1.09	up	3.88E-01	8.95E-01	-	-
1386683_at	Atrx	alpha thalassemia/mental retardation syndrome X-linked (RAD54 homolog, S	246284	Rn.107838	BF562870	5.73	6.05	6.18	6.82	4.95	6.57	1.09	up	8.41E-01	9.50E-01	-	-
1374011_at	Ercc3	excision repair cross-complementing rodent repair deficiency, complementatic	291703	Rn.44012	BM388758	5.47	6.23	5.72	5.68	5.35	6.01	1.09	down	6.83E-01	9.03E-01	-	-
1387852_at	Thrsp	thyroid hormone responsive	25357	Rn.81145	NM_012703	2.75	2.40	2.41	2.39	2.40	2.37	1.09	down	3.32E-01	8.95E-01	-	-
1398180_at	---	---	---	Rn.146192	BF567681	2.87	2.75	3.06	2.82	3.02	2.22	1.09	up	4.28E-01	8.95E-01	-	-
1374453_at	RGD1560871	similar to plexin 1	362398	---	AW917568	3.25	3.23	4.30	3.81	3.26	3.33	1.09	down	7.80E-01	9.22E-01	-	-
1372085_at	Arl6ip2	ADP-ribosylation factor-like 6 interacting protein 2	298757	Rn.203081	AI237657	6.88	6.90	7.08	7.02	7.28	6.95	1.09	up	3.37E-01	8.95E-01	-	-
1371353_at	Sqstm1	sequestosome 1	113894	Rn.107103	BG663093	8.82	9.02	9.12	9.24	9.06	9.05	1.09	up	2.91E-01	8.95E-01	-	-
1397865_at	---	---	---	Rn.162609	AI138056	2.46	2.45	2.46	2.42	2.46	2.88	1.09	up	4.30E-01	8.95E-01	-	-
1397818_at	---	---	---	Rn.156145	BF565302	2.35	2.34	2.35	2.75	2.35	2.32	1.09	up	4.12E-01	8.95E-01	-	-
1390787_at	Gart	phosphoribosylglycinamide formyltransferase	288259	Rn.55532	AI103888	2.49	2.68	2.60	2.60	2.96	2.59	1.09	up	3.86E-01	8.95E-01	-	-
1383649_a_at	---	---	---	---	BI291080	2.45	2.46	3.31	2.87	2.53	2.43	1.09	down	7.02E-01	9.07E-01	-	-
1380192_at	Amn1	antagonist of mitotic exit network 1 homolog (S. cerevisiae)	302032	Rn.104358	AI105297	3.23	2.71	2.76	2.91	2.71	2.70	1.09	down	5.14E-01	8.95E-01	-	-
1372530_at	Hcfc1	host cell factor C1	363519	Rn.94043	AA944190	6.46	6.85	7.61	6.97	6.64	6.91	1.09	down	7.34E-01	9.15E-01	-	-
1369340_at	Snip	SNAP25-interacting protein	56029	Rn.207205	NM_019378	2.32	2.30	2.31	2.71	2.31	2.30	1.09	up	3.98E-01	8.95E-01	-	-
1391282_at	RGD1306962	Similar to dJ55C23.6 gene product	309570	Rn.13192	AI029285	8.03	8.08	7.48	7.61	8.04	8.32	1.09	up	6.73E-01	9.01E-01	-	-
1389778_a_at	Tceb3	transcription elongation factor B (SIII), polypeptide 3	25562	Rn.37427	AI227515	5.48	6.05	5.27	5.67	5.76	5.76	1.09	up	6.15E-01	8.95E-01	-	-
1392939_at	Slc41a3	solute carrier family 41, member 3	641603	Rn.190829	BM388933	5.79	6.46	6.20	6.21	5.94	6.68	1.09	up	6.81E-01	9.03E-01	-	-
1398417_at	Fem1a	feminization 1 homolog a (C. elegans)	316131	Rn.97265	BE104341	4.52	4.51	4.14	5.42	3.47	4.66	1.09	up	8.35E-01	9.48E-01	-	-
1395438_at	---	---	---	Rn.52062	BF408726	2.87	2.42	2.43	2.49	2.43	2.42	1.09	down	4.37E-01	8.95E-01	-	-
1371738_at	Ano10	anoctamin 10	301111	Rn.104231	BI287983	5.06	4.70	4.54	4.89	4.53	4.49	1.09	down	5.56E-01	8.95E-01	-	-
1387036_at	Hes1	hairy and enhancer of split 1 (Drosophila)	29577	Rn.19727	NM_024360	4.01	4.33	3.74	3.67	4.25	3.78	1.09	down	6.28E-01	8.95E-01	-	-
1390531_at	Pric285	peroxisomal proliferator-activated receptor A interacting complex 285	296474	Rn.47450	BE098021	2.33	2.32	2.73	2.33	2.34	2.33	1.09	down	3.89E-01	8.95E-01	-	-
1388852_at	Nono1	nodal modulator 1	361578	Rn.8989	AI406307	7.75	8.07	7.84	8.09	7.90	8.05	1.09	up	3.10E-01	8.95E-01	-	-
1390113_a_at	Larp1	La ribonucleoprotein domain family, member 1	303158	Rn.98804	BI300539	7.83	7.65	8.77	7.79	8.10	7.98	1.09	down	7.38E-01	9.16E-01	-	-
1398188_at	---	---	---	Rn.207839	BE121116	2.44	2.44	3.03	2.66	2.44	2.42	1.09	down	5.78E-01	8.95E-01	-	-
1370773_a_at	Kcnip2	Kv channel-interacting protein 2	56817	Rn.98384	AF269283	2.45	2.44	2.84	2.44	2.46	2.44	1.09	down	3.93E-01	8.95E-01	-	-
1380432_at	Cmah	cytidine monophosphate-N-acetylneuraminic acid hydroxylase (CMP-N-acetyl	361245	Rn.14280	AI014030	2.46	2.45	2.47	2.72	2.46	2.57	1.09	up	1.70E-01	8.95E-01	-	-
1389729_at	Rilpl2	Rab interacting lysosomal protein-like 2	288652	Rn.12933	AI408907	6.42	6.38	5.93	6.37	5.47	6.50	1.09	down	7.39E-01	9.16E-01	-	-
1373930_at	LOC687681	similar to pericentrin	687681	Rn.199175	BM388963	3.73	4.04	4.08	4.32	3.93	3.99	1.09	up	4.76E-01	8.95E-01	-	-
1398946_at	Mrps18	mitochondrial ribosomal protein S18	689912	Rn.8846	AI230278	6.91	6.69	7.14	6.87	6.62	6.87	1.09	down	4.58E-01	8.95E-01	-	-
1369510_at	Gapdhs	glyceraldehyde-3-phosphate dehydrogenase, spermatogenic	66020	Rn.64496	NM_023964	2.60	2.47	2.65	2.59	2.91	2.59	1.09	up	3.48E-01	8.95E-01	-	-
1369922_at	P76	mannose-6-phosphate protein p76	246120	Rn.72896	NM_139255	2.40	3.97	3.41	3.29	3.40	3.48	1.09	up	7.95E-01	9.34E-01	-	-
1385990_at	RGD1565545	similar to zinc finger protein ZFP	308337	Rn.198482	BG665161	3.58	3.19	3.31	3.23	3.24	3.22	1.09	down	3.25E-01	8.95E-01	-	-
1390415_at	Trip13	thyroid hormone receptor interactor 13	292206	Rn.11751	BM392319	2.38	2.36	2.39	2.77	2.38	2.36	1.09	up	3.95E-01	8.95E-01	-	-
1395367_at	Rnf215	ring finger protein 215	305478	Rn.41695	BF408110	5.57	4.03	5.75	5.73	5.56	3.68	1.09	down	8.88E-01	9.65E-01	-	-
1373195_at	Fus	fusion, derived from t(12;16) malignant liposarcoma (human)	317385	Rn.100218	AW532485	10.97	11.30	10.95	11.29	11.13	11.18	1.09	up	3.54E-01	8.95E-01	-	-
1372309_at	---	---	---	Rn.203769	BI296558	6.17	5.38	5.83	5.75	5.05	6.19	1.09	down	7.66E-01	9.23E-01	-	-
1371322_at	Lamc1	Laminin, gamma 1	117036	Rn.7145	BI275624	4.44	4.58	3.70	3.87	4.61	3.85	1.09	down	7.48E-01	9.18E-01	-	-
1396751_at	Necab2	N-terminal EF-hand calcium binding protein 2	170928	Rn.62703	BF403666	2.47	2.36	2.47	2.47	2.76	2.46	1.09	up	2.85E-01	8.95E-01	-	-
1397916_s_at	Ptpn1	protein tyrosine phosphatase, non-receptor type 1	24697	Rn.11317	AI924431	3.08	3.05	3.07	3.06	3.06	3.06	1.09	up	3.96E-01	8.95E-01	-	-
1396813_at	---	---	---	Rn.46994	AW528749	2.34	2.34	2.35	2.73	2.35	2.33	1.09	up	3.85E-01	8.95E-01	-	-
1378356_at	Slc24a4	solute carrier family 24 (sodium/potassium/calcium exchanger), member 4	314396	Rn.198754	AI556625	2.60	2.52	2.61	2.94	2.61	2.57	1.09	up	3.56E-01	8.95E-01	-	-
1375288_at	Gcn1l1	GCN1 general control of amino-acid synthesis 1-like 1 (yeast)	690632	Rn.98494	BI299737	2.68	3.10	2.72	2.67	2.71	2.73	1.09	down	4.03E-01	8.95E-01	-	-
1391329_at	---	---	---	Rn.146644	BM387817	2.38	2.37	2.38	2.36	2.38	2.76	1.09	up	3.82E-01	8.95E-01	-	-
1371657_at	Uba2	ubiquitin-like modifier activating enzyme 2	308508	Rn.198150	AA799692	7.92	8.29	8.09	8.36	8.07	8.25	1.09	up	4.02E-01	8.95E-01	-	-
1375689_at	---	---	---	Rn.205048	BI300470	4.55	5.39	6.11	6.63	4.70	4.34	1.09	down	8.86E-01	9.65E-01	-	-
1371489_at	---	---	---	Rn.30015	AI017748	5.60	4.60	4.66	4.95	5.21	5.08	1.09	up	7.19E-01	9.11E-01	-	-
1398791_at	Txnrd1	thioredoxin reductase 1	58819	Rn.67581	NM_031614	9.28	9.28	9.31	9.21	9.34	8.94	1.09	down	3.36E-01	8.95E-01	-	-
1370648_a_at	Wipf3	WAS/WASL interacting protein family, member 3	259242	Rn.11272	U25281	2.35	2.73	2.35	2.34	2.36	2.34	1.09	down	3.76E-01	8.95E-01	-	-
1372350_at	Supv3l1	suppressor of var1, 3-like 1 (S. cerevisiae)	294385	Rn.19830	BI297676	3.57	3.80	3.92	3.71	2.84	4.36	1.09	down	7.92E-01	9.33E-01	-	-
1378156_at	LOC690489	similar to cystin 1	690489	Rn.170218	BE109002	7.37	7.45	7.89	7.91	7.41	7.77	1.09	up	5.92E-01	8.95E-01	-	-
1397489_at	---	---	---	Rn.207404	BE099670	2.58	2.56	2.57	2.97	2.57	2.56	1.09	up	4.05E-01	8.95E-01	-	-
1378620_at	---	---	---	Rn.156052	BE104164	2.54	2.53	2.60	2.56	2.55	2.94	1.09	up	3.79E-01	8.95E-01	-	-
1371646_at	Cort /// Pgd	cortistatin /// phosphogluconate dehydrogenase	25305 /// 362660	Rn.10490	AI008441	4.47	4.63	4.44	4.39	4.30	4.46	1.09	down	1.68E-01	8.95E-01	-	-
1373136_at	Zufsp	zinc finger with UFM1-specific peptidase domain	294390	Rn.3372	AI013609	4.92	5.26	4.60	4.97	4.92	5.27	1.09	up	5.94E-01	8.95E-01	-	-
1370427_at	Pdgfa	platelet-derived growth factor alpha polypeptide	25266	Rn.10999	L06238	2.59	2.66	2.99	2.84	2.87	2.91	1.09	up	3.61E-01	8.95E-01	-	-
1377490_at	Tbx1	T-box 1	360737	Rn.41347	BE103482	2.80	2.51	2.48	2.45	2.48	2.47	1.09	down	2.91E-01	8.95E-01	-	-
1388818_at	---	---	---	Rn.203416	AA946074	4.13	4.29	4.24	4.06	4.15	4.06	1.09	down	8.12E-02	8.95E-01	-	-
1375238_at	Stk11	Serine/threonine kinase 11	314621	Rn.12052	BM385814	4.91	4.55	4.52	4.50	4.69	5.18	1.09	up	6.23E-01	8.95E-01	-	-
1383400_at	LOC682097	similar to TBP-associated factor 4	682097	Rn.12115	BI293535	6.60	8.09	8.52	8.21	7.16	8.23	1.09	up	8.61E-01	9.57E-01	-	-
1379450_at	Ctnbp2nl	CTNBP2 N-terminal like	310780	Rn.25049	BM383195	2.65	2.83	2.84	2.90	2.84	2.95	1.09	up	1.38E-01	8.95E-01	-	-
1369148_at	Hnf1a	HNF1 homeobox A	24817	Rn.9660	NM_012669	7.94	8.14	7.61	8.56	7.12	8.40	1.09	up	8.05E-01	9.37E-01	-	-
1380363_at	Klf7	Kruppel-like factor 7 (ubiquitous)	363243	Rn.219339	BF420490	2.45	2.44	2.45	2.82	2.55	2.36	1.09	up	3.92E-01	8.95E-01	-	-
1388304_at	Ndufb5	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 5	294964	Rn.3367	BI281307	11.46	11.20	11.15	11.19	11.15	11.10	1.09	down	2.78E-01	8.95E-01	-	-
1385869_at	---	---	---	Rn.22651	AA897980	5.97	6.45	6.37	5.43	7.27	6.48	1.09	up	8.30E-01	9.46E-01	-	-
1389971_at	Sgce	sarcoglycan, epsilon	432360	Rn.185815	AI179438	2.40	2.39	2.78	2.40	2.40	2.39	1.09	down	3.74E-01	8.95E-01	-	-
1370854_at	Nexn	nexilin (F actin binding protein)	246172	Rn.107975	AA799423	2.50	2.49	2.51	2.49	2.76	2.64	1.09	up	1.77E-01	8.95E-01	-	-
1383927_at	---	---	---	Rn.119594	AW528112	2.66	2.58	2.72	3.04	2.68	2.63	1.09	up	4.05E-01	8.95E-01	-	-
1368963_at	Mxi1	MAX interactor 1	25701	Rn.37510	NM_013160	6.29	8.90	6.85	7.40	6.91	7.35	1.09	down	8.83E-01	9.64E-01	-	-
1393625_at	Itsn2	intersectin 2	313934	Rn.37673	AA998540	2.63	3.18	2.76	2.73	2.74	2.72	1.09	down	4.87E-01	8.95E-01	-	-
1390923_a_at	Osbpl1a	oxysterol binding protein-like 1A	259221	Rn.78864	AI137224	6.07	7.62	5.92	6.18	6.80	7.00	1.09	up	8.42E-01	9.51E-01	-	-
1375270_at	---	---	---	Rn.223376	BM384026	2.87	3.08	2.48	3.31	2.55	2.95	1.09	up	6.77E-01	9.02E-01	-	-
1392274_at	---	---	---	Rn.18332	BE118653	4.60	4.86	4.84	4.72	4.61	4.58	1.09	down	2.51E-01	8.95E-01	-	-
1367851_at	Ptgds	prostaglandin D2 synthase (brain)	25526	Rn.11400	J04488	2.43	2.79	2.44	2.43	2.44	2.41	1.09	down	3.42E-01	8.95E-01	-	-
1384705_at	Phf17	PHD finger protein 17	310352	Rn.90858	BI296885	7.42	7.52	7.00	7.26	7.48	7.58	1.09	up	5.31E-01	8.95E-01	-	-
1379496_at	---	---	---	Rn.178387	AI029460	2.34	2.33	2.35	2.63	2.35	2.43	1.09	up	2.10E-01	8.95E-01	-	-
1368419_at	Cp	ceruloplasmin	24268	Rn.32777	AF202115	4.06	4.99	5.31	5.84	4.95	3.96	1.09	up	8.57E-01	9.55E-01	-	-
1369769_at	Kcne1	potassium voltage-gated channel, Isk-related subfamily, member 1	25471	Rn.9734	M36461	2.67	2.40	3.04	2.61	2.56	2.55	1.09	down	5.34E-01	8.95E-01	-	-
1380136_at	---	---	---	Rn.50224	AW433986	4.79	4.90	4.80	6.54	3.17	5.15	1.09	up	9.03E-01	9.70E-01	-	-
1374506_at	Ddx31	DEAD (Asp-Glu-Ala-Asp) box polypeptide 31	311835	Rn.63648	BI296403	3.17	2.81	2.83	2.82	2.83	2.79	1.09	down	3.46E-01	8.95E-01	-	-
1389331_at	---	---	---	Rn.22818	AI104371	6.52	6.31	6.38	6.40	6.52	6.68	1.09	up	2.83E-01	8.95E-01	-	-
1390247_at	Arid3b	AT rich interactive domain 3B (Bright like)	367092	Rn.18259	BI275999	2.70	2.33	2.34	2.33	2.34	2.32	1.09	down	3.55E-01	8.95E-01	-	-
1372265_at	RGD1304719	similar to RIKEN cDNA 2810002N01	299341	Rn.3813	AI172218	9.43	9.97	9.64	9.65	9.74	10.03	1.09	up	5.52E-01	8.95E-01	-	-
1376801_at	RGD1564450	RGD1564450	294291	Rn.220072	AW915035	4.38	4.01	4.45	4.35	4.66	4.21	1.09	up	5.43E-01	8.95E-01	-	-
1387223_at	Aadat	aminoadipate aminotransferase	29416	Rn.11133	NM_017193	12.91	12.95	13.11	12.84	12.88	12.88	1.09	down	1.08E-01	8.95E-01	-	-
1384926_at	---	---	---	Rn.160428	AA964975	4.21	4.10	4.18	4.13	4.40	4.34	1.09	up	2.23E-01	8.95E-01	-	-
1377959_at	Fam

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1372990_at	Creb3	cAMP responsive element binding protein 3	298400	Rn.104043	AI179264	6.36	6.31	6.45	6.22	6.21	6.31	1.09	down	7.36E-02	8.95E-01	-	-
1377664_at	Kab	KARP-1 binding protein 1	171457	Rn.6424	AI101205	2.88	2.50	2.51	2.50	2.52	2.49	1.09	down	3.73E-01	8.95E-01	-	-
1378929_at	---	---	---	Rn.16728	BE116137	2.52	2.47	2.46	2.46	2.54	2.83	1.09	up	3.25E-01	8.95E-01	-	-
1376243_at	Serpinb12	serine (or cysteine) peptidase inhibitor, clade B (ovalbumin), member 12	304692	Rn.34266	BI278780	2.53	2.78	2.53	2.53	2.53	2.41	1.09	down	2.52E-01	8.95E-01	-	-
1393294_at	Cpeb4	cytoplasmic polyadenylation element binding protein 4	303010	Rn.218260	BG671389	8.61	8.71	8.65	8.63	8.41	8.56	1.09	down	1.43E-01	8.95E-01	-	-
1387237_at	Exoc7	exocyst complex component 7	64632	Rn.45761	BM388722	3.42	3.36	4.03	3.85	3.20	3.38	1.09	down	6.84E-01	9.03E-01	-	-
1383089_at	Rab21	RAB21, member RAS oncogene family	299799	Rn.162952	BM386284	9.89	9.54	9.73	9.91	9.86	9.77	1.09	up	3.20E-01	8.95E-01	-	-
1375541_at	LOC687656	hypothetical protein LOC687656	687656	---	AA900525	5.78	5.83	5.67	5.66	5.58	5.65	1.09	down	8.50E-02	8.95E-01	-	-
1370708_a_at	Akr1c14	aldo-keto reductase family 1, member C14	191574	Rn.10021	M61937	2.51	2.47	2.52	2.48	2.51	2.88	1.09	up	3.87E-01	8.95E-01	-	-
1369586_at	Atpif1	ATPase inhibitory factor 1	25392	Rn.1658	NM_012915	10.01	10.19	10.25	10.33	10.18	10.31	1.09	up	2.19E-01	8.95E-01	-	-
1372017_at	Diablo	diablo homolog (Drosophila)	288753	Rn.9090	BE110572	6.82	6.91	7.30	6.94	6.59	7.13	1.09	down	5.90E-01	8.95E-01	-	-
1395794_at	Tpm1	tropomyosin 1, alpha	24851	Rn.87540	BF395218	2.42	2.44	2.38	2.38	2.90	2.34	1.09	up	5.29E-01	8.95E-01	-	-
1388904_at	Dtl25	hypothetical protein Dtl25	360883	Rn.84751	AI236597	6.98	7.46	7.98	7.27	7.07	7.72	1.09	down	7.37E-01	9.15E-01	-	-
1376144_at	Parp9	poly (ADP-ribose) polymerase family, member 9	303905	Rn.2158	AA819679	3.34	3.26	3.62	3.56	3.46	3.57	1.09	up	3.27E-01	8.95E-01	-	-
1398799_at	Eif4e	eukaryotic translation initiation factor 4E	117045	Rn.11275	NM_053974	8.54	8.85	8.68	8.50	8.56	8.63	1.09	down	2.57E-01	8.95E-01	-	-
1374335_at	Gata6	GATA binding protein 6	29300	Rn.8701	AA800786	2.39	2.36	2.37	2.76	2.36	2.38	1.09	up	3.86E-01	8.95E-01	-	-
1388414_at	Ndufs5	NADH dehydrogenase (ubiquinone) Fe-S protein 5	362588	Rn.156413	AI410498	9.56	9.70	9.78	9.51	9.60	9.55	1.09	down	1.52E-01	8.95E-01	-	-
1371091_at	Irs2	insulin receptor substrate 2	29376	Rn.10718	BE118080	6.11	6.20	6.05	6.03	6.71	5.99	1.09	up	6.26E-01	8.95E-01	-	-
1382196_at	RGD1307394	similar to hypothetical protein ET	360667	Rn.16739	BI293505	2.51	2.52	2.53	2.91	2.52	2.52	1.09	up	3.88E-01	8.95E-01	-	-
1392702_at	---	---	---	---	BM387858	3.61	2.60	2.69	2.78	2.67	3.83	1.09	up	8.11E-01	9.39E-01	-	-
1395587_at	Phca	phytoceramidase, alkaline	499210	Rn.19122	BF388640	2.47	2.46	2.42	2.47	2.53	2.72	1.09	up	1.83E-01	8.95E-01	-	-
1381261_at	---	---	---	Rn.206211	BE113729	2.24	2.40	2.42	2.40	2.63	2.39	1.09	up	2.64E-01	8.95E-01	-	-
1371556_at	Pias4	protein inhibitor of activated STAT, 4	362827	Rn.12810	BE108748	2.35	2.34	2.36	2.35	2.75	2.33	1.09	up	4.13E-01	8.95E-01	-	-
1371280_at	LOC497995	high sulfur protein B2F	497995	Rn.190823	AB003753	2.36	2.35	2.37	2.35	2.75	2.35	1.09	up	4.02E-01	8.95E-01	-	-
1395877_at	---	---	---	Rn.168368	AW919687	5.22	5.60	5.05	4.95	5.12	5.42	1.09	down	5.89E-01	8.95E-01	-	-
1367971_at	Ptp4a2	protein tyrosine phosphatase 4a2	85237	Rn.167750	NM_053475	8.77	9.31	9.08	9.13	8.98	9.42	1.09	up	5.70E-01	8.95E-01	-	-
1383083_a_at	---	---	---	Rn.164799	AI137878	3.86	2.76	2.65	2.72	2.76	3.41	1.09	down	7.94E-01	9.34E-01	-	-
1384382_at	Osgepl1	O-sialoglycoprotein endopeptidase-like 1	314548	Rn.210040	BF393066	5.00	5.12	5.98	6.04	3.72	5.97	1.09	down	8.87E-01	9.65E-01	-	-
1380121_at	Nek7	NIMA (never in mitosis gene a)-related kinase 7	360850	Rn.3649	BE117215	3.82	4.57	5.74	4.45	4.53	4.77	1.09	down	8.36E-01	9.48E-01	-	-
1382362_at	---	---	---	Rn.199234	AA997890	4.63	4.79	4.63	5.69	3.65	5.09	1.09	up	8.47E-01	9.52E-01	-	-
1391169_at	Tmem117	transmembrane protein 117	500921	Rn.88857	BE120139	2.58	2.50	2.51	2.96	2.50	2.49	1.09	up	4.72E-01	8.95E-01	-	-
1395505_at	RGD1309388	similar to DIP13 alpha	290537	Rn.34413	AI229654	2.45	2.46	2.53	2.48	2.57	2.78	1.09	up	2.46E-01	8.95E-01	-	-
1374512_at	LOC684314	similar to CG9886-like	684314	Rn.202605	AI232341	8.79	8.95	8.51	8.32	9.14	9.16	1.09	up	7.06E-01	9.08E-01	-	-
1395621_at	RGD1565119	similar to Mitochondrial carrier triple repeat 1	305350	---	H33102	4.78	4.57	5.24	4.44	4.10	4.42	1.09	up	8.14E-01	9.40E-01	-	-
1383977_a_at	---	---	---	---	BM388500	5.89	6.41	5.84	6.26	6.43	5.83	1.09	up	6.51E-01	8.98E-01	-	-
1367991_at	Gcs1	glucosidase 1	78947	Rn.22161	NM_031749	6.80	6.85	7.98	7.12	6.86	7.27	1.09	down	7.74E-01	9.26E-01	-	-
1380796_at	Spire1	spire homolog 1 (Drosophila)	307348	Rn.98481	AW521390	3.55	2.90	2.95	2.93	2.94	3.15	1.09	down	6.02E-01	8.95E-01	-	-
1372894_at	Tmem115	transmembrane protein 115	363136	Rn.7749	BI284175	5.52	5.58	5.62	5.69	5.64	5.76	1.09	up	4.50E-02	8.95E-01	-	-
1378986_at	---	---	---	Rn.46057	AW525997	5.35	4.71	4.51	4.77	4.74	5.42	1.09	up	7.30E-01	9.14E-01	-	-
1386898_at	Hspe1	heat shock protein 1 (chaperonin 10)	25462	Rn.106093	NM_012966	11.77	11.60	11.96	11.69	11.60	11.67	1.09	down	3.13E-01	8.95E-01	-	-
1386902_at	Vdac3	voltage-dependent anion channel 3	83532	Rn.107287	NM_031355	9.94	9.89	9.72	9.79	10.10	10.03	1.09	up	3.36E-01	8.95E-01	-	-
1387153_at	Ril	reversion induced LIM gene	24915	Rn.34221	NM_017062	2.80	2.71	2.64	2.70	3.20	2.63	1.09	up	5.40E-01	8.95E-01	-	-
1388351_at	Pomp	proteasome maturation protein	288455	Rn.28242	BM384128	8.89	8.91	8.82	8.84	8.51	8.89	1.09	down	3.68E-01	8.95E-01	-	-
1377413_at	---	---	---	Rn.163733	BF548480	8.65	8.40	9.11	8.47	8.17	9.15	1.09	down	7.45E-01	9.17E-01	-	-
1386991_a_at	Bad	Bcl2-antagonist of cell death	64639	Rn.36696	AF279911	6.97	7.96	6.91	7.76	7.08	7.37	1.09	up	7.68E-01	9.24E-01	-	-
1371641_at	Cct7	chaperonin containing Tcp1, subunit 7 (eta)	297406	Rn.62267	BM388827	8.61	9.02	9.15	8.71	8.79	8.90	1.09	down	5.08E-01	8.95E-01	-	-
1397485_at	---	---	---	Rn.176861	BI298636	7.65	8.30	8.00	7.42	7.80	8.37	1.09	down	7.29E-01	9.14E-01	-	-
1376335_at	Tfip11	tuftelin interacting protein 11	288718	Rn.161710	BI282368	5.24	5.77	5.07	5.22	5.22	5.26	1.09	down	5.90E-01	8.95E-01	-	-
1377148_at	---	---	---	---	AI412344	2.93	3.02	2.76	3.31	2.86	2.91	1.09	up	4.83E-01	8.95E-01	-	-
1392901_at	Lrrc1	Leucine rich repeat containing 1	367113	Rn.15622	BM385213	5.02	5.11	5.03	5.42	5.04	5.08	1.09	up	3.66E-01	8.95E-01	-	-
1370528_at	Csnk1d	casein kinase 1, delta	64462	Rn.8046	L07578	2.45	2.44	2.46	2.44	2.86	2.42	1.09	up	4.36E-01	8.95E-01	-	-
1392048_at	---	---	---	Rn.57374	BI288401	2.47	2.47	2.40	2.84	2.47	2.41	1.09	up	4.10E-01	8.95E-01	-	-
1373870_at	Fam98a	family with sequence similarity 98, member A	313873	Rn.12770	BE110630	6.77	5.80	6.16	5.91	6.28	6.18	1.09	down	7.04E-01	9.07E-01	-	-
1394834_at	Wdfy3	WD repeat and FYVE domain containing 3	305164	Rn.57981	BF393831	5.36	6.85	6.45	6.30	5.60	6.38	1.09	down	8.20E-01	9.42E-01	-	-
1380254_at	---	---	---	---	AA893529	5.37	5.87	5.12	5.12	5.57	6.04	1.09	up	7.38E-01	9.16E-01	-	-
1371889_at	Slc22a17	solute carrier family 22, member 17	305886	Rn.7312	AW915448	3.72	3.92	4.93	4.28	4.03	3.89	1.09	down	7.69E-01	9.24E-01	-	-
1398936_at	Eif2s3x	eukaryotic translation initiation factor 2, subunit 3, structural gene X-linked	299027	Rn.87025	AI598546	4.93	5.48	5.66	5.40	5.12	5.93	1.09	up	7.21E-01	9.11E-01	-	-
1388508_at	Fam32a	family with sequence similarity 32, member A	498600	Rn.7484	BM384233	5.79	6.43	5.75	6.10	6.35	5.90	1.09	up	6.53E-01	8.97E-01	-	-
1381870_at	---	---	---	Rn.212079	BG377539	4.18	2.94	3.00	4.12	3.02	2.60	1.09	down	8.48E-01	9.53E-01	-	-
1396118_at	RGD1564942	RGD1564942	---	298409	Rn.92043	AI410171	3.41	3.43	3.22	3.72	3.31	3.40	1.09	up	4.27E-01	8.95E-01	-	-
1390880_at	Eif3s6ip	eukaryotic translation initiation factor 3, subunit 6 interacting protein	300069	Rn.22102	BF420467	7.86	7.46	6.65	7.31	7.44	7.59	1.09	up	7.50E-01	9.19E-01	-	-
1382729_at	RGD1564019	similar to GTPase activating RANGAP domain-like 3	499783	---	BE098382	2.52	2.51	2.91	2.57	2.47	2.52	1.09	down	4.10E-01	8.95E-01	-	-
1375918_at	Znf830	zinc finger protein 830	497967	Rn.137587	AW917682	4.17	4.62	5.37	4.78	4.90	4.85	1.09	up	7.43E-01	9.17E-01	-	-
1396002_at	---	---	---	Rn.53540	BF403333	2.78	2.75	2.99	2.73	2.79	2.62	1.09	down	2.48E-01	8.95E-01	-	-
1388839_at	Rgl2	ral guanine nucleotide dissociation stimulator-like 2	294283	Rn.27644	AI233143	3.11	3.56	2.96	3.04	3.24	2.98	1.09	down	5.61E-01	8.95E-01	-	-
1381803_at	---	---	---	---	BE110472	2.42	2.72	2.43	2.42	2.43	2.35	1.09	down	2.80E-01	8.95E-01	-	-
1375544_at	---	---	---	Rn.145256	AI172543	2.54	2.62	2.43	2.41	2.42	2.39	1.09	down	9.27E-02	8.95E-01	-	-
1397185_at	---	---	---	Rn.170815	BE102060	9.12	9.26	9.13	9.07	9.02	9.05	1.09	down	5.92E-02	8.95E-01	-	-
1370229_at	Ndrg4	N-myc downstream regulated gene 4	64457	Rn.81250	BG866709	2.71	2.72	2.55	2.54	2.55	2.52	1.09	down	8.72E-02	8.95E-01	-	-
1377412_at	---	---	---	Rn.22217	AI146237	3.00	3.05	3.55	3.02	3.92	3.03	1.09	up	7.38E-01	9.16E-01	-	-
1374222_at	Slc22a18	solute carrier family 22, member 18	309131	Rn.3575	BM391436	7.84	8.51	9.13	8.68	7.85	8.57	1.09	down	7.98E-01	9.35E-01	-	-
1374095_at	---	---	---	Rn.203145	BM385244	3.05	3.43	3.33	3.21	4.17	2.81	1.09	up	7.82E-01	9.30E-01	-	-
1375086_at	---	---	---	---	BF393881	2.67	2.73	2.85	2.52	2.72	2.65	1.09	down	1.96E-01	8.95E-01	-	-
1374158_at	---	---	---	Rn.18902	BF398160	3.70	3.74	3.84	3.77	3.29	4.59	1.09	up	7.61E-01	9.22E-01	-	-
1398174_at	Mecp2	methyl CpG binding protein 2	29386	Rn.9680	BE114216	2.40	2.39	2.40	2.40	2.40	2.76	1.09	up	3.64E-01	8.95E-01	-	-
1389693_at	RGD1310893	similar to hypothetical protein 3010020C06	362514	Rn.7748	AA944526	4.00	3.98	6.05	3.99	5.77	3.91	1.09	down	8.99E-01	9.69E-01	-	-
1388710_at	Rreb1	ras responsive element binding protein 1	306873	Rn.37	BI281986	7.29	7.37	7.19	7.03	7.24	7.95	1.09	up	6.84E-01	9.03E-01	-	-
1376045_at	---	---	---	Rn.14919	AW529960	2.35	2.42	2.79	2.35	2.36	2.49	1.09	down	4.35E-01	8.95E-01	-	-
1376019_at	Atp9b	ATPase, class II, type 9B	291411	Rn.217953	AI598367	4.81	4.88	4.43	4.68	5.38	4.42	1.09	up	7.19E-01	9.11E-01	-	-
1390291_at	---	---	---	Rn.160263	BG375126	4.10	4.51	4.46	3.21	4.47	5.02	1.09	down	8.34E-01	9.48E-01	-	-
1384907_at	LOC306096	similar to Dachshund homolog 1 (Dach1)	306096	Rn.170849	AI411835	8.42	9.05	8.29	8.43	8.63	8.34	1.09	down	6.47E-01	8.95E-01	-	-
1395667_at	---	---	---	---	BF287710	2.50	2.49	2.50	2.85	2.53	2.49	1.09	up	3.37E-01	8.95E-01	-	-
1380152_at	---	---	---	Rn.163595	BF407782	7.26	7.03	6.25	6.96	6.81	7.15	1.09	up	7.19E-01	9.11E-01	-	-
1390116_at	---	---	---	Rn.164609	AA899937	6.25	6.53	6.28	6.44	6.89	6.10	1.09	up	6.43E-01	8.95E-01	-	-
1399001_at	RGD1305481	hypothetical LOC294030	294030	Rn.233	BI285943	8.27	8.53	8.09	8.33	8.25	8.69	1.09	up	5.45E-01	8.95E-01	-	-
1397454_at	---	---	---	Rn.205821	AW526622	3.00	2.83	2.86	2.69	2.84	2.80	1.09	down	1.43E-01	8.95E-01	-	-
1367817_at	Hdgf	hepatoma-derived growth factor	114499	Rn.860	NM_053707	8.51	8.31	8.03	8.45	7.97	8.79	1.09	up	6.77E-01	9.02E-01	-	-
1397250_at	---	---	---	---	AA850799	2.68	2.31	2.32	2.31	2.33	2.30	1.09	down	3.66E-01	8.95E-01	-	-
1382100_at	RGD1309605	similar to RIKEN cDNA 2310047O13	291320	Rn.106046	AA997169	7.65	8.11	7.99	7.83	7.95	8.34	1.09	up	5.81E-01	8.95E-01	-	-
1368074_at	Gale	UDP-galactose-4-epimerase	114860	Rn.29908	NM_080783	2.51	2.87	2.52	2.51	2.51	2.51	1.09	down	3.57E-01	8.95E-01	-	-
1373705_at	Mrpl28	mitochondrial ribosomal protein L28	497876	Rn.163110	AI235502	6.81	7.60	7.38	7.65	6.98	6.80	1.09	down	7.42E-01	9.17E-01	-	-
1381591_at	---	---	---	Rn.38617	BI302903	4.61	3.59	3.77	4.38	3.50	4.46	1.09	up	7.93E-01	9.34E-01	-	-
1387420_at	Clic4	chloride intracellular channel 4 (mitochondrial)	83718	Rn.162115	NM_031818	9.31	9.78	9.30	9.68	8.90	9.45	1.09	down	6.83E-01	9.03E-01	-	-
1393495_at	---	---	---	Rn.147542	AI043752	3.75	4.08	3.28	3.56	3.75	3.44	1.09	down	6.48E-01	8.96E-01	-	-
1373551_at	RGD1309762	similar to KIAA0614 protein	304503	Rn.2635	AA817753	2.61	2.49	2.24	2.24	2.70	2.77	1.09	up	5.68E-01	8.95E-01	-	-
1377666_at	Chdh	choline dehydrogenase	299551	Rn.22857	BI293004	10.12	10.36	10.46	10.33	9.87	10.36	1.09	down	5.49E-01	8.95E-01	-	-
1392902_at	Esf1	ESF1, nucleolar pre-rRNA processing protein, homolog (S. cerevisiae)	366203	Rn.22208	AW141642	5.82	6.59	6.33	6.41	6.40	6.30	1.09	up	6.22E-01	8.95E-01	-	-
1377829_at	Cep57	centrosomal protein 57kDa	315423	Rn.94972	BI291153	4.88	5.66	5.35	5.34	5.49	5.44	1.09	up	6.22E-01	8.95E-01	-	-
1383163_at	Igj	immunoglobulin joining chain	360922	Rn.17804	AA817898	2.54	2.79	2.55	2.50	2.53	2.48	1.09	down	2.16E-01	8.95E-01	-	-
1394874_at	RGD1310935	similar to Dermal papilla derived protein 7	360707	Rn.162057	BI282780	2.80	2.84	3.01	2.80	2.84	2.64	1.09	down	2.38E-01	8.95E-01	-	-
1388241_at	Insl3	insulin-like 3	114215	Rn.48700	AF139918	3.36	3.54	3.23	3.35	3.27	3.15	1.09	down	3.09E-01	8.95E-01	-	-
1396569_at	Agpat3	1-acylglycerol-3-phosphate O-acyltransferase 3	294324	Rn.100251	AI716045	2.68	2.32	2.33	2.32	2.33	2.31	1.09	down	3.57E-01	8.95E-01	-	-
1385343_at	---	---	---	Rn.216783	AW523620	2.34	2.33	2.34	2.33	2.71	2.33	1.09	up	3.87E-01	8.95E-01	-	-
1392889_at	---	---	---	Rn.40320	AI112294	2.75	3.04	2.73	2.71	2.73	2.70	1.09	down	2.81E-01	8.95E-01	-	-
1377649_at	---	---	---	Rn.16215	BM383391	5.58	5.49	5.50	5.39	4.79	6.02	1.09	down	7.48E-01	9.19E-01	-	-
1378046_at	Fuk	fucokinase	307848	Rn.160636	AI407320	2.35	2.35	2.36	2.35	2.72	2.35	1.09	up	3.81E-01	8.95E-01	-	-
1382642_at	Zfp281	zinc finger protein 281	305083	Rn.204958	BI291753	4.17	4.88	4.41	4.35	5.09	4.38	1.09	up	7.18E-01	9.11E-01	-	-
1395937_at	Arfgef1	ADP-ribosylation factor guanine nucleotide-exchange factor 1(brefeldin A-inhi	312915	Rn.6834	AI045928	6.92	6.41	7.08	6.57	7.45	6.76	1.09	up	7.33E-01	9.14E-01	-	-
1371649_at	Mrps24	mitochondrial ribosomal protein S24	498406	Rn.1914	BI289411	6.75	7.25	6.61	7.01	6.94	7.03	1.09	up	5.63E-01	8.95E-01	-	-
1377733_at	RGD1310769	similar to HSPC288	299207	Rn.162887	BF290890	5.79	5.07	5.14	5.07	5.83	5.47	1.09	up	7.20E-01	9.11E-01	-	-
1369990_at	Ptpmt1	protein tyrosine phosphatase, mitochondrial 1	29390	Rn.108023	NM_022183	7.60	6.92	7.45	7.30	7.54	7.49	1.09	up	6.06E-01	8.95E-01	-	-
1398606_at	Golim4	golgi integral membrane protein 4	310526	Rn.24186	BM391878	5.22	5.11	5.37	4.39	5.56	6.13	1.09	up	8.24E-01	9.44E-01	-	-
1381311_at	Emr1	EGF-like module containing, mucin-like, hormone receptor-like 1	316137	Rn.205894	BE100625	2.98	2.97	2.66	2.89	2.91	3.18	1.09	up	4.29E-01	8.95E-01	-	-
1377845_at	Aff3	AF4/FMR2 family, member 3	363220	Rn.203251	BM391291	2.67	2.49	2.43	2.40	2.45	2.37	1.09	down	1.77E-01	8.95E-01	-	-
1384288_at	---	---	---	---	BI292470	2.43	2.42	2.44	2.42	2.83	2.41	1.09	up	4.23E-01	8.95E-01	-	-
1389585_at	---	---	---	---	BG377510	2.47	2.44	2.82	2.47	2.47	2.43	1.09	down	3.78E-01	8.95E-01	-	-
1375660_at	08-Sep	septin 8	303135	Rn.23507	AA943694	3.68	3.63	4.41	3.91	3.66	3.78	1.09	down	8.63E-01	8.98E-01	-	-
1370043_at	Alcam	activated leukocyte cell adhesion molecule	79559	Rn.5789	NM_031753	4.43	3.82	4.23	3.70	4.50	3.90	1.09	down	7.02E-01	9.07E-01	-	-
1378155_at	Bat2d1	BAT2 domain containing 1	360865	Rn.206334	BI289641	6.95	7.10	7.38	7.59	6.38	7.10	1.09	down	7.58E-01	9.21E-01	-	-
1389619_at	---	---	---	Rn.51642	BG669808	2.54	2.50	2.59	2.56	2.87	2.56	1.09	up	3.22E-01	8.95E-01	-	-
1389433_at	Mkks	McKusick-Kaufman syndrome	311456	Rn.8839	BI298816	4.50	4.00	3.51	4.01	3.97	3.65	1.09	down	7.10E-01	9.09E-01	-	-
1382033_at	Klf1	Kruppel-like factor 1 (erythroid)	304666	Rn.23089	AA926284	2.37	2.36	2.73	2.36	2.37	2.36	1.09	down	3.77E-01	8.95E-01	-	-
1372604_at	RGD1309808	similar to apolipoprotein L2; apolipoprotein L-II	362951	Rn.195551	BI289459	2.30	2.30	2.31	2.30	2.68	2.29	1.09	up	3.90E-01	8.95E-01	-	-
1368599_at	Slc9a2	solute carrier family 9 (sodium/hydrogen exchanger), member 2	24783	Rn.11047	NM_012653	3.02	2.62	2.58	2.63	2.63	2.59	1.09	down	4.31E-01	8.95E-01	-	-
1383837_at	Yipf3	Yip1 domain family, member 3	301245	Rn.104143	AI102932	3.50	3.86	3.52	3.51	3.51	3.50	1.09	down	3.58E-01	8.95E-01	-	-
1377118_at	RGD1308517	similar to KIAA1712 protein	290722	Rn.18903	AW916012	4.65	5.08	6.13	5.86	4.77	5.60	1.09	up	8.34E-01	9.48E-01	-	-
1387227_at	Wipf1	WAS/WASL interacting protein family, member 1	117538	Rn.161803	NM_057192	4.92	3.78	4.83	4.41	4.55	4.20	1.09	down	7.63E-01	9.23E-01	-	-
1389832_at	Gsto1	glutathione S-transferase omega 1	114846	Rn.25166	BE113459	9.66	10.18	10.12	10.12	9.96	10.25	1.09	up	5.41E-01	8.95E-01	-	-
1379981_at	---	---	---	---	BI304043	2.52	2.54	2.56	2.59	2.54	2.86	1.09	up	2.92E-01	8.95E-01	-	-
1379139_x_at	---	---	---	---	BF406217	2.86	2.74	3.14	2.85	2.89	2.83	1.09	down	4.34E-01	8.95E-01	-	-
1380498_at	RGD1561067	similar to RNA binding protein gene with multiple splicing	498642	Rn.8565	AW141174	2.73	2.37	2.40	2.38	2.39	2.37	1.09	down	3.50E-01	8.95E-01	-	-
1369955_at	Col5a1	collagen, type V, alpha 1	85490	Rn.117	NM_134452	2.68	2.52	2.51	3.03	2.55	2.50	1.09	up	5.26E-01	8.95E-01	-	-
1387233_at	Hsd17b7	hydroxysteroid (17-beta) dehydrogenase 7	29540	Rn.7040	NM_017235	2.43	2.43	2.45	2.42	2.83	2.43	1.09	up	4.11E-01	8.95E-01	-	-
1390796_at	LOC688211	hypothetical protein LOC688211	688211	---	AA998424	2.66	2.61	2.51	2.48	2.49	2.45	1.09	down	5.41E-02	8.95E-01	-	-
1395719_at	Tufm	Tu translation elongation factor, mitochondrial	293481	Rn.48850	AI763950	5.11	5.00	5.78	6.33	4.64	4.55	1.09	down	8.55E-01	9.55E-01	-	-
1378618_at	---	---	---	Rn.209812	BF392356	2.66	2.72	2.74	3.05	2.72	2.71	1.09	up	3.36E-01	8.95E-01	-	-
1391684_at	Tmem14a	transmembrane protein 14A	363206	Rn.45035	AW521094	2.41	2.39	2.43	2.80	2.41	2.38	1.09	up	4.16E-01	8.95E-01	-	-
1368903_at	Sfrbp	spermatid perinuclear RNA binding protein	84476	Rn.98476	NM_053416	10.07	10.27	10.18	10.20	10.18	10.51	1.09	up	3.71E-01	8.95E-01	-	-
1369669_at	Nln	neurolysin (metallopeptidase M3 family)	117041	Rn.11029	NM_053970	4.21	4.61	5.00	4.40	5.06	4.73	1.09	up	7.01E-01	9.07E-01	-	-
1372697_at	Mrps15	mitochondrial ribosomal protein S15	298517	Rn.12127	AW254612	6.67	6.28	6.10	5.76	6.29	6.63	1.09	down	7.10E-01	9.09E-01	-	-
1373734_at	Slco3a1	Solute carrier organic anion transporter family, member 3a1	140915	Rn.102164	AI101171	2.52	2.51	2.54	2.70	2.73	2.51	1.09	up	1.48E-01	8.95E-01	-	-
1397339_at	---	---

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)				REG	MTC
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval		
1377983_at	---	---	---	---	AA924175	2.28	2.28	2.29	2.63	2.29	2.30	1.09	up	3.44E-01	8.95E-01	-	-
1368835_at	Stat1	signal transducer and activator of transcription 1	25124	Rn.33229	NM_032612	7.35	7.23	5.34	6.26	7.17	6.86	1.09	up	8.72E-01	9.60E-01	-	-
1372136_at	Tspan14	tetraspanin 14	306324	Rn.199005	AA848776	4.49	4.64	5.05	4.42	4.71	4.69	1.09	down	5.64E-01	8.95E-01	-	-
1387778_at	Sdf4	stromal cell derived factor 4	155173	Rn.12964	NM_130412	8.18	8.79	8.52	8.17	8.83	8.85	1.09	up	6.90E-01	9.05E-01	-	-
1369276_at	Smad5	SMAD family member 5	59328	Rn.146857	NM_021692	2.72	2.64	3.13	2.71	2.72	2.69	1.09	down	4.75E-01	8.95E-01	-	-
1390669_at	---	---	---	Rn.15385	AI639410	5.07	5.25	5.13	4.92	5.41	5.48	1.09	up	5.44E-01	8.95E-01	-	-
1393113_at	Arhgap1	Rho GTPase activating protein 1	311193	Rn.64898	AA957578	2.58	4.28	2.64	3.00	2.57	3.57	1.09	down	8.56E-01	9.55E-01	-	-
1383387_at	Sec3l1	SEC3-like 1 (S. cerevisiae)	305287	Rn.204678	AI177465	3.07	2.60	2.70	2.78	2.66	2.56	1.09	down	4.83E-01	8.95E-01	-	-
1398860_at	Nedd8	neural precursor cell expressed, developmentally down-regulated 8	25490	Rn.216415	AF095740	9.81	9.72	9.77	9.72	9.99	9.95	1.09	up	2.50E-01	8.95E-01	-	-
1374660_at	Namce4a	non-SMC element 4 homolog A (S. cerevisiae)	295828	Rn.8643	BM385193	6.90	7.45	7.57	7.03	7.51	7.51	1.09	down	6.67E-01	8.95E-01	-	-
1384786_at	---	---	---	Rn.199332	AI073019	2.43	2.75	2.45	2.42	2.43	2.41	1.09	down	3.08E-01	8.95E-01	-	-
1388109_at	Gpr116	G protein-coupled receptor 116	245977	Rn.25073	BI290677	3.91	3.16	3.19	3.36	4.09	3.17	1.09	up	7.61E-01	9.22E-01	-	-
1374657_at	Anks4b	ankyrin repeat and sterile alpha motif domain containing 4B	687561	Rn.216488	AA848437	10.96	11.38	10.85	10.90	10.82	11.11	1.09	down	5.46E-01	8.95E-01	-	-
1372550_at	---	---	---	---	AI169278	8.31	8.33	9.00	8.82	8.35	8.83	1.09	up	6.85E-01	9.03E-01	-	-
1389859_at	Csnk1a1	Casein kinase 1, alpha 1	113927	Rn.23810	AI235291	4.91	6.45	5.97	4.84	6.36	5.76	1.09	down	8.59E-01	9.56E-01	-	-
1397696_at	RGD1307830	similar to cDNA sequence BC003331	304863	Rn.211806	BF546570	3.20	3.17	2.76	2.93	2.92	2.92	1.09	down	4.41E-01	8.95E-01	-	-
1367947_at	Prkag1	protein kinase, AMP-activated, gamma 1 non-catalytic subunit	25520	Rn.11089	U42413	5.94	5.88	5.51	5.85	5.97	5.87	1.09	up	4.34E-01	8.95E-01	-	-
1386526_at	Lhx5	LIM homeobox 5	124451	Rn.54653	BF561612	2.91	3.15	2.82	2.90	2.84	2.77	1.09	down	3.20E-01	8.95E-01	-	-
1390148_a_at	Zfp395	zinc finger protein 395	305972	Rn.13352	BM388100	3.77	4.14	2.73	3.04	4.33	3.63	1.09	up	8.41E-01	9.50E-01	-	-
1399094_at	Churc1	churchill domain containing 1	299154	Rn.2696	AA859919	9.30	9.54	10.04	10.04	9.25	9.95	1.09	up	7.34E-01	9.15E-01	-	-
1388617_at	Bphl	biphenyl hydrolase-like (serine hydrolase)	361239	Rn.220050	AW914486	8.89	9.21	9.85	9.12	8.91	9.55	1.09	down	7.39E-01	9.16E-01	-	-
1390307_at	561672 /// RGD15	similar to novel protein /// similar to echinoderm microtubule associated protei	305610 /// 498430	Rn.58044	BF404820	2.44	2.77	2.46	2.44	2.45	2.42	1.09	down	3.15E-01	8.95E-01	-	-
1384087_at	---	---	---	---	AA925049	3.39	3.43	3.42	3.60	3.47	3.53	1.09	up	3.65E-02	8.95E-01	-	-
1379809_at	---	---	---	Rn.203470	BF283568	2.82	2.54	2.56	2.54	2.57	2.45	1.09	down	2.87E-01	8.95E-01	-	-
1394154_at	Stt3a	STT3, subunit of the oligosaccharyltransferase complex, homolog A (S. cerev	500972	Rn.98525	AI008375	2.51	2.52	2.54	2.53	2.72	2.69	1.09	up	1.16E-01	8.95E-01	-	-
1369647_at	Calcrl	calcitonin receptor-like	25029	Rn.11202	L27487	2.43	2.59	2.34	2.34	2.34	2.32	1.09	down	1.74E-01	8.95E-01	-	-
1377735_at	Plekha3	pleckstrin homology domain-containing, family A (phosphoinositide binding sp	295674	Rn.204132	AI176309	5.41	6.12	6.94	5.93	5.52	6.66	1.09	down	8.38E-01	9.49E-01	-	-
1381422_at	---	---	---	Rn.33733	AA817889	2.39	2.36	2.38	2.76	2.38	2.35	1.09	up	4.06E-01	8.95E-01	-	-
1375373_at	---	---	---	Rn.199192	AI179744	4.19	4.18	3.97	4.18	4.31	4.20	1.09	up	2.08E-01	8.95E-01	-	-
1374219_at	Disp1	dispatched homolog 1 (Drosophila)	289338	Rn.41748	BI295135	2.52	2.52	2.54	2.52	2.92	2.50	1.09	up	4.23E-01	8.95E-01	-	-
1381423_at	Git2	G protein-coupled receptor kinase interacting ArfGAP 2	304546	Rn.77521	BI278770	4.56	3.91	3.64	3.92	3.73	4.83	1.09	up	7.96E-01	9.34E-01	-	-
1371531_at	LOC678880	similar to mammalian retrotransposon derived 8b	678880	---	AI012962	6.83	6.25	6.72	6.35	6.54	6.55	1.09	down	5.57E-01	8.95E-01	-	-
1397211_at	Grb10	growth factor receptor bound protein 10	498416	Rn.63942	AA874782	2.82	2.39	2.41	2.41	2.46	2.39	1.09	down	4.45E-01	8.95E-01	-	-
1388688_at	---	---	---	Rn.115416	BI296599	8.07	7.90	7.54	7.32	7.66	8.16	1.09	down	6.98E-01	9.07E-01	-	-
1380860_at	---	---	---	Rn.124103	AA819536	7.62	7.32	7.90	7.65	7.44	7.39	1.09	down	5.52E-01	8.95E-01	-	-
1378358_at	Repin1	Replication initiator 1	445541	Rn.204397	AI710449	2.84	2.82	2.96	2.62	2.82	2.82	1.09	down	2.10E-01	8.95E-01	-	-
1369933_at	Vdac2	voltage-dependent anion channel 2	83531	Rn.162037	AF268468	9.01	9.16	9.14	9.12	9.36	9.19	1.09	up	2.31E-01	8.95E-01	-	-
1382439_at	Itgb6	integrin, beta 6	311067	Rn.19823	AI070686	4.46	4.20	3.75	4.29	4.21	3.54	1.09	down	7.23E-01	9.12E-01	-	-
1379613_at	Parp14	Poly (ADP-ribose) polymerase family, member 14	309303	Rn.54182	BM390301	3.28	2.92	2.94	2.78	2.93	3.08	1.09	down	4.49E-01	8.95E-01	-	-
1373338_at	---	---	---	Rn.98471	AI175767	7.35	7.57	6.99	7.24	7.30	7.72	1.09	up	6.25E-01	8.95E-01	-	-
1377606_at	Pftk1	PFTAIRE protein kinase 1	362316	Rn.12982	AI500913	2.43	2.41	2.42	2.80	2.41	2.41	1.09	up	4.02E-01	8.95E-01	-	-
1387027_a_at	Lgals9	lectin, galactoside-binding, soluble, 9	25476	Rn.10706	U72741	2.46	2.46	2.47	2.82	2.48	2.45	1.09	up	3.68E-01	8.95E-01	-	-
1378753_at	Ocln	occludin	83497	Rn.31429	AI638971	5.37	5.33	5.37	5.34	5.03	5.34	1.09	down	3.18E-01	8.95E-01	-	-
1379219_at	RGD1308626	similar to 9630044O09Rik protein	361087	Rn.21577	AI045877	2.57	2.63	2.51	2.42	2.48	2.45	1.09	down	3.44E-02	8.95E-01	-	-
1371638_at	Rnf7	ring finger protein 7	303948	Rn.2768	AA858518	9.19	9.38	8.85	9.19	9.07	9.52	1.09	up	5.95E-01	8.95E-01	-	-
1368249_at	Klf15	Kruppel-like factor 15	85497	Rn.22556	NM_053536	7.90	8.17	5.99	7.00	7.06	7.63	1.09	down	8.75E-01	9.61E-01	-	-
1384930_at	LOC687047	similar to coiled-coil domain containing 13	687047	---	AI071862	3.45	3.11	3.14	3.08	3.19	3.08	1.09	down	3.51E-01	8.95E-01	-	-
1370796_at	Foxl2	forkhead box l2	246073	Rn.92429	L13205	2.69	2.67	2.68	2.67	3.06	2.65	1.09	up	4.21E-01	8.95E-01	-	-
1386990_at	Ebp	emopamil binding protein (sterol isomerase)	117278	Rn.19436	NM_057137	5.67	6.00	5.52	5.65	5.87	6.03	1.09	up	5.39E-01	8.95E-01	-	-
1396057_at	---	---	---	Rn.169319	AW521804	2.68	2.67	3.18	2.91	2.68	2.58	1.09	down	5.74E-01	8.95E-01	-	-
1374327_at	---	---	---	Rn.23552	AI180129	6.09	6.02	7.39	6.20	6.37	6.58	1.09	down	8.07E-01	9.38E-01	-	-
1372406_at	Mcm3	minichromosome maintenance complex component 3	316273	Rn.12916	BM383428	2.65	2.34	2.42	2.36	2.36	2.35	1.09	down	2.65E-01	8.95E-01	-	-
1371043_a_at	Pou3f3	POU class 3 homeobox 3	192109	Rn.11354	BE107327	9.02	9.56	8.96	8.78	9.18	9.23	1.09	down	6.41E-01	8.95E-01	-	-
1394935_at	Wasf2	WAS protein family, member 2	313024	Rn.162111	AI175684	7.41	6.40	6.49	6.18	6.79	6.96	1.09	down	7.80E-01	9.28E-01	-	-
1377420_at	Tll3	tolloid tyrosine ligase-like family, member 3	362415	Rn.198684	BE106848	3.52	3.51	3.53	3.52	3.52	3.16	1.09	down	3.77E-01	8.95E-01	-	-
1381157_at	---	---	---	Rn.148902	BF396928	2.50	2.49	2.87	2.49	2.52	2.49	1.09	down	3.90E-01	8.95E-01	-	-
1389988_at	LOC307347	hypothetical protein LOC307347	307347	---	BE110642	4.74	6.15	5.88	5.46	5.41	6.27	1.09	up	8.27E-01	9.45E-01	-	-
1377974_at	---	---	---	Rn.72676	AI502837	9.41	9.45	9.29	9.51	9.32	9.69	1.09	up	3.62E-01	8.95E-01	-	-
1373866_at	Coq10b	coenzyme Q10 homolog B (S. cerevisiae)	301416	Rn.101706	AI228596	10.38	9.94	10.21	10.42	10.18	10.30	1.09	up	4.54E-01	8.95E-01	-	-
1368623_at	Ceacam9	carcinoembryonic antigen-related cell adhesion molecule 9	116711	Rn.81017	NM_053919	2.40	2.39	2.75	2.40	2.41	2.39	1.09	down	3.71E-01	8.95E-01	-	-
1382734_at	---	---	---	Rn.205624	AI715578	2.62	2.55	3.18	2.77	2.63	2.59	1.09	down	5.94E-01	8.95E-01	-	-
1367812_at	Sptbn2	spectrin, beta, non-erythrocytic 2	29211	Rn.20389	NM_019167	3.62	2.56	2.56	2.48	3.55	2.34	1.09	down	8.29E-01	9.46E-01	-	-
1368464_at	Mgl1	macrophage galactose N-acetyl-galactosamine specific lectin 1	64195	Rn.779	NM_022393	2.39	2.38	2.39	2.38	2.77	2.37	1.09	up	4.15E-01	8.95E-01	-	-
1371041_at	Ndufv2	NADH dehydrogenase (ubiquinone) flavoprotein 2	81728	Rn.28882	M22756	8.14	8.61	8.45	8.42	7.88	8.54	1.09	down	6.50E-01	8.96E-01	-	-
1371434_at	rCG_28701	hypothetical protein LOC691807	691807	Rn.42365	AI172362	10.85	11.08	11.10	10.77	10.80	11.10	1.09	down	4.14E-01	8.95E-01	-	-
1393008_at	Arpp-19	Cyclic AMP phosphoprotein	60336	Rn.112577	BI290317	5.64	4.26	4.84	4.42	5.12	4.83	1.09	down	8.04E-01	9.37E-01	-	-
1395033_at	---	---	---	Rn.205595	AI713019	2.51	2.50	2.52	2.50	2.89	2.50	1.09	up	4.15E-01	8.95E-01	-	-
1372843_at	RGD1309410	LOC363020	363020	Rn.24677	BG377188	3.33	3.67	3.36	3.47	3.48	3.77	1.09	up	4.58E-01	8.95E-01	-	-
1394536_at	Usp4	ubiquitin specific peptidase 4 (proto-oncogene)	290864	Rn.92126	AI408662	2.58	3.37	3.10	3.54	3.09	2.78	1.09	up	7.28E-01	9.13E-01	-	-
1375074_at	Tbkbp1	TBK1 binding protein 1	266764	Rn.33571	BE113756	2.34	2.33	2.35	2.34	2.72	2.33	1.09	up	4.03E-01	8.95E-01	-	-
1371571_at	App	amyloid beta (A4) precursor protein	54226	Rn.2104	BM986220	9.72	9.59	9.48	9.36	9.72	10.07	1.09	up	6.08E-01	8.95E-01	-	-
1391544_at	---	---	---	Rn.212222	BI285941	3.81	3.87	4.06	3.33	4.47	4.30	1.09	up	7.58E-01	9.21E-01	-	-
1390312_at	3 /// RGD1561472	similar to sterile alpha motif domain containing 9-like /// similar to mKIAA2005	512 /// 500013 /// 50	Rn.98211	BG670441	2.46	2.45	2.46	2.73	2.46	2.54	1.09	up	2.05E-01	8.95E-01	-	-
1377619_at	Wdr36	WD repeat domain 36	361305	---	AI407932	4.63	5.15	4.36	5.07	3.72	4.99	1.09	down	8.21E-01	9.43E-01	-	-
1375302_at	Zbtb4	zinc finger and BTB domain containing 4	287441	Rn.15836	BM384146	5.79	6.18	4.72	5.10	5.11	5.13	1.09	down	7.18E-01	9.11E-01	-	-
1394963_at	Grsf1	G-rich RNA sequence binding factor 1	305256	Rn.66912	BG372371	2.61	2.80	3.40	2.80	2.61	3.04	1.09	down	6.82E-01	9.03E-01	-	-
1390222_at	RGD1308380	similar to RIKEN cDNA 2310079F23	305443	Rn.33422	BM388283	2.32	2.31	2.33	2.46	2.56	2.31	1.09	up	1.83E-01	8.95E-01	-	-
1395217_at	---	---	---	Rn.156826	AA899394	2.96	2.60	2.62	2.60	2.63	2.58	1.09	down	3.65E-01	8.95E-01	-	-
1389101_at	Ccnc	cyclin C	114839	Rn.106758	BE120340	2.58	2.56	3.12	2.57	3.48	2.57	1.09	up	7.54E-01	9.20E-01	-	-
1382291_at	---	---	---	Rn.76633	AI454332	9.15	9.29	9.03	9.14	8.84	9.85	1.09	up	7.20E-01	9.11E-01	-	-
1371534_at	Slc25a22	solute carrier family 25 (mitochondrial carrier, glutamate), member 22	309111	Rn.98367	AI407908	2.47	2.49	2.93	2.51	2.46	2.57	1.09	down	4.75E-01	8.95E-01	-	-
1371390_at	Tubb2c	tubulin, beta 2c	296554	Rn.110562	AA892044	8.13	8.14	7.91	8.26	8.00	8.28	1.09	up	3.66E-01	8.95E-01	-	-
1370234_at	Fn1	fibronectin 1	25661	Rn.1604	AA893484	2.37	2.39	2.34	2.72	2.38	2.37	1.09	up	3.60E-01	8.95E-01	-	-
1393636_at	---	---	---	Rn.147760	AW533462	2.78	2.78	2.98	2.76	2.93	2.50	1.09	down	4.42E-01	8.95E-01	-	-
1375967_a_at	Dusp22	dual specificity phosphatase 22	361242	Rn.162221	AI172067	3.63	4.86	6.15	4.85	4.78	5.38	1.09	up	8.81E-01	9.64E-01	-	-
1385219_a_at	LOC474147	RBSC-skeletrophin	474147	---	AI071110	2.73	2.38	2.39	2.38	2.39	2.38	1.09	down	3.59E-01	8.95E-01	-	-
1378208_at	---	---	---	Rn.175189	BE099836	2.62	2.65	2.66	2.65	2.89	2.74	1.09	up	1.72E-01	8.95E-01	-	-
1390274_at	---	---	---	Rn.12990	AI170313	4.50	4.69	5.23	4.90	4.48	4.68	1.09	down	6.58E-01	8.98E-01	-	-
1394127_at	---	---	---	---	AA943800	4.26	4.14	4.42	4.31	4.60	4.26	1.09	up	4.23E-01	8.95E-01	-	-
1368932_at	Rock1	Rho-associated coiled-coil containing protein kinase 1	81762	Rn.89756	NM_031098	2.40	2.74	2.42	2.39	2.42	2.40	1.09	down	3.44E-01	8.95E-01	-	-
1389212_at	---	---	---	Rn.11805	BI296278	2.84	2.80	2.81	2.83	2.78	3.20	1.09	up	4.20E-01	8.95E-01	-	-
1396822_at	Zbtb2	zinc finger and BTB domain containing 2	308126	Rn.36118	BE113214	2.73	2.37	2.38	2.37	2.38	2.37	1.09	down	3.70E-01	8.95E-01	-	-
1371416_at	Ndufv1	NADH dehydrogenase (ubiquinone) flavoprotein 1	293655	Rn.3159	AI231746	8.01	8.45	8.23	8.25	8.34	8.46	1.09	up	4.42E-01	8.95E-01	-	-
1374485_at	---	---	---	Rn.222016	AI137762	9.96	9.38	9.40	9.54	9.74	9.81	1.09	up	5.93E-01	8.95E-01	-	-
1391886_at	---	---	---	---	AW527166	4.36	4.08	4.30	4.18	4.03	4.17	1.09	down	2.89E-01	8.95E-01	-	-
1390561_at	---	---	---	Rn.153937	BF282191	4.26	4.15	3.93	4.20	3.93	3.86	1.09	down	4.58E-01	8.95E-01	-	-
1388095_at	LOC286987	hemiferrin, transferrin-like protein	286987	Rn.127831	M60388	2.45	2.44	2.80	2.44	2.45	2.43	1.09	down	3.71E-01	8.95E-01	-	-
1387447_at	Arf3	ADP-ribosylation factor 3	140940	Rn.106440	NM_080904	5.08	5.79	5.55	5.70	5.30	5.77	1.09	up	6.63E-01	8.99E-01	-	-
1384277_at	Plekhh1	pleckstrin homology domain containing, family H (with MyTH4 domain) membr	314262	Rn.205398	BM380018	3.25	2.95	3.42	2.94	3.34	3.70	1.09	up	6.72E-01	9.01E-01	-	-
1368546_at	Hivep2	human immunodeficiency virus type I enhancer binding protein 2	29732	Rn.9802	NM_024137	3.15	3.82	3.23	3.14	3.04	3.67	1.09	down	7.01E-01	9.07E-01	-	-
1374944_at	Znf691	zinc finger protein 691	313548	Rn.45006	BI275829	3.04	2.37	2.38	2.56	2.39	2.48	1.09	down	6.26E-01	8.95E-01	-	-
1369979_at	Skap2	src kinase associated phosphoprotein 2	155183	Rn.162747	NM_130413	7.52	7.46	6.82	7.32	7.39	7.45	1.09	up	6.25E-01	8.95E-01	-	-
1382083_at	Coch	coagulation factor C homolog, cochlin (Limulus polyphemus)	362735	Rn.8204	BF287593	2.44	2.71	2.45	2.40	2.44	2.40	1.09	down	2.51E-01	8.95E-01	-	-
1380452_at	---	---	---	Rn.11844	AA964564	2.98	2.99	2.98	3.37	2.98	2.97	1.09	up	4.18E-01	8.95E-01	-	-
1388815_at	Saps1	SAPS domain family, member 1	361502	Rn.138371	BE329438	6.95	8.08	7.49	7.65	6.58	7.94	1.09	down	8.33E-01	9.47E-01	-	-
1376207_at	Tao3	TAO kinase 3	304530	Rn.162145	BE098720	2.44	2.44	2.80	2.44	2.45	2.44	1.09	down	3.82E-01	8.95E-01	-	-
1395325_s_at	Tmem32	transmembrane protein 32	302864	Rn.64172	BF564628	10.04	10.19	9.99	9.78	9.88	10.20	1.09	down	4.48E-01	8.95E-01	-	-
1372693_at	Hnrnpa1	heterogeneous nuclear ribonucleoprotein A1	29578	Rn.25771	AI408833	7.88	7.79	7.89	8.01	7.81	8.10	1.09	up	2.74E-01	8.95E-01	-	-
1372128_at	Mrps12	mitochondrial ribosomal protein S12	292758	Rn.8526	BI294944	9.16	9.16	8.62	9.14	8.93	9.22	1.09	up	5.87E-01	8.95E-01	-	-
1368152_at	Slc27a2	solute carrier family 27 (fatty acid transporter), member 2	85192	Rn.3608	NM_031736	10.41	10.51	11.07	10.75	10.92	10.66	1.09	up	6.17E-01	8.95E-01	-	-
1379529_at	Nsbp1	nucleosomal binding protein 1	681284	Rn.25395	BE121400	3.55	3.85	3.47	3.64	3.73	3.85	1.09	up	4.09E-01	8.95E-01	-	-
1370299_at	Aldob	aldolase B, fructose-bisphosphate	24190	Rn.98207	M10149	12.93	12.75	12.70	12.71	12.64	12.66	1.09	down	1.70E-01	8.95E-01	-	-
1389362_at	Ptpn3	protein tyrosine phosphatase, non-receptor type 3	362524	Rn.22271	AI317821	7.90	7.37	8.11	7.77	7.55	7.71	1.09	down	6.34E-01	8.95E-01	-	-
1378919_at	Tcfe3	Transcription factor E3	317376	Rn.9231	BE329217	2.39	2.72	2.40	2.38	2.39	2.38	1.09	down	3.30E-01	8.95E-01	-	-
1381708_at	Zfyve1	Zinc finger, FYVE domain containing 1	299188	Rn.205587	BE097099	2.63	3.66	2.66	2.63	3.42	2.54	1.09	down	8.00E-01	9.35E-01	-	-
1392805_at	Ganc	glucosidase, alpha; neutral C	24382	Rn.23744	AI171867	2.73	2.83	2.76	2.72	2.76	3.20	1.09	up	4.96E-01	8.95E-01	-	-
1371665_at	Smarcd3	SWI/SNF related, matrix associated, actin dependent regulator of chromatin,	299732	Rn.20043	BG380496	2.48	2.48	2.49	2.83	2.48	2.48	1.09	up	3.65E-01	8.95E-01	-	-
1383264_at	RGD1306487	similar to RAB3 GTPase-activating protein	304759	---	BI294715	7.76	7.99	7.15	8.09	7.20	7.96	1.09	up	7.67E-01	9.24E-01	-	-
1390928_at	---	---	---	---	AI228340	5.63	5.67	4.73	5.33	4.52	5.82	1.09	down	8.20E-01	9.42E-01	-	-
1375224_at	Phda3	pleckstrin homology-like domain, family A, member 3	363989	Rn.17905	AW520812	2.53	2.52	2.88	2.52	2.52	2.50	1.09	down	3.55E-01	8.95E-01	-	-
1396038_at	Rtbdn	retbindin	304667	Rn.42054	AI763817	2.48	2.46	2.77	2.46	2.47	2.42	1.09	down	3.17E-01	8.95E-01	-	-
1391897_at	Rabgap1l	RAB GTPase activating protein 1-like	304914	Rn.219759	BG379295	2.65	2.90	4.16	3.32	3.93	2.82	1.09	up	8.45E-01	9.52E-01	-	-
1373956_at	Fundc1	FUN14 domain containing 1	363442	Rn.22678	BF284313	5.56	5.54	6.02	5.54	5.78	5.44	1.09	down	5.60E-01	8.95E-01	-	-
1376687_at	Usp1	ubiquitin specific peptidase 1	313387	Rn.155728	AI010241	3.50	4.13	3.19	3.19	3.66	4.33	1.09	up	7.97E-01	9.34E-01	-	-
1379226_at	Aim1l	absent in melanoma 1-like	298543	Rn.93581	BM386775	6.16	7.09	7.07	6.91	6.16	6.89	1.09	down	7.78E-01	9.28E-01	-	-
1380472_at	LOC679368	similar to carboxylesterase 5	679368	---	AI639486	2.46	2.44	2.80	2.45	2.47	2.42	1.09	down	3.76E-01	8.95E-01	-	-
1367973_at	Ccl2	chemokine (C-C motif) ligand 2	24770	Rn.4772	NM_031530	2.59	2.54	2.58	2.55	2.98	2.53	1.09	up	4.68E-01	8.95E-01	-	-
1379721_at	RGD1308026	similar to 2310047B19Rik protein	363029	Rn.21057	AA997421	2.35	2.34	2.35	2.71	2.35	2.34	1.09	up	3.92E-01	8.95E-01	-	-
1380453_at	Zswim5	zinc finger, SWIM domain containing 5	313524	Rn.134685	AW530611	2.76	2.54	2.67	2.57	2.49	2.57	1.09	down	1.62E-01	8.95E-01	-	-
1372453_at	Dr1	down-regulator of transcription 1	289881	Rn.6866	AI012637	7.16	6.92	7.30	6.54	6.99	7.50	1.09	down	7.10E-01	9.09E-01	-	-
1374400_at	Elf3a	EFR3 homolog A (S. cerevisiae)	362923	Rn.21009	BG373853	7.83	6.79	4.73	6.27	6.70	6.73	1.09	up	9.04E-01	9.71E-01	-	-
1379441_at	Znf294	zinc finger protein 294	288308	Rn.44204	AA965092	6.43	7.60	8.12	7.72	7.36	7.43	1.09	up	8.28E-01	9.46E-01	-	-
1381250_at	---	---	---	Rn.148171	BF399737	2.64	2.29	2.31	2.30	2.30	2.29	1.09	down	3.55E-01	8.95E-01	-	-
1398553_at	Tmed5	transmembrane emp24 protein transport domain containing 5	289883	Rn.204558	AI137113	6.84	6.86	6.81	6.74	5.96	7.46	1.09	down	7.99E-01	9.35E-01	-	-
1395405_at	---	---	---	Rn.35137	BE116248	2.34	2.33	2.35	2.33	2.71	2.33	1.09	up	4.02E-01	8.95E-01	-	-
1383433_at	Klhl23	kelch-like 23 (Drosophila)	311114	Rn.125724	BI281874	5.57	3.96	6.34	5.30	5.70	5.23	1.09	up	8.77E-01	9.62E-01	-	-
1390020_at	Ogdh	oxoglutarate (alpha-ketoglutarate) dehydrogenase (lipoamide)	360977	Rn.45985	BI277513	7.99	8.27	7.77	7.80	8.00	7.88	1.09	down	4.91E-01	8.95E-01	-	-
1375295_at	Cs	Citrate synthase	170587	Rn.66581	AI009657	6.56	7.01	5.98	6.91	6.32	6.67	1.09	up	7.49E-01	9.19E-01	-	-
1372261_at	---	---	---	Rn.3650	AI409087	11.88	12.17	12.39	12.16	12.25	12.38	1.09	up	5.03E-01	8.95E-01	-	-
1395152_

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1383691_at	---	---	---	Rn.173720	BF415419	2.83	2.54	2.66	2.56	2.60	2.52	1.08	down	2.48E-01	8.95E-01	-	-
1372130_at	Arfgef1	ADP-ribosylation factor guanine nucleotide-exchange factor 1(brefeldin A-inhi	312915	Rn.6834	AI408249	6.17	7.06	7.26	7.23	6.31	7.29	1.08	up	8.13E-01	9.40E-01	-	-
1372860_at	Lhpp	phospholysine phosphohistidine inorganic pyrophosphate phosphatase	361663	Rn.15275	BE112971	8.44	8.97	8.60	8.34	8.68	8.64	1.08	down	5.68E-01	8.95E-01	-	-
1384528_at	Rai14	retinoic acid induced 14	294804	Rn.67714	BF416474	2.86	2.77	2.63	2.72	2.57	2.62	1.08	down	2.14E-01	8.95E-01	-	-
1382853_at	LOC683844	similar to RING finger protein 11 (NEDD4 WW domain-binding protein 2) (Sid	683844	---	AW915066	2.87	2.85	2.94	2.85	3.31	2.85	1.08	up	4.98E-01	8.95E-01	-	-
1390043_at	Capza2	capping protein (actin filament) muscle Z-line, alpha 2	493810	Rn.17868	AI175286	8.77	9.38	9.01	8.79	9.30	9.41	1.08	up	6.78E-01	9.02E-01	-	-
1369403_at	Asah2	N-acylsphingosine amidohydrolase (non-lysosomal ceramidase) 2	114104	Rn.156958	NM_053846	3.40	3.40	3.58	3.54	3.10	3.39	1.08	down	4.53E-01	8.95E-01	-	-
1390447_at	Stx3	syntaxin 3	81802	Rn.10951	BI295918	4.85	5.27	5.25	5.20	4.34	5.48	1.08	down	7.66E-01	9.24E-01	-	-
1383466_at	---	---	---	Rn.164410	BG667930	2.49	2.49	2.51	2.49	2.52	2.84	1.08	up	3.58E-01	8.95E-01	-	-
1370921_at	Scamp3	secretory carrier membrane protein 3	65169	Rn.98518	BI285156	7.57	8.39	8.29	8.46	8.07	8.08	1.08	up	7.07E-01	9.08E-01	-	-
1392713_a_at	---	---	---	---	AA892541	6.52	6.55	6.66	6.57	7.13	6.38	1.08	up	6.41E-01	8.95E-01	-	-
1378455_at	---	---	---	Rn.205191	BE109654	2.41	2.60	2.49	2.40	2.36	2.39	1.08	down	1.06E-01	8.95E-01	-	-
1377807_a_at	Ipwd1	IQ motif and WD repeats 1	289181	Rn.3917	BF389856	9.49	9.19	9.22	9.33	9.24	8.98	1.08	down	4.56E-01	8.95E-01	-	-
1371420_at	LOC494529	92Aa-Protein	494529	Rn.162966	AI412054	5.81	7.30	6.64	6.68	6.47	6.95	1.08	up	8.10E-01	9.39E-01	-	-
1389173_at	Son	Son DNA binding protein	304092	Rn.7967	AI411575	2.35	2.34	2.36	2.71	2.36	2.34	1.08	up	3.83E-01	8.95E-01	-	-
1390390_at	Tcf20	transcription factor 20	366964	Rn.220442	BM386814	6.55	6.83	6.35	6.05	6.24	7.08	1.08	down	7.54E-01	9.20E-01	-	-
1383698_at	Pdha1	pyruvate dehydrogenase (lipoamide) alpha 1	29554	Rn.3655	BF561717	9.41	9.94	9.59	9.58	9.03	9.99	1.08	down	7.33E-01	9.15E-01	-	-
1379635_at	Syap1	synapse associated protein 1	302678	Rn.63210	BF399325	8.83	7.97	7.49	8.40	7.99	8.26	1.08	up	7.90E-01	9.33E-01	-	-
1378312_at	Mfsd9	major facilitator superfamily domain containing 9	316356	Rn.18430	AI070065	3.18	3.17	3.18	3.24	3.18	2.76	1.08	down	4.85E-01	8.95E-01	-	-
1374058_at	Tmem9b	TMEM9 domain family, member B	293415	Rn.219247	BM384945	7.80	8.17	8.01	7.78	8.19	8.35	1.08	up	5.91E-01	8.95E-01	-	-
1389247_at	Polr3a	polymerase (RNA) III (DNA directed) polypeptide A, 155kDa	361102	Rn.41904	BI274108	4.89	5.08	4.27	4.24	4.80	4.86	1.08	down	7.30E-01	9.14E-01	-	-
1368896_at	Smad7	SMAD family member 7	81516	Rn.29980	AV521447	4.24	4.87	3.96	4.93	4.12	4.37	1.08	up	7.63E-01	9.23E-01	-	-
1372734_at	Smagp	small cell adhesion glycoprotein	300236	Rn.162017	AI408095	9.38	9.56	9.51	9.45	9.69	9.65	1.08	up	2.69E-01	8.95E-01	-	-
1371456_at	Abcf3	ATP-binding cassette, sub-family F (GCN20), member 3	287982	Rn.98647	BI281218	6.44	7.11	5.88	6.97	6.17	6.64	1.08	up	7.96E-01	9.35E-01	-	-
1394945_at	Cwf19l2	CWF19-like 2, cell cycle control (S. pombe)	362804	Rn.58712	BF396909	2.95	2.66	2.69	2.63	2.67	2.66	1.08	down	2.79E-01	8.95E-01	-	-
1383492_at	Hoxd9	homeo box D9	688999	Rn.13330	BF397956	5.79	5.76	5.45	5.93	5.26	6.15	1.08	up	7.07E-01	9.08E-01	-	-
1393342_at	---	---	---	Rn.165480	BG380998	8.32	8.69	8.32	8.71	7.89	9.06	1.08	up	7.68E-01	9.24E-01	-	-
1379937_at	---	---	---	Rn.218381	AW526968	2.34	2.32	2.34	2.60	2.45	2.30	1.08	up	2.59E-01	8.95E-01	-	-
1375531_at	Lrig3	leucine-rich repeats and immunoglobulin-like domains 3	299830	Rn.204519	BI300956	2.77	3.60	2.38	2.95	2.52	3.63	1.08	up	8.21E-01	9.43E-01	-	-
1394706_at	---	---	---	Rn.220617	AI044545	4.43	4.67	5.06	5.18	4.56	4.76	1.08	up	6.78E-01	9.02E-01	-	-
1381592_at	---	---	---	Rn.156726	AA926244	4.75	5.05	4.39	4.78	5.45	4.32	1.08	up	7.74E-01	9.26E-01	-	-
1394714_at	Atp2b1	ATPase, Ca++ transporting, plasma membrane 1	29598	Rn.7208	BF386268	3.89	2.35	2.37	3.55	2.36	2.35	1.08	down	8.67E-01	9.58E-01	-	-
1384148_at	Rab20	RAB20, member RAS oncogene family	689377	Rn.140755	BI293985	8.31	7.47	6.96	8.07	7.26	7.07	1.08	down	8.27E-01	9.45E-01	-	-
1392768_at	Aaf1a	Aaf1 anti-silencing function 1 homolog A (S. cerevisiae)	294408	Rn.163427	AA900944	3.08	3.02	3.62	3.31	3.11	3.65	1.08	up	6.63E-01	8.98E-01	-	-
1376314_at	Ube2q2	ubiquitin-conjugating enzyme E2Q (putative) 2	363065	---	AI172148	6.75	6.95	7.23	7.13	7.08	7.07	1.08	up	4.56E-01	8.95E-01	-	-
1367983_at	Fen1	flap structure-specific endonuclease 1	84490	Rn.16664	NM_053430	5.19	4.67	4.65	4.77	4.71	4.69	1.08	down	5.47E-01	8.95E-01	-	-
1389198_at	Sh2d3c	SH2 domain containing 3C	362111	Rn.16537	AI179893	2.34	2.30	2.39	2.55	2.39	2.45	1.08	up	9.23E-02	8.95E-01	-	-
1383276_at	Lanc2	LanC lantibiotic synthetase component C-like 2 (bacterial)	362375	Rn.104463	BG664988	2.50	2.45	2.96	2.60	2.49	2.48	1.08	down	5.28E-01	8.95E-01	-	-
1378355_a_at	Slc24a4	solute carrier family 24 (sodium/potassium/calcium exchanger), mem	314396	Rn.198754	AI556625	3.10	3.10	3.11	3.51	3.11	3.04	1.08	up	4.71E-01	8.95E-01	-	-
1393596_at	Atrx	alpha thalassemia/mental retardation syndrome X-linked (RAD54 homolog, S	246284	Rn.107838	BF390064	4.95	6.36	6.99	6.38	5.33	6.94	1.08	up	8.87E-01	9.65E-01	-	-
1397275_at	---	---	---	Rn.199290	BF386708	3.04	3.05	3.34	3.09	3.07	3.62	1.08	up	6.02E-01	8.95E-01	-	-
1370115_at	Slc7a10	solute carrier family 7, (neutral amino acid transporter, y+ system) member 10	114518	Rn.128083	NM_053726	2.48	2.46	2.48	2.47	2.83	2.46	1.08	up	3.98E-01	8.95E-01	-	-
1373585_at	Synj2bp	synaptojanin 2 binding protein	64531	Rn.6258	BE116774	9.73	9.25	9.40	9.22	9.20	9.62	1.08	down	5.90E-01	8.95E-01	-	-
1370230_at	Atp5j	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit F6	94271	Rn.5790	BG666602	10.70	10.93	10.72	10.70	11.05	10.95	1.08	up	4.09E-01	8.95E-01	-	-
1374877_at	LOC687295	similar to translocase of inner mitochondrial membrane 50 homolog	687295	---	AI112752	5.43	6.05	5.59	5.59	5.75	5.38	1.08	down	6.17E-01	8.95E-01	-	-
1383448_at	Irf9	interferon regulatory factor 9	305896	Rn.163277	AI029121	2.38	2.37	2.39	2.53	2.39	2.58	1.08	up	1.08E-01	8.95E-01	-	-
1383184_at	Znrf1	zinc and ring finger 1	362367	Rn.32245	AW916773	2.40	2.74	2.40	2.39	2.40	2.40	1.08	down	3.63E-01	8.95E-01	-	-
1378503_at	LOC100125371	hypothetical LOC100125371	100125371	Rn.34289	BF404403	2.37	2.34	2.71	2.40	2.34	2.33	1.08	down	3.91E-01	8.95E-01	-	-
1367689_a_at	Cd36	CD36 molecule (thrombospondin receptor)	29184	Rn.102418	NM_031561	2.79	2.78	2.85	2.66	3.21	2.89	1.08	up	5.11E-01	8.95E-01	-	-
1386511_x_at	---	---	---	---	AI231356	4.59	4.57	4.91	4.56	4.74	4.41	1.08	down	4.72E-01	8.95E-01	-	-
1388197_at	Hoxa4	homeo box A4	24453	---	AA900970	3.84	3.51	3.51	3.50	3.51	3.50	1.08	down	3.48E-01	8.95E-01	-	-
1371728_at	rCG_21212	similar to ubiquitin protein ligase E3B	687633	Rn.216438	BF281133	7.28	7.80	7.08	7.76	7.20	7.55	1.08	up	6.92E-01	9.05E-01	-	-
1386587_at	Btbd12	BTB (POZ) domain containing 12	302953	Rn.25408	AW144448	2.33	2.32	2.34	2.45	2.57	2.31	1.08	up	1.87E-01	8.95E-01	-	-
1369092_at	Sec22a	SEC22 vesicle trafficking protein homolog A (S. cerevisiae)	117513	Rn.34191	NM_057147	2.55	2.49	2.46	2.85	2.50	2.49	1.08	up	3.99E-01	8.95E-01	-	-
1394352_at	Ifih1	interferon induced with helicase C domain 1	499801	Rn.151974	BF543871	2.35	2.68	2.35	2.34	2.35	2.35	1.08	down	3.53E-01	8.95E-01	-	-
1388258_at	Nrg1	neuregulin 1	112400	Rn.37438	AF194443	2.57	2.38	2.81	2.38	2.66	2.37	1.08	down	5.00E-01	8.95E-01	-	-
1377791_at	---	---	---	Rn.209947	BI299500	2.43	2.44	2.43	2.40	2.82	2.42	1.08	up	4.48E-01	8.95E-01	-	-
1369801_at	Nyw1	wybemia related factor NYW-1	59319	Rn.133954	NM_021683	3.18	3.20	3.83	3.55	3.17	3.13	1.08	down	6.71E-01	9.00E-01	-	-
1382679_at	Wdr43	WD repeat domain 43	362703	Rn.101883	BF396190	7.10	6.65	6.35	6.25	6.60	7.58	1.08	up	8.11E-01	9.39E-01	-	-
1375687_at	---	---	---	Rn.163656	BE097926	10.34	10.30	10.26	10.37	10.34	10.52	1.08	up	1.26E-01	8.95E-01	-	-
1374875_at	---	---	---	Rn.23642	AW915273	3.73	3.46	3.25	3.42	3.43	3.94	1.08	up	6.30E-01	8.95E-01	-	-
1392662_at	Cisd2	CDGSH iron sulfur domain 2	295457	Rn.24858	AI229905	5.61	5.49	5.22	5.56	5.44	5.57	1.08	up	3.29E-01	8.95E-01	-	-
1387780_at	Dnaja2	DnaJ (Hsp40) homolog, subfamily A, member 2	84026	Rn.3904	NM_032079	8.06	8.41	8.09	8.53	7.87	8.50	1.08	up	6.58E-01	8.98E-01	-	-
1398979_at	Angel2	angel homolog 2 (Drosophila)	305035	Rn.62	BF405079	2.51	2.81	2.51	2.49	3.17	2.53	1.08	up	6.58E-01	8.98E-01	-	-
1388694_at	H2-T24	histocompatibility 2, T region locus 24	414784	---	AI233121	4.86	2.37	2.68	3.46	2.91	3.20	1.08	down	8.92E-01	9.66E-01	-	-
1387314_at	Sult1b1	sulfotransferase family, cytosolic, 1B, member 1	64305	Rn.1183	NM_022513	10.17	10.22	10.21	10.01	10.17	10.76	1.08	up	6.40E-01	8.95E-01	-	-
1368118_at	Bcl10	B-cell CLL/lymphoma 10	83477	Rn.13007	NM_031328	4.80	5.63	6.22	5.76	5.25	5.97	1.08	up	8.16E-01	9.41E-01	-	-
1382591_at	---	---	---	Rn.23346	AI045562	2.42	2.40	2.46	2.40	2.83	2.39	1.08	up	4.71E-01	8.95E-01	-	-
1382781_at	---	---	---	Rn.20540	AI784744	2.31	2.61	2.34	2.31	2.30	2.30	1.08	down	2.95E-01	8.95E-01	-	-
1392870_at	---	---	---	Rn.18442	AI406729	2.51	2.49	2.55	2.61	2.54	2.76	1.08	up	1.62E-01	8.95E-01	-	-
1378974_at	---	---	---	Rn.40955	AI709944	2.64	2.30	2.31	2.30	2.31	2.29	1.08	down	3.67E-01	8.95E-01	-	-
1372227_at	Muted	muted homolog (mouse)	306868	Rn.1373	AI177863	7.74	7.63	7.24	7.35	7.33	7.59	1.08	down	5.43E-01	8.95E-01	-	-
1376157_at	Uba6	Ubiquitin-like modifier activating enzyme 6	305268	Rn.94245	AI236782	2.84	5.10	5.23	4.66	3.89	4.96	1.08	up	8.97E-01	9.68E-01	-	-
1383549_at	RGD1310794	similar to RIKEN cDNA C030048B08	296840	Rn.24927	AW533221	2.84	3.53	2.63	2.84	2.84	2.97	1.08	down	6.96E-01	9.07E-01	-	-
1389336_at	Pop5	processing of precursor 5, ribonuclease P/MRP subunit (S. cerevisiae)	117241	Rn.41651	BM390893	6.22	6.34	6.42	6.40	6.41	6.51	1.08	up	1.63E-01	8.95E-01	-	-
1374107_at	Elac2	elaC homolog 2 (E. coli)	282826	Rn.163124	AI229668	4.49	5.16	3.74	4.50	4.28	4.96	1.08	up	8.14E-01	9.40E-01	-	-
1372823_at	---	---	---	Rn.198956	BE117126	4.86	5.20	5.22	5.50	5.21	4.91	1.08	up	6.07E-01	8.95E-01	-	-
1396285_at	RGD1306344	Similar to Ab1-133	296384	Rn.202742	BE097728	3.36	4.26	4.11	4.16	3.95	3.97	1.08	up	7.08E-01	9.09E-01	-	-
1397414_at	---	---	---	Rn.169146	BF388307	3.03	2.47	2.61	2.59	2.60	2.58	1.08	down	5.31E-01	8.95E-01	-	-
1378853_at	Mtmr14	myotubularin related protein 14	312634	Rn.49772	BG377853	5.54	5.06	5.22	5.61	4.99	5.56	1.08	up	6.61E-01	8.98E-01	-	-
1395486_at	Gtf3c1	general transcription factor III C 1	171063	Rn.11288	BF413851	3.43	2.90	2.94	2.74	2.93	3.25	1.08	down	6.36E-01	8.95E-01	-	-
1379775_at	Brf1	BRF1 homolog, subunit of RNA polymerase III transcription initiation factor IIIB	299347	Rn.205393	AI556888	7.23	7.42	6.87	7.23	7.67	6.96	1.08	up	6.84E-01	9.03E-01	-	-
1379132_at	---	---	---	Rn.207011	BE107317	3.11	2.52	2.56	2.58	2.82	2.45	1.08	down	6.29E-01	8.95E-01	-	-
1381141_at	---	---	---	Rn.203338	BF396613	2.58	2.56	2.61	2.98	2.60	2.52	1.08	up	4.69E-01	8.95E-01	-	-
1371615_at	Dgat2	diacylglycerol O-acyltransferase homolog 2 (mouse)	252900	Rn.9523	BI279069	6.40	5.88	6.58	5.76	6.28	6.47	1.08	down	7.20E-01	9.11E-01	-	-
1372509_at	---	---	---	Rn.22487	AI172024	4.02	4.37	4.19	3.81	4.01	4.40	1.08	down	5.97E-01	8.95E-01	-	-
1382174_at	---	---	---	Rn.108166	AI227996	8.94	8.52	8.39	8.99	8.29	8.91	1.08	up	7.01E-01	9.07E-01	-	-
1399030_at	Wdr45	WD repeat domain 45	302559	Rn.25900	AA800682	7.79	7.25	7.68	7.68	7.72	7.67	1.08	up	5.22E-01	8.95E-01	-	-
1394897_at	---	---	---	Rn.16878	AA858696	2.99	2.70	2.64	2.72	2.58	2.69	1.08	down	3.76E-01	8.95E-01	-	-
1398347_at	Axl /// LOC687188	Axl receptor tyrosine kinase /// similar to AXL receptor tyrosine kinase	308444 /// 687188	Rn.161805	AI406520	2.51	2.49	2.37	2.49	2.64	2.58	1.08	up	1.32E-01	8.95E-01	-	-
1377400_at	Hrb2	HIV-1 Rev binding protein 2	314830	Rn.162939	BF391890	6.10	5.66	5.13	6.23	5.17	5.85	1.08	up	7.97E-01	9.34E-01	-	-
1381263_at	---	---	---	---	H33747	2.59	2.57	2.90	2.57	2.60	2.55	1.08	down	3.52E-01	8.95E-01	-	-
1375595_at	Arih1	ariadne ubiquitin-conjugating enzyme E2 binding protein homolog 1 (Drosoph	300756	Rn.29865	AI231433	7.33	7.56	7.28	7.57	7.38	7.58	1.08	up	3.48E-01	8.95E-01	-	-
1383496_at	RGD1560481	similar to hypothetical protein FLJ20171	500409	Rn.161971	BM387466	2.38	2.38	2.39	2.38	2.75	2.37	1.08	up	4.09E-01	8.95E-01	-	-
1372109_at	Pnkd	paroxysmal nonkinesiogenic dyskinesia	100188944	Rn.50364	AI102715	6.23	6.31	6.28	6.27	6.34	6.55	1.08	up	2.57E-01	8.95E-01	-	-
1391135_at	---	---	---	Rn.167228	AI175443	4.04	3.55	3.50	4.04	3.21	4.08	1.08	down	7.17E-01	9.10E-01	-	-
1372237_at	---	---	---	Rn.199495	BI298306	2.41	2.42	2.42	2.76	2.42	2.41	1.08	up	3.78E-01	8.95E-01	-	-
1367507_at	Nudt22	nudix (nucleoside diphosphate linked moiety X)-type motif 22	293703	Rn.1934	BI281661	4.73	4.90	4.43	5.22	4.42	4.76	1.08	up	6.92E-01	9.05E-01	-	-
1367607_at	Cox4i1	cytochrome c oxidase subunit IV isoform 1	29445	Rn.2528	NM_017202	11.20	11.39	11.23	11.22	11.48	11.46	1.08	up	3.20E-01	8.95E-01	-	-
1376081_at	Lonf2	leucine carboxyl methyltransferase 2	296098	Rn.17983	AI059661	4.07	4.32	3.89	4.18	4.19	4.25	1.08	up	4.15E-01	8.95E-01	-	-
1393503_at	---	---	---	---	BE099137	2.38	2.70	2.38	2.37	2.38	2.36	1.08	down	3.44E-01	8.95E-01	-	-
1384463_at	Tex264	testis expressed 264	300988	Rn.13429	AW252660	7.95	7.89	7.23	7.58	7.94	7.89	1.08	up	6.79E-01	9.02E-01	-	-
1371281_at	doxc9 /// rCG_5076	homeobox C9 /// homeo box C8	24460 /// 368178	Rn.101733	M37568	2.50	2.68	2.62	2.49	2.52	2.45	1.08	down	1.02E-01	8.95E-01	-	-
1380411_at	Got1l1	glutamic-oxaloacetic transaminase 1-like 1	306540	Rn.36169	BI293378	2.39	2.38	2.46	2.39	2.81	2.38	1.08	up	4.75E-01	8.95E-01	-	-
1387809_at	Map2k6	mitogen-activated protein kinase kinase 6	114495	Rn.17256	NM_053703	2.40	2.44	2.43	2.43	2.57	2.63	1.08	up	1.35E-01	8.95E-01	-	-
1391279_at	Scin	Scinderin	298975	Rn.28816	AI112564	2.59	2.59	2.67	2.76	2.78	2.66	1.08	up	6.91E-02	8.95E-01	-	-
1392460_at	---	---	---	---	BF283685	5.32	5.61	5.79	4.94	6.00	6.12	1.08	up	7.89E-01	9.32E-01	-	-
1372121_at	Usp9x	ubiquitin specific peptidase 9, X-linked	363445	Rn.7273	BF284408	8.44	8.61	8.62	8.60	8.63	8.77	1.08	up	2.21E-01	8.95E-01	-	-
1375899_at	---	---	---	Rn.96103	BF283736	2.92	3.77	4.18	3.92	3.44	3.86	1.08	up	7.89E-01	9.32E-01	-	-
1398340_at	Ccndbp1	cyclin D-type binding-protein 1	362201	Rn.162679	AI317832	6.21	5.56	5.97	5.86	5.83	5.70	1.08	down	5.94E-01	8.95E-01	-	-
1379604_at	apol3 /// LOC68135	apolipoprotein L, 3 /// similar to apolipoprotein L, 3	315108 /// 681351	Rn.119914	BF284937	3.14	3.18	3.03	3.06	3.47	3.15	1.08	up	4.35E-01	8.95E-01	-	-
1372024_at	---	---	---	Rn.23401	AI104846	2.56	2.55	2.57	2.64	2.84	2.54	1.08	up	2.75E-01	8.95E-01	-	-
1398385_at	Thoc7	THO complex 7 homolog (Drosophila)	305714	Rn.22227	AI199641	7.58	8.41	8.70	8.14	8.15	8.75	1.08	up	7.65E-01	9.30E-01	-	-
1376401_at	---	---	---	Rn.7709	AI412569	5.28	5.74	5.94	5.50	5.22	5.90	1.08	down	7.00E-01	9.07E-01	-	-
1389574_at	Gtf3c2	general transcription factor IIIC, polypeptide 2, beta	313914	Rn.22450	AI014004	4.95	4.94	4.93	4.47	5.41	5.29	1.08	up	7.17E-01	9.10E-01	-	-
1376764_at	---	---	---	Rn.136571	AI406412	2.29	2.27	2.29	2.28	2.48	2.44	1.08	up	1.44E-01	8.95E-01	-	-
1372103_at	LOC498996	similar to DnaJ (Hsp40) homolog, subfamily A, member 4	498996	Rn.196543	AI104324	6.96	6.78	6.41	7.05	6.21	6.56	1.08	down	7.17E-01	9.10E-01	-	-
1374162_at	---	---	---	Rn.17670	AI112255	2.57	2.58	2.43	2.42	2.42	2.40	1.08	down	8.37E-02	8.95E-01	-	-
1384639_at	Reep6	receptor accessory protein 6	362835	Rn.9353	AI070350	3.33	3.82	4.26	3.79	3.51	3.78	1.08	down	7.08E-01	9.09E-01	-	-
1377162_at	---	---	---	Rn.153689	BF390386	4.82	4.60	4.40	4.22	4.45	4.80	1.08	down	6.16E-01	8.95E-01	-	-
1390358_at	Cacna2d3	calcium channel, voltage-dependent, alpha2/delta subunit 3	306243	Rn.206369	BF405996	2.84	2.50	2.53	2.52	2.53	2.49	1.08	down	3.55E-01	8.95E-01	-	-
1375650_at	Brd4	bromodomain containing 4	362844	Rn.12110	BM389207	8.17	8.36	7.68	7.88	8.11	7.88	1.08	down	6.24E-01	8.95E-01	-	-
1398583_at	Snapc5	small nuclear RNA activating complex, polypeptide 5	691501	Rn.47597	BE114791	6.39	6.83	7.09	6.78	6.83	7.04	1.08	up	6.30E-01	8.95E-01	-	-
1372217_at	Tmem199	transmembrane protein 199	303332	Rn.160826	BM385348	5.49	5.71	5.71	5.71	5.66	5.89	1.08	up	3.31E-01	8.95E-01	-	-
1392219_at	---	---	---	Rn.199373	AI145523	2.43	2.75	2.45	2.43	2.44	2.42	1.08	down	3.26E-01	8.95E-01	-	-
1374999_at	---	---	---	Rn.14884	BF399489	3.01	3.15	3.16	3.16	3.30	3.21	1.08	up	1.53E-01	8.95E-01	-	-
1373746_at	Wdr91	WD repeat domain 91	312225	Rn.158722	BM390756	6.37	6.34	6.97	6.20	7.28	6.54	1.08	up	7.77E-01	9.28E-01	-	-
1375161_at	Mrpl55	mitochondrial ribosomal protein L55	287356	Rn.4271	BM386389	6.31	5.97	6.19	5.92	6.13	6.08	1.08	down	3.96E-01	8.95E-01	-	-
1390653_at	Wdr89	WD repeat domain 89	314243	Rn.20078	AI171174	3.06	3.54	5.07	3.65	4.36	3.32	1.08	down	8.75E-01	9.61E-01	-	-
1377808_at	Ipwd1	IQ motif and WD repeats 1	289181	Rn.3917	BF389856	11.06	10.83	10.65	10.91	11.03	10.95	1.08	up	4.01E-01	8.95E-01	-	-
1389883_at	RGD1563224	similar to 4930438D12Rik protein	500874	Rn.7349	BF284719	2.64	2.55	2.57	2.35	2.49	2.57	1.08	down	1.75E-01	8.95E-01	-	-
1389603_at	---	---	---	Rn.11837	AA964544	2.48	2.47	2.38	2.47	2.66	2.54	1.08	up	1.43E-01	8.95E-01	-	-
1397859_x_at	RT1-A2 /// RT1-A3	RT1 class Ia, locus A2 /// RT1 class I, A3	24974 /// 309627	---	BI291927	2.87	2.86	2.85	2.87	3.28	2.78	1.08	up	5.00E-01	8.95E-01	-	-
1383863_at	Lmo2	LIM domain only 2	362171	Rn.155591	BF288303	2.89	2.76	3.09	3.18	3.04	2.88	1.08	up	4.28E-01	8.95E-01	-	-
1368410_at	Mpg	N-methylpurine-DNA glycosylase	24561	Rn.11241	NM_012601	2.41	2.43	2.42	2.74	2.44	2.42	1.08	up	3.23E-01	8.95E-01	-	-
1389912_at	Ensa	endosulfine alpha	60334	Rn.27154	BI289922	6.63	6.54	4.59	5.77	6.17	5.48	1.08	down	8.78E-01	9.62E-01	-	-
1373429_at	Atf6b	activating transcription factor 6 beta	406169	Rn.18179	BI295832	5.28	4.24	5.75	5.00	4.81	5.12	1.08	down	8.16E-01	9.41E-01	-	-
1369898_a_at	Gip	gastric inhibitory polypeptide	25040	Rn.10446	L08831	2.42	2.74	2.43	2.42	2.43	2.40	1.08	up	3.44E-01	8.95E-01	-

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1378746_at	---	---	---	---	AI013683	5.24	5.02	5.13	5.04	5.63	5.06	1.08	up	6.08E-01	8.95E-01	-	-
1377336_at	Sema3b	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (se	363142	Rn.26859	BI275485	5.24	5.98	5.33	5.22	5.23	5.76	1.08	down	7.21E-01	9.11E-01	-	-
1389167_at	Mapkap1	mitogen-activated protein kinase associated protein 1	296648	Rn.105886	BI275749	5.08	6.53	5.81	5.81	5.74	6.21	1.08	up	8.12E-01	9.39E-01	-	-
1390329_at	---	---	---	Rn.209165	BF398845	2.53	2.79	2.59	3.19	2.56	2.50	1.08	up	6.56E-01	8.98E-01	-	-
1391744_at	---	---	---	Rn.171558	AI548028	3.72	3.77	3.40	3.45	3.37	3.73	1.08	down	5.14E-01	8.95E-01	-	-
1386984_at	Smad4	SMAD family member 4	50554	Rn.9774	NM_019275	7.49	7.25	7.14	7.49	7.30	7.42	1.08	up	3.94E-01	8.95E-01	-	-
1367774_at	Gsta3	glutathione S-transferase A3	24421	Rn.10400	NM_031509	12.10	11.87	11.94	11.98	11.71	11.89	1.08	down	3.36E-01	8.95E-01	-	-
1391539_at	---	---	---	Rn.49247	BI291849	6.27	6.68	6.74	6.37	7.10	6.55	1.08	up	6.94E-01	9.05E-01	-	-
1374897_at	Thoc4	THO complex 4	690585	Rn.6994	AI406842	5.34	5.82	7.33	6.48	6.75	5.61	1.08	up	8.78E-01	9.62E-01	-	-
1385857_at	Ophn1	oligophrenin 1	312108	Rn.51019	AA998681	2.79	2.50	2.56	2.51	2.54	2.46	1.08	down	2.94E-01	8.95E-01	-	-
1389348_at	Catf1	cleavage stimulation factor, 3' pre-RNA, subunit 1	311670	Rn.8860	BF282442	5.44	4.74	4.98	4.75	5.32	4.76	1.08	down	7.07E-01	9.08E-01	-	-
1395634_at	---	---	---	Rn.168253	AI576190	3.29	2.68	2.65	3.02	2.65	2.62	1.08	down	6.71E-01	9.00E-01	-	-
1384535_at	---	---	---	Rn.205201	BF406790	2.46	2.44	2.77	2.46	2.49	2.38	1.08	down	3.67E-01	8.95E-01	-	-
1383306_at	---	---	---	Rn.22089	AI013468	7.57	7.34	7.94	7.31	7.24	7.96	1.08	down	7.15E-01	9.10E-01	-	-
1389062_at	Ik /// Wdr55	IK cytokine /// WD repeat domain 55	291659 /// 307494	Rn.162302	BE109152	7.61	8.33	8.15	8.37	7.55	8.51	1.08	up	7.76E-01	9.27E-01	-	-
1376537_at	Ptpn3	Protein tyrosine phosphatase, non-receptor type 3	362524	Rn.22271	AW435010	4.29	4.02	4.42	3.97	4.23	4.18	1.08	down	4.72E-01	8.95E-01	-	-
1377819_at	RGD1561065	similar to mKIAA1111 protein	317425	Rn.22904	AA955441	5.04	5.79	5.18	5.98	4.42	5.94	1.08	up	8.52E-01	9.54E-01	-	-
1388873_at	Trip12	thyroid hormone receptor interactor 12	316575	Rn.8277	AA891883	8.49	8.78	8.82	8.58	8.30	8.87	1.08	down	5.95E-01	8.95E-01	-	-
1380135_at	---	---	---	Rn.206928	AW531996	2.66	2.58	2.60	2.58	2.69	2.91	1.08	up	3.19E-01	8.95E-01	-	-
1398034_at	---	---	---	Rn.210940	BF403840	2.59	2.39	2.53	2.39	2.38	2.40	1.08	down	1.41E-01	8.95E-01	-	-
1390937_at	RGD1309051	similar to chromosome 14 open reading frame 50	299153	Rn.203121	AW523875	7.65	8.71	8.41	8.37	8.09	8.65	1.08	up	7.67E-01	9.24E-01	-	-
1378748_at	LOC691984	similar to Glypican-6 precursor	691984	---	BF400032	2.41	2.59	2.42	2.41	2.94	2.40	1.08	up	5.79E-01	8.95E-01	-	-
1367728_at	Tsn	translin	60381	Rn.156195	NM_021762	2.34	2.69	2.34	2.33	2.35	2.35	1.08	down	3.89E-01	8.95E-01	-	-
1369165_at	Trpc3	transient receptor potential cation channel, subfamily C, member 3	60385	Rn.21862	NM_021771	2.40	2.27	2.28	2.48	2.42	2.39	1.08	up	8.32E-02	8.95E-01	-	-
1391604_at	Ncapd3	non-SMC condensin II complex, subunit D3	315508	Rn.48187	BF418841	3.26	2.61	2.51	3.73	2.49	2.49	1.08	up	8.25E-01	9.44E-01	-	-
1374628_at	Cryz	crystallin, zeta	362061	Rn.6746	AI232098	10.46	10.38	10.39	10.32	11.13	10.13	1.08	up	7.33E-01	9.14E-01	-	-
1376319_at	Sema3c	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (se	296787	Rn.98782	BM390322	4.37	5.99	5.79	4.29	6.22	5.99	1.08	up	8.94E-01	9.67E-01	-	-
1388306_at	RGD1305593	similar to RIKEN cDNA 1810042K04	288513	---	BM383758	4.87	5.77	5.54	5.24	4.94	5.67	1.08	down	7.61E-01	9.22E-01	-	-
1387929_at	Pmf31	PMF32 protein	171453	Rn.165271	AB020504	3.35	3.24	2.87	3.17	3.29	3.34	1.08	up	5.05E-01	8.95E-01	-	-
1373511_at	---	---	---	---	BI296596	7.22	7.47	7.11	6.91	7.72	7.50	1.08	up	6.91E-01	9.05E-01	-	-
1383248_at	Fmo5	flavin containing monooxygenase 5	246248	Rn.7038	AI454611	7.41	7.71	7.00	7.56	6.05	8.16	1.08	down	8.73E-01	9.61E-01	-	-
1394588_at	---	---	---	Rn.167464	BE113841	2.43	2.41	2.34	2.44	2.67	2.41	1.08	up	2.68E-01	8.95E-01	-	-
1388832_at	Dhrsx	dehydrogenase/reductase (SDR family) X-linked	288525	Rn.12762	AI104245	7.09	6.50	6.29	6.54	6.28	6.71	1.08	down	6.98E-01	9.07E-01	-	-
1391109_x_at	---	---	---	Rn.200363	BE108349	2.80	3.00	2.92	2.80	2.80	2.77	1.08	down	1.41E-01	8.95E-01	-	-
1390872_at	---	---	---	Rn.199320	AI178134	3.10	3.89	4.11	3.37	4.26	3.13	1.08	down	8.19E-01	9.42E-01	-	-
1380531_at	---	---	---	Rn.105909	AI102178	2.48	2.46	2.49	2.47	2.85	2.45	1.08	up	4.34E-01	8.95E-01	-	-
1367906_at	Acp2	acid phosphatase 2, lysosomal	24162	Rn.9816	NM_016988	7.41	7.66	7.84	7.21	7.53	7.82	1.08	down	6.31E-01	8.95E-01	-	-
1374829_at	Srf	serum response factor (c-fos serum response element-binding transcription fa	501099	Rn.1501	BF395579	2.33	2.62	2.32	2.31	2.32	2.30	1.08	down	3.15E-01	8.95E-01	-	-
1397693_at	Eif2s3x	eukaryotic translation initiation factor 2, subunit 3, structural gene X-linked	299027	Rn.87025	BG662620	6.43	7.48	7.62	6.60	6.76	7.84	1.08	down	8.46E-01	9.52E-01	-	-
1367528_at	Fbxw8	F-box and WD repeat domain containing 8	304522	Rn.812	BE103273	4.62	4.10	4.02	4.13	4.43	4.51	1.08	up	6.38E-01	8.95E-01	-	-
1397471_at	Mical2	microtubule associated monoxygenase, calponin and LIM domain containing	366352	Rn.203742	AW520988	2.56	2.55	2.97	2.55	2.63	2.56	1.08	down	4.75E-01	8.95E-01	-	-
1372555_at	Flywch1	FLYWCH-type zinc finger 1	360488	Rn.49088	AI171778	4.79	4.51	2.88	4.76	2.96	4.80	1.08	up	9.02E-01	9.70E-01	-	-
1372852_at	Ptprcap	protein tyrosine phosphatase, receptor type, C-associated protein	499300	Rn.4188	BF417048	2.63	2.74	2.64	2.63	2.39	2.66	1.08	down	2.85E-01	8.95E-01	-	-
1378183_at	---	---	---	Rn.23491	AW531387	3.06	3.38	3.04	3.08	3.03	3.03	1.08	down	3.69E-01	8.95E-01	-	-
1382056_at	Sfrs11	splicing factor, arginine/serine-rich 11	502603	Rn.11095	AI145768	9.66	8.61	8.09	9.09	8.56	8.38	1.08	down	8.37E-01	9.49E-01	-	-
1371983_at	Josd1	Josephin domain containing 1	315134	Rn.2495	AA945181	3.07	2.95	3.07	2.98	3.34	3.10	1.08	up	3.77E-01	8.95E-01	-	-
1388573_at	Alkbh	AlkB, alkylation repair homolog (E. coli)	362766	Rn.107927	BF288140	2.60	2.49	2.62	2.65	2.59	2.81	1.08	up	2.27E-01	8.95E-01	-	-
1394010_at	Rsf1	remodeling and spacing factor 1	308839	Rn.23988	H32100	5.35	5.72	4.17	4.81	5.78	4.97	1.08	up	8.50E-01	9.53E-01	-	-
1391556_at	Sema5a	sema domain, seven thrombospondin repeats (type 1 and type 1-like), transm	310207	Rn.14619	AW524218	4.02	3.98	4.01	3.77	4.20	4.37	1.08	up	5.64E-01	8.95E-01	-	-
1377750_at	Arhgef3	Rho guanine nucleotide exchange factor (GEF) 3	290541	Rn.11687	AI454536	5.69	5.10	5.20	5.38	5.82	5.13	1.08	up	7.04E-01	9.07E-01	-	-
1390524_at	Rnf12	ring finger protein 12	317241	Rn.85539	BM392295	5.44	6.05	6.05	5.32	6.27	6.28	1.08	up	7.83E-01	9.30E-01	-	-
1376005_at	---	---	---	Rn.203637	BE109334	2.46	2.99	2.31	2.46	2.51	3.13	1.08	up	7.26E-01	9.13E-01	-	-
1370936_at	Dmgdh	dimethylglycine dehydrogenase	245961	Rn.3646	AA892345	8.51	9.00	9.26	8.66	8.95	8.82	1.08	down	6.60E-01	8.98E-01	-	-
1398690_at	---	---	---	Rn.178143	BF284365	3.03	2.40	2.54	2.81	2.77	2.72	1.08	up	5.90E-01	8.95E-01	-	-
1390251_at	---	---	---	Rn.167766	BF397284	2.77	2.67	2.78	3.19	2.77	2.60	1.08	up	5.66E-01	8.95E-01	-	-
1384282_at	Zscan21	zinc finger and SCAN domain containing 21	304342	Rn.203972	BG379149	7.74	7.54	7.80	7.45	7.88	7.42	1.08	down	5.42E-01	8.95E-01	-	-
1368321_at	Egr1	early growth response 1	24330	Rn.9096	NM_012551	3.24	3.13	2.85	2.47	3.72	3.37	1.08	up	7.88E-01	9.32E-01	-	-
1367509_at	Gtf2h5	general transcription factor IIH, polypeptide 5	502227	Rn.25310	AI231812	8.20	8.07	8.83	8.43	7.79	8.55	1.08	down	7.53E-01	9.20E-01	-	-
1381734_at	LOC684258	similar to coiled-coil-helix-coiled-coil-helix domain containing 7	684258	---	BF400855	2.33	2.32	2.33	2.67	2.33	2.32	1.08	up	3.82E-01	8.95E-01	-	-
1388029_at	Anubl1	AN1, ubiquitin-like, homolog (Xenopus laevis)	286998	Rn.205939	AF315467	2.63	2.93	2.64	2.61	2.64	2.62	1.08	down	3.23E-01	8.95E-01	-	-
1382957_at	Crop	cisplatin resistance-associated overexpressed protein	360602	Rn.15676	BF408881	9.58	9.80	9.11	9.72	9.64	9.45	1.08	up	6.36E-01	8.95E-01	-	-
1389705_at	Rag1ap1	recombination activating gene 1 activating protein 1	295245	Rn.823	AI136061	4.22	4.85	4.31	4.36	4.29	4.40	1.08	down	6.10E-01	8.95E-01	-	-
1374828_at	Pdia5	protein disulfide isomerase family A, member 5	360722	Rn.162053	AI045590	2.35	2.35	2.36	2.35	2.36	2.69	1.08	up	3.67E-01	8.95E-01	-	-
1367984_at	Scaf1	SR-related CTD-associated factor 1	56081	Rn.93	NM_019384	3.86	3.91	3.88	3.60	3.82	3.89	1.08	down	2.72E-01	8.95E-01	-	-
1374332_at	Ddx49	DEAD (Asp-Glu-Ala-Asp) box polypeptide 49	290660	Rn.95332	AI171365	6.37	6.25	5.82	5.66	6.45	6.68	1.08	up	7.67E-01	9.24E-01	-	-
1373422_at	Larp1	La ribonucleoprotein domain family, member 1	303158	Rn.98804	BE108280	7.67	7.97	7.47	7.29	8.00	8.15	1.08	up	7.31E-01	9.14E-01	-	-
1385838_a_at	Tm2d1	TM2 domain containing 1	362545	Rn.198278	BF287928	8.74	8.72	9.40	8.92	9.19	8.41	1.08	down	7.44E-01	9.17E-01	-	-
1375763_at	Heatr6	HEAT repeat containing 6	497972	Rn.27022	BF407879	2.93	2.77	2.74	2.72	2.69	3.38	1.08	up	6.55E-01	8.98E-01	-	-
1388120_at	Pdcd6ip	programmed cell death 6 interacting protein	501083	Rn.101328	BE328942	5.86	6.65	6.14	6.15	5.86	6.29	1.08	down	6.83E-01	9.05E-01	-	-
1382476_x_at	---	---	---	Rn.79888	AI060133	4.39	3.96	4.16	4.61	4.16	4.07	1.08	up	6.25E-01	8.95E-01	-	-
1385970_at	Ctr9	Ctr9, Paf1/RNA polymerase II complex component, homolog (S. cerevisiae)	293184	Rn.102000	BF289079	2.95	2.91	3.09	3.02	3.20	3.07	1.08	up	2.17E-01	8.95E-01	-	-
1392934_at	---	---	---	Rn.153589	BM394509	7.82	8.86	8.54	8.45	8.13	8.31	1.08	down	7.46E-01	9.18E-01	-	-
1373616_at	Crebl2	cAMP responsive element binding protein-like 2	362453	Rn.107553	BE113210	6.06	5.98	5.52	5.47	5.90	5.85	1.08	down	6.33E-01	8.95E-01	-	-
1389649_at	---	---	---	Rn.12537	AI411897	8.48	7.90	8.18	8.43	8.39	8.07	1.08	up	6.12E-01	8.95E-01	-	-
1374526_at	Ankfy1	ankyrin repeat and FYVE domain containing 1	303292	Rn.98554	BF396420	6.14	6.58	6.08	5.97	5.59	6.91	1.08	down	8.05E-01	9.37E-01	-	-
1379805_at	Slc41a2	solute carrier family 41, member 2	362861	Rn.7329	BF410740	2.32	2.31	2.64	2.31	2.32	2.30	1.08	down	3.66E-01	8.95E-01	-	-
1369785_at	Ppat	phosphoribosyl pyrophosphate amidotransferase	117544	Rn.18690	NM_057198	4.00	5.14	5.36	4.97	5.05	4.81	1.08	up	8.08E-01	9.38E-01	-	-
1370907_at	St6gal1	ST6 beta-galactosamide alpha-2,6-sialyltranferase 1	25197	Rn.54567	M83143	10.90	11.49	11.13	11.02	11.07	11.10	1.08	down	5.58E-01	8.95E-01	-	-
1379375_at	Pdgfa	Platelet derived growth factor alpha polypeptide	25260	Rn.10999	BE100812	3.54	3.87	3.34	4.06	3.46	3.55	1.08	up	6.71E-01	9.01E-01	-	-
1388837_at	Slc44a2	solute carrier family 44, member 2	363024	Rn.140320	AI408306	2.47	2.64	2.46	2.49	2.95	2.46	1.08	up	5.46E-01	8.95E-01	-	-
1374187_at	---	---	---	---	AI233361	2.45	2.47	2.53	2.80	2.46	2.54	1.08	up	3.49E-01	8.95E-01	-	-
1384451_at	---	---	---	Rn.161443	BE116574	5.62	6.08	6.94	6.08	5.54	6.69	1.08	down	8.38E-01	9.49E-01	-	-
1387530_a_at	Fosb /// Fosl2	FBJ osteosarcoma oncogene B /// fos-like antigen 2	25446 /// 308411	Rn.163577	NM_012954	2.74	3.37	3.00	2.82	3.84	2.79	1.08	up	7.90E-01	9.32E-01	-	-
1371231_at	Sptbn1	spectrin, beta, non-erythrocytic 1	305614	Rn.93208	AJ242018	3.14	3.13	3.19	3.13	3.15	2.84	1.08	down	3.39E-01	8.95E-01	-	-
1372204_at	Elk4	ELK4, member of ETS oncogene family	304786	Rn.204345	BM391843	6.00	6.75	8.40	7.73	6.85	6.91	1.08	up	8.91E-01	9.66E-01	-	-
1376141_at	---	---	---	Rn.146754	BF394672	4.25	4.51	3.32	4.25	3.09	4.40	1.08	down	8.49E-01	9.53E-01	-	-
1379501_at	---	---	---	Rn.203652	AA963993	2.46	2.44	2.47	2.80	2.46	2.45	1.08	up	3.83E-01	8.95E-01	-	-
1388789_at	RGD1563325	similar to hypothetical protein MGC17943	362857	Rn.19351	AI410352	5.66	5.71	6.99	6.07	5.40	7.22	1.08	up	8.79E-01	9.63E-01	-	-
1393450_at	---	---	---	Rn.202748	BI292896	6.26	6.31	6.67	5.79	6.68	6.45	1.08	down	7.26E-01	9.13E-01	-	-
1368252_at	Kbtbd10	kelch repeat and BTB (POZ) domain containing 10	117537	Rn.28875	NM_057191	2.46	2.74	3.90	3.32	2.76	2.68	1.08	down	8.30E-01	9.46E-01	-	-
1376578_at	Ehmt1	euchromatic histone-lysine N-methyltransferase 1	362078	Rn.7645	BM389055	4.41	4.42	4.30	4.42	4.43	4.60	1.08	up	1.89E-01	8.95E-01	-	-
1371438_at	---	---	---	Rn.1929	BE113144	5.57	5.83	5.96	6.00	5.86	5.83	1.08	up	4.33E-01	8.95E-01	-	-
1369791_at	Clcn4-2	chloride channel 4-2	60586	Rn.44406	NM_022198	2.33	2.29	2.31	2.39	2.57	2.31	1.08	up	2.32E-01	8.95E-01	-	-
1371564_at	Atp6v1e1	ATPase, H+ transporting, lysosomal V1 subunit E1	297566	Rn.103171	AI169159	7.97	8.00	7.40	7.64	8.04	8.02	1.08	up	6.61E-01	8.98E-01	-	-
1388653_at	Sin3b	SIN3 homolog B, transcription regulator (yeast)	683381	Rn.216472	AA849552	3.73	3.26	3.64	4.04	3.10	3.82	1.08	up	7.45E-01	9.18E-01	-	-
1395600_at	Ccdc117	Coiled-coil domain containing 117	498404	Rn.20128	AI227694	2.48	2.52	2.34	2.34	2.34	2.33	1.08	down	1.21E-01	8.95E-01	-	-
1372150_at	Usp10	ubiquitin specific peptidase 10	307905	Rn.24862	AI229488	9.81	10.43	9.82	9.96	9.93	10.50	1.08	up	7.09E-01	9.09E-01	-	-
1398513_at	---	---	---	Rn.25315	AI556479	3.49	3.65	3.66	3.66	3.79	3.69	1.08	up	1.86E-01	8.95E-01	-	-
1368388_at	Maf	v-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian)	54267	Rn.10726	NM_019318	2.69	2.51	2.52	2.57	2.43	2.38	1.08	down	2.37E-01	8.95E-01	-	-
1390074_at	Nup214	nucleoporin 214	296634	Rn.101794	BE111736	2.55	2.54	2.55	2.54	2.22	2.54	1.08	down	3.51E-01	8.95E-01	-	-
1371624_at	Zc3h7b	zinc finger CCCH-type containing 7B	315158	Rn.91605	AW142595	5.87	6.41	6.19	6.16	5.94	6.71	1.08	up	7.10E-01	9.09E-01	-	-
1383843_at	Hlcs	holocarboxylase synthetase (biotin-(propriony-Coenzyme A-carboxylase (ATI	288240	Rn.17293	AA945568	3.16	3.83	3.16	3.45	3.23	3.15	1.08	down	6.70E-01	9.00E-01	-	-
1391899_at	---	---	---	Rn.165121	BI303858	7.51	8.07	8.19	7.85	7.32	8.28	1.08	down	7.66E-01	9.23E-01	-	-
1375579_at	LOC690871	hypothetical protein LOC690871	690871	Rn.41151	BG377374	8.79	9.29	9.34	9.27	9.10	9.37	1.08	up	5.95E-01	8.95E-01	-	-
1393568_at	Cugbp1	CUG triplet repeat, RNA binding protein 1	362160	Rn.203134	BF404793	6.94	7.68	8.83	7.45	8.15	7.51	1.08	down	8.62E-01	9.57E-01	-	-
1382082_at	Nfyb	nuclear transcription factor Y beta	25336	Rn.90077	AI145337	4.98	4.49	4.51	3.59	4.54	5.52	1.08	down	8.58E-01	9.55E-01	-	-
1372731_at	Rhot1 /// Rnf135	ras homolog gene family, member T1 /// ring finger protein 135	303350 /// 303351	Rn.7462	AI228628	7.10	7.82	7.78	7.30	7.31	7.75	1.08	down	7.11E-01	9.09E-01	-	-
1377745_at	Lrrc40	leucine rich repeat containing 40	310946	Rn.106141	BE349673	3.16	3.86	3.14	3.16	3.25	4.10	1.08	up	7.86E-01	9.31E-01	-	-
1394932_at	---	---	---	Rn.170066	AW534255	5.49	4.57	4.24	4.38	5.49	4.76	1.08	up	8.34E-01	9.47E-01	-	-
1382333_at	Ifk /// RGD1560962	riboflavin kinase /// similar to RIKEN cDNA 0610038L10 gene	311241 /// 499328	Rn.145048	AI180421	8.75	8.91	8.60	8.85	8.86	8.88	1.08	up	2.86E-01	8.95E-01	-	-
1383964_at	Ankrd50	ankyrin repeat domain 50	294988	Rn.7482	AI549551	3.02	2.87	3.18	3.38	2.65	2.72	1.08	down	6.81E-01	9.03E-01	-	-
1388672_at	Zcchc24	zinc finger, CCHC domain containing 24	361104	Rn.219261	AI101373	2.29	2.61	2.30	2.29	2.30	2.28	1.08	down	3.51E-01	8.95E-01	-	-
1370516_at	Slc15a3	solute carrier family 15, member 3	246239	Rn.17317	AB026995	2.39	2.70	2.40	2.39	2.40	2.38	1.08	down	3.40E-01	8.95E-01	-	-
1374019_at	RGD1564379	RGD1564379	499758	Rn.7256	BF284939	5.77	4.95	4.79	5.72	4.63	5.49	1.08	up	8.17E-01	9.41E-01	-	-
1371619_at	RGD1310352	similar to HTGN29 protein; keratinocytes associated transmembrane protein 2	303122	Rn.106999	BI296718	8.75	9.22	9.62	9.35	9.27	9.30	1.08	up	6.83E-01	9.03E-01	-	-
1395038_at	Ccdc101	Coiled-coil domain containing 101	293488	Rn.34983	BI279631	2.44	2.45	3.30	2.46	2.47	2.94	1.08	down	7.51E-01	9.19E-01	-	-
1395861_at	LOC688535	hypothetical protein LOC688535	688535	Rn.18562	BG379884	2.40	2.40	2.45	2.79	2.40	2.38	1.08	up	4.59E-01	8.95E-01	-	-
1367585_a_at	Atp1a1	ATPase, Na+/K+ transporting, alpha 1 polypeptide	24211	Rn.2992	M28647	11.00	10.81	10.88	10.83	10.75	10.78	1.08	down	1.37E-01	8.95E-01	-	-
1385014_at	BC683238 /// Nudt	similar to Diphosphoinositol polyphosphate phosphohydrolase 3 alpha (DIPP-6	680248 /// 683238	Rn.153531	BG377996	2.59	2.54	2.64	2.59	3.01	2.51	1.08	up	5.23E-01	8.95E-01	-	-
1372360_at	Abi1	abl-interactor 1	79249	Rn.43675	AA817862	5.99	6.31	6.51	6.00	5.89	6.60	1.08	down	7.00E-01	9.07E-01	-	-
1388933_at	---	---	---	Rn.8858	AI233748	4.44	4.28	4.33	3.89	4.48	4.34	1.08	down	5.82E-01	8.95E-01	-	-
1370588_a_at	Slc8a1	solute carrier family 8 (sodium/calcium exchanger), member 1	29715	Rn.118972	U04933	2.77	2.39	2.45	2.41	2.44	2.43	1.08	down	3.99E-01	8.95E-01	-	-
1373106_at	Zfp362	zinc finger protein 36, C3H type-like 2	298765	Rn.22055	AI178069	8.54	8.88	8.23	8.21	8.56	8.56	1.08	down	6.44E-01	8.95E-01	-	-
1373531_at	Cpsf1	cleavage and polyadenylation specific factor 1	366952	Rn.40455	AI600198	2.99	3.00	3.00	3.34	2.98	3.00	1.08	up	3.96E-01	8.95E-01	-	-
1391423_at	Hsf2	Heat shock factor 2	64441	Rn.163428	AA944812	4.90	5.15	5.24	4.60	5.12	5.23	1.08	down	6.42E-01	8.95E-01	-	-
1379258_at	Klhl5	kelch-like 5 (Drosophila)	305351	Rn.13334	AA998367	2.49	2.68	2.69	2.68	2.69	2.82	1.08	up	2.33E-01	8.95E-01	-	-
1398699_at	---	---	---	Rn.51667	BE109091	2.39	2.68	2.41	2.38	2.39	2.38	1.08	down	3.09E-01	8.95E-01	-	-
1371350_at	Mat2a	methionine adenosyltransferase II, alpha	171347	Rn.144658	AI412159	11.32	11.63	11.16	11.36	11.50	11.59	1.08	up	5.15E-01	8.95E-01	-	-
1379220_at	---	---	---	Rn.29878	AI764398	2.48	3.27	2.47	2.46	2.45	2.98	1.08	down	7.46E-01	9.18E-01	-	-
1385809_at	---	---	---	---	AA996771	3.79	4.36	4.30	3.72	4.77	4.29	1.08	up	7.70E-01	9.25E-01	-	-
1368042_a_at	3681718 /// RGD1	high-mobility group (nonhistone chromosomal) protein 1-like 1 /// high mobility	0 /// 678705 /// 67	Rn.4121	AF275734	11.33	11.35	11.51	11.32	11.61	11.60	1.08	up	3.76E-01	8.95E-01	-	-
1370226_at	Cstb	cystatin B (stefin B)	25308	Rn.1233	AI409867	9.14	9.17	9.08	8.97	9.31	9.43	1.08	up	4.80E-01	8.95E-01	-	-
1368058_at	Safb	scaffold attachment factor B	64198	Rn.88640	NM_022394	5.21	6.23	7.17	7.09	5.59	5.60	1.08	down	8.91E-01	9.66E-01	-	-
1382210_at	LOC302495	hypothetical LOC302495	302495	Rn.204468	BE117392	4.02	5.06	4.81	4.39	4.09	5.08	1.08	down	8.10E-01	9.39E-01	-	-
1371468_at	LOC312502	similar to RAB11 family interacting protein 5 (class I) isoform 1	312502	Rn.3496	BI296378	7.23	6.93	7.55	7.89	6.83	6.66	1.08	down	8.07E-01	9.38E-01	-	-
1371320_at	Itm2b	integral membrane protein 2B	290364	Rn.107335	BF282337	10.61	10.75	10.62	10.34	10.58	10.73	1.08	down	4.13E-01	8.95E-01	-	-
1374777_at	LOC502894	hypothetical protein LOC502894	502894	Rn.15200	BG380800	3.14	2.88	2.42	2.88	3.31	2.57

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1373105_at	Tmed1	transmembrane emp24 protein transport domain containing 1	315461	Rn.162983	BG375429	3.12	3.12	2.86	2.72	3.51	3.20	1.08	up	6.80E-01	9.03E-01	-	-
1382426_at	Psma7	Proteasome (prosome, macropain) subunit, alpha type 7	29674	Rn.105784	AA997406	7.59	7.59	7.65	7.72	7.89	7.55	1.08	up	3.39E-01	8.95E-01	-	-
1371995_at	Klhl21	kelch-like 21 (Drosophila)	313743	Rn.87563	AI599225	2.66	2.65	2.54	2.86	2.66	2.66	1.08	up	2.34E-01	8.95E-01	-	-
1399165_a_at	Ccdc97	coiled-coil domain containing 97	292724	Rn.44186	AA943500	8.20	8.78	7.50	7.28	8.29	7.23	1.08	up	8.49E-01	9.53E-01	-	-
1377671_at	---	---	---	Rn.164677	BI279816	10.23	10.32	10.17	10.56	9.73	10.76	1.08	up	7.49E-01	9.19E-01	-	-
1384659_at	---	---	---	---	AI058540	3.04	3.06	5.58	3.39	3.74	4.22	1.08	down	9.07E-01	9.72E-01	-	-
1392696_at	---	---	---	Rn.6558	BF288234	2.35	2.35	2.35	2.68	2.35	2.34	1.08	up	3.77E-01	8.95E-01	-	-
1394493_at	---	---	---	Rn.206251	AW524359	3.50	3.89	3.81	3.98	3.44	3.47	1.08	down	6.33E-01	8.95E-01	-	-
1380840_at	---	---	---	Rn.210976	BF412081	2.48	2.48	2.79	2.47	2.50	2.45	1.08	down	3.53E-01	8.95E-01	-	-
1373283_at	---	---	---	Rn.203323	BE113158	3.00	3.13	4.10	3.00	3.85	3.71	1.08	up	8.16E-01	9.41E-01	-	-
1398510_at	Gapvd1	GTPase activating protein and VPS9 domains 1	311880	Rn.22293	BI295013	3.51	3.49	3.54	3.74	3.33	3.79	1.08	up	4.99E-01	8.95E-01	-	-
1373591_at	Arfip2	ADP-ribosylation factor interacting protein 2	293344	Rn.73878	BG375435	3.91	3.92	3.73	3.92	4.05	3.91	1.08	up	2.25E-01	8.95E-01	-	-
1368709_at	Fut1	fucosyltransferase 1 (galactoside 2-alpha-L-fucosyltransferase)	81919	Rn.11382	NM_031236	2.38	2.37	2.39	2.38	2.39	2.71	1.08	up	3.70E-01	8.95E-01	-	-
1367461_at	Copb1	coatomer protein complex, subunit beta 1	114023	Rn.4327	NM_080781	8.36	7.86	8.28	8.31	8.13	8.38	1.08	up	5.64E-01	8.95E-01	-	-
1376135_at	Dars2	aspartyl-tRNA synthetase 2 (mitochondrial)	304919	Rn.137838	BI294730	3.07	3.72	2.82	2.88	3.07	3.33	1.08	down	7.33E-01	9.15E-01	-	-
1371736_at	RGD1565192	similar to 1810013D10Rik protein	501923	Rn.3288	AI411283	8.03	8.44	8.01	7.94	8.17	8.70	1.08	up	7.02E-01	9.07E-01	-	-
1380771_at	---	---	---	Rn.208275	BM385539	2.73	2.40	2.43	2.41	2.43	2.39	1.08	down	3.65E-01	8.95E-01	-	-
1368056_at	Tsc2	tuberous sclerosis 2	24855	Rn.5875	U24150	4.90	6.73	6.11	6.13	5.69	6.25	1.08	up	8.57E-01	9.55E-01	-	-
1376384_at	Dusp19	dual specificity phosphatase 19	311151	Rn.65563	BE111118	3.53	3.22	3.23	3.22	3.21	3.22	1.08	down	3.54E-01	8.95E-01	-	-
1382018_at	Fam113a	family with sequence similarity 113, member A	296158	Rn.31861	AA999062	3.51	3.47	3.71	3.47	4.12	3.42	1.08	up	6.74E-01	9.01E-01	-	-
1394487_at	---	---	---	Rn.29945	AW526344	3.51	3.05	3.71	3.53	3.54	3.52	1.08	up	6.07E-01	8.95E-01	-	-
1378230_at	---	---	---	Rn.205411	AI575447	2.75	2.47	2.51	2.47	2.50	2.44	1.08	down	2.99E-01	8.95E-01	-	-
1376430_at	---	---	---	Rn.163649	AA925921	7.44	7.71	7.59	7.25	7.59	7.58	1.08	down	4.69E-01	8.95E-01	-	-
1374820_at	---	---	---	Rn.43962	AI598946	5.51	6.08	7.50	6.22	5.97	6.58	1.08	down	8.69E-01	9.59E-01	-	-
1383120_at	Arsk	arylsulfatase family, member K	365619	Rn.202360	BE107993	4.76	3.52	3.67	3.68	3.78	4.16	1.08	down	8.09E-01	9.38E-01	-	-
1373221_at	Diaph1	Diaphanous homolog 1 (Drosophila)	307483	Rn.3004	BI278478	4.78	4.97	4.84	4.83	4.88	5.19	1.08	up	4.36E-01	8.95E-01	-	-
1372767_at	h168b /// LOC503	family with sequence similarity 168, member B /// similar to Protein KIAA0280	503175 /// 690188	Rn.120228	AI231284	6.76	7.18	7.07	7.01	6.68	7.00	1.08	down	5.53E-01	8.95E-01	-	-
1368460_at	Slc2a5	solute carrier family 2 (facilitated glucose/fructose transporter), member 5	65197	Rn.10900	NM_031741	7.70	8.19	7.95	7.49	7.97	8.06	1.08	down	6.59E-01	8.98E-01	-	-
1373378_at	Agtpbp1	ATP/GTP binding protein 1	290986	Rn.33035	BF410522	6.58	6.29	6.56	6.92	5.42	6.75	1.08	down	8.34E-01	9.47E-01	-	-
1371321_at	Cox6b1	cytochrome c oxidase, subunit VIb polypeptide 1	502592	---	AI230604	10.70	10.85	10.98	10.77	10.77	10.67	1.08	down	2.83E-01	8.95E-01	-	-
1389004_at	Josd2	Josephin domain containing 2	292876	Rn.22861	BG868333	5.30	5.32	5.53	5.37	5.21	5.25	1.08	down	2.77E-01	8.95E-01	-	-
1371008_at	Pmpca	peptidase (mitochondrial processing) alpha	296588	Rn.11175	BE099971	8.79	8.46	8.41	8.63	8.27	8.43	1.08	down	5.31E-01	8.95E-01	-	-
1373199_at	Gla	galactosidase, alpha	363494	Rn.98982	AA943573	3.15	2.87	2.89	2.80	2.66	3.11	1.08	down	5.31E-01	8.95E-01	-	-
1385132_at	---	---	---	Rn.15847	AI044253	6.25	8.90	9.33	8.27	7.81	8.07	1.08	down	9.17E-01	9.75E-01	-	-
1367837_at	Psma4	proteasome (prosome, macropain) subunit, alpha type 4	29671	Rn.11076	NM_017281	7.53	7.67	7.70	7.50	7.17	7.91	1.08	down	6.50E-01	8.96E-01	-	-
1377700_at	Atrx	alpha thalassemia/mental retardation syndrome X-linked (RAD54 homolog, S	246284	Rn.107838	BE111648	6.28	6.07	5.92	5.76	5.88	6.32	1.08	down	6.19E-01	8.95E-01	-	-
1396965_at	---	---	---	Rn.211124	BF406350	2.42	2.41	2.45	2.42	2.81	2.38	1.08	up	4.72E-01	8.95E-01	-	-
1394659_at	---	---	---	---	BF289445	2.49	2.50	2.50	2.48	2.87	2.46	1.08	up	4.67E-01	8.95E-01	-	-
1377655_at	Fgf12	Fibroblast growth factor 12	170630	Rn.45965	BF562838	2.57	2.54	2.65	2.54	3.01	2.53	1.08	up	5.36E-01	8.95E-01	-	-
1383379_at	LOC684112	similar to KIAA0999 protein	684112	Rn.216596	AI059153	3.67	3.74	3.57	3.82	3.65	3.84	1.08	up	2.37E-01	8.95E-01	-	-
1387062_a_at	Chek1	CHK1 checkpoint homolog (S. pombe)	140583	Rn.33267	NM_080400	2.47	2.80	2.48	2.43	2.49	2.50	1.08	down	3.81E-01	8.95E-01	-	-
1382062_at	Gstcd	glutathione S-transferase, C-terminal domain containing	310855	Rn.38009	AA943385	4.69	4.18	2.75	3.54	2.60	5.82	1.08	up	9.28E-01	9.79E-01	-	-
1380963_at	---	---	---	Rn.146601	BE121320	2.35	2.34	2.35	2.35	2.36	2.65	1.08	up	3.39E-01	8.95E-01	-	-
1372058_at	---	---	---	---	AI177914	8.74	8.73	8.68	8.89	8.36	8.57	1.08	down	5.26E-01	8.95E-01	-	-
1379657_at	---	---	---	Rn.144180	BE107438	7.33	5.04	5.93	5.78	6.30	5.90	1.08	down	8.82E-01	9.64E-01	-	-
1389271_at	Vasn	vasorin	679921	Rn.198255	BI274567	3.51	3.47	3.38	3.51	2.96	3.56	1.08	down	6.09E-01	8.95E-01	-	-
1376270_at	---	---	---	Rn.129183	AI059493	8.95	8.78	8.64	9.01	8.99	8.70	1.08	up	4.88E-01	8.95E-01	-	-
1377667_at	Rtf1	Rtf1, Paf1/RNA polymerase II complex component, homolog (S. cerevisiae)	366169	Rn.22569	AW141706	6.33	5.49	5.51	5.32	6.18	6.14	1.08	up	7.97E-01	9.34E-01	-	-
1367814_at	Atp1b1	ATPase, Na+/K+ transporting, beta 1 polypeptide	25650	Rn.8925	AI232036	11.37	11.38	11.50	11.52	11.48	11.56	1.08	up	8.54E-02	8.95E-01	-	-
1384339_s_at	Csnk2a1	casein kinase 2, alpha 1 polypeptide	116549	Rn.4231	BF288177	9.84	10.24	9.77	10.34	8.96	10.23	1.08	down	8.28E-01	9.46E-01	-	-
1394876_at	---	---	---	---	AI454929	2.71	2.42	2.44	2.41	2.43	2.40	1.08	down	3.22E-01	8.95E-01	-	-
1377439_at	679830 /// RGD13	hypothetical protein LOC679830 /// similar to hypothetical protein FLJ13231	310137 /// 679830	Rn.207007	BF408617	3.00	2.81	2.77	2.75	2.77	2.73	1.08	down	2.12E-01	8.95E-01	-	-
1388908_at	Peci	peroxisomal D3,D2-enoyl-CoA isomerase	291075	Rn.108029	BI278268	8.61	9.32	8.55	8.33	8.69	9.12	1.08	down	7.66E-01	9.23E-01	-	-
1388194_at	Dlat	dihydrolipoamide S-acetyltransferase	81654	Rn.15413	BI295900	8.26	8.56	8.24	8.39	8.14	8.86	1.08	up	6.70E-01	9.00E-01	-	-
1388461_at	---	---	---	---	AI639079	2.95	2.67	2.69	2.68	2.68	2.62	1.08	down	2.98E-01	8.95E-01	-	-
1393006_at	---	---	---	Rn.166773	BF282112	6.56	6.27	6.11	6.50	5.25	6.87	1.08	down	8.41E-01	9.50E-01	-	-
1382388_at	Tmem143	transmembrane protein 143	308593	Rn.48200	AW533941	5.46	5.69	5.29	5.54	5.35	5.22	1.08	down	5.07E-01	8.95E-01	-	-
1379889_at	Rc3h2	Ring finger and CCCH-type zinc finger domains 2	311909	Rn.134067	AI071930	4.44	5.48	5.16	4.80	4.92	5.04	1.08	down	7.48E-01	9.18E-01	-	-
1385719_at	---	---	---	Rn.149950	AW531176	3.62	4.09	4.58	3.91	3.92	4.79	1.08	up	8.02E-01	9.38E-01	-	-
1375600_at	Pigo	phosphatidylinositol glycan anchor biosynthesis, class O	313341	Rn.123611	AI535065	2.44	2.40	2.43	2.43	2.46	2.70	1.08	up	2.82E-01	8.95E-01	-	-
1383543_at	Golt1b	golgi transport 1 homolog B (S. cerevisiae)	362460	Rn.1895	AW918220	4.21	4.81	4.52	5.27	3.14	4.80	1.08	down	8.80E-01	9.63E-01	-	-
1379861_at	Dcakd	dephospho-CoA kinase domain containing	360839	Rn.102152	BE107793	2.48	2.48	2.49	2.48	2.49	2.81	1.08	up	3.69E-01	8.95E-01	-	-
1382068_at	Tulp4	tubby like protein 4	499016	Rn.198109	AA963991	4.26	4.88	6.36	5.06	4.68	5.43	1.08	down	8.78E-01	9.62E-01	-	-
1373537_at	---	---	---	Rn.204287	BE113175	3.52	3.23	3.17	3.21	3.17	3.21	1.08	down	3.73E-01	8.95E-01	-	-
1386709_at	---	---	---	Rn.13039	AW916606	2.74	2.74	2.83	2.77	2.77	3.11	1.08	up	4.11E-01	8.95E-01	-	-
1389406_at	rCG_40784	chromosome 1 open reading frame, human C6orf35	292228	Rn.18853	BI296349	8.17	7.34	7.58	8.01	7.62	7.14	1.08	down	7.74E-01	9.26E-01	-	-
1395818_at	LOC499110	similar to Zinc finger protein 354A (Transcription factor 17) (Renal transcriptio	499110	Rn.161813	BF542853	2.99	2.96	3.02	3.32	2.98	2.99	1.08	up	3.90E-01	8.95E-01	-	-
1393744_at	Tssk2	testis-specific serine kinase 2	304181	Rn.163190	BE110023	2.54	2.83	2.54	2.53	2.58	2.49	1.08	down	3.32E-01	8.95E-01	-	-
1388817_at	Fam63a	family with sequence similarity 63, member A	310665	Rn.7768	BI284848	3.03	3.02	3.43	3.02	3.10	3.03	1.08	down	4.80E-01	8.95E-01	-	-
1393893_at	Morn5	MORN repeat containing 5	362122	Rn.57435	BF404146	2.43	2.41	2.44	2.42	2.77	2.41	1.08	up	4.18E-01	8.95E-01	-	-
1387399_at	Pclo	piccolo (presynaptic cytomatrix protein)	56768	Rn.53925	AF138789	2.83	2.55	2.59	2.56	2.56	2.53	1.08	down	2.92E-01	8.95E-01	-	-
1380232_at	---	---	---	---	BE119516	6.23	6.87	6.14	6.05	5.63	7.24	1.08	down	8.50E-01	9.53E-01	-	-
1379644_at	LOC686506	hypothetical protein LOC686506	686506	Rn.34277	BE100978	2.72	3.02	2.73	2.72	2.72	2.71	1.08	down	3.33E-01	8.95E-01	-	-
1371217_at	Apex1	APEX nuclease (multifunctional DNA repair enzyme) 1	79116	Rn.5949	AF311054	5.37	4.36	7.93	5.39	6.77	5.82	1.08	up	9.29E-01	9.80E-01	-	-
1372191_at	---	---	---	Rn.165910	BI303656	3.40	3.40	3.41	3.40	3.63	3.73	1.08	up	3.78E-01	8.95E-01	-	-
1388195_at	Cugbp2	CUG triplet repeat, RNA binding protein 2	29428	Rn.162247	AW140475	5.45	5.12	4.57	3.51	5.61	5.69	1.08	down	8.94E-01	9.67E-01	-	-
1398377_at	Znf672	zinc finger protein 672	303165	Rn.143913	AI172116	2.77	2.77	2.79	2.99	2.70	2.96	1.08	up	3.08E-01	8.95E-01	-	-
1372651_at	---	---	---	Rn.203069	AI144726	2.57	2.49	2.39	2.55	2.59	2.63	1.08	up	1.26E-01	8.95E-01	-	-
1380042_at	---	---	---	---	AA864012	2.63	2.44	2.49	2.45	2.35	2.44	1.08	down	1.73E-01	8.95E-01	-	-
1370313_at	Acot7	acyl-CoA thioesterase 7	26759	Rn.6024	D88891	5.75	5.95	4.03	5.36	4.00	6.05	1.08	down	9.06E-01	9.71E-01	-	-
1388648_at	---	---	---	Rn.103327	AA799764	4.43	5.89	6.21	5.43	5.39	6.04	1.08	up	8.64E-01	9.58E-01	-	-
1392739_a_at	Eepd1	endonuclease/exonuclease/phosphatase family domain containing 1	315500	Rn.110716	AI454794	5.08	4.10	4.08	5.41	4.08	4.09	1.08	up	8.55E-01	9.55E-01	-	-
1392596_at	---	---	---	Rn.19996	BF420447	2.57	2.67	2.77	2.82	2.55	2.96	1.08	up	4.64E-01	8.95E-01	-	-
1369134_x_at	Kcnc3	potassium voltage gated channel, Shaw-related subfamily, member 3	117101	Rn.9885	NM_053997	2.78	2.58	2.79	2.94	2.78	2.76	1.08	up	2.95E-01	8.95E-01	-	-
1387885_at	Fcgrt	Fc fragment of IgG, receptor, transporter, alpha	29558	Rn.15845	BE110597	6.82	7.22	6.55	6.99	6.74	7.20	1.08	up	6.71E-01	9.00E-01	-	-
1393724_at	Spata1	spermatogenesis associated 1	362056	Rn.207388	BE113911	6.42	7.46	8.13	7.65	7.13	7.55	1.08	up	8.47E-01	9.52E-01	-	-
1371485_at	---	---	---	---	BI283695	2.63	2.35	2.38	2.34	2.35	2.35	1.08	down	2.98E-01	8.95E-01	-	-
1390072_at	Fibp	fibroblast growth factor (acidic) intracellular binding protein	282837	Rn.18229	BI283002	5.83	6.19	5.95	6.28	5.73	6.28	1.08	up	6.36E-01	8.95E-01	-	-
1380166_at	---	---	---	Rn.50095	BE101632	2.54	2.78	2.54	2.53	2.53	2.49	1.08	down	2.52E-01	8.95E-01	-	-
1395901_at	---	---	---	Rn.220678	AW532049	5.61	6.06	5.87	5.89	5.81	6.17	1.08	up	5.61E-01	8.95E-01	-	-
1391677_at	Ifnar1	Interferon (alpha, beta and omega) receptor 1	288264	Rn.105738	AA900818	3.12	3.21	3.31	2.56	3.65	3.75	1.08	up	7.94E-01	9.34E-01	-	-
1368934_at	cyp4a1 /// Cyp4a1	cytochrome P450, family 4, subfamily a, polypeptide 1 /// cytochrome P450, fa	170544 /// 50549	Rn.92401	NM_016999	5.25	5.80	5.03	5.51	4.63	5.61	1.08	down	7.95E-01	9.34E-01	-	-
1397169_at	---	---	---	---	BF283075	2.43	2.38	2.40	2.76	2.40	2.37	1.08	up	4.41E-01	8.95E-01	-	-
1376016_at	RGD1311660	similar to RIKEN cDNA 1110007L15	288518	Rn.102176	BF285425	6.35	5.95	5.77	6.00	5.93	6.46	1.08	up	6.81E-01	9.03E-01	-	-
1397812_at	Senp6	SUMO/sentrin specific peptidase 6	300860	Rn.98553	H32530	5.49	5.08	5.78	4.94	5.25	5.84	1.08	down	7.65E-01	9.23E-01	-	-
1390426_at	Notch1	Notch homolog 1, translocation-associated (Drosophila)	25496	Rn.25046	BF389398	2.60	2.90	2.28	2.35	2.36	2.76	1.08	down	6.60E-01	8.98E-01	-	-
1369472_a_at	Atf2	activating transcription factor 2	81647	Rn.9825	NM_031018	5.91	4.28	4.42	5.41	4.66	4.85	1.08	up	8.60E-01	9.57E-01	-	-
1398596_at	---	---	---	Rn.3832	AA925896	4.87	4.94	5.72	5.03	4.86	5.33	1.08	down	7.44E-01	9.17E-01	-	-
1376881_at	---	---	---	Rn.11259	AW528057	2.41	2.39	2.41	2.40	2.42	2.70	1.08	up	3.37E-01	8.95E-01	-	-
1398848_at	St13	suppression of tumorigenicity 13	81800	Rn.8756	BG377057	9.60	10.00	10.11	9.80	9.96	10.26	1.08	up	8.29E-01	8.95E-01	-	-
1396586_at	---	---	---	Rn.205404	AI764632	2.88	2.63	2.86	2.67	2.82	2.56	1.08	down	3.79E-01	8.95E-01	-	-
1398098_at	---	---	---	Rn.206115	AW522192	2.65	2.32	2.41	2.34	2.39	2.33	1.08	down	3.53E-01	8.95E-01	-	-
1383736_at	Fancl	Fanconi anemia, complementation group L	305600	Rn.82534	BI274202	3.77	3.79	4.62	3.28	4.76	3.83	1.08	down	8.46E-01	9.52E-01	-	-
1373711_at	Orc5l	origin recognition complex, subunit 5-like (yeast)	362304	Rn.137519	BI296681	2.97	2.97	2.88	2.79	2.83	2.88	1.08	down	5.38E-02	8.95E-01	-	-
1373672_at	Serpinb9	Serine (or cysteine) peptidase inhibitor, clade B, member 9	361241	Rn.95177	BM384419	2.29	2.28	2.60	2.29	2.29	2.28	1.08	down	3.73E-01	8.95E-01	-	-
1385681_at	MGC94542	similar to RIKEN cDNA 5430437P03	290631	Rn.74107	BG868520	3.32	3.33	3.19	3.32	3.16	3.68	1.08	up	5.46E-01	8.95E-01	-	-
1388319_at	---	---	---	Rn.207992	BE108642	2.46	2.81	2.61	2.45	2.49	2.60	1.08	down	3.87E-01	8.95E-01	-	-
1370331_at	Il11ra1	interleukin 11 receptor, alpha chain 1	245983	Rn.29849	AF347936	5.64	6.37	4.27	5.60	5.54	5.47	1.08	up	8.71E-01	9.60E-01	-	-
1376411_at	Arl13b	ADP-ribosylation factor-like 13B	304037	Rn.30700	BE107062	2.83	2.83	4.01	2.75	3.75	2.85	1.08	down	8.44E-01	9.51E-01	-	-
1378741_at	LOC684441	similar to Peptidyl-prolyl cis-trans isomerase NIMA-interacting 4 (Rotamase P	684441	---	BE106252	9.30	9.28	9.32	9.28	9.32	9.61	1.08	up	3.69E-01	8.95E-01	-	-
1372873_at	Fbxo38	F-box protein 38	307390	Rn.13347	BM385705	3.65	3.97	3.56	3.43	3.64	4.43	1.08	up	7.61E-01	9.22E-01	-	-
1395708_at	---	---	---	---	BF288845	2.41	2.71	2.42	2.39	2.41	2.42	1.08	down	3.39E-01	8.95E-01	-	-
1373433_at	Nsbp1	nucleosomal binding protein 1	681284	Rn.25395	BE108745	6.70	6.74	5.62	5.43	6.86	6.46	1.08	down	8.59E-01	9.56E-01	-	-
1394715_at	Dicer1	dicer 1, ribonuclease type III	299284	Rn.205881	AI406925	2.60	2.48	3.21	2.95	2.51	2.52	1.08	down	7.12E-01	9.10E-01	-	-
1392694_at	RGD1562344	similar to Gm566 protein	295337	Rn.44158	AW526101	3.99	3.56	3.50	3.50	3.53	3.70	1.08	down	5.51E-01	8.95E-01	-	-
1383759_at	Agtpbp1	ATP/GTP binding protein 1	290986	Rn.33035	BF553179	5.78	5.21	4.46	5.52	5.20	5.05	1.08	up	8.07E-01	9.38E-01	-	-
1371580_at	Erlin1	ER lipid raft associated 1	293939	Rn.3674	AI102725	7.54	8.07	8.53	7.53	7.70	8.59	1.08	down	8.19E-01	9.42E-01	-	-
1398144_at	---	---	---	Rn.154184	BF406256	2.34	2.33	2.34	2.33	2.67	2.32	1.08	up	4.00E-01	8.95E-01	-	-
1371679_at	Sympo2	synaptopodin 2	499702	Rn.205751	BE113393	2.75	2.75	2.75	3.08	2.74	2.74	1.08	up	4.05E-01	8.95E-01	-	-
1374983_at	RGD1561676	similar to Ketch domain containing 4	307917	Rn.67594	BI289414	5.74	6.27	6.21	5.66	6.14	6.11	1.08	down	6.66E-01	8.96E-01	-	-
1388380_at	Samm50	sorting and assembly machinery component 50 homolog (S. cerevisiae)	300111	Rn.12611	BI278122	7.75	8.05	8.09	7.88	8.27	8.05	1.08	up	5.28E-01	8.95E-01	-	-
1369528_at	Smad3	SMAD family member 3	25631	Rn.10636	NM_013095	2.33	2.64	2.34	2.33	2.33	2.32	1.08	down	3.48E-01	8.95E-01	-	-
1374347_at	Cdkal1	CDK5 regulatory subunit associated protein 1-like 1	361243	Rn.198339	BF412225	4.00	4.92	4.26	4.62	3.65	4.59	1.08	down	8.13E-01	9.40E-01	-	-
1395399_at	Zcchc17	zinc finger, CCHC domain containing 17	500555	Rn.63831	BM387829	5.96	6.27	5.75	5.73	5.96	5.97	1.08	down	5.64E-01	8.95E-01	-	-
1369262_at	Casp8	caspase 8	64044	Rn.54474	NM_022277	3.57	3.52	3.58	3.48	3.95	3.56	1.08	up	5.10E-01	8.95E-01	-	-
1383918_at	---	---	---	Rn.129479	AI070651	2.42	2.41	2.42	2.68	2.44	2.45	1.08	up	2.48E-01	8.95E-01	-	-
1373530_at	Ccne1	cyclin E1	25729	Rn.15455	AW913890	2.41	2.40	2.42	2.40	2.41	2.73	1.08	up	3.75E-01	8.95E-01	-	-
1384877_at	Aqp11	aquaporin 11	286758	Rn.20144	AI072405	5.35	5.44	5.97	5.15	5.60	5.69	1.08	down	6.99E-01	9.07E-01	-	-
1375791_at	RGD1309821	Similar to KIAA1161 protein	366360	Rn.106115	AW252675	2.48	2.44	2.49	2.60	2.49	2.65	1.08	up	1.00E-01	8.95E-01	-	-
1371960_at	Ythdf2	YTH domain family, member 2	310353	Rn.21737	AI230548	8.12	7.45	7.81	8.01	7.78	7.91	1.08	up	6.30E-01	8.95E-01	-	-
1369634_at	Slc4a1	solute carrier family 4 (anion exchanger), member 1	24779	Rn.32202	BE113640	3.23	2.91	2.72	2.78	2.95	2.81	1.08	down	5.37E-01	8.95E-01	-	-
1392177_at	---	---	---	Rn.209485	BF400937	2.74	2.74	2.74	3.05	3.09	2.40	1.08	up	6.58E-01	8.98E-01	-	-
1372970_at	Shkbp1	Sh3kbp1 binding protein 1	292735	Rn.16376	BM389664	2.52	2.52	2.52	2.52	2.53	2.83	1.08	up	3.56E-01	8.95E-01	-	-
1389156_at	LOC498606	hypothetical protein LOC498606	498606	Rn.822	BM384589	5.11	5.02	4.84	5.29	5.01	4.98	1.08	up	4.54E-01	8.95E-01	-	-
1395391_at	LOC680045	hypothetical protein LOC680045	680045	Rn.64455	BF412774	2.81	2.44	2.48	2.49	2.48	2.45	1.08	down	4.16E-01	8.95E-01	-	-
1388039_a_at	Gabbr1	gamma-aminobutyric acid (GABA) B receptor 1	81657	Rn.30059	AF283276	2.24	2.83	2.24	2.38	2.24	2.37	1.08	down	6.24E-01	8.95E-01	-	-
1374942_at	Cpxm2	carboxypeptidase X (M14 family), member 2	293566	Rn.24920	BI285086	2.40	2.82	2.41	2.39	2.47	2.45	1.08	down	4.97E-01	8.95E-01	-	-
1393627_at	Oaap	ovary-specific acidic protein	689931	Rn.105851	AA957929	2.60	2.57	2.64	2.58	2.68	2.88	1.08	up	3.05E-01	8.95E-01	-	-
1372474_at	Syp1	Synaptophysin-like 1	366595	Rn.17193	AI172184	10.31	10.32	10.55	10.21	10.31	10.35	1.08	down	2.97E-01	8.95E-01	-	-
1395702_at	4g1 /// RGD1562	eukaryotic translation initiation factor 4 gamma,

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)				REG	MTC
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval		
1389763_at	---	---	---	---	BF397229	2.46	2.44	2.48	2.51	2.71	2.45	1.08	up	2.56E-01	8.95E-01	-	-
1390723_at	---	---	---	Rn.205113	BF386742	2.46	2.84	2.49	2.46	2.47	2.53	1.08	down	4.40E-01	8.95E-01	-	-
1376505_at	---	---	---	---	AA819112	2.76	2.67	3.02	2.71	2.72	2.70	1.08	down	3.73E-01	8.95E-01	-	-
1368216_at	Rab28	RAB28, member RAS oncogene family	117049	Rn.4023	NM_053978	8.39	8.39	8.35	8.40	8.35	8.70	1.08	up	3.91E-01	8.95E-01	-	-
1370170_at	Hnrnpu	heterogeneous nuclear ribonucleoprotein U	117280	Rn.4328	AI058964	10.51	10.46	10.42	10.66	10.54	10.50	1.08	up	1.34E-01	8.95E-01	-	-
1381471_at	---	---	---	Rn.21181	AI060117	6.75	7.07	6.08	6.60	7.24	6.38	1.08	up	8.00E-01	9.35E-01	-	-
1375997_at	---	---	---	Rn.3768	AA799503	8.12	8.12	8.08	8.35	6.53	7.02	1.08	up	9.08E-01	9.72E-01	-	-
1373292_at	hai3 /// RGD13116	ORAI calcium release-activated calcium modulator 3 /// similar to KIAA0339 p	309000 /// 309001	Rn.112692	AI176553	3.12	3.43	4.10	4.41	3.12	3.43	1.08	up	8.39E-01	9.50E-01	-	-
1383730_at	Ttc9c	Tetratricopeptide repeat domain 9C	309196	Rn.162477	BG668930	2.76	3.11	3.17	2.95	3.33	3.07	1.08	up	5.69E-01	8.95E-01	-	-
1381487_at	Angpt1	angiopoietin 1	Rn.161953	BF402869	2.55	2.80	2.59	2.54	2.58	2.50	1.08	down	2.72E-01	8.95E-01	-	-
1398476_at	Vcl	vinculin	305679	Rn.164613	AW527349	4.72	4.60	4.60	4.60	4.18	4.82	1.08	down	6.17E-01	8.95E-01	-	-
1392708_at	Stard6	StAR-related lipid transfer (START) domain containing 6	291527	Rn.204855	AI175745	2.44	2.43	2.44	2.44	2.46	2.72	1.08	up	3.12E-01	8.95E-01	-	-
1372234_at	Lix1l	Lix1 homolog (mouse)-like	499677	Rn.3632	AA800950	2.79	4.05	2.74	3.76	2.72	2.77	1.08	down	8.57E-01	9.55E-01	-	-
1373942_at	---	---	---	Rn.2860	BF396312	4.55	4.80	3.40	3.73	4.27	4.44	1.08	down	8.38E-01	9.49E-01	-	-
1381666_at	---	---	---	---	BF411434	2.41	2.39	2.41	2.42	2.71	2.40	1.08	up	3.59E-01	8.95E-01	-	-
1368245_at	Upb1	ureidopropionase, beta	116593	Rn.11110	NM_053845	9.19	9.78	9.80	9.49	9.41	9.56	1.08	down	6.33E-01	8.95E-01	-	-
1388311_at	Mrfap1	Morf4 family associated protein 1	282585	Rn.3393	AA799550	11.16	11.51	11.58	11.27	11.21	11.46	1.08	down	5.23E-01	8.95E-01	-	-
1378034_at	Mterfd3	MTERF domain containing 3	366856	Rn.138073	BF552141	3.56	2.73	2.74	3.12	2.73	2.87	1.08	down	7.42E-01	9.17E-01	-	-
1391430_at	Cyb5r2	cytochrome b5 reductase 2	365345	Rn.16198	BE105855	2.53	2.40	2.52	2.73	2.53	2.50	1.08	up	2.83E-01	8.95E-01	-	-
1398755_at	Atp6v0c	ATPase, H+ transporting, lysosomal 16kDa, V0 subunit c	170667	Rn.1869	NM_130823	8.84	9.13	9.45	9.02	8.98	9.11	1.08	down	5.91E-01	8.95E-01	-	-
1395878_at	---	---	---	Rn.217726	AI706643	2.33	2.56	2.60	2.71	2.59	2.51	1.08	up	3.65E-01	8.95E-01	-	-
1382623_at	Rhebl1	Ras homolog enriched in brain like 1	359959	Rn.43211	AI409262	2.32	2.31	2.62	2.31	2.32	2.30	1.08	down	3.70E-01	8.95E-01	-	-
1381715_at	---	---	---	Rn.207838	BE107590	2.42	2.40	2.44	2.72	2.43	2.42	1.08	up	3.51E-01	8.95E-01	-	-
1388102_at	Ptgr1	prostaglandin reductase 1	192227	Rn.10656	U66322	5.83	4.73	3.69	5.16	4.91	4.49	1.08	up	8.80E-01	9.63E-01	-	-
1393765_at	---	---	---	Rn.153224	AI043706	2.89	2.85	3.02	2.87	2.89	2.69	1.08	down	2.59E-01	8.95E-01	-	-
1390010_at	Ncoa1	nuclear receptor coactivator 1	313929	Rn.165307	AI454081	5.84	4.04	4.31	4.41	4.23	5.24	1.08	down	8.78E-01	9.62E-01	-	-
1398252_at	Mecr	mitochondrial trans-2-enoyl-CoA reductase	29470	Rn.15375	NM_017209	5.32	4.41	4.18	4.39	5.48	4.34	1.08	up	8.48E-01	9.53E-01	-	-
1387946_at	Lgals3bp	lectin, galactoside-binding, soluble, 3 binding protein	245955	Rn.3251	AF065438	2.36	2.36	2.77	3.09	2.37	2.35	1.08	up	7.28E-01	9.13E-01	-	-
1395376_at	Ddx11	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 11 (CHL1-like helicase homo	316767	Rn.33391	BE104111	2.62	2.61	2.62	2.49	2.62	3.06	1.08	up	5.73E-01	8.95E-01	-	-
1393364_at	Slc12a8	solute carrier family 12 (potassium/chloride transporters), member 8	266733	Rn.15381	BM385460	5.11	5.04	6.56	5.82	5.00	5.58	1.08	down	8.59E-01	9.56E-01	-	-
1376584_at	Ppm1l	protein phosphatase 1 (formerly 2C)-like	310506	Rn.133275	BE116408	2.55	2.54	3.02	2.68	2.55	2.56	1.08	down	5.54E-01	8.95E-01	-	-
1390076_at	---	---	---	---	BE109608	2.84	2.97	2.86	2.89	3.23	2.87	1.08	up	4.49E-01	8.95E-01	-	-
1399161_a_at	Erap1	endoplasmic reticulum aminopeptidase 1	80897	Rn.22516	AF148323	3.97	3.61	3.71	3.13	3.96	4.51	1.08	up	8.14E-01	9.40E-01	-	-
1369160_a_at	Slc4a7	solute carrier family 4, sodium bicarbonate cotransporter, member 7	117955	Rn.26858	AF070475	2.95	2.35	2.36	2.36	2.65	2.35	1.08	down	6.63E-01	8.98E-01	-	-
1387005_at	Ctss	cathepsin S	50654	Rn.11347	NM_017320	7.51	7.37	7.51	7.90	7.30	7.51	1.08	up	5.97E-01	8.95E-01	-	-
1371663_at	RGD1305138	similar to expressed sequence AW556797	315329	Rn.17060	AI232361	2.68	2.51	2.67	2.41	2.52	2.62	1.08	down	2.77E-01	8.95E-01	-	-
1384504_at	Magi1	membrane associated guanylate kinase, WW and PDZ domain containing 1	500261	Rn.95239	BI286449	2.76	3.05	2.83	2.78	2.80	2.75	1.08	down	3.04E-01	8.95E-01	-	-
1393041_at	Smc2	structural maintenance of chromosomes 2	362519	Rn.94452	AW550052	2.58	2.61	2.82	2.74	2.78	2.81	1.08	up	2.60E-01	8.95E-01	-	-
1386111_at	Dpm1	Dolichyl-phosphate mannosyltransferase polypeptide 1, catalytic subunit	296394	Rn.7840	AA998619	2.98	2.69	2.72	2.69	2.70	2.69	1.08	down	3.25E-01	8.95E-01	-	-
1372935_at	Tmem119	transmembrane protein 119	304581	Rn.155038	AI598550	2.62	2.31	2.32	2.31	2.32	2.31	1.08	down	3.57E-01	8.95E-01	-	-
1391913_at	---	---	---	Rn.43467	AI407496	2.70	2.41	2.42	2.40	2.42	2.39	1.08	down	3.31E-01	8.95E-01	-	-
1386172_at	---	---	---	Rn.133644	AI639019	2.56	2.58	2.44	2.43	2.44	2.40	1.07	down	8.13E-02	8.95E-01	-	-
1389037_at	Rit1	Ras-like without CAAX 1	499652	Rn.50417	BM986252	3.36	3.61	3.36	3.39	3.36	3.27	1.07	down	3.16E-01	8.95E-01	-	-
1394095_at	Gin1	gypsy retrotransposon integrase 1	316687	Rn.55553	AA850714	3.01	2.87	2.61	2.74	2.60	3.46	1.07	up	7.39E-01	9.16E-01	-	-
1381835_at	---	---	---	Rn.164254	BF420021	2.36	2.35	2.36	2.36	2.67	2.36	1.07	up	3.69E-01	8.95E-01	-	-
1389617_at	Elk3	ELK3, member of ETS oncogene family	362871	Rn.196088	BM392135	4.43	3.18	2.50	3.26	3.20	3.96	1.07	up	8.74E-01	9.61E-01	-	-
1392102_at	---	---	---	---	BE118959	2.86	2.85	2.67	2.85	3.12	2.92	1.07	up	2.69E-01	8.95E-01	-	-
1375527_at	Chd8	chromodomain helicase DNA binding protein 8	65027	Rn.98337	BF282681	7.39	7.22	7.16	7.14	7.02	7.31	1.07	down	3.87E-01	8.95E-01	-	-
1398794_at	Tceb1	transcription elongation factor B (SIII), polypeptide 1	64525	Rn.5996	NM_022593	10.39	10.32	10.37	10.20	10.18	10.38	1.07	down	1.95E-01	8.95E-01	-	-
1369302_at	Gper	G protein-coupled estrogen receptor 1	171104	Rn.9806	NM_133573	2.90	2.87	3.22	2.91	2.90	2.86	1.07	down	4.08E-01	8.95E-01	-	-
1381808_at	rCG_34148	alanine-glyoxylate aminotransferase 2-like 2	100169747	Rn.217734	AI411255	4.76	3.88	2.67	4.39	4.50	2.75	1.07	up	9.06E-01	9.71E-01	-	-
1389463_at	Prkar1b	protein kinase, cAMP dependent regulatory, type I, beta	25521	Rn.145151	BG375376	3.04	2.37	2.40	2.39	2.40	2.70	1.07	down	6.91E-01	9.05E-01	-	-
1387540_at	Brca1	breast cancer 1	497672	Rn.217584	NM_012514	2.51	2.51	2.52	2.50	2.52	2.83	1.07	up	3.89E-01	8.95E-01	-	-
1374541_at	Gys1	glycogen synthase 1, muscle	690987	Rn.95278	BM392117	3.56	3.24	3.26	3.22	3.25	3.28	1.07	down	3.82E-01	8.95E-01	-	-
1387159_at	Ager	advanced glycosylation end product-specific receptor	81722	Rn.9829	NM_053336	2.83	2.50	2.53	2.52	2.45	2.58	1.07	down	4.06E-01	8.95E-01	-	-
1370913_at	Rsad2	radical S-adenosyl methionine domain containing 2	65190	Rn.14882	AI409634	2.72	2.44	2.44	2.44	2.41	2.41	1.07	down	3.38E-01	8.95E-01	-	-
1391085_at	---	---	---	Rn.206506	BE118077	2.43	2.55	2.47	2.40	2.46	2.89	1.07	up	5.49E-01	8.95E-01	-	-
1369065_a_at	Atp2a2	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2	29693	Rn.2305	NM_017290	8.05	8.54	8.26	8.12	7.71	8.72	1.07	down	7.66E-01	9.24E-01	-	-
1376521_at	---	---	---	Rn.176439	BG378315	2.43	2.42	2.46	2.76	2.44	2.42	1.07	up	4.05E-01	8.95E-01	-	-
1395206_at	---	---	---	Rn.47031	AW528854	2.59	2.55	2.55	2.55	2.94	2.51	1.07	up	4.91E-01	8.95E-01	-	-
1376249_at	Fuca2	fucosidase, alpha-L- 2, plasma	292485	Rn.47769	BM389993	3.82	3.91	5.51	4.52	3.98	4.43	1.07	down	8.65E-01	9.58E-01	-	-
1372678_at	Zfp828	zinc finger protein 828	309547	Rn.3851	AA800044	3.67	4.11	3.79	3.75	4.16	3.97	1.07	up	5.89E-01	8.95E-01	-	-
1391640_at	---	---	---	---	BF290284	2.42	2.71	2.42	2.42	2.42	2.41	1.07	down	3.46E-01	8.95E-01	-	-
1385017_at	Aqr /// Znf770	aquarius homolog (mouse) /// zinc finger protein 770	366163 /// 691610	Rn.37299	AW553683	3.32	3.14	2.86	2.98	2.79	3.23	1.07	down	6.04E-01	8.95E-01	-	-
1383655_at	Tnip2	TNFAIP3 interacting protein 2	305451	Rn.17607	BF545192	2.39	2.37	2.71	2.38	2.38	2.40	1.07	down	3.96E-01	8.95E-01	-	-
1377908_at	---	---	---	Rn.168837	AI408225	2.47	2.46	2.61	2.60	2.51	2.74	1.07	up	2.80E-01	8.95E-01	-	-
1391970_at	Car11	carbonic anhydrase 11	308588	Rn.44281	AM385197	2.66	2.55	2.31	2.41	2.41	2.39	1.07	down	3.66E-01	8.95E-01	-	-
1384550_at	RGD1565685	similar to RIKEN cDNA 1810030O07	317344	Rn.12981	AW917943	6.65	6.70	7.15	6.47	6.75	6.97	1.07	down	6.54E-01	8.97E-01	-	-
1395422_at	---	---	---	Rn.172080	BF288357	2.85	3.20	2.86	2.82	2.71	3.06	1.07	down	5.39E-01	8.95E-01	-	-
1369543_s_at	Dnajc21	DnaJ (Hsp40) homolog, subfamily C, member 21	192210	Rn.53644	NM_138856	4.96	3.94	4.76	4.62	3.26	5.46	1.07	down	8.91E-01	9.66E-01	-	-
1395817_at	---	---	---	Rn.46375	BI290516	2.32	2.31	2.61	2.31	2.30	2.31	1.07	down	3.47E-01	8.95E-01	-	-
1371675_at	Chd2	Chromodomain helicase DNA binding protein 2	308738	Rn.1779	AA893193	4.58	4.64	4.73	4.34	4.53	4.77	1.07	down	4.78E-01	8.95E-01	-	-
1372649_at	Hspb7	heat shock protein family, member 7 (cardiovascular)	50565	Rn.21809	BM390305	2.28	2.28	2.60	2.28	2.29	2.28	1.07	down	3.80E-01	8.95E-01	-	-
1391397_at	LOC684055	hypothetical protein LOC684055	684055	---	BF418393	2.35	2.34	2.37	2.43	2.60	2.33	1.07	up	2.71E-01	8.95E-01	-	-
1370171_at	Hnrnpu	heterogeneous nuclear ribonucleoprotein U	117280	Rn.4328	AI058964	7.73	7.84	7.88	7.84	7.91	8.02	1.07	up	2.07E-01	8.95E-01	-	-
1371524_at	Gli3	gene trap locus 3	307642	Rn.6708	AI009608	3.64	4.43	4.01	4.02	3.14	4.62	1.07	down	8.42E-01	9.51E-01	-	-
1371921_at	Ctnna1	catenin (cadherin associated protein), alpha 1	307505	Rn.103790	BM986272	7.67	8.15	7.84	8.00	7.30	8.05	1.07	down	7.31E-01	9.14E-01	-	-
1383431_at	---	---	---	Rn.199793	BF404209	6.96	6.10	5.38	5.00	6.98	6.76	1.07	up	9.00E-01	9.69E-01	-	-
1378583_at	RGD1566215	similar to Coatomer gamma-2 subunit (Gamma-2 coat protein) (Gamma-2 CO	301742	Rn.216502	BI278145	2.79	2.50	2.51	2.50	2.52	2.47	1.07	down	3.41E-01	8.95E-01	-	-
1373392_at	Tmem165	transmembrane protein 165	364137	Rn.2779	AW523924	6.20	6.59	5.98	5.89	6.42	6.15	1.07	down	6.83E-01	9.03E-01	-	-
1393189_at	Maoa	Monoamine oxidase A	29253	Rn.163443	BF414665	4.09	4.25	4.61	4.38	4.17	4.70	1.07	up	6.59E-01	8.98E-01	-	-
1385212_at	---	---	---	Rn.204944	AI603192	4.36	3.10	3.89	4.04	2.94	4.68	1.07	up	8.77E-01	9.62E-01	-	-
1380929_at	RGD1560244	Similar to hypothetical protein FLJ34512	302996	Rn.144920	BF393940	2.81	2.46	2.48	2.46	2.52	2.45	1.07	down	4.22E-01	8.95E-01	-	-
1388842_at	Srf	serum response factor (c-fos serum response element-binding transcription fa	501099	Rn.1501	BG380385	7.64	7.51	7.26	7.34	7.39	7.37	1.07	down	4.06E-01	8.95E-01	-	-
1398989_at	Son	Son DNA binding protein	304092	Rn.7967	BI275248	9.72	9.44	9.51	9.55	9.32	9.50	1.07	down	3.96E-01	8.95E-01	-	-
1391494_at	---	---	---	---	AW527503	4.53	5.73	5.50	4.71	4.67	5.07	1.07	down	8.89E-01	9.59E-01	-	-
1374607_at	---	---	---	Rn.23786	AI599854	3.74	3.74	3.74	3.34	4.18	4.02	1.07	up	7.08E-01	9.08E-01	-	-
1395332_at	Tbx2	T-box 2	303398	Rn.38282	AW917757	2.51	2.50	2.54	2.85	2.51	2.50	1.07	up	4.19E-01	8.95E-01	-	-
1380178_at	---	---	---	Rn.22982	AI228334	3.06	3.09	2.84	2.82	2.93	2.93	1.07	down	3.01E-01	8.95E-01	-	-
1395273_at	Ahcyl1	S-adenosylhomocysteine hydrolase-like 1	362013	Rn.17493	BE115782	9.94	9.56	9.31	9.45	9.13	9.91	1.07	down	7.41E-01	9.17E-01	-	-
1371189_x_at	25 /// LOC888911	similar to 40S ribosomal protein SA (p40) (34/67 kDa laminin receptor) /// simi	0 /// 367035 /// 68	Rn.159841	BG153272	10.46	10.25	10.50	10.47	10.54	10.51	1.07	up	2.64E-01	8.95E-01	-	-
1374774_at	Ptpn14	Protein tyrosine phosphatase, non-receptor type 14	305064	Rn.61069	BF552241	4.31	5.63	5.94	4.41	6.11	5.66	1.07	up	8.92E-01	9.66E-01	-	-
1374154_at	Sfrs2ip	splicing factor, arginine/serine-rich 2, interacting protein	312030	Rn.199124	AI411610	6.27	7.85	7.55	6.67	7.37	7.93	1.07	up	8.73E-01	9.61E-01	-	-
1371386_at	79485 /// LOC863	family with sequence similarity 120A /// similar to Protein CXorf17 homolog ///	679485 /// 683420	Rn.129434	AI407975	9.51	9.60	9.27	9.71	9.38	9.59	1.07	up	4.94E-01	8.95E-01	-	-
1383174_at	---	---	---	Rn.164342	AI576562	2.45	2.43	2.41	2.58	2.50	2.52	1.07	up	1.99E-02	8.95E-01	-	-
1381527_at	---	---	---	Rn.101986	AI535521	2.51	2.51	2.51	2.82	2.53	2.50	1.07	up	3.73E-01	8.95E-01	-	-
1383606_at	Tc2n	tandem C2 domains, nuclear	500707	Rn.43919	BI302544	2.50	3.05	2.54	2.48	2.68	3.25	1.07	up	7.41E-01	9.17E-01	-	-
1391757_at	---	---	---	Rn.25328	AA926072	2.91	3.37	3.96	3.79	3.41	3.36	1.07	up	7.71E-01	9.25E-01	-	-
1373129_at	---	---	---	Rn.39181	BF388415	5.60	5.28	4.57	5.41	4.98	5.39	1.07	up	7.74E-01	9.26E-01	-	-
1379710_at	---	---	---	Rn.18354	BE108372	2.87	2.43	2.44	2.44	2.57	2.42	1.07	down	5.31E-01	8.95E-01	-	-
1383867_at	---	---	---	Rn.206372	BE102803	2.42	2.44	3.70	2.46	2.47	2.32	1.07	down	8.50E-01	9.53E-01	-	-
1368583_a_at	Hrg	histidine-rich glycoprotein	171016	Rn.16100	NM_133428	3.04	2.41	2.43	2.70	2.42	2.45	1.07	down	6.69E-01	9.00E-01	-	-
1394490_at	Abca1	ATP-binding cassette, sub-family A (ABC1), member 1	313210	Rn.148916	AI502114	2.64	2.61	2.66	2.63	2.94	2.65	1.07	up	3.69E-01	8.95E-01	-	-
1398779_at	Arpc1a	actin related protein 2/3 complex, subunit 1A	81824	Rn.844	NM_031146	8.34	8.20	8.18	8.31	8.37	8.35	1.07	up	1.15E-01	8.95E-01	-	-
1381113_at	---	---	---	Rn.205010	BE102952	2.40	2.41	2.68	2.39	2.40	2.38	1.07	down	3.25E-01	8.95E-01	-	-
1388689_at	LOC682245	similar to Acylphosphatase, muscle type isozyme (Acylphosphate phosphohy	682245	---	AI170755	4.64	4.48	5.64	4.36	4.69	5.41	1.07	down	8.40E-01	9.50E-01	-	-
1379774_at	---	---	---	Rn.27512	AI137801	5.56	5.08	5.43	4.79	5.83	5.77	1.07	up	7.92E-01	9.33E-01	-	-
1379634_at	Uba7	ubiquitin-like modifier activating enzyme 7	301000	Rn.98275	AW921187	2.26	2.24	2.25	2.24	2.58	2.23	1.07	up	4.13E-01	8.95E-01	-	-
1377211_at	LOC288913	similar to LEYDIG CELL TUMOR 10 KD PROTEIN	288913	Rn.11148	BI279696	3.47	3.89	3.17	3.63	3.06	3.53	1.07	down	7.26E-01	9.13E-01	-	-
1398263_at	Abcc9	ATP-binding cassette, sub-family C (CFTR/MRP), member 9	25560	Rn.10528	NM_013040	2.46	2.46	2.49	2.46	2.83	2.43	1.07	up	4.73E-01	8.95E-01	-	-
1374783_at	---	---	---	Rn.1341	BI301183	3.11	4.03	3.12	3.10	3.15	4.32	1.07	up	8.48E-01	9.53E-01	-	-
1383740_at	---	---	---	Rn.165878	AI029740	6.34	4.86	4.72	4.71	5.16	6.36	1.07	up	8.93E-01	9.67E-01	-	-
1395374_at	---	---	---	Rn.203034	BF548045	2.76	2.48	2.57	2.49	2.55	2.46	1.07	down	3.08E-01	8.95E-01	-	-
1378100_at	Yeats4	YEATS domain containing 4	299810	Rn.103329	BG380660	5.22	6.17	5.71	5.78	5.79	5.84	1.07	up	7.29E-01	9.13E-01	-	-
1386176_at	Fam160b2	family with sequence similarity 160, member B2	306015	Rn.124637	AA892868	4.95	5.05	5.77	5.45	5.30	5.33	1.07	up	7.17E-01	9.10E-01	-	-
1379348_at	Exosc2	exosome component 2	366017	Rn.75292	BF420491	3.17	2.88	2.94	2.72	2.94	3.03	1.07	down	4.65E-01	8.95E-01	-	-
1381063_at	---	---	---	---	BE103485	2.56	2.87	2.56	2.51	2.56	2.61	1.07	down	3.98E-01	8.95E-01	-	-
1378344_at	---	---	---	Rn.147860	BF289238	2.64	2.34	2.36	2.35	2.36	2.33	1.07	down	3.48E-01	8.95E-01	-	-
1396135_at	---	---	---	Rn.206200	BF567887	2.41	2.40	2.42	2.72	2.42	2.40	1.07	up	3.88E-01	8.95E-01	-	-
1371810_at	Copg	Coatomer protein complex, subunit gamma	297428	Rn.50150	BF294093	7.55	7.05	7.18	6.78	7.54	7.47	1.07	up	7.75E-01	9.27E-01	-	-
1369930_at	Psma6	proteasome (prosome, macropain) subunit, alpha type 6	29673	Rn.107278	NM_017283	9.74	9.98	9.75	9.81	9.79	10.18	1.07	up	5.28E-01	8.95E-01	-	-
1382001_at	LOC502710	similar to Myeloid/lymphoid or mixed-lineage leukemia protein 3 homolog (His	502710	Rn.164602	AI227612	5.63	6.38	5.80	5.70	6.37	5.43	1.07	down	7.89E-01	9.32E-01	-	-
1396192_at	Npat	nuclear protein, ataxia-telangiectasia locus	315666	Rn.18968	H31517	4.64	5.83	4.10	4.39	5.51	4.97	1.07	up	8.74E-01	9.61E-01	-	-
1397289_at	---	---	---	---	AI228245	2.55	2.34	2.35	2.91	2.35	2.28	1.07	up	6.52E-01	8.97E-01	-	-
1388330_at	Vkorc1	vitamin K epoxide reductase complex, subunit 1	309004	Rn.97942	BM384958	8.09	7.41	6.49	7.45	7.00	7.84	1.07	up	8.55E-01	9.55E-01	-	-
1378587_at	Ankrd40	ankyrin repeat domain 40	690586	Rn.17667	BE105706	4.33	4.39	4.17	4.33	3.98	4.27	1.07	down	4.88E-01	8.95E-01	-	-
1393277_at	Nup155	Nucleoporin 155	117021	Rn.11328	AI579547	2.63	2.73	2.52	2.74	2.63	2.82	1.07	up	2.79E-01	8.95E-01	-	-
1390096_at	---	---	---	Rn.1097	BF284481	5.58	6.18	4.88	5.20	5.55	5.57	1.07	down	8.07E-01	9.38E-01	-	-
1386142_at	---	---	---	Rn.33741	AI102050	4.66	5.44	3.87	4.77	4.73	4.77	1.07	up	8.33E-01	9.47E-01	-	-
1393465_at	---	---	---	Rn.95697	BE103258	4.77	5.00	4.75	4.90	4.92	5.01	1.07	up	3.07E-01	8.95E-01	-	-
1391527_at	Stat6	Signal transducer and activator of transcription 6	362896	Rn.6880	BE109296	4.96	2.52	2.62	3.86	3.09	2.83	1.07	down	9.11E-01	9.73E-01	-	-
1376760_at	LOC683880	similar to GC-rich sequence DNA-binding factor homolog	683880	---	BF402128	3.53	3.62	3.40	3.44	3.60	3.81	1.07	up	4.55E-01	8.95E-01	-	-
1399085_at	Zmpste24	Zinc metallopeptidase, STE24 homolog (S. cerevisiae)	313564	Rn.25307	BM384770	7.88	8.32	7.98	7.70	7.80	8.37	1.07	down	7.01E-01	9.07E-01	-	-
1375932_at	---	---	---	Rn.163618	BF284677	4.49	4.22	4.23	4.19	4.22	4.21	1.07	down	3.13E-01	8.95E-01	-	-
1387213_at	Pcsk4	proprotein convertase subtilisin/kexin type 4	171085	Rn.2899	NM_133559	2.39	2.39	2.68	2.39	2.40	2.37	1.07	down	3.54E-01	8.95E-01	-	-
1374101_at	Tbc1d10a	TBC1 domain family, member 10a	360968	Rn.105859	BF282437	6.05	5.57	4.60	5.37	5.38	5.16	1.07	down	8.25E-01	9.45E-01	-	-
1373224_at	St3gal4	ST3 beta-galactoside alpha-2,3-sialyltransferase 4	363040	Rn.24125	BI285550	2.59	2.55	2.51	2.74	2.85	2.56	1.07	up	1.47E-01	8.95E-01	-	-
1376351_at	Jrk	jerky homolog (mouse)	315073	Rn.26833	BM383716	2.79	4.85	5.23	4.68	3.82	4.67	1.07	up	9.06E-01	9.71E-01	-	-
1374932_at	---	---	---	Rn.212163	BI282731	2.52	2.51	2.39	2.52	2.56	2.65	1.07	up	1.56E-01	8.95E-01	-	-
1385479_at	RGD1565512	similar to hypothetical protein

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1374018_at	Ascc2	activating signal cointegrator 1 complex subunit 2	498402	Rn.35208	AA851212	5.28	6.05	6.54	6.46	5.03	6.08	1.07	down	8.66E-01	9.58E-01	-	-
1395151_at	---	---	---	Rn.149066	AW527014	3.51	3.02	2.88	2.88	2.87	3.35	1.07	down	7.04E-01	9.07E-01	-	-
1371923_at	Lpcat1	lysophosphatidylcholine acyltransferase 1	361467	Rn.16547	BG380281	2.51	2.83	2.60	2.43	2.60	3.21	1.07	up	7.13E-01	9.10E-01	-	-
1385102_at	Ccdc127	coiled-coil domain containing 127	308060	Rn.21666	AI712625	2.66	3.84	4.04	3.53	3.22	4.10	1.07	up	8.50E-01	9.53E-01	-	-
1371968_at	Tmbim4	transmembrane BAX inhibitor motif containing 4	362884	Rn.104707	AI013781	7.87	8.00	8.11	8.01	7.60	8.67	1.07	up	7.67E-01	9.24E-01	-	-
1370154_at	Lyz2	lysozyme 2	25211	Rn.2283	L12458	9.11	9.30	9.41	9.36	9.47	9.29	1.07	up	3.75E-01	8.95E-01	-	-
1393604_at	Gpn3	GPN-loop GTPase 3	360810	Rn.162125	BE106064	4.36	3.60	3.22	3.76	3.42	3.70	1.07	down	7.87E-01	9.31E-01	-	-
1367487_at	B4galt3	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 3	494342	Rn.91751	BG378610	5.36	6.03	6.39	6.11	6.07	5.90	1.07	up	7.60E-01	9.22E-01	-	-
1395095_at	Letm2	leucine zipper-EF-hand containing transmembrane protein 2	361169	Rn.203805	BF407976	2.66	2.38	2.46	2.40	2.40	2.40	1.07	down	3.02E-01	8.95E-01	-	-
1384405_at	LOC682360	hypothetical protein LOC682360	682360	---	BI280128	6.13	4.56	4.04	4.57	5.33	4.53	1.07	down	8.88E-01	9.65E-01	-	-
1368043_at	Snx1	sorting nexin 1	84471	Rn.144614	NM_053411	4.71	7.47	6.77	5.30	6.85	7.09	1.07	up	9.24E-01	9.78E-01	-	-
1378389_at	---	---	---	Rn.148475	BM385157	2.94	2.99	2.77	2.94	3.16	2.90	1.07	up	3.96E-01	8.95E-01	-	-
1380471_at	---	---	---	Rn.48830	H31701	5.49	6.80	5.97	5.94	5.66	6.34	1.07	down	8.25E-01	9.45E-01	-	-
1367663_at	Psme1	proteasome (prosome, macropain) activator subunit 1	29630	Rn.2742	NM_017264	9.04	9.51	8.69	9.25	8.67	9.02	1.07	down	7.46E-01	9.18E-01	-	-
1372548_at	Cry2	cryptochrome 2 (photolyase-like)	170917	Rn.21150	AI412018	2.43	2.69	3.68	2.96	2.95	3.20	1.07	up	8.08E-01	9.38E-01	-	-
1367533_at	Elp2	elongation protein 2 homolog (S. cerevisiae)	307545	Rn.25007	BG663097	8.80	9.01	9.85	9.06	9.20	9.10	1.07	down	7.69E-01	9.25E-01	-	-
1374677_at	LOC684425	similar to Adenylosuccinate synthetase isozyme 1 (Adenylosuccinate synthetase	684425	---	AI577508	3.78	3.11	4.58	3.55	3.50	4.12	1.07	down	8.39E-01	9.50E-01	-	-
1380569_at	Rnf41	ring finger protein 41	362814	Rn.74790	BI281591	2.60	3.16	2.62	3.10	3.02	2.56	1.07	up	7.05E-01	9.08E-01	-	-
1372303_at	Fam49b	family with sequence similarity 49, member B	299909	Rn.105890	BE110633	4.15	4.02	3.97	3.92	4.62	3.90	1.07	up	6.99E-01	9.07E-01	-	-
1367914_at	Emp3	epithelial membrane protein 3	81505	Rn.6782	NM_030847	2.58	2.75	2.76	2.75	2.79	2.84	1.07	up	1.89E-01	8.95E-01	-	-
1375130_at	LOC679812	hypothetical protein LOC679612	679612	Rn.217698	AI410237	2.25	2.25	2.26	2.25	2.25	2.56	1.07	up	3.80E-01	8.95E-01	-	-
1372586_at	---	---	---	Rn.203335	AI411995	6.13	6.35	6.61	6.36	6.22	6.82	1.07	up	6.81E-01	9.03E-01	-	-
1387512_at	Zfp238	zinc finger protein 238	64619	Rn.207206	NM_022678	5.35	5.56	6.36	4.87	6.13	5.97	1.07	down	8.50E-01	9.53E-01	-	-
1393580_at	LOC691543	hypothetical protein LOC691543	691543	Rn.55420	AW531476	3.10	2.91	2.95	2.87	3.23	2.56	1.07	down	6.45E-01	8.95E-01	-	-
1375568_at	Socs1	Suppressor of cytokine signaling 1	25271	Rn.82754	AI029171	2.44	2.75	2.46	2.45	2.47	2.42	1.07	down	3.79E-01	8.95E-01	-	-
1374645_at	---	---	---	Rn.23413	AW535233	2.76	2.56	2.57	2.43	2.56	3.20	1.07	up	7.03E-01	9.07E-01	-	-
1379260_at	Heca	headcase homolog (Drosophila)	306824	Rn.8167	BE115626	5.97	5.75	6.00	5.35	5.93	6.13	1.07	down	7.04E-01	9.07E-01	-	-
1398248_s_at	Myh6 /// Myh7	myosin, heavy chain 6, cardiac muscle, alpha /// myosin, heavy chain 7, cardi	29556 /// 29557	Rn.54399	BF395647	2.72	2.48	2.51	2.45	2.55	2.41	1.07	down	3.17E-01	8.95E-01	-	-
1386930_at	Psmd4	proteasome (prosome, macropain) 26S subunit, non-ATPase, 4	83499	Rn.3830	NM_031331	7.32	6.59	6.63	6.95	6.89	7.01	1.07	up	6.97E-01	9.07E-01	-	-
1394157_at	---	---	---	Rn.221934	AI045190	4.19	4.16	3.98	3.89	4.38	3.77	1.07	down	6.38E-01	8.95E-01	-	-
1371214_at	Itga7	integrin alpha 7	81008	Rn.54492	X74293	2.56	2.73	2.35	2.54	2.45	2.95	1.07	up	6.22E-01	8.95E-01	-	-
1391462_at	Ebpl	emopamil binding protein-like	361054	Rn.99955	AI179635	5.68	5.42	5.19	5.40	4.92	5.67	1.07	down	7.22E-01	9.11E-01	-	-
1399006_at	Usf1	upstream transcription factor 1	83586	Rn.10845	BI285826	3.90	3.73	3.98	3.70	3.82	3.90	1.07	down	2.81E-01	8.95E-01	-	-
1367521_at	---	---	---	---	BI281185	6.19	6.62	5.76	4.50	6.37	6.37	1.07	down	9.21E-01	9.77E-01	-	-
1380212_at	---	---	---	Rn.203574	AA956814	4.90	6.20	5.35	5.32	5.32	5.52	1.07	down	8.07E-01	9.38E-01	-	-
1374102_at	---	---	---	Rn.199421	AI101299	2.49	2.48	2.50	2.48	2.81	2.47	1.07	up	4.19E-01	8.95E-01	-	-
1371380_at	Pdha1	pyruvate dehydrogenase (lipoamide) alpha 1	29554	Rn.3655	AI411413	10.47	10.17	10.61	10.31	10.26	10.37	1.07	down	4.97E-01	8.95E-01	-	-
1372705_at	Cherp	calcium homeostasis endoplasmic reticulum protein	290614	Rn.85994	BG376747	3.47	5.39	3.22	4.07	3.40	4.30	1.07	down	8.98E-01	9.68E-01	-	-
1383381_at	RGD1560394	RGD1560394	289728	Rn.101945	AI030756	2.36	2.35	2.37	2.35	2.68	2.34	1.07	up	4.23E-01	8.95E-01	-	-
1388216_at	Zfp423	zinc finger protein 423	94188	Rn.9981	L03386	2.42	2.40	2.67	2.40	2.40	2.39	1.07	down	3.17E-01	8.95E-01	-	-
1387911_at	Rabggtb	Rab geranylgeranyltransferase, beta subunit	25533	Rn.107818	L10416	7.13	7.92	8.22	7.89	7.85	7.83	1.07	up	7.72E-01	9.26E-01	-	-
1393543_at	Zfp426l2	zinc finger protein 426-like 2	363022	Rn.99479	BF399884	2.76	2.80	2.98	2.74	2.76	2.73	1.07	down	2.17E-01	8.95E-01	-	-
1397789_at	---	---	---	Rn.204991	BF392017	2.78	2.74	2.83	2.73	3.28	2.64	1.07	up	6.44E-01	8.95E-01	-	-
1369179_a_at	Pparg	peroxisome proliferator-activated receptor gamma	25864	Rn.23443	NM_013124	2.45	2.44	2.46	2.45	2.75	2.75	1.07	up	3.74E-01	8.95E-01	-	-
1372258_at	LOC100192313	hypothetical protein LOC100192313	100192313	Rn.98813	AI102935	9.17	9.24	9.16	9.18	9.17	9.52	1.07	up	4.50E-01	8.95E-01	-	-
1377754_at	---	---	---	Rn.15903	BF284038	2.43	3.12	3.01	2.87	2.57	3.42	1.07	up	7.77E-01	9.28E-01	-	-
1391383_at	Crtac1	cartilage acidic protein 1	171438	Rn.198566	BF413778	2.80	2.60	2.72	2.60	2.64	2.57	1.07	down	1.81E-01	8.95E-01	-	-
1387041_at	Ubqln1	ubiquilin 1	114590	Rn.94864	NM_053747	8.16	8.06	8.23	8.09	7.86	8.19	1.07	down	4.08E-01	8.95E-01	-	-
1377072_at	---	---	---	Rn.201858	BE115516	3.10	3.58	4.59	3.70	3.64	3.63	1.07	down	8.31E-01	9.47E-01	-	-
1367480_at	Eif4a3	eukaryotic translation initiation factor 4A, isoform 3	688288	Rn.202617	AI230248	7.48	7.97	7.81	7.91	7.29	8.37	1.07	up	7.86E-01	9.31E-01	-	-
1373838_at	Fut4	fucosyltransferase 4 (alpha (1,3) fucosyltransferase, myeloid-specific)	60670	Rn.44467	AI237192	2.83	2.82	2.83	2.84	2.80	3.14	1.07	up	4.08E-01	8.95E-01	-	-
1373021_at	---	---	---	Rn.163210	AI171823	6.64	5.74	5.67	6.43	5.65	5.66	1.07	down	8.18E-01	9.42E-01	-	-
1386957_at	Pom121	nuclear pore membrane protein 121	113975	Rn.10474	NM_053622	4.90	4.87	5.60	5.32	4.90	5.44	1.07	up	7.47E-01	9.18E-01	-	-
1370327_at	Commd5	COMM domain containing 5	245974	Rn.24747	AF290194	4.37	4.09	4.48	4.14	4.29	4.81	1.07	up	6.91E-01	9.05E-01	-	-
1371595_at	---	---	---	Rn.153998	BM384301	9.34	9.62	9.62	9.66	10.05	9.17	1.07	up	7.33E-01	9.14E-01	-	-
1396335_at	---	---	---	Rn.216999	BF405922	2.67	2.36	2.39	2.37	2.39	2.36	1.07	down	3.78E-01	8.95E-01	-	-
1384954_at	a3st3a1 /// Hs3st3	heparan sulfate (glucosamine) 3-O-sulfotransferase 3A1 /// heparan sulfate (g	303218 /// 363618	Rn.72525	AI548686	2.41	2.42	2.70	2.41	2.42	2.40	1.07	down	3.55E-01	8.95E-01	-	-
1384392_at	Cyp26b1	cytochrome P450, family 26, subfamily b, polypeptide 1	312495	Rn.19898	BF397093	2.49	2.40	2.51	2.49	2.69	2.52	1.07	up	2.26E-01	8.95E-01	-	-
1386860_at	---	---	---	---	BF565021	2.47	2.44	2.48	2.70	2.47	2.52	1.07	up	2.31E-01	8.95E-01	-	-
1397670_at	Atg12	ATG12 autophagy related 12 homolog (S. cerevisiae)	361321	Rn.6224	BG664324	3.05	2.94	3.07	3.16	2.66	3.54	1.07	up	7.21E-01	9.11E-01	-	-
1392584_at	---	---	---	Rn.204022	BF415201	3.80	3.94	3.76	3.75	3.76	3.70	1.07	down	1.51E-01	8.95E-01	-	-
1389802_at	---	---	---	Rn.211667	BF416288	6.04	6.31	6.19	6.17	6.18	5.89	1.07	down	4.71E-01	8.95E-01	-	-
1374464_at	Tfg	Trk-fused gene	360709	Rn.24822	BI287875	5.89	5.79	5.96	5.90	5.78	6.26	1.07	up	5.47E-01	8.95E-01	-	-
1376463_at	---	---	---	Rn.17336	AA955579	2.38	2.58	2.43	2.37	2.37	2.35	1.07	down	1.69E-01	8.95E-01	-	-
1382904_at	Ccdc55	coiled-coil domain containing 55	303346	Rn.145937	BF397274	6.74	6.53	6.57	7.01	6.36	6.77	1.07	up	6.44E-01	8.95E-01	-	-
1378667_at	---	---	---	Rn.206268	BF411828	2.35	2.34	2.36	2.34	2.67	2.33	1.07	up	4.20E-01	8.95E-01	-	-
1384905_at	Cd209g	CD209g molecule	688750	Rn.137828	AI578098	2.44	2.42	2.46	2.43	2.45	2.74	1.07	up	3.74E-01	8.95E-01	-	-
1390473_at	Kcng2	potassium voltage-gated channel, subfamily G, member 2	307234	Rn.163389	AI407741	2.74	2.54	2.58	2.58	3.02	2.57	1.07	up	5.70E-01	8.95E-01	-	-
1370808_at	Cyb5r3	cytochrome b5 reductase 3	25035	Rn.35998	J03867	7.55	8.30	8.12	8.03	8.15	7.50	1.07	down	7.60E-01	9.22E-01	-	-
1391997_at	LOC301128	Similar to jumonji domain containing 2B	301128	Rn.6679	AA523656	4.11	2.38	3.07	3.42	3.08	2.76	1.07	down	8.62E-01	9.57E-01	-	-
1378223_at	---	---	---	Rn.205676	AI717058	2.84	2.59	2.66	2.57	2.64	2.57	1.07	down	2.68E-01	8.95E-01	-	-
1390491_at	Coq9	coenzyme Q9 homolog (S. cerevisiae)	498909	Rn.22044	BM390772	2.38	2.61	2.36	2.35	2.35	2.94	1.07	up	6.65E-01	8.96E-01	-	-
1389783_s_at	RGD1311906	similar to Fc fragment of IgG binding protein; IgG Fc binding protein	292746	Rn.103230	BI280865	2.71	2.69	2.74	2.68	2.76	3.01	1.07	up	3.78E-01	8.95E-01	-	-
1368904_at	Capn10	calpain 10	63834	Rn.216532	NM_031673	2.45	2.57	2.48	2.42	2.47	2.92	1.07	up	5.76E-01	8.95E-01	-	-
1386925_at	Arpc1b	actin related protein 2/3 complex, subunit 1B	54227	Rn.2090	NM_019289	5.59	5.70	5.69	5.55	5.78	5.95	1.07	up	4.64E-01	8.95E-01	-	-
1373860_at	Sox4	SRY (sex determining region Y)-box 4	364712	Rn.163667	BI297183	2.44	2.30	2.37	2.76	2.30	2.34	1.07	up	5.52E-01	8.95E-01	-	-
1391516_at	LOC303140	up-regulator of carnitine transporter, OCTN2	303140	---	AI058429	2.58	2.58	2.60	2.91	2.59	2.56	1.07	up	4.27E-01	8.95E-01	-	-
1374708_at	RGD1565043	similar to Rho guanine nucleotide exchange factor (GEF) 10	306618	---	BF408594	2.28	2.27	2.28	2.58	2.28	2.27	1.07	up	3.85E-01	8.95E-01	-	-
1370599_a_at	Ptprs	protein tyrosine phosphatase, receptor type, S	25029	Rn.91202	L19933	2.48	2.46	3.11	2.47	2.48	2.79	1.07	down	6.97E-01	9.07E-01	-	-
1388393_at	Plp2	proteolipid protein 2 (colonic epithelium-enriched)	302562	Rn.96974	BM385031	7.62	7.28	8.17	8.33	7.01	8.03	1.07	up	8.45E-01	9.52E-01	-	-
1385776_at	---	---	---	Rn.208170	BE111954	3.04	2.40	2.42	2.75	2.42	2.39	1.07	down	7.00E-01	9.07E-01	-	-
1391258_at	---	---	---	---	AI178337	2.91	2.38	2.35	2.59	2.38	2.37	1.07	down	6.37E-01	8.95E-01	-	-
1389724_at	Dolpp1	dolichyl pyrophosphate phosphatase 1	296624	Rn.93101	BI274507	4.22	4.02	4.19	4.03	4.06	4.03	1.07	down	1.93E-01	8.95E-01	-	-
1375503_at	Ifit0	intermediate filament family orphan 1	362437	Rn.38932	AI411183	2.50	2.49	2.50	2.49	2.81	2.48	1.07	up	4.04E-01	8.95E-01	-	-
1388317_at	---	---	---	Rn.114933	BE110655	7.29	7.52	6.92	6.60	7.50	7.93	1.07	up	8.28E-01	9.46E-01	-	-
1389077_at	Golt1b	golgi transport 1 homolog B (S. cerevisiae)	362460	Rn.1895	AI179974	3.09	3.30	3.08	3.06	3.08	3.04	1.07	down	2.40E-01	8.95E-01	-	-
1375880_at	Appbp2	amyloid beta precursor protein (cytoplasmic tail) binding protein 2	303396	Rn.104856	AI170384	5.63	6.45	5.87	4.93	6.41	6.30	1.07	down	8.62E-01	9.57E-01	-	-
1373737_at	---	---	---	Rn.209875	BF415808	2.33	2.62	2.33	2.33	2.33	2.32	1.07	down	3.58E-01	8.95E-01	-	-
1382015_at	---	---	---	Rn.93165	AI172613	6.08	6.13	6.14	6.01	6.02	6.02	1.07	down	7.78E-03	8.95E-01	-	-
1382705_at	---	---	---	Rn.171506	BE116909	6.74	6.19	6.21	6.65	6.19	6.01	1.07	down	7.24E-01	9.12E-01	-	-
1373110_at	---	---	---	Rn.1452	AI407487	8.63	8.82	7.84	8.39	8.51	8.69	1.07	up	7.67E-01	9.24E-01	-	-
1384937_at	Rbak	RB-associated KRAB zinc finger	288489	Rn.137256	AI715121	3.74	2.73	2.77	3.14	3.67	2.73	1.07	up	8.28E-01	9.45E-01	-	-
1397519_at	Adipor2	adiponectin receptor 2	312670	Rn.101984	BF547596	2.46	2.52	2.48	2.66	2.48	2.61	1.07	up	1.53E-01	8.95E-01	-	-
1378433_at	Ankrd33b	ankyrin repeat domain 33B	310200	Rn.205946	BI296242	3.99	4.61	4.01	3.85	3.96	4.50	1.07	down	7.46E-01	9.18E-01	-	-
1397290_at	RGD1308759	similar to KIAA0892 protein	290668	Rn.49215	AI408310	2.86	2.77	2.86	3.04	2.89	2.86	1.07	up	2.01E-01	8.95E-01	-	-
1379575_at	---	---	---	Rn.204910	BF412271	3.03	2.97	2.91	3.36	2.95	2.89	1.07	up	5.47E-01	8.95E-01	-	-
1388432_at	Optn	optineurin	246294	Rn.63435	BI294994	7.36	7.16	6.73	6.97	7.34	7.23	1.07	up	6.70E-01	9.00E-01	-	-
1395994_at	---	---	---	Rn.115701	BE116471	2.64	2.69	2.70	2.50	2.90	2.92	1.07	up	5.12E-01	8.95E-01	-	-
1367531_at	Eif4h	eukaryotic translation initiation factor 4H	288599	Rn.79423	BG666846	7.35	7.81	7.20	7.68	7.56	7.42	1.07	up	6.45E-01	8.95E-01	-	-
1379148_at	---	---	---	Rn.210988	BF404371	2.43	2.41	2.44	2.74	2.43	2.40	1.07	up	4.10E-01	8.95E-01	-	-
1392833_at	---	---	---	---	BF289062	2.27	2.27	2.28	2.27	2.59	2.26	1.07	up	4.05E-01	8.95E-01	-	-
1382891_at	Usp27x	ubiquitin specific peptidase 27, X-linked	302566	Rn.61758	BE108241	2.97	2.97	3.04	2.99	3.03	3.27	1.07	up	3.34E-01	8.95E-01	-	-
1380139_at	---	---	---	Rn.8110	AI500762	2.49	2.44	2.50	2.82	2.48	2.42	1.07	up	4.88E-01	8.95E-01	-	-
1385521_at	---	---	---	Rn.150075	AI603505	7.86	8.42	9.02	8.23	8.54	8.84	1.07	up	8.06E-01	9.38E-01	-	-
1372962_at	Tarbp2	TAR (HIV-1) RNA binding protein 2	363006	Rn.17227	AI599123	3.00	3.57	3.15	3.31	3.51	3.19	1.07	up	6.36E-01	8.95E-01	-	-
1387598_at	Thpo	thrombopoietin	81811	Rn.10576	NM_013133	3.48	3.27	3.26	3.79	3.27	3.24	1.07	up	6.35E-01	8.95E-01	-	-
1389593_at	---	---	---	Rn.219292	BM392287	2.50	2.51	3.43	2.56	2.59	3.00	1.07	down	7.84E-01	9.30E-01	-	-
1388929_at	---	---	---	Rn.117671	AI011716	4.80	5.55	7.53	6.17	5.46	5.95	1.07	down	9.12E-01	9.74E-01	-	-
1370729_at	Ss18l1	synovial sarcoma translocation gene on chromosome 18-like 1	192352	Rn.81037	AY034073	2.95	3.26	2.95	2.94	2.95	2.97	1.07	down	3.91E-01	8.95E-01	-	-
1388844_at	---	---	---	Rn.145438	BM390767	2.73	2.69	2.85	2.71	2.72	2.54	1.07	down	2.58E-01	8.95E-01	-	-
1380128_at	---	---	---	Rn.61106	AI237408	2.95	2.65	2.85	3.40	2.55	2.79	1.07	up	7.32E-01	9.14E-01	-	-
1380362_at	Sephs1	Selenophosphate synthetase 1	291314	Rn.100803	AW534019	2.34	2.32	2.65	2.34	2.34	2.32	1.07	down	4.03E-01	8.95E-01	-	-
1371587_at	Map2k1ip1	mitogen-activated protein kinase kinase 1 interacting protein 1	362045	Rn.1123	AA817829	5.92	6.50	5.39	5.19	6.12	6.20	1.07	down	8.39E-01	9.50E-01	-	-
1372683_at	Mocos	molybdenum cofactor sulfurase	361300	Rn.51875	BI291252	5.30	5.29	5.30	5.50	4.81	5.29	1.07	down	6.56E-01	8.98E-01	-	-
1372529_at	---	---	---	Rn.12839	BE116914	4.68	5.58	5.80	6.02	4.79	5.54	1.07	up	8.52E-01	9.54E-01	-	-
1368399_s_at	Pgcp	plasma glutamate carboxypeptidase	58952	Rn.17112	NM_031640	7.86	7.93	7.64	7.64	7.70	8.38	1.07	up	7.15E-01	9.10E-01	-	-
1382272_at	Agtrap	angiotensin II receptor-associated protein	298646	Rn.8471	BE349785	8.69	8.89	8.64	8.63	8.72	9.18	1.07	up	6.27E-01	8.95E-01	-	-
1384983_at	Zdhhc5	zinc finger, DHHC-type containing 5	362156	Rn.4240	BI294693	3.59	3.57	3.63	3.59	3.60	3.89	1.07	up	3.85E-01	8.95E-01	-	-
1372346_at	Znf513	zinc finger protein 513	313913	Rn.15926	AI230729	4.71	4.43	4.46	4.10	4.53	4.68	1.07	down	6.40E-01	8.95E-01	-	-
1376998_a_at	RGD1308093	similar to FLJ00128 protein	361034	Rn.98243	BI276006	2.33	2.49	2.33	2.57	2.44	2.42	1.07	up	2.39E-01	8.95E-01	-	-
1388440_at	Aph1b	anterior pharynx defective 1 homolog B (C. elegans)	300802	Rn.103390	AI408482	5.54	4.31	4.11	4.65	4.11	4.91	1.07	down	8.55E-01	9.55E-01	-	-
1376957_at	Lzic	leucine zipper and CTNNBIP1 domain containing	366507	Rn.162132	AI178922	2.87	3.32	2.44	3.11	2.92	2.90	1.07	up	7.26E-01	9.13E-01	-	-
1384766_a_at	Phf14	PHD finger protein 14	500030	Rn.117647	AI717644	6.52	5.99	5.94	6.51	5.66	5.99	1.07	down	7.67E-01	9.24E-01	-	-
1379138_at	---	---	---	---	BF391688	2.60	2.60	2.68	2.98	2.61	2.59	1.07	up	4.87E-01	8.95E-01	-	-
1397473_at	Dtnbp1	distrobrevin binding protein 1	641528	Rn.187290	AI029288	3.67	3.38	3.29	3.35	3.93	3.37	1.07	up	6.79E-01	9.02E-01	-	-
1376259_at	Prkcq	protein kinase C, theta	85420	Rn.8227	AI171093	5.09	6.13	5.90	5.33	5.65	6.44	1.07	up	8.39E-01	9.50E-01	-	-
1395171_at	---	---	---	Rn.148906	BI281135	2.47	2.45	2.54	2.46	2.86	2.43	1.07	up	5.30E-01	8.95E-01	-	-
1372005_at	---	---	---	Rn.114418	BI294361	2.57	2.50	2.75	2.96	2.58	2.57	1.07	up	5.48E-01	8.95E-01	-	-
1368698_at	Atp2b2	ATPase, Ca++ transporting, plasma membrane 2	24215	Rn.90982	NM_012508	2.68	2.38	2.40	2.38	2.40	2.37	1.07	down	3.68E-01	8.95E-01	-	-
1384425_at	LOC304131	similar to C21ORF7	304131	Rn.32787	BI297081	2.80	3.06	2.80	2.77	2.80	2.80	1.07	down	3.29E-01	8.95E-01	-	-
1383833_at	Fam55b	family with sequence similarity 55, member B	500991	Rn.29872	BI291641	2.72	2.40	2.42	2.42	2.43	2.40	1.07	down	4.02E-01	8.95E-01	-	-
1392974_at	Wasf1	WAS protein family, member 1	294568	Rn.7692	BI295427	3.37	2.97	2.68	3.52	3.02	2.77	1.07	up	7.59E-01	9.21E-01	-	-
1381810_at	---	---	---	Rn.200151	BF406753	5.35	6.37	5.75	6.79	4.87	6.10	1.07	up	8.84E-01	9.64E-01	-	-
1371839_at	Sfrs2	splicing factor, arginine/serine-rich 2	494445	Rn.136644	AA819369	7.12	6.28	6.57	6.96	6.46	6.25	1.07	down	7.77E-01	9.27E-01	-	-
1371842_at	Zmat2	zinc finger, matrin type 2	679898	Rn.203095	AI227747	8.94	8.77	8.91	8.46	8.83	9.05	1.07	down	6.16E-01	8.95E-01	-	-
1373013_at	Paip2	poly(A) binding protein interacting protein 2	361309	Rn.1073	AI178191	8.24	8.52	8.51	8.22	8.39	8.38	1.07	down	4.14E-01	8.95E-01	-	-
1375484_at	---	---	---	Rn.166596	BG376458	3.31	4.45	3.10	3.47	3.58	3.51	1.07	down	8.27E-01	9.45E-01	-	-
1383399_at	Sv2a	synaptic vesicle glycoprotein 2a	117559	Rn.11264	AI574728	2.37	2.36	2.66	2.36	2.38	2.36	1.07	down	3.70E-01	8.95E-01	-	-
1382260_at	---	---	---	Rn.203223	AW531471	2.43	3.00	2.43	2.42	2.72	2.41	1.07	down	6.72E-01	9.01E-01	-	-
1397369_at	---	---	---	---	BF387226	2.56	2.27	2.28	2.28	2.28	2.26	1.07	down	3.51E-01	8.95E-01	-	-
1375202_at	Ier5	immediate early response 5	498256	Rn.8590	AA800604	2.43	2.36	2.39	2.39	2.74

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1371789_at	Clpp	ClpP caseinolytic peptidase, ATP-dependent, proteolytic subunit homolog (E.	301117	Rn.12681	AI411601	6.87	6.66	6.15	6.67	6.54	6.77	1.07	up	6.86E-01	9.04E-01	-	-
1371345_at	Mbd3	methyl-CpG binding domain protein 3	362834	Rn.1737	AI008699	6.74	7.84	7.07	7.56	7.01	7.37	1.07	up	8.01E-01	9.36E-01	-	-
1370371_a_at	acam1 /// Ceacam	carcinoembryonic antigen-related cell adhesion molecule 1 (biliary glycoprote	287009 /// 81613	Rn.92160	U32056	2.86	2.88	3.06	3.17	2.79	3.13	1.07	up	5.17E-01	8.95E-01	-	-
1375180_at	---	---	---	---	BF419280	2.32	2.61	2.33	2.32	2.33	2.32	1.07	down	3.57E-01	8.95E-01	-	-
1380619_at	RGD1305537	similar to RIKEN cDNA 3110001I22	363528	Rn.122064	AI177390	2.75	2.43	2.45	2.43	2.49	2.42	1.07	down	4.17E-01	8.95E-01	-	-
1389115_at	Evpl	envoplakin	303687	Rn.19832	AI716245	2.46	2.45	2.71	2.45	2.46	2.43	1.07	down	3.24E-01	8.95E-01	-	-
1386823_at	Irx5	Iroquois homeobox 5	498918	Rn.141335	BF545481	2.92	4.34	2.84	3.01	3.08	4.30	1.07	up	8.87E-01	9.65E-01	-	-
1371549_at	Wdr23	WD repeat domain 23	305895	Rn.16542	AI228630	10.62	10.28	10.75	10.75	10.15	10.47	1.07	down	6.86E-01	9.04E-01	-	-
1369505_at	Cds2	CDP-diacylglycerol synthase (phosphatidate cytidylyltransferase) 2	114101	Rn.212746	NM_053643	5.51	5.25	5.31	6.00	4.95	5.42	1.07	up	7.74E-01	9.26E-01	-	-
1382463_at	---	---	---	Rn.165691	AI757104	4.68	4.66	4.69	4.57	4.70	5.05	1.07	up	5.32E-01	8.95E-01	-	-
1381855_at	Tube1	tubulin, epsilon 1	361856	Rn.101545	AA851436	2.58	2.59	2.74	2.54	2.58	2.50	1.07	down	1.59E-01	8.95E-01	-	-
1389274_at	Dcakd	dephospho-CoA kinase domain containing	360639	Rn.102152	AA800803	2.62	2.62	2.54	2.72	2.73	2.61	1.07	up	1.05E-01	8.95E-01	-	-
1372364_a_at	Ntan1	N-terminal asparagine amidase	360462	Rn.1273	AA894101	8.29	8.29	7.91	8.03	7.84	8.33	1.07	down	6.35E-01	8.95E-01	-	-
1371066_at	Snrk	SNF related kinase	170837	Rn.10245	X89383	2.33	2.32	2.33	2.63	2.33	2.32	1.07	up	3.93E-01	8.95E-01	-	-
1396671_at	---	---	---	Rn.154193	BF400889	2.43	2.77	2.43	2.52	2.43	2.40	1.07	down	4.57E-01	8.95E-01	-	-
1394856_at	---	---	---	---	BM383417	2.54	2.77	2.56	2.54	2.52	2.53	1.07	down	2.61E-01	8.95E-01	-	-
1373397_at	Mapre1	microtubule-associated protein, RP/EB family, member 1	114764	Rn.7652	AI180161	8.64	8.76	9.29	8.94	8.42	9.05	1.07	down	7.44E-01	9.17E-01	-	-
1383402_at	---	---	---	Rn.163601	BE107427	2.38	2.38	2.40	2.37	2.39	2.68	1.07	up	3.90E-01	8.95E-01	-	-
1392855_x_at	ab1b /// Rab1b-ps	RAB1B, member RAS oncogene family /// RAB1B, member RAS oncogene fa	00126191 /// 3617	Rn.105979	AI711306	5.77	5.35	5.91	4.57	7.22	4.96	1.07	down	9.14E-01	9.74E-01	-	-
1375695_at	Ythdf2	YTH domain family, member 2	313053	Rn.21737	AW535358	3.90	4.23	3.92	3.54	3.63	4.58	1.07	down	7.94E-01	9.34E-01	-	-
1383136_a_at	---	---	---	---	AI764288	2.67	2.52	2.53	2.53	2.53	2.95	1.07	up	5.52E-01	8.95E-01	-	-
1387791_at	Ace	angiotensin I converting enzyme (peptidyl-dipeptidase A) 1	24310	Rn.10149	AF201331	2.95	4.76	2.93	3.34	4.37	3.23	1.07	up	8.98E-01	9.68E-01	-	-
1391198_at	Car12	carbonic anhydrase 12	363085	Rn.18638	BF401433	5.08	5.64	5.25	5.23	5.25	5.21	1.07	down	5.90E-01	8.95E-01	-	-
1374710_at	---	---	---	Rn.41040	BI289549	2.34	2.33	2.62	2.33	2.34	2.32	1.07	down	3.68E-01	8.95E-01	-	-
1389933_at	Smek1	SMEK homolog 1, suppressor of mek1 (Dictyostelium)	314388	Rn.22873	AI176476	2.51	2.35	2.32	2.31	2.32	2.26	1.07	down	1.94E-01	8.95E-01	-	-
1367972_at	Cand1	cullin-associated and neddylation-dissociated 1	117152	Rn.32934	NM_054004	7.87	7.72	7.72	7.88	7.60	7.55	1.07	down	4.42E-01	8.95E-01	-	-
1397468_at	Hsd12	3-hydroxysteroid dehydrogenase like 2	313200	Rn.203684	BI288527	6.28	7.43	7.57	7.47	6.11	7.42	1.07	down	8.80E-01	9.63E-01	-	-
1391467_at	Pknox1	PBX/knotted 1 homeobox 1	294322	Rn.204913	BE111698	2.51	2.51	2.57	2.49	2.50	2.89	1.07	up	5.05E-01	8.95E-01	-	-
1380605_at	---	---	---	Rn.173545	BM387149	3.37	3.30	3.38	3.58	3.38	3.39	1.07	up	2.38E-01	8.95E-01	-	-
1376038_at	Tex2	testis expressed 2	303611	Rn.94152	AI411054	8.64	9.26	9.28	9.14	8.28	9.47	1.07	down	8.26E-01	9.45E-01	-	-
1384694_at	---	---	---	---	AI169393	2.33	2.33	2.34	2.48	2.33	2.47	1.07	up	1.12E-01	8.95E-01	-	-
1376102_at	Tmbim1	transmembrane BAX inhibitor motif containing 1	316516	Rn.204023	BI292351	7.37	5.95	7.41	7.06	7.01	6.37	1.07	down	8.64E-01	9.58E-01	-	-
1387855_at	Gdi1	GDP dissociation inhibitor 1	25183	Rn.4000	BI278628	8.61	8.22	8.54	8.53	8.17	8.38	1.07	down	5.74E-01	8.95E-01	-	-
1398977_at	---	---	---	---	BF558116	6.77	7.19	7.13	6.66	7.50	7.22	1.07	up	7.46E-01	9.18E-01	-	-
1367632_at	Glul	glutamate-ammonia ligase (glutamine synthetase)	24957	Rn.2204	BI275294	12.04	12.09	12.21	12.30	12.23	12.11	1.07	up	2.72E-01	8.95E-01	-	-
1378524_at	Rnf19a	ring finger protein 19A	362900	Rn.204043	AW533310	6.98	6.50	6.48	7.03	6.02	7.19	1.07	up	8.22E-01	9.43E-01	-	-
1383849_at	Rtx7	regulatory factor X, 7	315804	Rn.58758	AW143311	4.13	4.76	4.16	4.14	3.97	4.64	1.07	down	7.55E-01	9.20E-01	-	-
1392650_at	Csnk2a1	casein kinase 2, alpha 1 polypeptide	116549	Rn.4231	AI059343	2.57	2.77	2.68	2.98	2.68	2.65	1.07	up	4.68E-01	8.95E-01	-	-
1384975_at	Ermp1	endoplasmic reticulum metallopeptidase 1	373544	Rn.99609	BM387447	2.31	2.59	2.32	2.31	2.31	2.31	1.07	down	3.60E-01	8.95E-01	-	-
1376301_at	---	---	---	Rn.107201	BE110719	3.23	2.95	2.96	2.95	2.96	2.93	1.07	down	3.46E-01	8.95E-01	-	-
1372573_at	---	---	---	---	BI300206	2.66	2.35	2.37	2.38	2.37	2.34	1.07	down	3.98E-01	8.95E-01	-	-
1375755_at	B4galt1	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 1	24390	Rn.17157	BE098673	2.55	2.43	2.59	2.62	2.56	2.68	1.07	up	1.73E-01	8.95E-01	-	-
1380743_at	---	---	---	Rn.171475	BE116508	2.49	2.88	2.49	2.49	2.48	2.59	1.07	down	5.15E-01	8.95E-01	-	-
1368271_a_at	Fabp4	fatty acid binding protein 4, adipocyte	79451	Rn.4258	NM_053365	2.52	2.54	2.55	2.54	2.82	2.54	1.07	up	3.63E-01	8.95E-01	-	-
1372482_at	Slc39a13	solute carrier family 39 (metal ion transporter), member 13	299520	Rn.17295	AI600216	4.52	4.75	4.46	4.75	4.53	4.75	1.07	up	4.45E-01	8.95E-01	-	-
1370017_at	Emd	emerin	25437	Rn.10968	NM_012948	2.64	2.63	2.67	2.66	2.92	2.64	1.07	up	3.46E-01	8.95E-01	-	-
1371209_at	RT1-CE5	RT1 class I, CE5	309607	---	AJ243338	2.49	2.47	2.52	2.49	2.82	2.47	1.07	up	4.54E-01	8.95E-01	-	-
1393777_at	---	---	---	Rn.92969	AA998104	8.51	7.51	8.02	7.79	7.75	8.22	1.07	down	7.81E-01	9.29E-01	-	-
1372381_at	---	---	---	Rn.16382	BM383457	4.84	4.68	4.27	4.23	4.97	4.87	1.07	up	7.53E-01	9.20E-01	-	-
1387139_at	Hao2	hydroxyacid oxidase 2 (long chain)	84029	Rn.198611	NM_032082	13.23	13.23	13.36	13.20	13.20	13.14	1.07	down	1.11E-01	8.95E-01	-	-
1392773_at	Psk5	proprotein convertase subtilisin/kexin type 5	116548	Rn.104002	AA859578	2.43	2.59	2.43	2.45	2.44	2.86	1.07	up	5.48E-01	8.95E-01	-	-
1369626_at	Sv2b	synaptic vesicle glycoprotein 2b	117556	Rn.58137	BG672437	10.43	10.32	10.37	10.63	10.56	10.21	1.07	up	5.11E-01	8.95E-01	-	-
1374833_at	---	---	---	Rn.24673	BF290953	4.12	4.84	5.46	4.96	3.23	5.94	1.07	down	9.19E-01	9.76E-01	-	-
1378964_at	Ttc9c	Tetratricopeptide repeat domain 9C	309196	Rn.162477	AI709953	3.73	4.44	5.44	4.05	4.32	4.96	1.07	down	8.73E-01	9.61E-01	-	-
1392897_at	---	---	---	---	AA924586	7.01	7.11	7.33	7.35	7.21	7.19	1.07	up	4.23E-01	8.95E-01	-	-
1369862_at	Pim1	pim-1 oncogene	24649	Rn.34888	NM_017034	2.49	2.56	2.60	2.62	2.75	2.57	1.07	up	1.98E-01	8.95E-01	-	-
1377509_at	---	---	---	---	BI295894	2.68	2.56	2.70	2.53	2.71	2.41	1.07	down	3.71E-01	8.95E-01	-	-
1388884_at	RGD1310224	similar to RIKEN cDNA 1810022C23	291076	Rn.3194	BM390774	12.33	12.40	12.32	12.29	12.14	12.33	1.07	down	2.06E-01	8.95E-01	-	-
1392903_at	---	---	---	Rn.164361	BG665185	4.69	4.09	4.57	4.10	4.86	4.09	1.07	down	7.74E-01	9.26E-01	-	-
1374227_at	Ttc27	tetratricopeptide repeat domain 27	298782	Rn.13205	BM386851	3.74	5.94	5.32	4.85	4.62	5.25	1.07	down	8.95E-01	9.67E-01	-	-
1381033_at	---	---	---	Rn.173653	BF413686	2.74	2.54	2.58	2.53	2.57	2.48	1.07	down	2.18E-01	8.95E-01	-	-
1376961_at	Lrfn2	leucine rich repeat and fibronectin type III domain containing 2	316205	Rn.219938	BG380772	2.44	2.43	2.44	2.43	2.76	2.41	1.07	up	4.45E-01	8.95E-01	-	-
1397226_at	---	---	---	---	AI100942	2.70	2.42	2.45	2.43	2.44	2.41	1.07	down	3.39E-01	8.95E-01	-	-
1385696_at	---	---	---	Rn.126019	BI274471	3.22	2.85	2.87	2.41	3.40	2.85	1.07	down	7.73E-01	9.26E-01	-	-
1383171_at	Tfb2m	transcription factor B2, mitochondrial	289307	Rn.96104	BG373674	6.39	6.38	6.06	6.22	6.54	6.34	1.07	up	5.41E-01	8.95E-01	-	-
1389262_at	---	---	---	Rn.22489	AI172156	2.69	2.68	3.03	2.69	2.71	2.72	1.07	down	4.57E-01	8.95E-01	-	-
1371284_at	Igha	immunoglobulin heavy chain, alpha	314487	Rn.219258	AJ391310	2.79	2.58	2.60	2.56	2.62	2.50	1.07	down	2.85E-01	8.95E-01	-	-
1383591_at	Sf3a2	splicing factor 3a, subunit 2	299620	Rn.102569	BM391839	3.28	3.88	3.50	4.43	3.50	3.02	1.07	up	8.41E-01	9.50E-01	-	-
1393171_at	RGD1564799	similar to transmembrane 4 superfamily member 10	501589	Rn.1643	BG664080	2.65	2.51	2.68	2.55	2.55	2.45	1.07	down	1.97E-01	8.95E-01	-	-
1380789_at	---	---	---	Rn.146943	AF416254	2.53	2.68	2.59	2.53	2.57	2.41	1.07	down	2.14E-01	8.95E-01	-	-
1398430_at	---	---	---	Rn.8814	AW524711	7.23	7.98	8.83	7.67	7.53	8.55	1.07	down	8.73E-01	9.61E-01	-	-
1370368_at	Cabin1	calcineurin binding protein 1	94165	Rn.4	AF061947	3.74	4.18	3.65	3.85	3.62	3.81	1.07	down	6.16E-01	8.95E-01	-	-
1390340_a_at	Eif4g1	eukaryotic translation initiation factor 4 gamma, 1	287986	Rn.101803	AA899256	8.24	7.97	7.95	7.94	7.89	8.04	1.07	down	4.06E-01	8.95E-01	-	-
1374176_at	RGD1308059	similar to DNA segment, Chr 4, Brigham & Womens Genetics 0951 expresse	362535	Rn.36366	AI408727	2.58	2.42	2.59	2.57	2.58	2.72	1.07	up	2.65E-01	8.95E-01	-	-
1393298_at	---	---	---	Rn.17029	BF566249	4.20	4.63	3.71	3.55	3.60	5.10	1.07	down	8.76E-01	9.61E-01	-	-
1392183_at	Hoxc9	homeobox C9	368178	Rn.101733	AI547389	2.74	2.45	2.49	2.46	2.49	2.44	1.07	down	3.49E-01	8.95E-01	-	-
1371542_at	Tuba4a	tubulin, alpha 4A	316531	Rn.92961	BI284599	7.03	8.39	7.26	7.39	7.40	8.18	1.07	up	8.56E-01	9.55E-01	-	-
1368229_at	Sip1	survival of motor neuron protein interacting protein 1	84404	Rn.34143	NM_053389	4.73	4.66	3.76	4.87	4.12	4.46	1.07	up	8.14E-01	9.40E-01	-	-
1377581_at	Galnt1	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltran	362760	An.40168	AW526899	2.47	2.36	2.51	2.35	2.37	2.33	1.07	down	1.23E-01	8.95E-01	-	-
1376077_at	Mxd1	max dimerization protein 1	362391	Rn.19241	BG374774	2.80	3.34	3.13	3.20	2.82	2.96	1.07	down	6.44E-01	8.95E-01	-	-
1375261_at	Man1a2	Mannosidase, alpha, class 1A, member 2	295319	Rn.218006	AI011360	3.21	3.13	3.62	3.41	3.17	3.09	1.07	down	6.24E-01	8.95E-01	-	-
1380057_at	---	---	---	Rn.45104	BE097091	2.76	2.32	2.30	2.29	2.48	2.31	1.07	down	5.85E-01	8.95E-01	-	-
1386720_at	Tmprss8	transmembrane protease, serine 8 (intestinal)	287106	Rn.102783	BF555392	2.49	3.10	2.51	2.51	2.53	2.76	1.07	down	6.81E-01	9.03E-01	-	-
1378822_at	---	---	---	Rn.152983	BF563999	2.58	2.46	2.33	2.37	2.38	2.32	1.07	down	2.63E-01	8.95E-01	-	-
1377580_at	RGD1565474	similar to mKIAA0738 protein	362353	Rn.44698	AA964744	3.06	2.92	3.08	3.04	3.25	3.06	1.07	up	3.11E-01	8.95E-01	-	-
1379436_a_at	---	---	---	Rn.203412	AA945875	2.61	2.91	2.62	2.62	2.61	2.63	1.07	down	3.82E-01	8.95E-01	-	-
1380004_at	---	---	---	Rn.209013	BG373440	2.68	2.44	2.45	2.43	2.45	2.40	1.07	down	3.07E-01	8.95E-01	-	-
1396331_at	---	---	---	---	BF387074	2.66	2.58	2.63	2.63	3.01	2.52	1.07	up	5.64E-01	8.95E-01	-	-
1375116_at	---	---	---	Rn.216548	AI548989	3.53	2.89	4.06	4.20	3.32	3.25	1.07	up	8.45E-01	9.52E-01	-	-
1397766_at	---	---	---	Rn.160933	BI291982	8.32	7.19	7.35	7.74	7.54	7.86	1.07	up	8.07E-01	9.38E-01	-	-
1397262_at	---	---	---	Rn.148131	AI144961	2.66	2.37	2.38	2.37	2.38	2.36	1.07	down	3.73E-01	8.95E-01	-	-
1394130_at	Trim44	Tripartite motif-containing 44	362172	Rn.8005	AA946190	3.05	3.25	2.69	3.09	3.10	3.09	1.07	up	5.96E-01	8.95E-01	-	-
1372446_at	Ppp1r2	protein phosphatase 1, regulatory (inhibitor) subunit 2	192361	Rn.4016	AI172726	7.45	8.10	8.37	7.76	8.24	8.20	1.07	up	7.75E-01	9.27E-01	-	-
1381762_at	---	---	---	Rn.46190	AW526420	2.51	2.48	2.53	2.84	2.52	2.46	1.07	up	4.65E-01	8.95E-01	-	-
1374390_at	LOC686324	similar to Protein UNQ655/PRO1286 homolog precursor	686324	---	AI716420	7.45	8.49	8.55	7.89	7.90	8.41	1.07	down	8.23E-01	9.43E-01	-	-
1398919_at	RGD1304704	similar to hypothetical protein CGI-99	302247	Rn.1434	BI296033	9.39	9.18	9.61	9.02	9.41	8.47	1.07	down	6.40E-01	8.95E-01	-	-
1372380_at	RGD1561067	similar to RNA binding protein gene with multiple splicing	498842	Rn.8565	AI231308	6.49	4.65	5.53	6.73	6.04	4.20	1.07	up	9.23E-01	9.77E-01	-	-
1384249_at	---	---	---	Rn.23570	AI111958	2.30	2.30	2.57	2.29	2.30	2.29	1.07	down	3.66E-01	8.95E-01	-	-
1396589_at	Slc35a3	solute carrier family 35 (UDP-N-acetylglucosamine (UDP-GlcNAc) transporter	310808	Rn.162630	AW141632	2.95	2.94	2.78	2.94	2.95	3.06	1.07	up	2.22E-01	8.95E-01	-	-
1396804_at	Clasp2	cytoplasmic linker associated protein 2	114514	Rn.19943	BF399424	2.70	2.43	2.47	2.44	2.46	2.41	1.07	down	3.30E-01	8.95E-01	-	-
1379152_at	---	---	---	---	BF404953	2.40	2.37	2.38	2.49	2.56	2.39	1.07	up	1.29E-01	8.95E-01	-	-
1389963_at	LOC652956	p55 protein	652956	Rn.189455	BI283388	6.88	7.30	7.83	8.22	7.11	6.97	1.07	up	8.54E-01	9.55E-01	-	-
1393840_at	Gnat2	guanine nucleotide binding protein, alpha transducing 2	365901	Rn.219804	BE095728	2.49	2.47	2.49	2.71	2.49	2.53	1.07	up	2.46E-01	8.95E-01	-	-
1370943_at	Sult1c2a	sulfotransferase family, cytosolic, 1C, member 2a	316153	Rn.205998	AI168953	10.99	11.05	10.94	10.97	11.15	11.14	1.07	up	2.17E-01	8.95E-01	-	-
1378926_at	---	---	---	---	BF415792	2.43	2.43	2.65	2.43	2.43	2.36	1.07	down	2.89E-01	8.95E-01	-	-
1388913_at	Ppap2c	phosphatidic acid phosphatase type 2c	246115	Rn.3301	AA893191	6.49	6.84	7.06	6.87	6.75	7.05	1.07	up	6.40E-01	8.95E-01	-	-
1375622_at	Zfyve20	zinc finger, FYVE domain containing 20	312562	Rn.172475	BF402692	2.82	2.91	2.91	2.97	2.92	3.03	1.07	up	9.21E-02	8.95E-01	-	-
1399045_at	Galnt1	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltran	79214	Rn.10266	AI236745	5.64	6.40	5.65	5.83	4.91	6.66	1.07	down	8.75E-01	9.61E-01	-	-
1367514_at	LOC361635	similar to RIKEN cDNA 9030624J02	361635	Rn.6279	AI235508	3.46	4.09	3.47	3.56	3.44	3.73	1.07	down	6.94E-01	9.05E-01	-	-
1375974_at	---	---	---	Rn.15886	AI010423	5.43	5.74	5.23	5.74	5.49	5.46	1.07	up	6.14E-01	8.95E-01	-	-
1377414_at	RGD1307934	similar to DNA segment, Chr 19, ERATO Doi 386, expressed	293953	Rn.45195	BF400262	3.95	4.20	3.24	3.55	3.63	3.93	1.07	down	7.76E-01	9.27E-01	-	-
1382817_at	Mcm3ap	minichromosome maintenance deficient 3 (S. cerevisiae) associated protein	294339	Rn.55967	AA891758	2.33	2.32	2.34	2.62	2.34	2.32	1.07	up	3.91E-01	8.95E-01	-	-
1391822_at	---	---	---	Rn.153833	AW523356	2.50	2.48	2.50	2.49	2.52	2.76	1.07	up	3.38E-01	8.95E-01	-	-
1380726_at	Aspn	Asporin	306805	Rn.160633	BI290633	2.86	2.60	2.68	2.60	2.68	2.57	1.07	down	3.13E-01	8.95E-01	-	-
1393693_at	Doxl1	diamine oxidase-like protein 1	312316	Rn.79162	BI290553	2.67	2.40	2.41	2.41	2.41	2.39	1.07	down	3.44E-01	8.95E-01	-	-
1375220_at	Ndufa11	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 11	301123	Rn.96380	AA818971	8.42	8.73	8.52	8.70	8.15	8.53	1.07	down	6.40E-01	8.95E-01	-	-
1396876_at	---	---	---	Rn.210075	---	2.91	2.96	3.10	2.89	3.46	3.01	1.07	up	6.21E-01	8.95E-01	-	-
1377614_at	Ccdc95	coiled-coil domain containing 95	293494	Rn.3179	BI283147	2.65	2.65	2.38	2.68	2.65	2.63	1.07	up	3.47E-01	8.95E-01	-	-
1378672_at	---	---	---	Rn.52800	BG381207	2.42	2.41	2.37	2.60	2.48	2.40	1.07	up	1.89E-01	8.95E-01	-	-
1379245_at	Txndc9	thioredoxin domain containing 9	280671	Rn.4272	BI283491	6.02	5.98	6.75	6.31	5.87	6.28	1.07	down	7.59E-01	9.21E-01	-	-
1383374_at	Galnt1	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltran	79214	Rn.10266	BE111170	2.81	3.36	3.43	3.71	2.82	3.36	1.07	up	7.85E-01	9.30E-01	-	-
1380246_at	---	---	---	Rn.43949	AI548945	2.41	2.41	2.42	2.41	2.78	2.34	1.07	up	5.29E-01	8.95E-01	-	-
1399156_at	Arid2	AT rich interactive domain 2 (Arid-rfx like)	366980	Rn.42849	AA900891	6.31	5.98	6.50	6.23	6.05	6.23	1.07	down	5.91E-01	8.95E-01	-	-
1372063_at	---	---	---	Rn.203827	BG377807	2.81	2.54	2.60	2.60	2.51	2.55	1.07	down	3.33E-01	8.95E-01	-	-
1385999_at	Ytne1l1	YME1-like 1 (S. cerevisiae)	114217	Rn.8153	AA849923	3.82	3.90	4.77	4.05	4.18	4.54	1.07	up	7.94E-01	9.34E-01	-	-
1388457_at	Fam125a	family with sequence similarity 125, member A	290635	Rn.106	AI176633	7.30	7.07	6.49	6.66	6.88	7.03	1.07	down	7.38E-01	9.16E-01	-	-
1377276_at	Cdk5r2	Cyclin-dependent kinase 5, regulatory subunit 2 (p39)	50164	Rn.219411	BF390413	2.32	2.36	2.57	2.32	2.33	2.32	1.07	down	2.84E-01	8.95E-01	-	-
1398014_at	---	---	---	Rn.18429	BG371918	2.56	2.52	2.58	2.58	2.82	2.55	1.07	up	3.45E-01	8.95E-01	-	-
1372419_at	Vrk3	vaccinia related kinase 3	361565	Rn.6570	BG380296	8.87	8.82	8.32	8.47	8.59	8.67	1.07	down	6.38E-01	8.95E-01	-	-
1375953_at	---	---	---	Rn.156340	AI012884	2.71	2.70	2.75	2.92	2.73	2.78	1.07	up	1.86E-01	8.95E-01	-	-
1373755_at	Lrrc39	leucine rich repeat containing 39	691307	Rn.79735	AI717543	2.41	2.40	2.43	2.40	2.44	2.69	1.07	up	3.52E-01	8.95E-01	-	-
1383283_at	Ocrl	oculocerebrorenal syndrome of Lowe	317576	Rn.36925	BM385645	2.74	2.71	2.58	2.93	2.55	2.84	1.07	up	4.90E-01	8.95E-01	-	-
1372717_at	---	---	---	---	BI296012	6.22	6.11	6.14	6.15	6.16	6.43	1.07	up	3.74E-01	8.95E-01	-	-
1390054_at	---	---	---	---	BF412571	2.64	2.63	3.09	2.81	2.65	2.62	1.07	down	5.91E-01	8.95E-01	-	-
1377680_at	Gfra3	GDNF family receptor alpha 3	84422	Rn.15499	BG377887	4.71	3.51	5.34	5.04	4.39	4.42	1.07	up	8.78E-01	9.62E-01	-	-
1384150_at	Mid1	Midline 1	54252	Rn.15169	AA901038	2.84	2.52	2.56	2.57	2.56	2.50	1.07	down	4.09E-01	8.95E-01	-	-
1394920_at	---	---	---	Rn.205385	AI556704	2.72	2.57	2.59	2.58	2.60	2.42	1.07	down	2.63E-01	8.95E-01	-	-
1380179_at	---	---	---	Rn.203879	AI548649	2.53	2.42	2.78	2.78	2.54	2.68	1.07	up	4.93E-01	8.95E-01	-	-
1379020_at	Prdm15	PR domain containing 15	304054	Rn.7986	AI454024	2.76	2.96	2.78	2.76	2.79	2.67	1.07	down	2.64E-01	8.95E-01	-	-
1368606_at	Cyp2f4	cytochrome P450, family 2, subfamily f, polypeptide 4	54246	Rn.10817	NM_019303	2.53	2.25	2.26	2.25	2.26	2.25	1.07	down	3.62E-01	8.95E-01	-	-
1384174_at	---	---	---	---	AI028874

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1370553_at	Stx2	syntaxin 2	25130	Rn.10623	L20823	2.51	3.91	2.94	2.83	3.00	3.24	1.07	down	8.39E-01	9.50E-01	-	-
1377604_a_at	Pftk1	PFTAIRE protein kinase 1	362316	Rn.12908	BF549046	2.48	2.47	2.49	2.77	2.48	2.47	1.07	up	3.90E-01	8.95E-01	-	-
1391980_at	LOC360990	similar to ubiquitin specific protease 34	360990	Rn.16057	BF394201	4.15	3.57	4.45	3.65	4.21	4.60	1.07	up	8.17E-01	9.41E-01	-	-
1371612_at	Tsen34	tRNA splicing endonuclease 34 homolog (S. cerevisiae)	292534	Rn.1591	AI177656	9.22	9.27	9.33	9.37	9.29	9.44	1.07	up	1.68E-01	8.95E-01	-	-
1378001_at	---	---	---	Rn.26537	AI548615	2.40	2.38	2.40	2.39	2.69	2.38	1.07	up	4.21E-01	8.95E-01	-	-
1394452_at	---	---	---	Rn.168586	BM391487	4.60	4.25	4.23	4.09	4.44	4.28	1.07	down	5.82E-01	8.95E-01	-	-
1388639_at	Bcas3	Breast carcinoma amplified sequence 3	363662	Rn.203379	BF284148	5.13	4.92	5.30	5.06	5.33	5.23	1.07	up	5.31E-01	8.95E-01	-	-
1373989_at	Rassf1	Ras association (RalGDS/AF-6) domain family member 1	363140	Rn.83042	AI103943	4.83	5.45	4.63	5.44	4.68	5.07	1.07	up	7.91E-01	9.33E-01	-	-
1370038_at	Npvf	neuropeptide VF precursor	60570	Rn.62354	NM_023952	3.44	3.23	3.28	3.20	3.24	3.23	1.07	down	2.33E-01	8.95E-01	-	-
1367964_at	Tnni2	troponin I type 2 (skeletal, fast)	29389	Rn.9924	NM_017185	2.70	2.39	2.55	2.40	2.57	2.39	1.07	down	4.39E-01	8.95E-01	-	-
1369799_at	Abat	4-aminobutyrate aminotransferase	81632	Rn.10090	U29701	7.02	7.48	6.82	6.97	6.88	7.20	1.07	down	6.93E-01	9.05E-01	-	-
1379516_at	RGD1559896	similar to RIKEN cDNA 2310022B05	498967	Rn.6137	AW253651	3.46	4.87	3.18	3.19	4.77	3.84	1.07	up	9.00E-01	9.69E-01	-	-
1369759_at	Slc5a1	solute carrier family 5 (sodium/glucose cotransporter), member 1	25552	Rn.10224	AB000729	4.95	5.76	5.45	6.25	4.37	5.26	1.07	down	8.83E-01	9.64E-01	-	-
1391314_at	Kcnq5l	potassium voltage-gated channel, subfamily Q, member 5-like	259273	Rn.211385	BF414224	3.98	3.72	4.18	3.97	4.11	3.53	1.07	down	6.96E-01	9.06E-01	-	-
1387933_s_at	Podxl	podocalyxin-like	192181	Rn.162741	AB020726	2.37	2.36	2.46	2.37	2.39	2.16	1.07	down	3.06E-01	8.95E-01	-	-
1391558_at	Znf608	zinc finger protein 608	307296	Rn.106300	BF290997	2.69	2.84	2.71	2.65	2.70	2.62	1.07	down	1.57E-01	8.95E-01	-	-
1387109_at	Por	P450 (cytochrome) oxidoreductase	29441	Rn.11359	NM_031576	8.80	7.96	7.51	8.37	7.57	8.61	1.07	up	8.60E-01	9.57E-01	-	-
1394563_at	---	---	---	---	AI230657	2.40	2.39	2.42	2.39	2.70	2.39	1.07	up	4.27E-01	8.95E-01	-	-
1368872_a_at	Homer2	homer homolog 2 (Drosophila)	29547	Rn.30014	NM_053309	3.38	3.32	3.47	3.81	3.22	3.42	1.07	up	6.32E-01	8.95E-01	-	-
1392837_at	LOC498912	similar to Alpha- and gamma-adaptin-binding protein p34	498912	Rn.196542	AA859108	6.52	6.66	7.49	6.63	7.04	6.71	1.07	down	7.90E-01	9.33E-01	-	-
1387599_a_at	Nqo1	NAD(P)H dehydrogenase, quinone 1	24314	Rn.11234	J02670	2.63	3.90	3.04	3.43	2.26	4.15	1.07	up	8.96E-01	9.67E-01	-	-
1371181_x_at	Grm1	glutamate receptor, metabotropic 1	24414	Rn.87787	Y18810	2.53	2.50	2.52	2.52	2.82	2.50	1.07	up	4.24E-01	8.95E-01	-	-
1367462_at	Capns1	calpain, small subunit 1	29156	Rn.3430	U10861	7.09	6.86	7.26	6.91	6.88	7.14	1.07	down	5.47E-01	8.95E-01	-	-
1390311_at	Tll	Tubulin tyrosine ligase	171572	Rn.205120	AW526802	4.53	5.32	5.55	5.30	5.19	5.19	1.07	up	7.79E-01	9.28E-01	-	-
1371933_at	---	---	---	---	AI228039	2.70	2.84	2.89	2.52	2.90	2.73	1.07	down	5.00E-01	8.95E-01	-	-
1368567_at	Ndufv3	NADH dehydrogenase (ubiquinone) flavoprotein 3	64539	Rn.6452	NM_022607	5.83	5.73	5.84	5.83	6.01	5.84	1.07	up	2.45E-01	8.95E-01	-	-
1384379_at	---	---	---	Rn.203994	BG669700	2.35	2.34	2.63	2.34	2.36	2.35	1.07	down	3.84E-01	8.95E-01	-	-
1380447_a_at	Mrps18c	mitochondrial ribosomal protein S18C	289469	Rn.105741	AI071722	6.04	7.85	9.95	8.10	7.59	8.43	1.07	up	9.40E-01	9.83E-01	-	-
1383498_at	---	---	---	Rn.43744	BG373354	4.84	3.68	2.51	2.62	3.69	4.44	1.07	down	9.19E-01	9.76E-01	-	-
1393358_at	---	---	---	Rn.164771	AA957379	2.48	2.52	2.71	2.48	2.49	2.47	1.07	down	2.63E-01	8.95E-01	-	-
1392498_at	Ppp2r5c	protein phosphatase 2, regulatory subunit B' gamma isoform	691318	Rn.2153	BG670494	5.83	7.16	6.59	6.22	6.32	6.77	1.07	down	8.36E-01	9.48E-01	-	-
1398394_at	---	---	---	Rn.222044	AI411809	8.25	8.37	8.26	7.97	8.69	8.50	1.07	up	6.96E-01	9.06E-01	-	-
1398833_at	Mtitps1	membrane-bound transcription factor peptidase, site 1	89842	Rn.2362	NM_053569	5.29	5.68	5.89	5.45	5.70	6.00	1.07	up	7.18E-01	9.11E-01	-	-
1367522_at	Fbx1	coagulation factor VIII-associated (intronic transcript) 1	501661	Rn.41311	AA894324	5.25	5.24	5.53	5.05	5.21	5.47	1.07	down	5.80E-01	8.95E-01	-	-
1383538_at	RGD1565257	Similar to zinc finger protein 650	311115	Rn.16154	BF545850	7.38	7.08	7.50	7.50	7.01	7.72	1.07	up	7.24E-01	9.12E-01	-	-
1395449_at	RGD1309784	similar to ribosomal protein L24-like; 60S ribosomal protein L30 isolog; myo024	363099	Rn.105523	BG673211	5.30	5.19	5.35	5.21	5.18	5.18	1.07	down	1.22E-01	8.95E-01	-	-
1378770_at	---	---	---	Rn.207540	BE102513	2.77	2.82	2.83	2.77	2.77	2.60	1.07	down	1.86E-01	8.95E-01	-	-
1388246_at	Clu	clusterin	24854	Rn.1780	AF314657	5.40	5.86	6.35	6.83	4.76	6.28	1.07	up	8.98E-01	9.68E-01	-	-
1390204_at	---	---	---	---	AI227856	2.40	2.41	2.41	2.35	2.46	2.69	1.07	up	4.07E-01	8.95E-01	-	-
1383881_at	---	---	---	Rn.62409	BG665316	4.63	5.39	5.12	4.01	4.86	5.99	1.07	down	8.88E-01	9.65E-01	-	-
1389444_at	Zdhhc20	Zinc finger, DHHC-type containing 20	305923	Rn.22849	AI179665	7.44	7.66	8.12	7.84	7.68	7.96	1.07	up	6.91E-01	9.05E-01	-	-
1390282_at	Cyp2s1	cytochrome P450, family 2, subfamily s, polypeptide 1	308445	Rn.6389	BI274639	2.40	2.37	2.42	2.39	2.71	2.37	1.07	up	4.48E-01	8.95E-01	-	-
1398693_at	Man1c1	mannosidase, alpha, class 1C, member 1	362625	Rn.29300	BF289500	2.71	2.45	2.46	2.45	2.46	2.44	1.07	down	3.50E-01	8.95E-01	-	-
1397573_at	---	---	---	Rn.165714	BM391779	11.28	10.93	10.62	11.23	11.04	10.27	1.07	down	8.05E-01	9.37E-01	-	-
1374826_at	---	---	---	Rn.15239	BE118972	2.62	2.32	2.35	2.33	2.35	2.33	1.07	down	3.88E-01	8.95E-01	-	-
1394000_at	---	---	---	Rn.217118	BM391003	2.39	2.32	2.39	2.59	2.43	2.36	1.07	up	2.64E-01	8.95E-01	-	-
1372215_at	Mrps11	mitochondrial ribosomal protein S11	499185	Rn.759	AA859788	3.19	2.70	2.70	2.90	2.70	2.72	1.07	down	6.27E-01	8.95E-01	-	-
1368181_at	Mthfd1	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1, methenylte	64300	Rn.1114	NM_022508	8.53	8.83	8.24	8.66	8.17	8.49	1.07	down	7.00E-01	9.07E-01	-	-
1376213_at	MGC124740	similar to Rap2-binding protein 9	688590	Rn.147469	AI007838	2.38	2.31	2.38	2.57	2.38	2.39	1.07	up	2.31E-01	8.95E-01	-	-
1379337_at	Fastkd2	FAST kinase domains 2	301463	Rn.24905	BI284334	4.55	4.27	4.75	4.55	4.50	4.80	1.07	up	6.06E-01	8.95E-01	-	-
1394047_at	---	---	---	Rn.20135	BE107848	2.36	2.35	2.69	2.36	2.43	2.34	1.07	down	4.66E-01	8.95E-01	-	-
1374571_at	Pigx	phosphatidylinositol glycan anchor biosynthesis, class X	288041	Rn.34037	AI172192	5.21	6.09	6.62	5.91	6.09	6.21	1.07	up	8.37E-01	9.49E-01	-	-
1371597_at	Rnf187	ring finger protein 187	360533	Rn.100245	BI281621	7.08	7.33	7.00	7.14	7.09	7.46	1.07	up	5.79E-01	8.95E-01	-	-
1371127_at	Bmp1	bone morphogenetic protein 1	83470	Rn.9305	AB012139	2.53	2.49	2.54	2.64	2.67	2.53	1.07	up	1.05E-01	8.95E-01	-	-
1385596_at	Tbc1d15	TBC1 domain family, member 15	366896	Rn.15910	BF392191	4.57	4.15	4.15	4.28	4.13	4.73	1.07	up	7.08E-01	9.09E-01	-	-
1381925_x_at	LOC497729	hypothetical gene supported by NM_172157	497729	---	AI412401	6.79	6.72	6.79	6.74	6.62	7.24	1.07	up	6.55E-01	8.97E-01	-	-
1369176_at	Slc36a1	solute carrier family 36 (proton/amino acid symporter), member 1	155205	Rn.76305	NM_130415	5.46	5.71	5.33	4.95	5.99	5.29	1.07	down	7.93E-01	9.33E-01	-	-
1377655_at	Ccdc41	coiled-coil domain containing 41	366872	Rn.45405	BE111774	2.75	2.75	3.31	3.07	2.75	2.71	1.07	down	6.95E-01	9.06E-01	-	-
1374740_at	LOC588966	similar to K11B4.2	688966	Rn.27139	BF408740	6.33	6.64	6.62	6.67	6.34	6.31	1.07	down	5.79E-01	8.95E-01	-	-
1391224_at	RGD1311678	similar to 4921517L17Rik protein	296311	---	AI169436	7.65	7.16	7.23	6.85	7.43	7.49	1.07	down	7.36E-01	9.15E-01	-	-
1381793_at	---	---	---	---	BE098864	2.52	2.38	2.41	2.41	2.81	2.37	1.07	up	5.88E-01	8.95E-01	-	-
1392339_at	---	---	---	Rn.120448	BF406130	2.80	4.58	3.52	3.48	3.10	4.05	1.07	down	8.82E-01	9.64E-01	-	-
1382646_at	Prpf4b	PRP4 pre-mRNA processing factor 4 homolog B (yeast)	291078	Rn.32654	AI145475	6.09	6.13	3.26	5.22	4.65	5.33	1.07	down	9.29E-01	9.80E-01	-	-
1388607_at	Smurf2	SMAD specific E3 ubiquitin protein ligase 2	303614	Rn.92843	AI177408	4.03	4.23	4.46	4.62	4.40	3.98	1.07	up	7.05E-01	9.08E-01	-	-
1372567_at	R3hcc1	R3H domain and coiled-coil containing 1	361064	Rn.30496	BI274544	4.89	5.15	5.84	4.88	6.11	5.61	1.07	down	9.03E-01	9.70E-01	-	-
1375076_at	Lrrc46	leucine rich repeat containing 46	287653	Rn.26693	AI112007	3.12	2.75	2.87	2.76	2.84	2.87	1.07	down	4.65E-01	8.95E-01	-	-
1371076_at	Cyp2b1 /// Cyp2b2	cytochrome P450, family 2, subfamily b, polypeptide 1 /// cytochrome P450, fa	24300 /// 361523	Rn.91353	AI454613	2.42	2.69	2.43	2.42	2.43	2.41	1.07	down	3.52E-01	8.95E-01	-	-
1378961_at	---	---	---	---	AW523012	2.43	2.66	2.43	2.43	2.41	2.41	1.07	down	2.96E-01	8.95E-01	-	-
1372403_at	RGD1560011	similar to Nuclear membrane binding protein NUCLING	315732	---	BI276339	2.58	2.84	2.59	2.59	2.99	2.71	1.07	up	5.64E-01	8.95E-01	-	-
1371031_at	Mat1a	methionine adenosyltransferase I, alpha	25331	Rn.10418	AI454484	2.66	2.45	2.67	2.56	2.84	2.65	1.07	up	4.56E-01	8.95E-01	-	-
1376623_at	Tmem204	transmembrane protein 204	287129	Rn.16780	AI409186	2.55	2.60	2.45	2.44	2.45	2.44	1.07	down	1.05E-01	8.95E-01	-	-
1374962_at	Rtn4ip1	reticulon 4 interacting protein 1	309912	Rn.220185	BM385683	4.74	6.53	6.73	4.61	6.67	6.44	1.07	down	9.24E-01	9.78E-01	-	-
1396110_at	---	---	---	Rn.7641	BE107839	2.40	2.40	2.41	2.40	2.40	2.69	1.07	up	3.95E-01	8.95E-01	-	-
1393000_at	---	---	---	---	AI045970	2.79	2.50	2.52	2.53	2.50	2.50	1.07	down	3.83E-01	8.95E-01	-	-
1374442_at	Sfrs9	splicing factor, arginine/serine rich 9	288701	Rn.136718	AI227831	5.59	6.40	7.04	6.32	6.74	6.25	1.07	up	8.47E-01	9.52E-01	-	-
1398964_at	---	---	---	Rn.18892	AI231773	9.25	9.45	9.27	9.31	8.97	9.40	1.07	down	5.61E-01	8.95E-01	-	-
1389118_s_at	LOC685385	similar to S100 calcium binding protein A14	685385	Rn.160952	BM387197	2.70	2.89	2.78	2.68	2.76	2.66	1.07	down	2.27E-01	8.95E-01	-	-
1383595_at	---	---	---	---	AW533961	3.14	2.73	2.57	2.72	2.73	2.72	1.07	down	6.20E-01	8.95E-01	-	-
1393136_at	Tmem57	transmembrane protein 57	313618	Rn.214009	BF393285	7.30	6.28	6.49	6.80	6.59	6.96	1.07	up	7.95E-01	9.34E-01	-	-
1398697_at	---	---	---	Rn.168017	BE117321	5.51	5.96	5.96	5.85	5.83	6.02	1.07	up	6.04E-01	8.95E-01	-	-
1380583_s_at	Csf1	colony stimulating factor 1 (macrophage)	78965	Rn.83632	AW535553	2.79	2.53	2.56	2.54	2.54	2.52	1.07	down	3.24E-01	8.95E-01	-	-
1397714_at	RGD1307235	similar to RIKEN cDNA 2310035C23	309053	Rn.38292	BF565706	2.42	2.73	2.43	2.41	2.50	2.39	1.07	down	4.36E-01	8.95E-01	-	-
1368080_at	Rgc32	response gene to complement 32	117183	Rn.3504	NM_054008	2.98	2.98	2.85	3.14	2.99	2.96	1.07	up	2.73E-01	8.95E-01	-	-
1391097_at	---	---	---	---	BF418831	2.42	2.42	2.44	2.42	2.72	2.41	1.07	up	4.19E-01	8.95E-01	-	-
1381495_at	---	---	---	Rn.206435	BF393718	2.63	2.83	2.64	2.62	2.63	2.57	1.07	down	2.54E-01	8.95E-01	-	-
1395655_at	---	---	---	Rn.172593	BM383435	7.80	8.13	8.45	7.91	8.26	8.48	1.07	up	7.32E-01	9.14E-01	-	-
1396445_at	Ribc2	RIB43A domain with coiled-coils 2	300122	Rn.96045	BI288520	2.84	2.61	2.64	2.61	2.66	2.55	1.07	down	3.16E-01	8.95E-01	-	-
1372389_at	Ier2	immediate early response 2	494344	Rn.4298	BF420059	3.42	3.52	3.42	3.41	3.42	3.80	1.07	up	5.20E-01	8.95E-01	-	-
1369737_at	Crem	cAMP responsive element modulator	25620	Rn.10251	NM_017334	3.82	4.36	4.11	4.39	3.94	4.24	1.07	up	6.78E-01	9.02E-01	-	-
1368334_at	Grb7	growth factor receptor bound protein 7	84427	Rn.28109	NM_053403	2.45	2.41	2.51	2.58	2.59	2.48	1.07	up	1.17E-01	8.95E-01	-	-
1383817_at	---	---	---	---	AA817688	5.19	2.57	3.39	3.29	3.38	4.20	1.07	down	9.17E-01	9.75E-01	-	-
1377916_at	Slfn2	schlafen 2	303380	Rn.105052	AW915529	5.33	6.27	5.86	6.23	5.19	6.32	1.07	up	8.50E-01	9.53E-01	-	-
1370179_at	Dynlrb1	dynein light chain roadblock-type 1	170714	Rn.3560	AI102949	9.71	9.77	9.63	9.61	9.78	10.00	1.07	up	4.89E-01	8.95E-01	-	-
1380979_a_at	RGD1309414	similar to KIAA0913 protein	361004	Rn.24931	AW523336	2.65	2.26	4.47	2.75	3.86	2.48	1.07	down	9.15E-01	9.75E-01	-	-
1379801_at	---	---	---	Rn.23792	AI137954	5.54	7.38	6.07	5.99	6.51	6.21	1.07	down	8.80E-01	9.63E-01	-	-
1390382_at	Hyjk	Huntingtin interacting protein K	311359	Rn.17258	BF414043	10.47	10.59	10.61	10.64	10.50	10.80	1.07	up	4.07E-01	8.95E-01	-	-
1389547_at	Pphln1	periphilin 1	366975	Rn.8935	BE107375	5.71	5.38	5.27	5.43	5.38	5.83	1.07	up	6.64E-01	8.99E-01	-	-
1368315_at	Entpd6	ectonucleoside triphosphate diphosphohydrolase 6	85260	Rn.27017	NM_053498	3.44	3.73	2.85	3.58	2.85	3.32	1.07	down	8.00E-01	9.35E-01	-	-
1371535_at	Pmm2	phosphomannomutase 2	302915	Rn.56278	AI411161	5.02	5.25	5.61	5.13	5.19	5.29	1.07	down	6.40E-01	8.95E-01	-	-
1393223_a_at	RGD1306772	similar to RIKEN cDNA 1110008J03	288683	Rn.20168	BE115227	3.26	2.83	2.84	2.83	2.84	2.99	1.07	down	5.82E-01	8.95E-01	-	-
1372059_at	RGD1309437	similar to RIKEN cDNA 2610528E23	288176	Rn.3487	AA891759	4.85	5.50	6.09	4.93	4.83	6.41	1.07	down	8.91E-01	9.66E-01	-	-
1389369_at	---	---	---	---	BF289017	4.36	5.84	5.25	5.73	4.52	5.46	1.07	up	8.80E-01	9.63E-01	-	-
1394758_at	---	---	---	Rn.55697	BF402131	2.45	2.64	2.52	2.45	2.46	2.42	1.07	down	1.80E-01	8.95E-01	-	-
1391652_at	Glyat	glycine-N-acyltransferase	293779	Rn.21872	AI411140	10.99	11.32	11.14	11.24	11.11	11.37	1.07	up	4.93E-01	8.95E-01	-	-
1383383_at	---	---	---	Rn.168356	BE115992	3.90	4.20	4.18	3.90	3.89	4.77	1.07	up	7.82E-01	9.29E-01	-	-
1372088_at	Ppfibp1	PTPRF interacting protein, binding protein 1 (liprin beta 1)	312855	Rn.22871	AI012434	7.01	7.55	7.13	7.10	7.23	7.08	1.07	down	6.24E-01	8.95E-01	-	-
1370150_a_at	Thrsp	thyroid hormone responsive	25357	Rn.81140	NM_012703	2.44	2.71	2.45	2.43	2.47	2.43	1.07	down	3.59E-01	8.95E-01	-	-
1379074_at	Oraov1	oral cancer overexpressed 1	309136	Rn.15258	BE329032	4.04	4.91	3.84	4.42	3.98	4.11	1.07	down	8.09E-01	9.38E-01	-	-
1373992_at	MGC108823	similar to interferon-inducible GTPase	307414	Rn.201788	AI408440	2.67	2.53	2.55	2.55	2.98	2.50	1.07	up	5.93E-01	8.95E-01	-	-
1368280_at	Ctsc	cathepsin C	25423	Rn.203177	BF415370	8.17	6.59	6.47	6.73	6.62	6.61	1.06	down	9.10E-01	9.73E-01	-	-
1375337_at	Adam9	ADAM metallopeptidase domain 9 (meltrin gamma)	290834	Rn.25221	AI011712	6.57	7.33	7.88	7.82	6.73	7.51	1.06	up	8.65E-01	9.58E-01	-	-
1397704_at	LOC691979	similar to N-acetyltransferase ESCO2 (Establishment of cohesion 1 homolog	691979	Rn.145486	BF407449	2.49	2.67	2.60	2.47	2.51	2.50	1.06	down	1.60E-01	8.95E-01	-	-
1393801_at	LOC367808	similar to Sid3177p	367808	Rn.211968	AI111841	3.76	3.52	3.55	3.53	3.55	3.48	1.06	down	3.09E-01	8.95E-01	-	-
1377255_at	---	---	---	Rn.28290	AI410434	2.59	2.32	2.34	2.33	2.34	2.31	1.06	down	3.57E-01	8.95E-01	-	-
1383944_at	---	---	---	Rn.204640	AI144970	2.53	2.47	2.88	2.50	2.58	2.52	1.06	down	5.28E-01	8.95E-01	-	-
1388333_at	Rbx1	ring-box 1	300084	Rn.8068	BF291171	8.56	9.18	9.04	8.64	8.83	9.05	1.06	down	7.03E-01	9.07E-01	-	-
1375812_at	Otud7a	OTU domain containing 7A	309252	Rn.207098	BG376824	3.36	3.29	3.29	3.24	3.14	3.29	1.06	down	1.38E-01	8.95E-01	-	-
1372933_at	Sirt7	sirtuin 7 (silent mating type information regulation 2, homolog) 7 (S. cerevisiae	303745	Rn.23064	AA892780	5.33	5.37	4.91	5.26	5.21	5.41	1.06	up	6.01E-01	8.95E-01	-	-
1372180_at	Sdc3	syndecan 3	116673	Rn.10504	AI112985	2.66	2.59	2.87	2.60	2.67	2.58	1.06	down	3.51E-01	8.95E-01	-	-
1371567_at	Aldh7a1	aldehyde dehydrogenase 7 family, member A1	291450	Rn.7330	AI411279	9.88	9.80	9.77	9.74	9.47	9.97	1.06	down	5.79E-01	8.95E-01	-	-
1372592_at	dac6 /// LOC67966	histone deacetylase 6 /// similar to ES cell-expressed Ras	679682 /// 84581	Rn.218605	AI411391	8.84	9.47	9.20	9.28	8.85	9.11	1.06	down	7.02E-01	9.07E-01	-	-
1370651_a_at	Inpp1	inositol polyphosphate phosphatase-like 1	65038	Rn.42902	AB011439	2.46	2.54	2.45	2.82	2.45	2.45	1.06	up	5.07E-01	8.95E-01	-	-
1398765_at	Ap2m1	adaptor-related protein complex 2, mu 1 subunit	116563	Rn.3172	NM_053837	9.93	9.84	9.64	10.10	9.98	9.60	1.06	up	6.30E-01	8.95E-01	-	-
1378791_at	Map3k4	mitogen activated protein kinase kinase kinase 4	308106	Rn.66102	BF398201	4.89	4.92	4.62	4.66	4.81	5.23	1.06	up	6.65E-01	8.99E-01	-	-
1372774_at	Coq6	Coenzyme Q6 homolog (yeast)	299195	Rn.9283	AI170570	10.42	10.55	10.44	10.43	10.07	10.63	1.06	down	6.20E-01	8.95E-01	-	-
1394571_at	RGD1305939	hypothetical LOC300074	300074	Rn.72811	BF419402	2.40	2.42	2.42	2.39	2.43	2.70	1.06	up	4.14E-01	8.95E-01	-	-
1398419_at	LOC683470	similar to growth arrest specific 1	683470	---	AI235956	2.34	2.33	2.61	2.34	2.34	2.33	1.06	down	3.78E-01	8.95E-01	-	-
1376725_at	Lrp6	low density lipoprotein receptor-related protein 6	312781	Rn.32960	BM391816	3.85	4.08	3.85	3.75	3.85	3.90	1.06	down	3.69E-01	8.95E-01	-	-
1397380_at	---	---	---	Rn.212066	BG376947	2.41	2.67	2.42	2.41	2.42	2.40	1.06	down	3.40E-01	8.95E-01	-	-
1395559_at	---	---	---	Rn.67375	BF543323	2.50	2.48	2.52	2.50	2.58	2.70	1.06	up	2.11E-01	8.95E-01	-	-
1373135_at	Aarsd1	alanyl-tRNA synthetase domain containing 1	619440	Rn.153971	AW531123	8.74	9.57	9.29	9.43	8.91	8.99	1.06	down	7.73E-01	9.26E-01	-	-
1369084_a_at	Bok	BCL2-related ovarian killer	29884	Rn.44461	AF051093	2.67	2.67	2.80	2.66	3.03	2.71	1.06	up	5.04E-01	8.95E-01	-	-
1384764_at	RGD1563574	similar to Hypothetical protein MGC30332	499126	Rn.161831	BF418343	2.72	2.45	2.50	2.48	2.50	2.43	1.06	down	3.50E-01	8.95E-01	-	-
1383364_at	Sugt1	SGT1, suppressor of G2 allele of SKP1 (S. cerevisiae)	290408	Rn.101758	BG672604	2.66	2.39	2.40	2.39	2.40	2.39	1.06	down	3.58E-01	8.95E-01	-	-
1374531_at	---	---	---	Rn.163580	AA926305	8.61	8.94	7.70	8.25	8.51	8.77	1.06	up	8.33E-01	9.47E-01	-	-
1380862_at	---	---	---	Rn.47139	BF386273	2.55	2.79	2.56	2.52	2.55	2.55	1.06	down	3.31E-01	8.95E-01	-	-
1369702_at	Ensa	endosulfine alpha	60334	Rn.27154	NM_021842	2.83	3.16	2.40	2.42	2.98	2.73	1.06	down	7.59E-01	9.22E-01	-	-
1370844_at	Hnrnpf	heterogeneous nuclear ribonucleoprotein F	64200	Rn.144596	BM387425	7.90	8.47	8.38	8.43	7.98	8.60	1.06	up	7.42E-01	9.17E-01	-	-
1376989_at	---	---	---	Rn.14653	BE099568	2.42	2.54	2.42	2.37	2.37	2.36	1.06	down	1.02E-01	8.95E-01	-	-

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1381641_at	Bcas3	Breast carcinoma amplified sequence 3	363662	Rn.203379	BE097328	2.32	2.63	2.32	2.37	2.32	2.32	1.06	down	4.38E-01	8.95E-01	-	-
1393011_at	LOC361041	similar to hypothetical protein	361041	Rn.201786	BE104363	2.94	2.88	2.89	2.91	2.82	2.71	1.06	down	2.15E-01	8.95E-01	-	-
1379878_at	Hmgxb4	HMG box domain containing 4	307667	Rn.2796	AI547695	2.53	2.52	2.88	2.53	2.60	2.53	1.06	down	4.93E-01	8.95E-01	-	-
1380687_at	---	---	---	Rn.210165	BI295176	2.95	2.46	2.88	2.87	2.88	2.82	1.06	up	5.90E-01	8.95E-01	-	-
1383479_at	---	---	---	Rn.203146	BE109730	2.60	2.34	2.36	2.35	2.33	1.06	down	3.39E-01	8.95E-01	-	-
1367723_a_at	Sh2b3	SH2B adaptor protein 3	58838	Rn.11228	NM_031621	3.55	3.07	2.57	2.98	2.96	2.98	1.06	down	7.68E-01	9.24E-01	-	-
1376265_at	Steap2	six transmembrane epithelial antigen of the prostate 2	312052	Rn.203614	AI411542	5.71	5.51	4.93	5.82	5.35	5.25	1.06	up	7.76E-01	9.27E-01	-	-
1393435_at	Plch2	Phospholipase C, eta 2	313756	Rn.37890	AI575267	2.83	2.61	2.64	2.59	2.62	2.60	1.06	down	2.59E-01	8.95E-01	-	-
1389329_at	Lgals8	lectin, galactoside-binding, soluble, 8	116641	Rn.10069	AI411914	8.83	8.96	9.30	8.92	9.04	8.86	1.06	down	5.82E-01	8.95E-01	-	-
1398548_at	---	---	---	Rn.20936	BF389746	2.71	2.81	2.66	2.66	2.67	2.58	1.06	down	1.72E-01	8.95E-01	-	-
1378689_at	---	---	---	Rn.208712	BF409044	4.09	5.26	3.72	5.63	3.93	3.78	1.06	up	9.12E-01	9.73E-01	-	-
1385637_at	Svep1	Sushi, von Willebrand factor type A, EGF and pentraxin domain containing 1	685899	Rn.96258	AI029494	4.09	4.10	3.92	4.42	3.76	3.67	1.06	down	7.33E-01	9.14E-01	-	-
1393816_at	LOC689399	hypothetical protein LOC689399	689399	Rn.51	AI555801	2.92	2.88	3.02	2.86	3.44	2.79	1.06	up	6.95E-01	9.06E-01	-	-
1394831_at	---	---	---	Rn.44677	AW524225	3.04	2.66	2.86	2.79	2.83	2.67	1.06	down	4.94E-01	8.95E-01	-	-
1389017_at	LOC305633	similar to Antxr2 protein	305633	Rn.203300	AI013888	2.82	2.60	2.42	2.42	3.27	2.42	1.06	up	7.85E-01	9.30E-01	-	-
1394558_at	---	---	---	Rn.154269	BF391665	2.39	2.63	2.39	2.39	2.39	2.36	1.06	down	3.36E-01	8.95E-01	-	-
1369517_at	Cyth1	cytohesin 1	116691	Rn.10672	NM_053910	2.65	2.65	2.66	2.65	2.66	2.39	1.06	down	3.73E-01	8.95E-01	-	-
1382815_at	---	---	---	Rn.7019	AA850547	2.42	2.41	2.69	2.43	2.41	2.40	1.06	down	3.87E-01	8.95E-01	-	-
1394368_x_at	RGD1311823	Similar to RIKEN cDNA 1700016G05	362346	Rn.28920	BF288608	2.79	2.87	2.97	2.76	2.84	2.77	1.06	down	1.98E-01	8.95E-01	-	-
1383069_at	LOC680726	similar to RNA binding motif, single stranded interacting protein 3 isoform 1	680726	Rn.135990	AW144676	2.95	2.95	3.36	3.10	2.96	2.94	1.06	down	5.69E-01	8.95E-01	-	-
1394390_at	---	---	---	Rn.51029	BF394739	3.47	3.58	3.59	3.56	3.66	3.70	1.06	up	1.85E-01	8.95E-01	-	-
1374119_at	Elf3	E74-like factor 3	304815	Rn.3063	BI279615	2.95	3.45	2.96	2.95	2.96	3.19	1.06	down	6.54E-01	8.97E-01	-	-
1379486_at	---	---	---	Rn.201609	AW528261	2.69	2.43	2.45	2.44	2.45	2.41	1.06	down	3.53E-01	8.95E-01	-	-
1387521_at	Pdcd4	programmed cell death 4	64031	Rn.206228	NM_022265	4.45	5.31	5.60	5.28	5.38	4.97	1.06	up	8.20E-01	9.42E-01	-	-
1395396_at	Rcc2	regulator of chromosome condensation 2	298594	Rn.98282	AA848942	2.49	2.38	2.57	2.48	2.49	2.75	1.06	up	4.36E-01	8.95E-01	-	-
1375208_at	Tmem86a	transmembrane protein 86A	308602	Rn.23056	BE109619	2.36	2.32	2.38	2.61	2.37	2.35	1.06	up	3.57E-01	8.95E-01	-	-
1378891_at	Kif3c	Kinesin family member 3C	85248	Rn.10894	AI576222	2.68	2.66	2.60	2.58	2.58	2.51	1.06	down	5.17E-02	8.95E-01	-	-
1371672_at	Cbx7	chromobox homolog 7	362962	Rn.12512	AI406275	3.85	3.62	3.93	3.85	3.91	3.91	1.06	up	3.99E-01	8.95E-01	-	-
1371414_at	Gsn	gelsolin	296654	Rn.103770	BI285576	6.65	5.80	5.57	6.54	6.44	5.30	1.06	up	8.71E-01	9.60E-01	-	-
1379908_at	---	---	---	Rn.166081	BE104836	2.53	2.52	2.72	2.52	2.52	2.46	1.06	down	2.65E-01	8.95E-01	-	-
1382079_at	Mapk8	mitogen-activated protein kinase 8	116554	Rn.4090	AI511007	6.35	7.40	8.18	7.34	6.80	7.52	1.06	down	8.84E-01	9.64E-01	-	-
1374434_at	LOC498222	similar to specifically androgen-regulated protein	498222	Rn.28408	BI291703	2.32	2.32	2.33	2.32	2.60	2.31	1.06	up	4.04E-01	8.95E-01	-	-
1385062_at	RGD1306072	hypothetical LOC304654	304654	Rn.110163	BG379388	2.97	2.97	2.98	2.99	3.24	2.96	1.06	up	3.74E-01	8.95E-01	-	-
1377641_at	---	---	---	Rn.47423	BE100646	2.37	2.36	2.38	2.51	2.48	2.39	1.06	up	7.61E-02	8.95E-01	-	-
1398870_at	Tomm20	translocase of outer mitochondrial membrane 20 homolog (yeast)	266601	Rn.2143	AI177295	9.31	9.91	9.75	9.79	9.63	9.81	1.06	up	6.62E-01	8.98E-01	-	-
1375171_at	LOC691036	Similar to SET binding factor 2	691036	Rn.37595	BF396622	4.44	4.80	4.89	4.45	4.59	5.35	1.06	up	7.92E-01	9.33E-01	-	-
1382108_at	---	---	---	Rn.164638	AA800536	2.69	2.63	2.66	2.65	2.95	2.64	1.06	up	4.42E-01	8.95E-01	-	-
1376646_at	Popdc2	popeye domain containing 2	360718	Rn.145147	BF285164	2.51	2.73	2.52	2.51	2.47	1.06	down	2.93E-01	8.95E-01	-	-
1376747_at	---	---	---	Rn.201797	BE107075	2.94	2.50	2.52	2.50	2.50	2.70	1.06	down	6.04E-01	8.95E-01	-	-
1397808_at	---	---	---	Rn.209056	AW920064	2.60	2.45	2.83	2.59	2.40	2.62	1.06	down	5.39E-01	8.95E-01	-	-
1382198_at	Pum2	pumilio homolog 2 (Drosophila)	298874	Rn.8622	AI233267	7.04	7.02	7.18	6.86	6.69	7.41	1.06	down	7.12E-01	9.10E-01	-	-
1377206_at	Lhx1	LIM homeobox 1	257634	Rn.127825	BI282093	2.35	2.47	3.22	2.57	2.48	2.72	1.06	down	7.68E-01	9.24E-01	-	-
1390098_at	N6amt2	N-6 adenine-specific DNA methyltransferase 2 (putative)	290279	Rn.7240	AA955687	3.88	3.55	3.17	3.74	3.29	3.83	1.06	up	7.54E-01	9.20E-01	-	-
1379835_at	---	---	---	Rn.166248	BF558512	2.47	3.14	3.63	2.80	3.26	3.44	1.06	up	8.31E-01	9.47E-01	-	-
1383949_at	Med13l	mediator complex subunit 13-like	360817	Rn.41407	AI703880	4.31	5.08	4.28	4.41	4.50	5.03	1.06	up	8.00E-01	9.35E-01	-	-
1383025_at	Mgea5	meningioma expressed antigen 5 (hyaluronidase)	154968	Rn.162539	BE097791	6.92	6.49	3.45	5.93	5.37	5.83	1.06	up	9.40E-01	9.83E-01	-	-
1385256_at	---	---	---	Rn.152480	BE106225	2.54	2.53	2.55	2.53	2.54	2.80	1.06	up	3.77E-01	8.95E-01	-	-
1373738_at	LOC686999	similar to M phase phosphoprotein 6	686999	Rn.216565	BG379494	4.43	4.69	4.46	4.50	4.52	4.82	1.06	up	5.41E-01	8.95E-01	-	-
1394925_at	RGD1307235	similar to RIKEN cDNA 2310035C23	309053	Rn.38292	AI578037	2.67	2.76	2.68	2.67	2.67	2.51	1.06	down	2.22E-01	8.95E-01	-	-
1381572_at	RGD1565787	similar to RIKEN cDNA 1810065E05	308429	Rn.12333	BG375279	2.90	2.59	2.63	2.62	2.63	2.61	1.06	down	4.05E-01	8.95E-01	-	-
1379819_at	---	---	---	Rn.171604	BF392928	2.64	2.39	2.42	2.40	2.41	2.37	1.06	down	3.28E-01	8.95E-01	-	-
1382013_at	---	---	---	---	AI071118	7.33	7.64	7.86	7.52	7.32	8.25	1.06	up	7.97E-01	9.34E-01	-	-
1372556_at	Polr2l	polymerase (RNA) II (DNA directed) polypeptide L	502374	Rn.30672	AA924509	8.61	9.20	8.48	8.62	8.70	9.24	1.06	up	7.79E-01	9.28E-01	-	-
1377035_at	Mospd4	motile sperm domain containing 4	317161	Rn.63770	BF400026	2.48	2.77	2.49	2.45	2.55	2.47	1.06	down	4.26E-01	8.95E-01	-	-
1367917_at	Cyp2d2	cytochrome P450, family 2, subfamily d, polypeptide 2	25053	Rn.91355	NM_012730	9.97	9.51	9.37	9.67	9.84	9.60	1.06	up	6.74E-01	9.01E-01	-	-
1382003_at	Slc16a13	solute carrier family 16, member 13 (monocarboxylic acid transporter 13)	287451	Rn.23260	AI704067	6.67	7.43	6.73	7.18	7.12	6.79	1.06	up	7.61E-01	9.22E-01	-	-
1370265_at	Aerb2	arrestin, beta 2	25388	Rn.32973	BF285345	3.54	3.53	3.41	3.57	3.66	3.51	1.06	up	1.98E-01	8.95E-01	-	-
1373549_at	Ddx10	DEAD (Asp-Glu-Ala-Asp) box polypeptide 10	360710	Rn.99481	BE105899	3.01	3.46	2.95	2.88	2.43	3.83	1.06	down	8.52E-01	9.54E-01	-	-
1374517_at	Recql	RecQ protein-like (DNA helicase Q1-like)	312824	Rn.203166	AA891612	7.43	6.34	6.48	6.10	7.09	6.80	1.06	down	8.54E-01	9.55E-01	-	-
1369022_at	Svop	SV2 related protein	171442	Rn.162148	NM_134404	2.38	2.62	2.38	2.37	2.37	2.37	1.06	down	3.33E-01	8.95E-01	-	-
1387450_at	Tgfa	transforming growth factor alpha	24827	Rn.9952	NM_012671	2.48	3.13	2.49	2.51	2.92	2.94	1.06	up	7.50E-01	9.19E-01	-	-
1396551_at	---	---	---	Rn.206819	AW536501	2.67	2.68	2.99	2.72	2.80	2.66	1.06	down	4.27E-01	8.95E-01	-	-
1379165_at	---	---	---	---	BE098949	2.98	2.70	2.83	2.73	2.77	2.74	1.06	down	3.34E-01	8.95E-01	-	-
1397066_at	---	---	---	Rn.45416	BF567364	2.62	2.58	2.73	2.49	2.62	2.55	1.06	down	2.01E-01	8.95E-01	-	-
1373980_at	LOC688393	similar to XPA binding protein 1	688393	Rn.16253	AW916138	4.10	4.44	5.43	5.34	3.50	4.86	1.06	down	9.03E-01	9.70E-01	-	-
1394539_at	---	---	---	Rn.211448	BF413362	2.50	2.48	2.52	2.49	2.50	2.77	1.06	up	3.86E-01	8.95E-01	-	-
1373653_at	Papd1	PAP associated domain containing 1	307050	Rn.16216	BF550883	3.23	4.84	3.54	3.74	3.32	4.82	1.06	up	9.01E-01	9.69E-01	-	-
1375496_at	---	---	---	---	BI295329	2.30	2.30	2.31	2.30	2.58	2.29	1.06	up	3.96E-01	8.95E-01	-	-
1386174_at	---	---	---	Rn.167657	AI235918	2.72	2.49	2.51	2.47	2.50	2.49	1.06	down	2.96E-01	8.95E-01	-	-
1370241_at	Cyp2c7	cytochrome P450, family 2, subfamily c, polypeptide 7	29298	Rn.1247	AA800502	2.37	2.59	2.39	2.37	2.37	2.34	1.06	down	2.82E-01	8.95E-01	-	-
1384167_at	LOC681647	similar to F43G9.2	681647	---	AW522260	4.39	4.85	5.89	4.63	4.95	5.29	1.06	down	8.64E-01	9.58E-01	-	-
1389800_at	Pwwp2b	PWWP domain containing 2B	361671	Rn.29879	BF420629	2.83	2.38	2.40	2.40	2.55	2.40	1.06	down	6.00E-01	8.95E-01	-	-
1387084_at	Dpp4	dipeptidylpeptidase 4	25253	Rn.91364	NM_012789	9.03	9.44	9.47	9.22	9.15	9.84	1.06	up	7.54E-01	9.20E-01	-	-
1368077_at	Fbp1	fructose-1,6- biphosphatase 1	24362	Rn.33703	NM_012558	11.98	11.76	12.02	11.76	11.82	11.92	1.06	down	3.98E-01	8.95E-01	-	-
1397717_at	Isoc2b	isochorismatase domain containing 2b	361501	Rn.1804	BF285031	3.66	4.98	4.34	4.25	4.71	4.28	1.06	up	8.40E-01	9.50E-01	-	-
1390523_at	---	---	---	Rn.24008	BG373402	6.73	8.53	8.25	7.86	7.68	8.23	1.06	up	8.87E-01	9.65E-01	-	-
1381456_at	---	---	---	Rn.199741	BE096289	2.47	2.47	2.94	2.46	2.70	2.45	1.06	down	6.47E-01	8.95E-01	-	-
1376410_at	Mmp17	matrix metallopeptidase 17	288626	Rn.7971	BI291814	2.44	2.43	2.72	2.45	2.45	2.43	1.06	down	4.03E-01	8.95E-01	-	-
1396385_at	---	---	---	Rn.166637	BF387763	2.64	2.63	3.06	2.69	2.61	2.76	1.06	down	5.81E-01	8.95E-01	-	-
1397658_at	---	---	---	Rn.209930	BF414555	2.90	2.53	2.52	2.56	2.57	2.56	1.06	down	5.20E-01	8.95E-01	-	-
1384266_at	---	---	---	Rn.16810	AA817729	2.67	2.43	2.45	2.43	2.44	2.41	1.06	down	3.18E-01	8.95E-01	-	-
1373539_at	---	---	---	Rn.1552	BG380686	4.88	5.01	4.46	4.45	5.22	4.94	1.06	up	7.69E-01	9.24E-01	-	-
1393249_at	---	---	---	Rn.164402	BF407924	2.64	2.63	2.79	2.63	2.64	2.53	1.06	down	2.25E-01	8.95E-01	-	-
1381009_at	---	---	---	Rn.209990	BF403637	2.82	2.82	2.87	2.65	2.82	2.77	1.06	down	1.92E-01	8.95E-01	-	-
1392155_at	---	---	---	Rn.147947	AW523955	2.45	2.41	2.45	2.45	2.69	2.44	1.06	up	3.48E-01	8.95E-01	-	-
1370268_at	Kcna5	potassium voltage-gated channel, shaker-related subfamily, member 5	25470	Rn.162789	BM388694	2.41	2.39	2.67	2.40	2.42	2.40	1.06	down	3.86E-01	8.95E-01	-	-
1385394_at	Ms4a10	membrane-spanning 4-domains, subfamily A, member 10	293739	Rn.137647	AI555523	2.60	2.48	2.64	2.49	2.49	2.48	1.06	down	1.38E-01	8.95E-01	-	-
1394280_at	Rgs17	regulator of G-protein signaling 17	308118	Rn.166916	AW140991	2.90	2.58	2.59	2.58	2.68	2.55	1.06	down	4.81E-01	8.95E-01	-	-
1388392_at	Tax1bp3	Tax1 (human T-cell leukemia virus type I) binding protein 3	360564	Rn.34842	BI274159	3.90	3.68	3.57	3.53	3.55	3.80	1.06	down	5.39E-01	8.95E-01	-	-
1398366_at	---	---	---	Rn.220653	BF282644	5.10	5.62	5.67	4.60	6.16	5.36	1.06	down	8.66E-01	9.58E-01	-	-
1373877_at	Picalm	Phosphatidylinositol binding clathrin assembly protein	89816	Rn.24871	BF401685	10.44	10.74	10.21	10.59	10.56	10.51	1.06	up	6.04E-01	8.95E-01	-	-
1398453_at	Klhl36	kelch-like 36 (Drosophila)	498957	Rn.139361	AI145037	3.19	3.77	4.52	4.07	3.85	3.83	1.06	up	8.34E-01	9.48E-01	-	-
1385281_at	Rbm9	RNA binding motif protein 9	362950	Rn.137551	BF388412	3.08	3.07	3.35	3.07	3.10	3.07	1.06	down	4.03E-01	8.95E-01	-	-
1371035_at	Gtf3a	general transcription factor III A	246299	Rn.195324	BE098763	8.16	7.19	7.08	7.10	7.51	7.55	1.06	down	8.25E-01	9.45E-01	-	-
1377656_at	Mak16	MAK16 homolog (S. cerevisiae)	306526	Rn.160904	BG375054	6.38	5.38	5.99	6.31	5.95	5.75	1.06	up	8.06E-01	9.38E-01	-	-
1396258_at	---	---	---	Rn.148848	AW921671	2.65	2.32	2.37	2.36	2.37	2.35	1.06	down	4.41E-01	8.95E-01	-	-
1395385_at	Garnl1	GTPase activating Rap/RanGAP domain-like 1	56785	Rn.86984	BF548145	8.97	9.35	9.49	9.92	8.71	8.90	1.06	down	8.40E-01	9.50E-01	-	-
1373712_at	Prdm2	PR domain containing 2, with ZNF domain	313678	Rn.202632	BI282710	4.25	4.09	4.11	3.74	4.37	4.08	1.06	down	6.69E-01	9.00E-01	-	-
1383687_at	---	---	---	Rn.155149	AW435306	8.17	8.95	8.42	8.69	7.67	8.92	1.06	down	8.55E-01	9.55E-01	-	-
1379356_at	---	---	---	---	AI574991	3.20	2.40	2.44	2.77	2.44	3.09	1.06	up	7.99E-01	9.35E-01	-	-
1381702_at	Sox30	SRY (sex determining region Y)-box 30	689918	Rn.198867	AW525063	2.34	2.41	2.30	2.28	2.27	2.23	1.06	down	6.87E-02	8.95E-01	-	-
1367546_at	Mrpl43	mitochondrial ribosomal protein L43	309440	Rn.126526	BM390298	7.54	7.12	7.68	7.18	7.65	7.25	1.06	down	7.16E-01	9.10E-01	-	-
1375509_at	---	---	---	---	BF388209	2.42	2.39	2.43	2.69	2.42	2.39	1.06	up	4.15E-01	8.95E-01	-	-
1369401_at	Slco1a6	solute carrier organic anion transporter family, member 1a6	84608	---	NM_130736	9.81	10.30	10.27	9.71	10.08	10.33	1.06	down	7.32E-01	9.14E-01	-	-
1390883_at	Akap11	A kinase (PRKA) anchor protein 11	498549	Rn.219324	AI501759	5.93	5.90	5.93	5.85	5.93	6.24	1.06	up	5.05E-01	8.95E-01	-	-
1388587_at	Ier3	immediate early response 3	294235	Rn.23638	AI176519	2.87	2.61	2.67	2.65	2.86	2.58	1.06	down	3.44E-01	8.95E-01	-	-
1389528_s_at	Jun	Jun oncogene	24516	Rn.93714	BI288619	8.72	9.01	9.58	8.93	9.34	9.30	1.06	up	7.74E-01	9.26E-01	-	-
1369277_at	Mecp2	methyl CpG binding protein 2	29386	Rn.9680	NM_022673	4.79	5.29	4.27	5.38	4.32	4.39	1.06	down	8.56E-01	9.55E-01	-	-
1383106_at	Cul2	cullin 2	361258	Rn.2970	BI295890	2.81	2.78	3.03	2.78	2.79	2.78	1.06	down	3.31E-01	8.95E-01	-	-
1376284_at	Nudcd1	NudC domain containing 1	362906	Rn.3282	AI408455	2.74	2.74	2.49	2.86	2.53	2.83	1.06	up	5.50E-01	8.95E-01	-	-
1380638_at	Ncoa3	nuclear receptor coactivator 3	84584	Rn.20691	BI294907	2.97	2.96	2.98	3.25	2.97	2.94	1.06	up	4.28E-01	8.95E-01	-	-
1369824_at	Nrp2	neuropilin 2	81527	Rn.10816	AF016297	2.61	2.39	2.40	2.38	2.39	2.35	1.06	down	2.98E-01	8.95E-01	-	-
1376579_at	Lap3	leucine aminopeptidase 3	289668	Rn.99730	AA945172	8.67	8.86	8.42	8.39	8.45	8.85	1.06	down	6.73E-01	9.01E-01	-	-
1377114_at	---	---	---	Rn.215881	AI410861	11.10	10.72	11.26	10.90	11.03	10.88	1.06	down	6.29E-01	8.95E-01	-	-
1380723_at	---	---	---	Rn.85814	AI179188	2.42	2.41	2.47	2.42	2.43	2.72	1.06	up	4.45E-01	8.95E-01	-	-
1368309_at	Txnrd2	thioredoxin reductase 2	50551	Rn.63054	NM_022584	4.13	4.17	4.17	3.97	4.13	4.10	1.06	down	1.73E-01	8.95E-01	-	-
1391054_at	Rbm15b	RNA binding motif protein 15B	315988	Rn.49808	BF418627	4.29	4.28	4.29	4.28	4.29	4.02	1.06	down	3.72E-01	8.95E-01	-	-
1375196_at	Ankrd11	Ankyrin repeat domain 11	365023	Rn.23844	AW253933	2.55	2.80	2.78	3.24	2.68	2.47	1.06	up	7.39E-01	9.16E-01	-	-
1380503_at	RGD1309634	hypothetical LOC305452	305452	Rn.7798	BI290590	2.47	2.89	2.49	2.48	2.50	2.60	1.06	down	5.70E-01	8.95E-01	-	-
1373845_at	---	---	---	Rn.165674	BM386246	6.04	7.48	8.40	7.04	7.42	7.20	1.06	down	9.06E-01	9.71E-01	-	-
1389434_at	Bbs9	Bardet-Biedl syndrome 9	315484	Rn.92828	BE110675	4.90	4.89	4.71	5.03	4.44	5.29	1.06	up	7.52E-01	9.20E-01	-	-
1395442_at	---	---	---	Rn.170878	BF398196	2.61	2.41	2.43	2.44	2.87	2.41	1.06	up	6.20E-01	8.95E-01	-	-
1370187_at	Pccb	propionyl coenzyme A carboxylase, beta polypeptide	24624	Rn.9732	AI502661	8.88	9.49	9.01	9.12	8.89	9.63	1.06	up	7.78E-01	9.28E-01	-	-
1380199_at	---	---	---	Rn.199698	BF564882	2.59	2.56	2.61	2.59	2.86	2.58	1.06	up	4.09E-01	8.95E-01	-	-
1379612_at	Mapk8	mitogen-activated protein kinase 8	116554	Rn.4090	BI276164	2.68	2.94	2.69	2.67	2.68	2.69	1.06	down	3.70E-01	8.95E-01	-	-
1391456_at	Jam3	junctional adhesion molecule 3	315509	Rn.104684	AW098207	2.46	2.38	2.37	2.38	2.40	2.69	1.06	up	4.51E-01	8.95E-01	-	-
1396230_at	---	---	---	Rn.205796	BM389821	2.39	2.38	2.40	2.67	2.39	2.37	1.06	up	4.14E-01	8.95E-01	-	-
1390785_at	Ubxd4	UBX domain containing 4	685859	Rn.25112	AI232339	6.37	6.03	6.44	5.82	6.62	6.14	1.06	down	7.60E-01	9.22E-01	-	-
1383925_at	Mtip	migration and invasion inhibitory protein	298643	Rn.27362	BG375810	3.51	3.33	3.14	3.75	3.30	3.18	1.06	up	6.94E-01	9.05E-01	-	-
1390229_at	---	---	---	Rn.164434	BF284176	6.68	6.21	6.95	6.13	6.53	6.91	1.06	down	7.94E-01	9.34E-01	-	-
1376773_at	---	---	---	Rn.19462	AI406968	2.73	2.35	3.90	2.93	2.65	3.15	1.06	down	8.67E-01	9.58E-01	-	-
1373087_at	07-Mar	Membrane-associated ring finger (C3HC4) 7	311059	Rn.117620	AI175452	7.57	7.29	7.04	6.94	7.25	7.46	1.06	down	7.06E-01	9.08E-01	-	-
1386272_at	---	---	---	Rn.220683	AI235835	6.97	5.58	5.12	5.88	6.05	5.48	1.06	down	8.88E-01	9.65E-01	-	-
1368886_at	Map3k12	mitogen activated protein kinase kinase kinase 12	25579	Rn.146082	NM_013055	5.04	5.07	5.02	4.84	4.99	5.05	1.06	down	2.44E-01	8.95E-01	-	-
1386850_x_at	Tlk1	tousled-like kinase 1	311118	Rn.6114	AW921365	7.32	7.33	7.26	7.35	7.65	7.17	1.06	up	5.69E-01	8.95E-01	-	-
1390033_at	Cadm3	cell adhesion molecule 3	360882	Rn.138884	BG378062	2.69	2.47	2.48	2.43	2.48	2.46	1.06	down	3.07E-01	8.95E-01	-	-
1375412_at	Arsb	arylsulfatase B	25227	Rn.94004	AI101331	4.76	5.40	5.48	4.63	4.52	5.23	1.06	down	8.92E-01	9.68E-01	-	-
1375323_a_at	Bat3	HLA-B-associated transcript 3	94342	Rn.203343	AA944698	3.00	3.00	3.23	2.99	3.01	2.98	1.06	down	3.27E-01	8.95E-01	-	-
1381088_at	Podn	podocan	313483	---	BE096686	2.36	2.56	2.57	2.56	2.62	2.56	1.06	up	2.92E-01	8.95E-01	-	-
1383766_at	Sgcb	sarcoglycan, beta (dystrophin-associated glycoprotein)	680229	Rn.98258	BG063336	3.91	3.91	4.93	5.15	3.98	3.89	1.06	up	8.78E-01	9.62E-01	-	-
1373857_at	---	---	---	Rn.98232	BM387116	7.28	7.14	5.01	7.26	6.03	6.40	1.06	up	9.21E-01	9.77E-01	-	-
1388827_at	35761 /// RGD156	similar to H2A histone family, member Y isoform 1 /// similar to H2A histone fa	498894 /// 685909	Rn.100938	AW523419	6.61	6.73	6.61	6.43	6.67	6.58	1.06	down	3.50E-01	8.95E-01	-	-
1386866_at	Ywhag	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicats)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1391864_at	Enpp6	ectonucleotide pyrophosphatase/phosphodiesterase 6	306460	Rn.8484	BF282495	7.89	8.80	7.10	7.51	8.24	8.30	1.06	up	8.84E-01	9.64E-01	-	-
1384647_at	Arhgef7	Rho guanine nucleotide exchange factor (GEF7)	114559	Rn.146763	AI071719	2.64	2.61	2.87	2.63	2.65	2.58	1.06	down	3.71E-01	8.95E-01	-	-
1393655_at	Rad54l	RAD54 like (S. cerevisiae)	298429	Rn.202025	BF397746	2.61	2.41	2.42	2.41	2.42	2.35	1.06	down	2.72E-01	8.95E-01	-	-
1395203_at	---	---	---	Rn.177330	BI290823	4.76	6.07	5.25	4.71	6.09	5.54	1.06	up	8.84E-01	9.64E-01	-	-
1397155_at	---	---	---	---	BF393137	2.76	2.91	2.71	2.74	3.30	2.58	1.06	up	7.23E-01	9.12E-01	-	-
1390224_at	---	---	---	---	BM387978	4.49	4.62	4.95	4.25	4.58	4.97	1.06	down	7.48E-01	9.18E-01	-	-
1396826_at	---	---	---	Rn.206131	AW522542	2.42	2.40	2.43	2.68	2.43	2.39	1.06	up	4.06E-01	8.95E-01	-	-
1390940_at	Zeb2	zinc finger E-box binding homeobox 2	311071	Rn.59710	AW529031	4.36	4.32	4.18	4.34	4.22	4.56	1.06	up	4.94E-01	8.95E-01	-	-
1385261_s_at	---	---	---	Rn.125849	BE103057	4.43	3.27	3.39	3.88	3.30	3.65	1.06	down	8.42E-01	9.51E-01	-	-
1385305_at	---	---	---	Rn.151804	BI278291	2.80	3.32	3.87	3.29	3.17	3.28	1.06	down	7.96E-01	9.34E-01	-	-
1395101_at	---	---	---	Rn.211440	BF396757	2.93	2.68	2.73	2.70	2.72	2.65	1.06	down	3.35E-01	8.95E-01	-	-
1384841_at	---	---	---	Rn.122504	AA858815	2.50	2.47	2.52	2.69	2.55	2.51	1.06	up	2.05E-01	8.95E-01	-	-
1386188_s_at	---	---	---	---	H31802	2.97	2.80	2.99	3.08	2.98	2.96	1.06	up	2.93E-01	8.95E-01	-	-
1374339_at	---	---	---	Rn.164881	BI303362	8.41	7.79	7.08	7.75	7.65	8.13	1.06	up	8.45E-01	9.52E-01	-	-
1368791_at	Oprd1	opioid receptor, delta 1	24613	Rn.10310	NM_012617	2.45	2.44	2.46	2.44	2.45	2.71	1.06	up	3.93E-01	8.95E-01	-	-
1393727_at	---	---	---	Rn.151578	BE117729	3.18	3.93	4.32	3.40	4.13	3.65	1.06	down	8.39E-01	9.50E-01	-	-
1381579_at	---	---	---	Rn.172295	BF386959	2.57	2.52	2.56	2.80	2.61	2.51	1.06	up	3.84E-01	8.95E-01	-	-
1381326_at	---	---	---	Rn.27851	AI013440	2.55	2.68	2.56	2.41	2.49	2.63	1.06	down	3.34E-01	8.95E-01	-	-
1370133_at	Rgs19	regulator of G-protein signaling 19	59293	Rn.88166	NM_021661	2.57	2.56	2.58	2.83	2.58	2.55	1.06	up	3.93E-01	8.95E-01	-	-
1388705_at	Selm	selenoprotein M	498398	Rn.8166	BI282694	2.81	2.81	2.86	2.81	2.85	2.56	1.06	down	4.13E-01	8.95E-01	-	-
1374368_at	Tmem164	transmembrane protein 164	367763	Rn.25222	BI291086	4.34	4.14	4.18	4.18	3.70	5.04	1.06	up	8.40E-01	9.50E-01	-	-
1379994_at	---	---	---	Rn.203567	AI070694	2.77	2.58	2.89	2.77	2.97	2.75	1.06	up	4.96E-01	8.95E-01	-	-
1369376_a_at	Lnpep	leucyl/cystinyl aminopeptidase	171105	Rn.10614	NM_133574	5.27	4.49	3.97	4.45	4.47	5.06	1.06	up	8.51E-01	9.54E-01	-	-
1384765_at	Rhbdl2	rhomboid 5 homolog 2 (Drosophila)	303690	Rn.141168	BI289371	2.50	2.57	2.57	2.56	2.60	2.73	1.06	up	1.99E-01	8.95E-01	-	-
1378671_at	---	---	---	Rn.209829	BF391144	2.61	2.60	2.95	2.72	2.62	2.57	1.06	down	5.23E-01	8.95E-01	-	-
1390852_x_at	Iqwd1	IQ motif and WD repeats 1	289181	Rn.3917	BF389856	10.85	10.66	10.47	10.80	10.75	10.69	1.06	up	4.93E-01	8.95E-01	-	-
1391650_at	Dido1	death inducer-obliterator 1	362286	Rn.219449	AA998699	2.50	2.98	2.40	2.50	3.15	2.50	1.06	up	7.76E-01	9.27E-01	-	-
1374497_at	Ncln	nicalin homolog (zebrafish)	314648	Rn.4202	AI102943	4.73	4.45	4.09	4.49	3.73	4.79	1.06	down	8.27E-01	9.45E-01	-	-
1371992_at	MGC94542	similar to RIKEN cDNA 5430437P03	290631	Rn.74107	BG378110	7.24	7.95	6.93	7.14	7.48	7.76	1.06	up	8.19E-01	9.42E-01	-	-
1369970_at	Vamp8	vesicle-associated membrane protein 8	83730	Rn.82672	NM_031827	8.92	9.45	9.11	9.06	8.79	9.38	1.06	down	7.28E-01	9.13E-01	-	-
1374519_at	Dock7	dedicator of cytokinesis 7	313388	Rn.23309	AI231782	2.83	2.82	3.08	2.61	3.16	2.70	1.06	down	6.76E-01	9.02E-01	-	-
1389543_at	Masp1	mannan-binding lectin serine peptidase 1	64023	Rn.203236	BE111083	2.80	2.60	2.70	2.66	2.64	2.54	1.06	down	2.69E-01	8.95E-01	-	-
1387786_at	Mtpn	myotrophin	79215	Rn.3239	AI711244	7.29	7.51	7.00	7.33	6.87	7.86	1.06	up	8.05E-01	9.37E-01	-	-
1385877_at	---	---	---	Rn.86588	BI294012	2.45	2.41	2.45	2.44	2.45	2.68	1.06	up	3.50E-01	8.95E-01	-	-
1389393_at	Fam108c1	family with sequence similarity 108, member C1	361601	Rn.198511	AI232269	6.98	6.89	6.82	6.94	7.09	6.92	1.06	up	2.97E-01	8.95E-01	-	-
1375620_at	Prkar2a	Protein kinase, cAMP dependent regulatory, type II alpha	29699	Rn.9742	AI059291	2.53	2.52	2.81	2.53	2.55	2.52	1.06	down	4.12E-01	8.95E-01	-	-
1383521_at	---	---	---	Rn.165361	AW915081	2.91	4.71	5.13	4.68	4.20	4.14	1.06	up	9.09E-01	9.72E-01	-	-
1388726_a_at	LOC100188932	dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 4	100188932	Rn.3416	AA800242	10.61	10.12	10.39	10.40	10.51	10.46	1.06	up	5.89E-01	8.95E-01	-	-
1372730_at	LOC684304	similar to Mitochondrial 39S ribosomal protein L39 (L39mt) (MRP-L39)	684304	---	BF282327	7.66	7.64	7.15	7.14	7.60	7.47	1.06	down	7.13E-01	9.10E-01	-	-
1389358_at	LOC679692	Similar to lysophosphatidylglycerol acyltransferase 1	679692	Rn.101953	BF282740	8.81	9.50	9.99	9.25	9.42	9.38	1.06	down	8.17E-01	9.42E-01	-	-
1372968_at	Sbf1	SET binding factor 1	300147	Rn.7632	BM385950	2.43	2.47	2.78	2.48	2.48	2.47	1.06	down	4.76E-01	8.95E-01	-	-
1386004_s_at	XC309220 /// Morf4	similar to mortality factor 4 like 1 isoform b /// mortality factor 4 like 1	300891 /// 309220	Rn.112847	BF286548	10.77	10.32	10.80	10.70	10.66	10.80	1.06	up	6.27E-01	8.95E-01	-	-
1377935_at	Cldnd1	Claudin domain containing 1	288182	Rn.101823	AI231223	4.82	6.77	6.76	6.02	5.41	6.66	1.06	down	9.14E-01	9.74E-01	-	-
1397967_at	---	---	---	Rn.173633	BF413391	2.40	2.58	2.42	2.39	2.37	2.37	1.06	down	2.11E-01	8.95E-01	-	-
1367679_at	Cd74	Cd74 molecule, major histocompatibility complex, class II invariant chain	25599	Rn.33804	NM_013069	10.88	9.71	10.12	10.95	10.19	9.83	1.06	up	8.67E-01	9.58E-01	-	-
1384394_at	---	---	---	---	BF548081	8.04	8.24	7.20	7.55	7.34	8.33	1.06	down	8.55E-01	9.55E-01	-	-
1376610_a_at	LOC304558	similar to TPR repeat-containing protein KIAA1043	304558	Rn.137233	BE109163	2.60	2.57	2.98	2.64	2.73	2.52	1.06	down	5.84E-01	8.95E-01	-	-
1398631_at	Gtpbp6	GTP binding protein 6 (putative)	363931	Rn.98504	AI136601	2.73	2.50	2.51	2.49	2.51	2.49	1.06	down	3.13E-01	8.95E-01	-	-
1384743_at	---	---	---	Rn.173547	BF418132	7.36	7.36	7.85	6.91	8.37	7.55	1.06	up	8.61E-01	9.57E-01	-	-
1379840_at	---	---	---	---	AI548086	2.27	2.30	2.47	2.27	2.27	2.26	1.06	down	2.49E-01	8.95E-01	-	-
1389732_at	Dram	damage-regulated autophagy modulator	679937	Rn.1826	BM386323	2.37	2.65	2.31	2.37	2.29	2.42	1.06	down	4.88E-01	8.95E-01	-	-
1375127_at	Cox5a	Cytochrome c oxidase, subunit Va	252934	Rn.11077	BI395849	12.08	11.82	12.00	11.79	11.90	11.96	1.06	down	4.16E-01	8.95E-01	-	-
1369382_at	Mertk	c-mer proto-oncogene tyrosine kinase	65037	Rn.207207	NM_022943	3.30	3.83	3.61	3.06	3.91	3.53	1.06	down	7.84E-01	9.30E-01	-	-
1387664_at	Atp6v1b2	ATPase, H transporting, lysosomal V1 subunit B2	117596	Rn.8109	NM_057213	7.59	7.67	7.71	7.30	7.54	7.86	1.06	down	6.33E-01	8.95E-01	-	-
1398850_at	Ppia	peptidylprolyl isomerase A (cyclophilin A)	25518	Rn.1463	BG671399	11.21	11.75	11.41	11.48	11.43	11.71	1.06	up	6.63E-01	8.99E-01	-	-
1383256_at	Dnttip2	deoxynucleotidyltransferase, terminal, interacting protein 2	295419	Rn.15094	BF410997	6.54	6.87	6.07	6.07	6.67	6.99	1.06	up	8.23E-01	9.43E-01	-	-
1393491_at	Tbl1x	transducin (beta)-like 1 X-linked	302711	Rn.107002	BF398496	2.73	2.70	3.23	2.50	2.77	3.65	1.06	up	8.38E-01	9.49E-01	-	-
1371900_at	Cugbp1	CUG-triplet repeat, RNA binding protein 1	362160	Rn.203194	BF408840	7.31	6.67	7.11	7.36	6.64	6.82	1.06	down	7.82E-01	9.29E-01	-	-
1370354_at	Parg	poly (ADP-ribose) glycohydrolase	83507	Rn.13634	AB019366	9.42	8.43	9.47	8.96	9.24	8.88	1.06	down	8.23E-01	9.43E-01	-	-
1398295_at	Slc29a1	solute carrier family 29 (nucleoside transporters), member 1	63997	Rn.5814	NM_031684	2.77	2.58	2.68	2.98	2.68	2.63	1.06	up	5.21E-01	8.95E-01	-	-
1373211_at	Fbxw4	F-box and WD repeat domain containing 4	309444	Rn.219325	BF283421	6.12	5.06	4.19	5.24	4.91	4.97	1.06	down	8.88E-01	9.65E-01	-	-
1399018_at	Crop	cisplatin resistance-associated overexpressed protein	360602	Rn.15676	AI410301	9.04	8.40	8.24	8.57	8.33	8.52	1.06	down	7.56E-01	9.21E-01	-	-
1386647_at	Map7	microtubule-associated protein 7	293016	Rn.23807	BF563299	9.13	9.68	9.63	9.53	8.62	10.04	1.06	down	8.60E-01	9.57E-01	-	-
1371242_at	Grm8	glutamate receptor, metabotropic 8	60590	Rn.44420	Y11153	2.77	2.43	2.51	2.49	2.49	2.48	1.06	down	4.60E-01	8.95E-01	-	-
1391664_at	Pigv	phosphatidylinositol glycan anchor biosynthesis, class V	366478	Rn.211496	BF414659	2.45	2.78	2.52	2.56	2.56	2.89	1.06	up	6.05E-01	8.95E-01	-	-
1372095_at	---	---	---	Rn.219291	BF281867	2.47	2.60	2.48	2.85	2.49	2.47	1.06	up	5.49E-01	8.95E-01	-	-
1386551_at	---	---	---	Rn.206138	BF562849	2.38	2.37	2.63	2.38	2.38	2.37	1.06	down	3.79E-01	8.95E-01	-	-
1389507_at	Nedd4l	neural precursor cell expressed, developmentally down-regulated 4-like	291553	Rn.72824	AI072446	5.16	6.31	6.40	6.75	5.26	6.12	1.06	up	8.92E-01	9.67E-01	-	-
1376587_at	Fbxl11	f-box protein 11	301674	Rn.36583	AA818128	3.77	3.57	3.82	3.77	3.80	3.84	1.06	up	3.40E-01	8.95E-01	-	-
1384556_at	Atp10a	ATPase, class V, type 10A	365266	Rn.208837	AI511244	2.74	2.50	2.52	2.50	2.51	2.49	1.06	down	3.32E-01	8.95E-01	-	-
1369997_at	Dvl1	dishevelled, dsh homolog 1 (Drosophila)	83721	Rn.144610	NM_031820	3.03	2.94	3.05	2.99	3.19	3.10	1.06	up	2.69E-01	8.95E-01	-	-
1379081_at	Noxo1	NADPH oxidase organizer 1	302976	Rn.13764	BE096731	2.48	2.46	2.50	2.47	2.76	2.46	1.06	up	4.49E-01	8.95E-01	-	-
1385817_at	Nek4	NIMA (never in mitosis gene a)-related kinase 4	306252	Rn.57768	BI288576	2.62	2.60	2.64	2.89	2.63	2.60	1.06	up	4.21E-01	8.95E-01	-	-
1390112_at	Efemp1	EGF-containing fibulin-like extracellular matrix protein 1	305604	Rn.163265	BF284634	2.53	2.50	2.57	2.82	2.56	2.48	1.06	up	4.72E-01	8.95E-01	-	-
1373091_at	Plagl2	pleiomorphic adenoma gene-like 2	296281	Rn.107493	AI102576	2.44	2.41	2.31	2.30	2.31	2.29	1.06	down	8.66E-02	8.95E-01	-	-
1393320_at	Utp15	UTP15, U3 small nucleolar ribonucleoprotein, homolog (S. cerevisiae)	310019	Rn.7959	BF396985	3.46	3.94	4.98	3.95	3.98	4.20	1.06	down	8.62E-01	9.57E-01	-	-
1394765_at	---	---	---	Rn.146935	BF397199	2.47	2.44	2.47	2.44	2.76	2.42	1.06	up	4.89E-01	8.95E-01	-	-
1397167_at	---	---	---	---	AW534046	2.46	2.34	2.36	2.34	2.75	2.33	1.06	up	5.86E-01	8.95E-01	-	-
1371329_at	Eif5a	eukaryotic translation initiation factor 5A	287444	Rn.128212	BI283681	10.12	9.80	10.06	10.23	9.87	9.63	1.06	down	6.93E-01	9.05E-01	-	-
1386038_x_at	---	---	---	---	BF288392	2.71	2.97	2.78	2.75	2.77	2.69	1.06	down	3.66E-01	8.95E-01	-	-
1376186_at	---	---	---	Rn.206748	BF393132	2.66	2.41	2.44	2.42	2.44	2.41	1.06	down	3.47E-01	8.95E-01	-	-
1394160_at	Tmem2	transmembrane protein 2	309400	Rn.107821	AI101945	2.91	2.42	2.49	2.47	2.48	3.12	1.06	up	7.65E-01	9.23E-01	-	-
1369347_s_at	Prom2	prominin 2	192211	Rn.82155	NM_138857	2.46	2.71	2.46	2.46	2.47	2.44	1.06	down	3.65E-01	8.95E-01	-	-
1386589_at	---	---	---	Rn.166079	AW143518	3.35	3.53	3.41	3.40	3.25	3.39	1.06	down	3.04E-01	8.95E-01	-	-
1377062_at	Cep250	centrosomal protein 250kDa	311573	Rn.41835	BE100468	2.46	2.46	2.48	2.43	2.45	2.77	1.06	up	4.79E-01	8.95E-01	-	-
1371253_at	Etfa	electron-transfer-flavoprotein, alpha polypeptide	300726	Rn.32496	AA942749	11.03	10.88	10.86	10.85	10.71	10.97	1.06	down	4.15E-01	8.95E-01	-	-
1387782_at	Dynll2	dynein light chain LC8-type 2	140734	Rn.36362	NM_080697	7.73	7.89	8.07	7.83	8.05	8.05	1.06	up	5.28E-01	8.95E-01	-	-
1399011_at	Copa6	COP9 constitutive photomorphogenic homolog subunit 6 (Arabidopsis)	304343	Rn.35643	AI409481	8.21	8.46	7.93	7.88	8.13	8.33	1.06	down	6.97E-01	9.07E-01	-	-
1377779_at	Pdcl3	phosducin-like 3	316348	Rn.103207	AI137175	2.62	3.13	3.35	3.38	3.05	2.93	1.06	up	7.59E-01	9.21E-01	-	-
1387209_at	Sec16b	SEC16 homolog B (S. cerevisiae)	89868	Rn.21873	NM_053571	5.69	6.35	6.72	6.44	5.99	6.58	1.06	up	8.22E-01	9.43E-01	-	-
1383020_at	Cntrob	centrobin, centrosomal BRCA2 interacting protein	303240	Rn.14900	AA899161	2.35	2.36	2.36	2.62	2.36	2.35	1.06	up	3.94E-01	8.95E-01	-	-
1370909_at	Nupr2	nucleoporin 62	65274	Rn.54450	BI286040	7.01	6.78	6.87	7.79	6.27	6.85	1.06	up	8.60E-01	9.57E-01	-	-
1393877_at	---	---	---	---	BM386887	2.59	2.57	2.65	2.56	2.63	2.87	1.06	up	4.25E-01	8.95E-01	-	-
1379408_at	RGD1305020	similar to Hepatocellular carcinoma-associated antigen 58 homolog	311575	Rn.38255	AW916148	2.72	2.67	2.82	2.68	2.72	2.55	1.06	down	2.86E-01	8.95E-01	-	-
1370034_at	Cdc25b	cell division cycle 25 homolog B (S. pombe)	171103	Rn.11312	NM_133572	2.56	2.38	2.42	2.37	2.38	2.37	1.06	down	2.57E-01	8.95E-01	-	-
1387426_at	Slc25a21	solute carrier family 25 (mitochondrial oxodicarboxylate carrier), member 21	171151	Rn.205044	NM_133614	3.30	3.32	3.14	3.30	3.36	3.35	1.06	up	2.44E-01	8.95E-01	-	-
1397031_at	---	---	---	Rn.173211	BE120561	2.33	2.33	2.34	2.59	2.34	2.33	1.06	up	3.73E-01	8.95E-01	-	-
1367666_at	Hnrph1	heterogeneous nuclear ribonucleoprotein H1	140931	Rn.23677	NM_080896	9.29	9.41	8.98	9.30	9.15	9.48	1.06	up	6.28E-01	8.95E-01	-	-
1393722_at	Fem1c	fem-1 homolog c (C.elegans)	302288	Rn.22697	BE108945	8.26	7.50	5.81	6.60	6.89	7.83	1.06	down	9.23E-01	9.77E-01	-	-
1378311_at	---	---	---	Rn.203767	BE115189	2.37	2.48	2.38	2.36	2.76	2.35	1.06	up	5.77E-01	8.95E-01	-	-
1377687_at	Zc4h2	zinc finger, C4H2 domain containing	367838	Rn.12889	AI009660	2.31	2.31	2.33	2.32	2.32	2.57	1.06	up	3.75E-01	8.95E-01	-	-
1385702_at	Ifi204	interferon activated gene 204	304988	Rn.15194	AA901151	2.50	2.45	2.55	2.50	2.54	2.71	1.06	up	3.03E-01	8.95E-01	-	-
1393099_at	Cox11	COX11 homolog, cytochrome c oxidase assembly protein (yeast)	690300	Rn.19469	BF400576	3.77	3.55	3.58	3.54	3.57	3.54	1.06	down	2.96E-01	8.95E-01	-	-
1397612_at	---	---	---	Rn.208461	BF391002	2.59	2.57	2.61	2.55	2.61	2.86	1.06	up	4.22E-01	8.95E-01	-	-
1367658_at	Shank3	SH3 and multiple ankyrin repeat domains 3	59312	Rn.42876	NM_021676	2.63	2.42	2.45	2.42	2.43	2.41	1.06	down	2.79E-01	8.95E-01	-	-
1376339_at	RGD1560666	Similar to KIAA1280 protein	317439	Rn.13256	BM385270	4.73	4.82	4.83	4.34	4.82	4.96	1.06	down	6.87E-01	9.04E-01	-	-
1370821_at	Tpmt	thiopurine S-methyltransferase	690050	Rn.112598	AF120100	11.48	11.33	11.54	11.36	11.27	11.48	1.06	down	3.88E-01	8.95E-01	-	-
1382184_at	Faim3	Fas apoptotic inhibitory molecule 3	548326	Rn.23441	AI410062	2.55	2.54	3.17	2.90	2.55	2.56	1.06	down	7.43E-01	9.17E-01	-	-
1388578_at	LOC289378	similar to B0432.8	289378	Rn.12992	BI288621	2.60	2.94	2.60	2.59	2.60	2.70	1.06	down	5.19E-01	8.95E-01	-	-
1383004_at	Ahcyl1	S-adenosylhomocysteine hydrolase-like 1	362013	Rn.17493	BF397074	9.04	9.45	9.08	9.39	8.53	9.40	1.06	down	8.04E-01	9.37E-01	-	-
1395921_at	Usp35	ubiquitin specific peptidase 35	308834	Rn.88266	BE097603	2.69	2.68	2.70	2.69	2.70	2.94	1.06	up	3.59E-01	8.95E-01	-	-
1395822_at	---	---	---	Rn.207190	BE098563	2.58	2.34	2.35	2.34	2.34	2.34	1.06	down	3.53E-01	8.95E-01	-	-
1383662_at	LOC500956	hypothetical protein LOC500956	500956	Rn.18715	AI043759	2.51	2.51	2.54	2.50	2.80	2.51	1.06	up	4.38E-01	8.95E-01	-	-
1375467_at	LOC683801	similar to zinc finger protein 740	683801	---	BI298372	2.96	3.53	2.53	3.01	2.87	2.90	1.06	down	7.88E-01	9.32E-01	-	-
1387560_a_at	Drp2	dystrophin related protein 2	66027	Rn.162341	NM_023971	2.49	2.47	2.72	2.48	2.49	2.46	1.06	down	3.60E-01	8.95E-01	-	-
1379926_at	---	---	---	Rn.203441	BG380347	2.37	2.37	2.38	2.61	2.42	2.34	1.06	up	3.56E-01	8.95E-01	-	-
1383657_at	Fscn3	fascin homolog 3, actin-bundling protein, testicular (Strongylocentrotus purpu	296947	Rn.3253	BI288276	2.44	2.43	2.66	2.41	2.43	2.43	1.06	down	3.28E-01	8.95E-01	-	-
1379183_at	Wdr62	WD repeat domain 62	308492	Rn.206015	BG379858	3.71	3.58	3.71	3.81	3.73	3.70	1.06	up	2.10E-01	8.95E-01	-	-
1390522_at	Fbxl11	F-box and leucine-rich repeat protein 11	361700	Rn.12228	BI278720	4.33	4.08	3.75	3.87	3.94	4.10	1.06	down	6.72E-01	9.01E-01	-	-
1367757_at	Cox6c	cytochrome c oxidase, subunit VIc	54322	Rn.846	NM_019360	11.75	11.82	11.89	11.72	11.71	11.78	1.06	down	1.59E-01	8.95E-01	-	-
1398177_at	Vps37c	vacuolar protein sorting 37 homolog C (S. cerevisiae)	308178	Rn.12915	BF400770	2.66	2.86	2.67	2.65	2.66	2.62	1.06	down	2.66E-01	8.95E-01	-	-
1380892_at	---	---	---	Rn.170618	BF412370	2.49	2.45	2.63	2.45	2.46	2.41	1.06	down	2.10E-01	8.95E-01	-	-
1399029_at	Usp48	ubiquitin specific protease 48	362636	Rn.100022	BI285965	2.42	2.88	2.37	2.41	2.51	2.49	1.06	down	6.40E-01	8.95E-01	-	-
1378938_at	LOC290577	hypothetical LOC290577	290577	Rn.8014	AI175581	6.85	6.83	6.93	6.53	6.99	6.83	1.06	down	5.79E-01	8.95E-01	-	-
1367704_at	Ap2b1	adaptor-related protein complex 2, beta 1 subunit	140670	Rn.56138	NM_080583	7.01	7.37	6.86	7.24	7.15	7.10	1.06	up	6.25E-01	8.95E-01	-	-
1369921_at	Gstm3	glutathione S-transferase mu 3	57298	Rn.209043	NM_020540	2.44	2.43	2.70	2.44	2.47	2.42	1.06	down	4.10E-01	8.95E-01	-	-
1390140_at	Lemd3	LEM domain containing 3	680066	Rn.22132	AI235493	2.32	2.31	2.32	2.32	2.55	2.34	1.06	up	3.27E-01	8.95E-01	-	-
1382673_at	---	---	---	Rn.16763	BE115812	3.23	3.25	3.34	3.56	3.35	3.16	1.06	up	5.24E-01	8.95E-01	-	-
1394907_at	---	---	---	Rn.7071	AW920883	3.17	2.30	2.32	2.92	2.33	2.30	1.06	down	8.24E-01	9.44E-01	-	-
1375474_at	Zcchc3	Zinc finger, CCHC domain containing 3	690005	Rn.198655	AW254459	2.35	2.34	2.36	2.35	2.55	2.41	1.06	up	2.30E-01	8.95E-01	-	-
1374542_at	---	---	---	Rn.1325	AI409904	2.80	2.58	2.61	2.59	2.58	2.57	1.06	down	2.81E-01	8.95E-01	-	-
1393629_at	Hlx	H2.0-like homeobox	364069	Rn.35243	AI501027	2.45	2.43	2.45	2.70	2.45	2.43	1.06	up	3.88E-01	8.95E-01	-	-
1383727_at	---	---	---	Rn.58317	BF564921	2.76	2.75	2.76	2.75	3.02	2.75	1.06	up	4.16E-01	8.95E-01	-	-
1375291_at	LOC502710	Similar to Myeloid/lymphoid or mixed-lineage leukemia protein 3 homolog (His	502710	Rn.164602	AA857992	2.96	3.01	3.07	2.93	2.96	2.90	1.06	down	8.66E-02	8.95E-01	-	-
1391538_at	Cideb	cell death-inducing DNA fragmentation factor, alpha subunit-like effector B	364388	Rn.204016	AI137938	9.29	9.66	9.50	9.19	9.55	9.45	1.06	down	6.13E-01	8.95E-01	-	-
1371917_at	Trmu	tRNA 5-methylaminomethyl-2-thiouridylate methyltransferase	362976	Rn.40588	AI411119	7.07	4.75	4.49	5.00	5.98	5.58	1.06	up	9.28E-01	9.80E-01	-	-
1379846_at	Gtf8a3	glycosyltransferase 8 domain containing 3	300173	Rn.14828	BF394502	2.74	2.78	2.71	2.82	2.86	2.80	1.06	up	4.45E-02	8.95E-01	-	-
1389257_at	Lancl2	LanC lantibiotic synthetase component C-like 2 (bacterial)	362375	Rn.104463	BI288578	2.94	3.57	5.16	3.45	3.95	4.03	1.06	down	9.09E-01	9.72E-01	-	-
1368029_at	Gnai3	guanine nucleotide binding protein (G protein), al

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1398605_at	RGD1306730	similar to cDNA sequence BC025641	309009	Rn.19042	BI289978	2.23	2.30	2.31	2.29	2.31	2.48	1.06	up	2.87E-01	8.95E-01	-	-
1379520_at	---	---	---	Rn.202718	BE103550	2.53	2.44	2.57	2.43	2.45	2.42	1.06	down	1.06E-01	8.95E-01	-	-
1388436_at	Snrpa	small nuclear ribonucleoprotein polypeptide A	292729	Rn.9347	AI230728	2.57	2.80	2.58	2.57	2.58	2.56	1.06	down	3.41E-01	8.95E-01	-	-
1387192_at	Shank1	SH3 and multiple ankyrin repeat domains 1	78957	Rn.144602	NM_031751	2.41	2.41	2.41	2.67	2.42	2.39	1.06	up	4.06E-01	8.95E-01	-	-
1375873_at	RGD1561149	similar to mKIAA1522 protein	500552	Rn.3216	AI231506	4.23	3.93	3.74	3.93	3.79	4.43	1.06	up	7.49E-01	9.19E-01	-	-
1384408_at	---	---	---	Rn.108921	BM386061	6.41	6.69	6.26	6.34	6.11	6.65	1.06	down	7.03E-01	9.07E-01	-	-
1393741_at	Mesp1	mesoderm posterior 1	308766	Rn.11951	BE108635	2.40	2.39	2.40	2.38	2.67	2.39	1.06	up	4.29E-01	8.95E-01	-	-
1381544_at	RGD1564534	similar to CHCHD4 protein	501576	Rn.29287	BI294859	2.40	2.40	2.66	2.45	2.39	2.38	1.06	down	4.05E-01	8.95E-01	-	-
1376868_at	Cobl1	Cobl-like 1	310088	Rn.38124	BM389293	6.78	6.76	6.68	6.76	6.77	6.92	1.06	up	2.39E-01	8.95E-01	-	-
1376072_at	Pafah1b1	family with sequence similarity 174, member A	301634	Rn.22362	AI170779	6.16	6.45	6.42	6.33	6.26	6.69	1.06	up	6.38E-01	8.95E-01	-	-
1392706_at	---	---	---	Rn.205980	AI548870	2.75	2.45	2.46	2.46	2.48	2.47	1.06	down	4.49E-01	8.95E-01	-	-
1379471_at	Uba6	ubiquitin-like modifier activating enzyme 6	305268	Rn.94245	BI275767	8.21	8.21	7.85	7.65	8.76	8.12	1.06	up	8.23E-01	9.43E-01	-	-
1377731_at	C1d	nuclear DNA binding protein	289810	Rn.102095	AI454091	10.25	10.10	9.89	10.03	10.12	9.84	1.06	down	5.74E-01	8.95E-01	-	-
1368710_at	Mark2	MAP/microtubule affinity-regulating kinase 2	60328	Rn.42926	NM_021699	5.33	5.39	5.43	5.65	5.58	4.70	1.06	down	8.02E-01	9.36E-01	-	-
1373036_at	RGD1561455	similar to Ras GTPase-activating-like protein IQGAP2	364885	Rn.3743	BF283621	6.88	6.71	7.06	6.80	6.59	7.01	1.06	down	6.35E-01	8.95E-01	-	-
1382786_at	---	---	---	Rn.167942	BF523557	2.60	2.37	2.39	2.38	2.39	2.35	1.06	down	3.37E-01	8.95E-01	-	-
1368745_at	Slc10a2	solute carrier family 10 (sodium/bile acid cotransporter family), member 2	29500	Rn.85891	NM_017222	2.81	2.74	3.06	2.77	2.97	3.12	1.06	up	5.90E-01	8.95E-01	-	-
1397079_at	---	---	---	Rn.156453	BF394313	2.75	2.70	2.87	2.72	2.80	2.55	1.06	down	4.15E-01	8.95E-01	-	-
1386622_at	RGD1565247	Similar to chromosome 16 open reading frame 28	302987	Rn.129828	BF542874	2.53	2.49	2.79	2.53	2.55	2.49	1.06	down	4.41E-01	8.95E-01	-	-
1377763_at	LOC687738	similar to Der1-like domain family, member 2	687738	---	BF283765	3.31	2.57	2.38	2.70	3.23	2.57	1.06	up	8.27E-01	9.45E-01	-	-
1387807_at	Pafah1b1	platelet-activating factor acetylhydrolase, isoform 1b, subunit 1	83572	Rn.5827	NM_031763	8.67	8.98	8.71	8.47	8.98	8.67	1.06	down	6.68E-01	9.00E-01	-	-
1393054_at	Dock3	dedicator of cyto-kinesis 3	315992	Rn.19982	AI070118	2.53	2.58	2.46	2.53	2.26	2.54	1.06	down	4.51E-01	8.95E-01	-	-
1372543_at	RGD1562502	similar to RIKEN cDNA 2610029G23	363485	Rn.12007	BI282107	5.52	4.98	4.29	6.14	3.16	5.73	1.06	up	9.39E-01	9.83E-01	-	-
1381390_at	RGD1564833	similar to 9630058J23Rik protein	498297	Rn.140701	AI459144	2.84	2.55	2.86	2.94	2.79	2.75	1.06	up	5.18E-01	8.95E-01	-	-
1381766_at	---	---	---	Rn.160470	AI711035	2.34	2.34	2.58	2.34	2.35	2.33	1.06	down	3.74E-01	8.95E-01	-	-
1393611_at	#308 /// LOC2894	DNA helicase HEL308 /// similar to DNA helicase HEL308	289471 /// 360912	Rn.84464	AA964538	2.70	2.69	2.71	2.69	2.89	2.76	1.06	up	2.36E-01	8.95E-01	-	-
1390055_at	RGD1308124	Similar to KIAA1357 protein	302830	Rn.22580	AI044108	5.39	5.77	6.14	5.94	6.29	5.32	1.06	up	8.30E-01	9.46E-01	-	-
1393340_at	Mlxip	MLX interacting protein	304479	Rn.166397	AI070775	2.25	2.24	2.26	2.24	2.51	2.24	1.06	up	4.11E-01	8.95E-01	-	-
1393637_at	Glb1l	galactosidase, beta 1-like	301525	Rn.159756	BF553039	7.30	5.75	6.64	6.12	7.05	6.27	1.06	down	8.86E-01	9.65E-01	-	-
1394727_at	---	---	---	Rn.181334	AI407942	2.50	2.71	2.56	2.93	2.52	2.57	1.06	up	6.00E-01	8.95E-01	-	-
1385315_at	Mtss1l	metastasis suppressor 1-like	307845	Rn.101261	AI145941	2.58	2.62	2.90	2.66	2.56	2.63	1.06	down	4.79E-01	8.95E-01	-	-
1392829_at	Cstf2	cleavage stimulation factor, 3' pre-RNA subunit 2	683927	Rn.170541	BI289495	2.52	3.01	2.56	2.64	2.60	2.61	1.06	down	6.35E-01	8.95E-01	-	-
1380940_at	---	---	---	Rn.210861	BF402603	2.47	2.47	2.48	2.47	2.87	2.33	1.06	up	6.38E-01	8.95E-01	-	-
1368335_at	Apoa1	apolipoprotein A-I	25081	Rn.10308	NM_012738	2.55	2.41	2.53	2.41	2.43	2.41	1.06	down	1.36E-01	8.95E-01	-	-
1383915_at	LOC686120	hypothetical protein LOC686120	686120	---	AI059630	8.91	8.93	9.17	8.64	9.07	9.06	1.06	down	6.48E-01	8.96E-01	-	-
1377784_at	Gatm	glycine amidinotransferase (L-arginine:glycine amidinotransferase)	81660	Rn.17661	AW915304	2.41	2.40	2.64	2.40	2.42	2.38	1.06	down	3.63E-01	8.95E-01	-	-
1376440_at	Rnf139	ring finger protein 139	315000	Rn.209127	BF391522	7.60	7.27	7.59	7.50	7.28	7.93	1.06	up	7.28E-01	9.13E-01	-	-
1374661_at	Aldh16a1	aldehyde dehydrogenase 16 family, member A1	361571	Rn.44200	AW524523	7.76	8.07	7.83	7.48	8.54	7.89	1.06	up	8.13E-01	9.40E-01	-	-
1391517_at	---	---	---	Rn.23264	AA996927	2.45	2.77	2.47	2.46	2.45	2.53	1.06	down	4.96E-01	8.95E-01	-	-
1371861_at	---	---	---	Rn.19802	BE117558	2.37	2.38	2.37	2.66	2.37	2.34	1.06	up	4.63E-01	8.95E-01	-	-
1393545_at	Kif11	Kinesin-like protein 11	313994	Rn.18589	AI043906	2.63	2.59	2.61	2.33	2.59	2.68	1.06	down	4.84E-01	8.95E-01	-	-
1375704_at	Atf7ip	activating transcription factor 7 interacting protein	312800	Rn.98469	AA817860	4.14	2.90	2.95	3.94	2.90	2.90	1.06	down	8.86E-01	9.65E-01	-	-
1398637_at	---	---	---	---	AA893390	2.66	2.68	2.84	2.61	2.78	2.53	1.06	down	4.24E-01	8.95E-01	-	-
1377639_at	Asam	adipocyte-specific adhesion molecule	286939	Rn.163013	BI276896	3.08	3.88	3.09	3.02	3.10	3.68	1.06	down	8.20E-01	9.42E-01	-	-
1374595_at	Tnks2	tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase 2	309512	Rn.75288	BF282323	8.70	9.32	9.18	9.12	9.00	9.32	1.06	up	7.17E-01	9.10E-01	-	-
1378499_at	---	---	---	Rn.58019	BF405148	2.36	2.36	2.36	2.61	2.36	2.36	1.06	up	3.80E-01	8.95E-01	-	-
1381788_at	---	---	---	---	BE097748	4.03	4.02	4.04	4.03	4.03	3.79	1.06	down	3.55E-01	8.95E-01	-	-
1372743_at	Snx5	sorting nexin 5	296199	Rn.86151	AI409727	9.43	9.80	9.88	9.49	9.56	9.81	1.06	down	6.53E-01	8.97E-01	-	-
1391565_at	Lsg1	large subunit GTPase 1 homolog (S. cerevisiae)	288029	Rn.41256	AA899663	2.86	2.49	2.55	2.55	2.59	2.52	1.06	down	5.23E-01	8.95E-01	-	-
1367508_at	RGD1565784	RGD1565784	497874	Rn.20990	BI281225	6.65	7.71	8.31	7.43	8.15	7.34	1.06	up	8.89E-01	9.65E-01	-	-
1394855_at	---	---	---	Rn.155850	AI232392	2.64	2.48	2.50	2.47	2.48	2.42	1.06	down	1.95E-01	8.95E-01	-	-
1388208_a_at	Ret	ret proto-oncogene	24716	Rn.93200	AJ299017	2.63	2.62	2.65	2.65	2.70	2.30	1.06	down	5.55E-01	8.95E-01	-	-
1388992_at	Ep400	E1A binding protein p400	304569	Rn.76053	AI169305	3.91	5.21	5.81	4.76	4.50	5.42	1.06	down	9.02E-01	9.70E-01	-	-
1369636_at	Sord	sorbitol dehydrogenase	24788	Rn.11334	BI285149	11.22	10.98	11.16	11.32	11.24	11.04	1.06	up	4.95E-01	8.95E-01	-	-
1380839_at	---	---	---	Rn.209415	BF401620	2.88	2.67	2.90	2.86	2.98	2.85	1.06	up	4.01E-01	8.95E-01	-	-
1388869_at	Tbce	tubulin folding cofactor E	361255	Rn.3547	BF281319	6.25	6.51	6.06	6.25	6.57	6.25	1.06	up	6.54E-01	8.97E-01	-	-
1384345_at	Ptgr2	prostaglandin reductase 2	299194	Rn.203285	AW527197	7.93	7.97	7.97	8.02	8.03	8.07	1.06	up	1.95E-02	8.95E-01	-	-
1396282_at	Ndufa9	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 9	362440	Rn.107963	BG864056	3.61	2.92	4.05	3.28	4.27	2.79	1.06	down	8.88E-01	9.65E-01	-	-
1381806_at	Ptgs1	prostaglandin-endoperoxide synthase 1	24693	Rn.44404	BF418208	2.74	2.48	2.54	2.51	2.52	2.49	1.06	down	3.67E-01	8.95E-01	-	-
1393271_at	Ihh	Indian hedgehog	84399	Rn.8711	AA955211	2.37	2.41	2.39	2.39	2.40	2.63	1.06	up	3.61E-01	8.95E-01	-	-
1371521_at	Sin3b	SIN3 homolog B, transcription regulator (yeast)	683381	Rn.216472	BI284797	6.94	6.49	5.81	6.54	6.60	6.34	1.06	up	8.23E-01	9.43E-01	-	-
1382073_at	Ifnk	interferon kappa	313152	Rn.104672	AI179042	2.56	2.54	2.57	2.56	2.56	2.79	1.06	up	3.53E-01	8.95E-01	-	-
1375439_at	Wdr18	WD repeat domain 18	314617	Rn.23448	BF417010	3.12	3.20	3.23	3.26	3.07	3.46	1.06	up	5.20E-01	8.95E-01	-	-
1390553_at	Tmem194b	transmembrane protein 194B	503257	Rn.168123	BE104167	2.42	2.38	2.60	2.38	2.41	2.37	1.06	down	3.03E-01	8.95E-01	-	-
1394917_at	---	---	---	Rn.198269	AI145806	2.64	2.64	2.67	2.64	2.93	2.62	1.06	up	4.60E-01	8.95E-01	-	-
1390943_at	RGD1359529	similar to chromosome 1 open reading frame 63	362626	Rn.3870	BE096504	2.85	2.91	2.85	3.23	2.78	2.84	1.06	up	5.98E-01	8.95E-01	-	-
1374618_at	---	---	---	Rn.16122	BI279751	7.19	7.11	6.29	7.11	6.77	6.96	1.06	up	8.03E-01	9.37E-01	-	-
1388854_at	LOC679934	similar to chromosome 3 open reading frame 10	679934	Rn.3501	AI233309	9.16	9.97	10.74	10.16	9.74	10.22	1.06	up	8.74E-01	9.61E-01	-	-
1391526_at	Kif16b	kinesin family member 16B	311478	Rn.70224	AI029006	3.62	4.11	3.78	3.71	3.81	3.74	1.06	down	6.08E-01	8.95E-01	-	-
1377173_at	---	---	---	Rn.203936	BE104535	4.10	5.45	5.07	5.05	4.48	5.34	1.06	up	8.73E-01	9.61E-01	-	-
1390464_at	Frmd4b	FERM domain containing 4B	252858	Rn.41044	BI291381	3.96	4.21	3.94	3.93	3.82	4.11	1.06	down	5.34E-01	8.95E-01	-	-
1396419_at	---	---	---	---	BF394908	2.68	2.45	2.46	2.45	2.46	2.43	1.06	down	3.42E-01	8.95E-01	-	-
1391166_at	---	---	---	Rn.164341	BG378332	2.66	3.23	2.61	2.66	2.94	2.65	1.06	down	7.35E-01	9.15E-01	-	-
1385068_at	---	---	---	Rn.147678	BF397283	2.73	2.48	2.62	2.57	2.59	2.43	1.06	down	3.96E-01	8.95E-01	-	-
1374504_at	Lsm6	LSM6 homolog, U6 small nuclear RNA associated (S. cerevisiae)	498934	Rn.139376	BF415402	2.71	2.50	2.52	2.48	2.51	2.50	1.06	down	2.93E-01	8.95E-01	-	-
1374170_at	Tirap	Traf and Tnf receptor associated protein	498749	Rn.115091	AI172069	7.38	7.91	7.55	7.96	7.04	7.61	1.06	down	8.07E-01	9.38E-01	-	-
1374843_at	765 /// LOC68898	chromobox homolog 3 (HP1 gamma homolog, Drosophila) /// hypothetical pro	681765 /// 688980	Rn.196455	BE095692	2.96	2.96	3.36	3.00	3.03	3.00	1.06	down	5.76E-01	8.95E-01	-	-
1372414_at	---	---	---	Rn.147163	BI281979	2.88	3.16	2.89	2.86	2.94	2.89	1.06	down	4.52E-01	8.95E-01	-	-
1374035_at	Rem2	RAS (RAD and GEM) like GTP binding 2	64626	Rn.48804	BI296482	2.37	2.36	2.37	2.39	2.60	2.36	1.06	up	3.49E-01	8.95E-01	-	-
1368231_at	Stat5a	signal transducer and activator of transcription 5A	24918	Rn.154399	NM_017064	2.68	2.38	3.24	2.62	3.17	2.27	1.06	down	8.34E-01	9.48E-01	-	-
1395360_at	Usp30	ubiquitin specific peptidase 30	304579	Rn.162152	AW916829	2.53	2.52	2.54	2.52	2.53	2.78	1.06	up	3.96E-01	8.95E-01	-	-
1374960_at	RGD1564887	similar to 9130011E15Rik protein	499363	Rn.23632	BM390080	7.29	6.35	5.70	6.35	6.36	6.39	1.06	down	8.70E-01	9.60E-01	-	-
1380097_at	---	---	---	Rn.204542	BE098726	2.42	2.41	2.57	2.41	2.42	2.32	1.06	down	2.66E-01	8.95E-01	-	-
1374382_at	---	---	---	Rn.59174	BF399385	2.50	2.26	2.28	2.27	2.27	2.26	1.06	down	3.65E-01	8.95E-01	-	-
1388412_at	RGD1307799	similar to RIKEN cDNA 2400003C14	307833	Rn.2250	BI284376	9.08	8.99	8.55	8.65	8.93	8.79	1.06	down	6.83E-01	9.03E-01	-	-
1380425_at	Rnasel	Ribonuclease L (2',5'-oligoisoadenylate synthetase-dependent)	359726	Rn.107928	AI012859	2.45	2.44	2.70	2.45	2.48	2.43	1.06	down	3.97E-01	8.95E-01	-	-
1390623_at	Gins3	GINS complex subunit 3 (Psf3 homolog)	307639	Rn.147049	BI279799	2.44	2.41	2.45	2.63	2.51	2.40	1.06	up	3.07E-01	8.95E-01	-	-
1373077_at	Cdkn2aipnl	CDKN2A interacting protein N-terminal like	287278	Rn.39094	BI285902	4.02	5.51	5.01	5.14	4.03	5.14	1.06	down	8.95E-01	9.67E-01	-	-
1385462_at	Map4k2	mitogen activated protein kinase kinase kinase kinase 2	293694	Rn.18710	AI555657	2.14	2.14	2.14	2.14	2.39	2.14	1.06	up	3.79E-01	8.95E-01	-	-
1375965_at	Ube2k	ubiquitin-conjugating enzyme E2K (UBC1 homolog, yeast)	289623	Rn.203330	AI229167	5.36	4.96	5.50	4.12	6.23	5.23	1.06	down	9.05E-01	9.71E-01	-	-
1375882_at	Ppp3cb	protein phosphatase 3, catalytic subunit, beta isoform	24675	Rn.11063	BG380745	4.49	5.15	4.45	4.06	4.71	5.55	1.06	up	8.76E-01	9.62E-01	-	-
1369421_at	Top1	topoisomerase (DNA) I	64550	Rn.91572	NM_022615	5.00	4.48	3.97	5.19	4.09	4.42	1.06	up	8.64E-01	9.58E-01	-	-
1393875_at	---	---	---	Rn.144756	AI500781	4.39	4.41	4.30	4.39	4.58	4.38	1.06	up	3.30E-01	8.95E-01	-	-
1397880_at	LOC679692	similar to lysophosphatidylglycerol acyltransferase 1	679692	Rn.101953	BF389592	7.44	8.89	9.28	8.70	8.81	8.33	1.06	up	8.96E-01	9.67E-01	-	-
1396275_at	Dusp18	dual specificity phosphatase 18	305477	Rn.19584	BE113872	2.82	3.18	2.70	2.94	2.69	2.83	1.06	down	6.42E-01	8.95E-01	-	-
1394384_at	Drd4	dopamine receptor D4	25432	Rn.10159	BI284462	2.67	2.69	2.71	2.97	2.71	2.63	1.06	up	4.79E-01	8.95E-01	-	-
1393797_at	---	---	---	---	AI113159	2.48	2.47	2.38	2.47	2.48	2.62	1.06	up	2.39E-01	8.95E-01	-	-
1374596_at	RGD1309594	similar to RIKEN cDNA 1810043G02; DNA segment, Chr 10, Johns Hopkins U	309681	Rn.128896	BG666593	2.77	2.57	2.71	2.47	2.56	2.77	1.06	down	4.97E-01	8.95E-01	-	-
1372277_at	LOC641316	similar to aldehyde dehydrogenase 4 family, member A1	641316	Rn.203318	BI274673	9.54	9.74	9.73	9.68	9.30	9.78	1.06	down	6.41E-01	8.95E-01	-	-
1379943_at	---	---	---	---	BM386570	2.38	2.37	2.39	2.65	2.36	2.36	1.06	up	4.36E-01	8.95E-01	-	-
1392523_at	Son	Son DNA binding protein	304092	Rn.7967	AW144637	10.74	10.72	10.44	10.75	10.24	10.67	1.06	down	6.89E-01	9.04E-01	-	-
1377968_at	---	---	---	Rn.13003	AI069912	2.31	2.30	2.32	2.31	2.57	2.30	1.06	up	4.04E-01	8.95E-01	-	-
1379415_at	---	---	---	---	BM386879	8.63	9.18	8.27	8.51	8.57	8.75	1.06	down	7.83E-01	9.30E-01	-	-
1375313_at	Mast4	Microtubule associated serine/threonine kinase family member 4	310040	Rn.43251	BF393156	2.45	2.44	2.45	2.44	2.45	2.69	1.06	up	3.76E-01	8.95E-01	-	-
1378301_at	---	---	---	Rn.204582	BG372184	2.60	2.36	2.37	2.36	2.37	2.36	1.06	down	3.69E-01	8.95E-01	-	-
1368019_at	Mtor	mechanistic target of rapamycin (serine/threonine kinase)	56718	Rn.11008	NM_019906	5.88	6.08	5.68	6.31	5.91	5.66	1.06	up	7.34E-01	9.15E-01	-	-
1377484_at	Fbxl3	F-box and leucine-rich repeat protein 3	306129	Rn.36356	BE096747	2.50	2.21	2.22	2.21	2.26	2.21	1.06	down	4.52E-01	8.95E-01	-	-
1388028_at	Ttl	tubulin tyrosine ligase	171572	Rn.205120	AF207605	2.58	2.56	2.58	2.65	2.76	2.55	1.06	up	2.66E-01	8.95E-01	-	-
1385228_x_at	Asap1	ArfGAP with SH3 domain, ankyrin repeat and PH domain 1	314961	Rn.63466	AI059117	3.35	3.67	2.73	3.75	2.94	3.31	1.06	up	8.34E-01	9.48E-01	-	-
1391598_at	---	---	---	Rn.38860	AI566642	2.41	2.40	2.64	2.40	2.41	2.39	1.06	down	3.64E-01	8.95E-01	-	-
1389036_at	Pisd	phosphatidylserine decarboxylase	681361	Rn.2904	BM385629	3.58	3.59	3.90	3.55	3.63	3.64	1.06	down	5.04E-01	8.95E-01	-	-
1398952_at	90331 /// RGD156	similar to CG18809-PA, isoform A /// similar to RIKEN cDNA 2310036O22	288920 /// 690331	Rn.121465	AI233222	8.68	9.40	8.77	9.01	8.87	9.21	1.06	up	7.61E-01	9.22E-01	-	-
1398742_at	---	---	---	Rn.212811	BM389610	2.51	2.28	2.29	2.28	2.28	2.27	1.06	down	3.49E-01	8.95E-01	-	-
1373844_at	Ppme1	protein phosphatase methylesterase 1	361613	Rn.137659	BE103921	5.48	6.53	6.77	6.51	5.65	6.37	1.06	down	8.74E-01	9.61E-01	-	-
1397220_at	---	---	---	---	AW534601	2.44	2.42	2.45	2.45	2.47	2.64	1.06	up	2.60E-01	8.95E-01	-	-
1371830_at	Sae1	SUMO1 activating enzyme subunit 1	308384	Rn.9014	BM986263	5.72	5.43	4.94	5.01	5.20	6.13	1.06	up	8.56E-01	9.55E-01	-	-
1385379_at	Znf287	zinc finger protein 287	303212	Rn.13149	AA998187	3.79	3.82	2.66	2.75	4.55	3.21	1.06	up	9.09E-01	9.73E-01	-	-
1381457_at	---	---	---	Rn.151889	BI294465	3.08	4.31	3.82	3.82	3.82	3.82	1.06	up	8.33E-01	9.47E-01	-	-
1397145_at	---	---	---	Rn.198971	BF387349	2.34	2.32	2.34	2.50	2.41	2.33	1.06	up	1.78E-01	8.95E-01	-	-
1376954_at	---	---	---	Rn.210820	BF406210	2.37	2.57	2.91	2.97	2.56	2.55	1.06	up	7.21E-01	9.11E-01	-	-
1382758_at	Slc10a7	solute carrier family 10 (sodium/bile acid cotransporter family), member 7	291942	Rn.23101	AA955094	2.50	2.58	2.60	2.73	2.63	2.56	1.06	up	2.52E-01	8.95E-01	-	-
1394005_s_at	Med21	mediator complex subunit 21	312849	Rn.6795	BE115762	3.22	2.87	2.66	2.99	3.11	2.88	1.06	up	6.72E-01	9.01E-01	-	-
1392591_at	MGC125002	Similar to RIKEN cDNA 5830433M19	500501	Rn.9502	AI170983	5.81	5.58	6.06	5.92	5.71	5.59	1.06	down	6.61E-01	8.98E-01	-	-
1380684_at	---	---	---	Rn.212400	BI303657	4.54	4.32	4.51	4.16	4.39	4.58	1.06	down	5.95E-01	8.95E-01	-	-
1377701_at	Zmym6	zinc finger, MYM-type 6	362602	Rn.221928	AI012404	5.92	5.65	5.46	5.92	5.48	5.87	1.06	up	6.96E-01	9.06E-01	-	-
1395939_at	---	---	---	---	BE103614	2.34	2.33	2.34	2.33	2.59	2.33	1.06	up	4.05E-01	8.95E-01	-	-
1386037_at	---	---	---	---	BF288392	2.66	2.63	2.78	2.65	2.65	2.54	1.06	down	2.46E-01	8.95E-01	-	-
1370463_x_at	RT1-CE16	RT1 class I, CE16	414819	---	U50449	4.06	4.06	4.42	4.11	4.34	3.85	1.06	down	6.89E-01	9.04E-01	-	-
1383144_at	Trnt1	tRNA nucleotidyl transferase, CCA-adding, 1	312616	Rn.159746	AI454550	7.83	7.96	8.08	7.95	7.97	8.18	1.06	up	4.80E-01	8.95E-01	-	-
1385676_at	Cd2bp2	Cd2 (cytoplasmic tail) binding protein 2	293505	Rn.14633	BG379822	7.33	6.26	6.26	7.27	5.36	6.99	1.06	down	9.14E-01	9.74E-01	-	-
1394810_at	---	---	---	---	BF289684	2.59	2.53	2.76	2.55	2.60	2.50	1.06	down	3.51E-01	8.95E-01	-	-
1388134_at	Eef1d	eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange	300033	Rn.71883	BG380216	8.36	9.17	8.63	8.79	8.25	9.36	1.06	up	8.51E-01	9.53E-01	-	-
1373134_at	Fahd2a	fumarylacetoacetate hydrolase domain containing 2A	296131	Rn.100583	BE329450	8.26	9.01	7.92	8.20	8.00	8.76	1.06	down	8.49E-01	9.53E-01	-	-
1390819_at	Tef	thyrotrophic embryonic factor	29362	Rn.59871	BF419374	6.43	7.01	6.89	6.91	6.43	7.23	1.06	up	7.99E-01	9.35E-01	-	-
1370602_at	Atp2b4	ATPase, Ca++ transporting, plasma membrane 4	29600	Rn.9986	U15408	2.59	2.35	2.36	2.35	2.37	2.34	1.06	down	3.74E-01	8.95E-01	-	-
1394437_at	---	---	---	Rn.18381	AI407319	3.07	3.45	4.12	3.36	3.59	3.46	1.06	down	8.12E-01	9.39E-01	-	-
1372000_at	Net1	neuroepithelial cell transforming 1	307098	Rn.3889	AI180187	8.85	9.00	8.79	8.69	8.38	9.33	1.06	down	7.95E-01	9.34E-01	-	-
1369458_at	Gab2	GRB2-associated binding protein 2	84477	Rn.211990	NM_053417	2.38	2.32	2.37	2.65	2.33	2.33	1.06	up	5.02E-01	8.95E-01	-	-
1390040_at	Bre	brain and reproductive organ-expressed protein	362704	Rn.1432	AA851481	5.08	6.03	2.72	3.98	5.31	4.79	1.06	up	9.43E-01	9.84E-01	-	-
1373467_at	Btaf1	BTAF1 RNA polymerase II, B

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1370078_at	Lin7b	lin-7 homolog b (C. elegans)	60377	Rn.44184	NM_021758	2.38	2.36	2.62	2.37	2.39	2.36	1.06	down	3.94E-01	8.95E-01	-	-
1391952_at	---	---	---	Rn.206012	BE110628	2.48	2.45	2.70	2.46	2.49	2.44	1.06	down	3.78E-01	8.95E-01	-	-
1368965_at	Slc16a3	solute carrier family 16, member 3 (monocarboxylic acid transporter 4)	80878	Rn.10826	NM_030834	2.39	2.37	2.44	2.37	2.70	2.36	1.06	up	5.17E-01	8.95E-01	-	-
1397312_at	Xpo7	exportin 7	361070	Rn.219364	AI574904	3.97	3.24	3.44	4.11	3.43	3.34	1.06	up	8.21E-01	9.43E-01	-	-
1378741_at	Ppp2r3c	protein phosphatase 2, regulatory subunit B", gamma	362739	Rn.162866	AA850260	5.86	5.90	4.91	5.60	5.30	6.01	1.06	up	8.47E-01	9.52E-01	-	-
1371108_a_at	Atp1a1	ATPase, Na+/K+ transporting, alpha 1 polypeptide	24211	Rn.217534	M74494	10.38	10.56	10.27	10.31	10.50	10.64	1.06	up	5.70E-01	8.95E-01	-	-
1398482_at	Bcl3	B-cell CLL/lymphoma 3	680611	Rn.198135	AI411774	3.17	3.10	3.16	3.27	3.12	3.28	1.06	up	2.31E-01	8.95E-01	-	-
1381211_at	---	---	---	---	BF414994	2.48	2.26	2.26	2.25	2.26	2.25	1.06	down	3.52E-01	8.95E-01	-	-
1370396_x_at	Rup2	urinary protein 2	619560	Rn.198813	AF198441	2.38	2.38	2.61	2.37	2.38	2.37	1.06	down	3.70E-01	8.95E-01	-	-
1376942_at	---	---	---	Rn.211570	BF394140	2.40	2.62	2.40	2.39	2.40	2.39	1.06	down	3.41E-01	8.95E-01	-	-
1383021_at	Galnt13	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltran	311039	Rn.39371	AI103845	2.54	2.53	2.75	2.53	2.56	2.49	1.06	down	3.45E-01	8.95E-01	-	-
1398336_at	Rnf25	ring finger protein 25	301515	Rn.101888	AI012577	3.44	4.25	3.59	3.89	3.77	3.86	1.06	up	7.70E-01	9.25E-01	-	-
1371304_a_at	/// Myl6b /// My	myosin, light chain 6, alkali, smooth muscle and non-muscle /// myosin, light ch	116 /// 685867 /// 68	Rn.146093	BI285502	11.61	11.84	11.69	11.75	11.68	11.95	1.06	up	4.83E-01	8.95E-01	-	-
1380874_at	---	---	---	Rn.206098	AW521752	2.63	2.40	2.42	2.41	2.42	2.38	1.06	down	3.58E-01	8.95E-01	-	-
1372666_at	---	---	---	Rn.1873	BI284861	6.90	6.63	7.50	6.94	6.89	6.96	1.06	down	7.75E-01	9.27E-01	-	-
1388279_at	Sry	sex determining region Y	25221	---	AF275682	2.47	2.64	2.52	2.47	2.48	2.44	1.06	down	2.02E-01	8.95E-01	-	-
1389280_at	---	---	---	Rn.205458	AI601965	2.66	2.63	2.85	2.64	2.66	2.61	1.06	down	3.29E-01	8.95E-01	-	-
1379451_at	---	---	---	Rn.147181	AI549081	2.65	2.41	2.44	2.41	2.45	2.39	1.06	down	3.63E-01	8.95E-01	-	-
1381696_at	---	---	---	Rn.47098	AW527867	2.41	2.86	2.42	2.42	2.41	2.63	1.06	down	6.59E-01	8.98E-01	-	-
1370570_at	Nrp1	neuropilin 1	246331	Rn.10815	AF016296	3.84	3.88	3.78	3.80	3.75	4.19	1.06	up	6.06E-01	8.95E-01	-	-
1384576_at	---	---	---	Rn.166607	AI716633	2.80	2.37	2.34	2.38	2.53	2.36	1.06	down	6.42E-01	8.95E-01	-	-
1396171_at	Ppil4	peptidylprolyl isomerase (cyclophilin)-like 4	361449	Rn.21237	BF552272	2.58	2.56	2.59	2.69	2.63	2.65	1.06	up	1.33E-02	8.95E-01	-	-
1385430_at	Lims1	LIM and senescent cell antigen-like domains 1	499443	Rn.100399	AA799637	5.14	5.11	5.26	5.10	5.16	5.02	1.06	down	2.57E-01	8.95E-01	-	-
1385808_at	Phf7	PHD finger protein 7	364510	Rn.24375	BF546046	2.57	2.47	2.85	2.48	2.57	2.60	1.06	down	5.46E-01	8.95E-01	-	-
1373246_at	Kif20a	Kinesin family member 20A	361308	Rn.101107	BF397920	2.46	2.68	2.46	2.45	2.46	2.45	1.06	down	3.59E-01	8.95E-01	-	-
1376350_at	---	---	---	Rn.147954	BF396151	2.53	2.29	2.31	2.29	2.32	2.29	1.06	down	3.62E-01	8.95E-01	-	-
1382551_at	Itsn2	intersectin 2	313934	Rn.37673	BF413245	7.03	6.91	6.64	7.62	6.29	6.91	1.06	up	8.54E-01	9.55E-01	-	-
1389325_at	Pdcd10	programmed cell death 10	494345	Rn.1176	AA848545	6.06	5.62	5.62	5.73	5.41	5.93	1.06	down	7.25E-01	9.13E-01	-	-
1389915_at	Klhl22	Kelch-like 22 (Drosophila)	303792	Rn.23143	AW520813	5.83	5.84	5.73	5.66	6.02	5.95	1.06	up	5.39E-01	8.95E-01	-	-
1385264_at	---	---	---	Rn.159002	AA892746	3.18	2.33	2.41	2.85	2.93	2.37	1.06	up	8.19E-01	9.42E-01	-	-
1392774_at	---	---	---	Rn.148299	BF284310	5.09	5.55	5.45	4.58	5.57	6.18	1.06	up	8.80E-01	9.63E-01	-	-
1370902_at	Akr1b8	aldo-keto reductase family 1, member B8	286921	Rn.23676	AI233740	2.43	2.58	2.60	2.59	2.68	2.57	1.06	up	2.89E-01	8.95E-01	-	-
1381604_at	RGD1307966	similar to hypothetical protein	287736	---	AI549557	2.47	2.45	2.70	2.47	2.47	2.45	1.06	down	3.84E-01	8.95E-01	-	-
1381892_at	Nav2	neuron navigator 2	171563	Rn.203786	BE097695	2.77	2.75	3.03	2.77	2.80	2.74	1.06	down	4.37E-01	8.95E-01	-	-
1372151_at	Tcerg1	transcription elongation regulator 1	307474	Rn.18770	AI317851	5.63	4.63	3.87	5.03	4.38	4.96	1.06	up	8.93E-01	9.67E-01	-	-
1391657_at	Aldh5a1	aldehyde dehydrogenase 5 family, member A1	291133	Rn.10070	AW525993	2.36	2.55	2.36	2.35	2.36	2.32	1.06	down	2.84E-01	8.95E-01	-	-
1393499_at	Pik3ca	Phosphatidylinositol 3-kinase, catalytic, alpha polypeptide	170911	Rn.44193	AA864375	2.99	2.98	3.10	2.81	2.71	3.79	1.06	up	8.32E-01	9.47E-01	-	-
1395543_at	---	---	---	Rn.168608	BG669430	3.60	3.91	3.58	4.22	3.64	3.47	1.06	up	7.71E-01	9.25E-01	-	-
1372495_at	RGD1565149	similar to chromosome 16 open reading frame 7	307923	Rn.204969	BI274679	4.81	4.60	5.09	5.54	4.13	5.07	1.06	up	8.66E-01	9.58E-01	-	-
1394420_at	---	---	---	Rn.91765	BF287027	2.51	3.03	2.51	2.68	2.51	2.63	1.06	down	6.89E-01	9.04E-01	-	-
1378563_at	RGD1309995	Similar to CG13957-PA	314690	Rn.22501	BF284358	8.57	8.62	8.84	8.34	8.69	8.77	1.06	down	6.41E-01	8.95E-01	-	-
1373332_at	Csnk1d	casein kinase 1, delta	64462	Rn.8046	AA946432	9.69	9.40	9.02	9.47	8.85	9.56	1.06	down	8.04E-01	9.37E-01	-	-
1382075_at	---	---	---	Rn.203392	BF386499	3.99	5.16	5.96	5.64	3.98	5.26	1.06	down	9.23E-01	9.77E-01	-	-
1379491_at	Mrap	melanocortin 2 receptor accessory protein	288271	Rn.45756	AW524012	7.38	6.71	6.69	7.15	6.61	7.26	1.06	up	8.10E-01	9.39E-01	-	-
1376558_at	LOC691429	hypothetical protein LOC691429	691429	Rn.50094	BE101628	2.47	2.63	2.48	2.46	2.41	2.46	1.06	down	2.27E-01	8.95E-01	-	-
1373030_at	---	---	---	Rn.13504	AJ225654	6.77	6.53	7.88	7.20	6.66	7.09	1.06	down	8.69E-01	9.59E-01	-	-
1398110_at	---	---	---	Rn.166591	AI717612	2.44	2.66	2.44	2.44	2.44	2.43	1.06	down	3.39E-01	8.95E-01	-	-
1375429_at	Zfr16	Zfr16 protein	100190937	Rn.199101	BI294768	6.09	6.84	6.58	6.51	6.11	6.65	1.06	down	7.88E-01	9.32E-01	-	-
1379902_at	---	---	---	Rn.148941	BE108170	2.46	3.66	3.51	2.39	2.61	4.40	1.06	down	9.21E-01	9.77E-01	-	-
1392296_at	---	---	---	Rn.131200	AI502798	2.60	2.55	2.80	2.56	2.63	2.52	1.06	down	4.06E-01	8.95E-01	-	-
1371412_a_at	Nreg	neuronal regeneration related protein	338475	Rn.8180	BE107405	8.38	8.07	8.10	7.98	8.56	7.77	1.06	down	7.75E-01	9.27E-01	-	-
1367844_at	Gnai2	guanine nucleotide binding protein (G protein), alpha inhibiting 2	81664	Rn.3036	M12672	6.01	6.30	5.64	5.69	6.03	6.00	1.06	down	7.41E-01	9.17E-01	-	-
1389227_at	Rhog	ras homolog gene family, member G (rho G)	308875	Rn.11976	BG375902	5.54	5.81	5.45	5.27	5.32	5.96	1.06	down	7.66E-01	9.24E-01	-	-
1373667_at	Ccbl1	cysteine conjugate-beta lyase, cytoplasmic	311844	Rn.110564	BF400674	10.35	10.49	10.68	10.48	10.39	10.42	1.06	down	4.82E-01	8.95E-01	-	-
1375143_at	Basp1	Brain abundant, membrane attached signal protein 1	64160	Rn.37779	AI576452	2.84	2.64	2.73	2.66	2.67	2.64	1.06	down	2.43E-01	8.95E-01	-	-
1398557_at	Ikzf5	IKAROS family zinc finger 5	309031	Rn.219422	BF389362	3.86	3.90	3.91	3.90	4.10	3.90	1.06	up	3.22E-01	8.95E-01	-	-
1386633_at	---	---	---	Rn.19125	BF549535	2.74	2.84	2.60	2.64	2.66	2.64	1.06	down	3.42E-01	8.95E-01	-	-
1378384_at	Ints6	integrator complex subunit 6	361057	Rn.202377	AW551141	2.33	2.31	2.32	2.31	2.57	2.31	1.06	up	4.19E-01	8.95E-01	-	-
1394186_at	---	---	---	---	AI638966	2.27	2.26	2.27	2.49	2.27	2.27	1.06	up	3.57E-01	8.95E-01	-	-
1371519_at	Etfdh	electron-transferring-flavoprotein dehydrogenase	295143	Rn.37277	AA851258	9.01	9.33	9.26	9.03	9.65	9.15	1.06	up	7.32E-01	9.14E-01	-	-
1394527_at	---	---	---	Rn.148928	AI501679	2.67	2.74	2.81	2.68	2.75	2.55	1.06	down	3.38E-01	8.95E-01	-	-
1382350_at	Stat6	signal transducer and activator of transcription 6	362896	Rn.6880	BG377827	3.03	3.01	4.17	3.13	3.84	3.00	1.06	down	8.76E-01	9.61E-01	-	-
1386919_at	Prl8a4	prolactin family 8, subfamily a, member 4	59088	Rn.203207	NM_021580	2.84	2.76	3.04	2.80	2.99	2.61	1.06	down	5.98E-01	8.95E-01	-	-
1377755_at	Ascc3	activating signal cointegrator 1 complex subunit 3	309887	Rn.24209	AI179403	4.12	4.14	3.71	4.15	3.10	4.96	1.06	up	8.95E-01	9.67E-01	-	-
1391535_at	---	---	---	Rn.164131	BF284610	2.67	2.39	2.53	2.50	2.84	2.49	1.06	up	6.08E-01	8.95E-01	-	-
1368777_at	Bard1	BRCA1 associated RING domain 1	64557	Rn.48735	NM_022622	2.48	2.38	2.30	2.38	2.63	2.37	1.06	up	4.79E-01	8.95E-01	-	-
1382468_at	RGD1311345	similar to CG9752-PA	361201	Rn.53930	AW143385	7.11	7.23	7.08	6.84	7.08	7.27	1.06	down	5.86E-01	8.95E-01	-	-
1371370_a_at	Svs6	seminal vesicle secretory protein 6	362267	---	BI284578	2.81	2.80	2.92	2.77	2.83	2.70	1.06	down	2.17E-01	8.95E-01	-	-
1390323_at	---	---	---	Rn.156524	AW527815	5.57	4.84	2.48	4.29	4.18	4.65	1.06	up	9.38E-01	9.83E-01	-	-
1393897_at	Cdh20	cadherin 20	363948	Rn.62576	BF419648	2.43	2.41	2.62	2.41	2.42	2.40	1.06	down	3.22E-01	8.95E-01	-	-
1378078_at	---	---	---	Rn.140563	BE095857	2.34	2.56	2.34	2.34	2.34	2.33	1.06	down	3.39E-01	8.95E-01	-	-
1384145_at	RGD1310495	similar to KIAA1919 protein	309809	Rn.24001	AI511200	9.29	9.78	10.03	9.82	9.45	9.59	1.06	down	7.66E-01	9.23E-01	-	-
1384586_x_at	LOC690418	similar to Acidic proline-rich protein PRP25 precursor	690418	---	BI279337	2.91	2.84	2.85	2.87	2.85	2.65	1.06	down	3.45E-01	8.95E-01	-	-
1397364_at	---	---	---	Rn.205597	AW521314	2.48	2.46	2.38	2.37	2.37	2.34	1.06	down	7.74E-02	8.95E-01	-	-
1372337_at	LOC100188932	dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 4	100188932	Rn.34416	AA800242	10.01	9.61	9.60	9.82	9.92	9.71	1.06	up	6.27E-01	8.95E-01	-	-
1388794_at	Rbmxrtl	RNA binding motif protein, X chromosome retrogene-like	307779	Rn.19966	BE107489	7.43	7.77	7.31	7.62	7.25	7.41	1.06	down	6.79E-01	9.02E-01	-	-
1394363_at	Riok3	RIO kinase 3 (yeast)	361293	Rn.203135	H34775	5.56	5.57	5.21	5.29	5.39	5.42	1.06	down	5.65E-01	8.95E-01	-	-
1376696_at	---	---	---	Rn.24077	AI175442	3.99	5.02	3.60	3.94	3.94	4.50	1.06	down	8.75E-01	9.61E-01	-	-
1374575_at	Creb3l1	cAMP responsive element binding protein 3-like 1	362166	Rn.24541	BI304123	2.45	2.44	2.46	2.69	2.45	2.44	1.06	up	3.93E-01	8.95E-01	-	-
1396052_at	Dhx8	DEAH (Asp-Glu-Ala-His) box polypeptide 8	287727	Rn.108087	BF554501	2.42	2.61	2.44	2.42	2.43	2.39	1.06	down	2.76E-01	8.95E-01	-	-
1381042_at	Anapc10	Anaphase promoting complex subunit 10	361389	Rn.9619	AA956336	2.64	3.20	2.71	2.64	3.09	2.59	1.06	down	7.59E-01	9.21E-01	-	-
1368374_at	Ggt1	gamma-glutamyltransferase 1	116568	Rn.10010	NM_053840	12.54	12.92	12.67	12.56	12.51	12.83	1.06	down	6.33E-01	8.95E-01	-	-
1378567_at	Tjp3	tight junction protein 3	314640	Rn.145098	BI295961	2.42	3.06	2.43	2.42	2.87	2.39	1.06	down	7.81E-01	9.29E-01	-	-
1396973_at	---	---	---	Rn.210999	BF404479	2.55	2.54	2.44	2.68	2.56	2.53	1.06	up	2.47E-01	8.95E-01	-	-
1379950_at	RGD1309362	similar to interferon-inducible GTPase	307415	Rn.160023	AA955213	6.30	3.97	4.10	5.71	4.97	3.92	1.06	up	9.37E-01	9.82E-01	-	-
1367641_at	Sod1	superoxide dismutase 1, soluble	24786	Rn.6059	NM_017050	12.60	12.67	12.62	12.55	12.40	12.71	1.06	down	4.47E-01	8.95E-01	-	-
1389854_at	Nr1h2	Nuclear receptor subfamily 1, group H, member 2	58851	Rn.786	AA956855	4.20	4.49	4.49	4.47	4.49	4.47	1.06	up	4.71E-01	8.95E-01	-	-
1371351_at	Rpo1-3	RNA polymerase 1-3	360762	Rn.6228	AI233192	7.47	7.60	8.87	8.08	8.01	8.07	1.06	up	8.71E-01	9.60E-01	-	-
1367985_at	Alas2	aminolevulinate, delta-, synthase 2	25748	Rn.32517	NM_013197	2.40	2.51	2.47	2.38	2.39	2.37	1.06	down	8.31E-02	8.95E-01	-	-
1384885_at	Tekt2	tektin 2 (testicular)	298532	Rn.47921	AW532312	2.51	2.43	2.59	2.43	2.45	2.42	1.06	down	1.85E-01	8.95E-01	-	-
1376745_at	Rabif	RAB interacting factor	304807	Rn.204985	BM383340	2.71	3.93	4.23	3.85	3.27	3.99	1.06	up	8.87E-01	9.65E-01	-	-
1370540_at	Nr1d2	nuclear receptor subfamily 1, group D, member 2	259241	Rn.10055	U20796	7.88	7.50	6.69	6.78	7.22	7.84	1.06	down	8.76E-01	9.62E-01	-	-
1389077_at	Slc35a1	Solute carrier family 35 (CMP-sialic acid transporter), member A1	313139	Rn.24337	AI228537	4.75	3.93	4.50	4.28	4.38	4.29	1.06	down	7.69E-01	9.24E-01	-	-
1371826_at	---	---	---	Rn.94891	BM390536	4.20	4.24	4.44	4.29	4.25	4.12	1.06	down	4.33E-01	8.95E-01	-	-
1370662_a_at	Ap2b1	adaptor-related protein complex 2, beta 1 subunit	140670	Rn.56138	M34176	6.34	5.63	6.87	6.14	6.37	6.10	1.06	down	8.45E-01	9.52E-01	-	-
1384808_at	Stox2	storkhead box 2	360459	Rn.61768	BF410724	2.41	2.40	2.48	2.69	2.44	2.40	1.06	up	4.53E-01	8.95E-01	-	-
1375117_at	Akt1s1	AKT1 substrate 1 (proline-rich)	292887	Rn.102669	AI102030	4.67	4.45	5.67	5.88	4.15	4.54	1.06	down	9.10E-01	9.73E-01	-	-
1369993_at	Camk2g	calcium/calmodulin-dependent protein kinase II gamma	171140	Rn.10961	NM_133605	2.40	2.39	2.41	2.45	2.45	2.53	1.06	up	4.91E-02	8.95E-01	-	-
1383564_at	Irf7	interferon regulatory factor 7	293624	Rn.101159	BF411036	3.18	3.11	4.31	4.25	3.30	3.29	1.06	up	8.85E-01	9.64E-01	-	-
1391344_at	---	---	---	Rn.206415	AW527134	2.63	2.84	2.72	3.11	2.69	2.61	1.06	up	6.65E-01	8.96E-01	-	-
1369432_at	Chrnb2	cholinergic receptor, nicotinic, beta 2 (neuronal)	54239	Rn.53978	NM_019297	2.79	2.56	2.57	2.56	2.56	2.56	1.05	down	3.62E-01	8.95E-01	-	-
1384803_at	Loc11	late cornified envelope 1F	499663	Rn.160543	BI283351	2.68	2.46	2.48	2.46	2.48	2.44	1.05	down	3.48E-01	8.95E-01	-	-
1388323_at	Ndufa9	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 9	362440	Rn.107963	BG381033	9.86	10.04	9.31	9.68	9.76	10.00	1.05	up	7.82E-01	9.22E-01	-	-
1380881_at	---	---	---	Rn.27730	AI112304	2.69	2.46	2.49	2.47	2.47	2.46	1.05	down	3.46E-01	8.95E-01	-	-
1375400_at	---	---	---	---	BF420605	2.52	2.42	2.73	2.42	2.61	2.41	1.05	down	5.23E-01	8.95E-01	-	-
1396439_at	---	---	---	Rn.173845	BF419397	2.32	2.31	2.33	2.55	2.34	2.31	1.05	up	3.62E-01	8.95E-01	-	-
1379195_s_at	Lig1	ligase I, DNA, ATP-dependent	81513	Rn.20467	AI556346	5.65	6.20	3.37	3.41	5.76	6.29	1.05	up	9.53E-01	9.86E-01	-	-
1367559_at	Ftl	ferritin, light polypeptide	29292	Rn.1905	L01122	12.05	12.13	12.27	12.30	12.14	12.25	1.05	up	3.94E-01	8.95E-01	-	-
1376728_at	---	---	---	Rn.203844	BM392264	9.17	9.12	9.09	9.19	8.82	9.60	1.05	up	7.53E-01	9.20E-01	-	-
1393253_at	Zfp365	zinc finger protein 365	499425	Rn.24356	BF408799	2.25	2.48	2.26	2.25	2.25	2.25	1.05	down	3.53E-01	8.95E-01	-	-
1397139_at	---	---	---	Rn.211466	BF413644	2.51	2.71	2.56	2.53	2.54	2.46	1.05	down	2.98E-01	8.95E-01	-	-
1372973_at	Lss	Lanosterol synthase (2,3-oxidosqualene-lanosterol cyclase)	81681	Rn.10211	BM390574	2.38	3.96	2.78	2.62	2.78	3.49	1.05	down	8.94E-01	9.67E-01	-	-
1395775_at	---	---	---	Rn.166932	BF391800	2.35	2.34	2.36	2.35	2.60	2.33	1.05	up	4.30E-01	8.95E-01	-	-
1369404_a_at	Nrxn1	neurexin 1	60391	Rn.54924	NM_021767	2.70	2.50	2.51	2.50	2.55	2.43	1.05	down	3.44E-01	8.95E-01	-	-
1390995_at	Fkbpl	FK506 binding protein-like	406168	Rn.54367	BF389385	4.82	4.23	4.40	4.71	3.96	4.54	1.05	down	8.02E-01	9.36E-01	-	-
1380829_at	---	---	---	Rn.79949	BM387795	2.62	2.83	2.62	2.62	2.63	2.60	1.05	down	3.35E-01	8.95E-01	-	-
1390578_at	LOC685286	Similar to brain-selective kinase 2 isoform gamma	685286	Rn.162481	AI578275	2.53	2.52	2.54	2.52	2.80	2.51	1.05	up	4.71E-01	8.95E-01	-	-
1370308_at	Xtp3tpa	XTP3-transactivated protein A	192252	Rn.8733	AY029335	4.45	4.47	4.36	3.71	4.87	4.47	1.05	down	8.34E-01	9.47E-01	-	-
1374641_at	Lmtk2	lemur tyrosine kinase 2	304286	Rn.26715	BF397653	4.72	5.37	5.59	5.15	5.03	5.25	1.05	down	7.89E-01	9.32E-01	-	-
1385841_at	---	---	---	Rn.153002	BM383983	2.43	2.51	2.46	2.38	2.45	2.35	1.05	down	1.29E-01	8.95E-01	-	-
1371512_at	---	---	---	---	AA818692	11.15	10.85	11.22	11.14	10.96	11.35	1.05	up	6.57E-01	8.98E-01	-	-
1393382_at	RGD1566386	similar to Hypothetical protein A430033K04	304336	Rn.47432	BE096740	3.37	2.77	2.86	2.77	2.81	3.65	1.05	up	8.33E-01	9.47E-01	-	-
1398355_at	Trpm7	Transient receptor potential cation channel, subfamily M, member 7	679906	Rn.86991	AI232142	5.64	5.66	5.79	5.63	5.65	5.58	1.05	down	2.03E-01	8.95E-01	-	-
1389986_at	---	---	---	Rn.119131	AI008409	11.38	11.28	10.42	11.73	11.24	10.34	1.05	up	6.87E-01	9.65E-01	-	-
1399049_at	RGD1308917	similar to RIKEN cDNA 1200003C05	299127	Rn.106021	AI230073	5.02	4.72	4.24	4.48	4.27	4.99	1.05	down	8.18E-01	9.42E-01	-	-
1370209_at	Klf9	Kruppel-like factor 9	117560	Rn.19481	AI071565	10.09	9.60	9.84	10.03	9.75	9.98	1.05	up	6.68E-01	9.00E-01	-	-
1381801_at	Facn2	fascin homolog 2, actin-bundling protein, retinal (Strongylocentrotus purpurat	303741	Rn.138713	AI771493	2.37	2.57	2.38	2.36	2.37	2.35	1.05	down	3.16E-01	8.95E-01	-	-
1383161_a_at	---	---	---	---	AI008646	10.79	10.45	11.18	10.73	10.93	11.00	1.05	up	7.49E-01	9.19E-01	-	-
1372245_at	Ciao1	cytosolic iron-sulfur protein assembly 1 homolog (S. cerevisiae)	29231	Rn.108832	AA894272	8.78	8.07	8.84	8.73	8.62	8.57	1.05	up	7.74E-01	9.26E-01	-	-
1387353_at	Akt2	v-akt murine thymoma viral oncogene homolog 2	25233	Rn.87086	AI105076	5.39	5.36	4.66	4.62	4.65	4.97	1.05	up	8.61E-01	9.57E-01	-	-
1372167_at	Snrpg	small nuclear ribonucleoprotein polypeptide G	681031	Rn.2397	AW525656	11.40	10.65	11.17	11.10	11.19	11.15	1.05	up	7.48E-01	9.19E-01	-	-
1371192_at	Nf2	neurofibromin 2 (merlin)	25744	Rn.46695	BF566236	7.25	5.90	6.09	6.95	6.06	6.00	1.05	down	8.90E-01	9.66E-01	-	-
1368281_at	Dpep1	dipeptidase 1 (renal)	94199	Rn.6051	NM_053591	2.41	2.42	2.34	2.54	2.51	2.36	1.05	up	2.84E-01	8.95E-01	-	-
1378379_at	Chic2	cysteine-rich hydrophobic domain 2	83835	Rn.106037	AI548933	2.55	2.54	2.74	2.55	2.55	2.50	1.05	down	3.06E-01	8.95E-01	-	-
1384829_at	---	---	---	Rn.166697	AI454917	7.82	7.32	6.54	7.43	7.27	7.21	1.05	up	8.49E-01	9.53E-01	-	-
1398763_at	Timm23	translocase of inner mitochondrial membrane 23 homolog (yeast)	54312	Rn.154974	NM_019352	8.67	8.75	8.80	8.72	8.54	8.73	1.05	down	3.62E-01	8.95E-01	-	-
1386781_at	---	---	---	---	BF544537	2.50	2.62	2.54	2.44	2.44	2.51	1.05	up	6.58E-01	8.98E-01	-	-
1388070_a_at	Akap1	A kinase (PRKA) anchor protein 1	114124	Rn.163146	AF092523	2.95	2.78	2.61	2.91	2.60	2.59	1.05	down	6.20E-01	8.95E-01	-	-
1373965_at	Ccdc124	coiled-coil domain containing 124	290642	Rn.14668	BM385251	4.59	4.77	4.88	4.60	4.46	4.95	1.05	down	6.74E-01	9.01E-01	-	-
1395555_at	Gosr1	golgi SNAP receptor complex member 1	94189	Rn.8228	AW916706	2.79	2.70	2.72	2.71	2.71	3.01	1.05	up	5.00E-01	8.95E-01	-	-

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1384691_at	---	---	---	---	BE113194	2.74	2.68	2.79	2.72	3.13	2.59	1.05	up	6.73E-01	9.01E-01	-	-
1390257_at	Vapb	VAMP (vesicle-associated membrane protein)-associated protein B and C	60431	Rn.52500	BG376956	8.63	8.51	8.23	8.46	8.32	8.36	1.05	down	5.77E-01	8.95E-01	-	-
1388032_a_at	Cxcl3	chemokine (C-X-C motif) ligand 3	171551	Rn.10525	D87927	3.00	3.14	3.12	3.02	3.07	2.93	1.05	down	2.83E-01	8.95E-01	-	-
1386733_at	---	---	---	Rn.167766	BF544390	2.45	2.68	2.46	2.45	2.46	2.45	1.05	down	3.68E-01	8.95E-01	-	-
1391112_at	Ggta1	Glycoprotein, alpha-galactosyltransferase 1	246766	Rn.916	BF405127	2.65	2.48	2.41	2.49	2.43	2.39	1.05	down	3.87E-01	8.95E-01	-	-
1387336_at	Cml4	camello-like 4	64570	Rn.204804	NM_022635	11.40	11.47	11.34	11.29	11.29	11.41	1.05	down	2.46E-01	8.95E-01	-	-
1367578_at	Prdx2	peroxiredoxin 2	29338	Rn.2511	NM_017169	9.76	9.98	9.28	9.48	9.68	9.63	1.05	down	7.41E-01	9.17E-01	-	-
1393116_at	Smyd4	SET and MYND domain containing 4	287525	Rn.137192	BI286804	4.72	4.06	4.08	3.97	4.03	4.63	1.05	down	8.15E-01	9.40E-01	-	-
1376362_at	Npbr	neuronal pentraxin receptor	81005	Rn.34907	BG380575	2.95	2.95	2.97	3.43	2.72	2.95	1.05	up	7.36E-01	9.15E-01	-	-
1371029_at	Pkd1	polycystic kidney disease 1 homolog (human)	24850	Rn.127770	AW916437	2.65	2.53	2.65	2.55	2.98	2.52	1.05	up	6.45E-01	8.95E-01	-	-
1389761_at	---	---	---	Rn.67006	BI297776	2.41	2.41	2.41	2.41	2.41	2.64	1.05	up	3.71E-01	8.95E-01	-	-
1390344_at	Trim11	tripartite motif-containing 11	360534	Rn.9308	BF393562	2.66	2.43	2.45	2.44	2.45	2.43	1.05	down	3.50E-01	8.95E-01	-	-
1392541_at	Ggct	gamma-glutamyl cyclotransferase	362368	Rn.129080	AW919608	12.17	12.51	12.17	12.48	12.32	12.28	1.05	up	5.91E-01	8.95E-01	-	-
1369945_at	Grid1	glutamate receptor, ionotropic, delta 1	79219	Rn.10040	NM_024378	2.57	2.55	2.54	2.55	2.55	2.33	1.05	down	3.55E-01	8.95E-01	-	-
1381453_at	---	---	---	Rn.204505	BE110814	2.36	2.35	2.36	2.58	2.36	2.36	1.05	up	3.63E-01	8.95E-01	-	-
1368015_at	Ptges	prostaglandin E synthase	59103	Rn.7730	AF280967	2.40	2.37	2.75	2.55	2.38	2.36	1.05	down	6.10E-01	8.95E-01	-	-
1390871_at	Toerg1	transcription elongation regulator 1	307474	Rn.18770	BF286230	2.68	2.75	2.80	2.67	2.68	2.65	1.05	down	9.82E-02	8.95E-01	-	-
1376445_at	Il17b	interleukin 17B	116472	Rn.50003	BF409208	2.41	2.40	2.42	2.40	2.66	2.40	1.05	up	4.37E-01	8.95E-01	-	-
1389294_at	Cyfip1	cytoplasmic FMR1 interacting protein 1	308666	Rn.143776	AI103084	8.34	8.67	8.64	8.40	8.42	8.60	1.05	down	5.72E-01	8.95E-01	-	-
1375914_at	Krba1	KRAB-A domain containing 1	362358	Rn.3134	BI285504	3.86	3.87	3.89	3.85	3.88	4.11	1.05	up	4.13E-01	8.95E-01	-	-
1367923_at	Acsbg1	acyl-CoA synthetase bubblegum family member 1	171410	Rn.17672	NM_134389	2.38	2.37	2.39	2.37	2.50	2.51	1.05	up	1.68E-01	8.95E-01	-	-
1382686_at	---	---	---	Rn.203383	BF285846	2.46	2.42	2.46	2.43	2.73	2.41	1.05	up	5.12E-01	8.95E-01	-	-
1378772_at	---	---	---	Rn.210952	BF403919	2.35	2.33	2.36	2.34	2.59	2.33	1.05	up	4.25E-01	8.95E-01	-	-
1376331_at	---	---	---	Rn.38226	BI295137	2.62	2.52	3.00	2.68	3.03	2.66	1.05	up	7.12E-01	9.10E-01	-	-
1367724_a_at	Atp6v0e1	ATPase, H+ transporting, lysosomal 9kDa, V0 subunit e1	94170	Rn.789	NM_053578	9.35	9.51	9.31	9.41	9.01	9.52	1.05	down	6.72E-01	9.01E-01	-	-
1380424_at	Ubxn11	UBX domain protein 11	192207	Rn.11961	AA964950	2.96	2.67	2.60	2.60	2.68	2.73	1.05	down	5.57E-01	8.95E-01	-	-
1392077_at	Mppe62	metallophosphoesterase domain containing 2	362185	Rn.206970	AW536022	2.45	2.39	2.41	2.71	2.39	2.38	1.05	up	5.27E-01	8.95E-01	-	-
1369610_at	Lin7c	lin-7 homolog C (C. elegans)	60442	Rn.44289	NM_021851	8.76	8.78	8.31	8.72	8.33	9.03	1.05	up	7.82E-01	9.29E-01	-	-
1378032_at	Nfkbiz	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, ze	304005	Rn.58420	AI176265	2.70	2.55	2.74	2.94	2.73	2.55	1.05	up	5.85E-01	8.95E-01	-	-
1373954_at	Suds3	suppressor of defective silencing 3 homolog (S. cerevisiae)	360819	Rn.98280	BG381520	3.18	3.56	3.78	3.76	3.43	3.55	1.05	up	7.25E-01	9.13E-01	-	-
1370183_at	Dyrk1a	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1A	25255	Rn.9354	BI303285	4.32	3.74	3.86	3.99	3.97	3.73	1.05	down	7.19E-01	9.11E-01	-	-
1398802_at	Ube2d3	ubiquitin-conjugating enzyme E2D 3 (UBC4/5 homolog, yeast)	81920	Rn.2778	NM_031237	7.90	8.29	8.69	8.25	8.12	8.74	1.05	up	8.11E-01	9.39E-01	-	-
1395459_at	---	---	---	Rn.26798	AI575802	2.54	2.41	2.32	2.35	2.36	2.33	1.05	down	3.08E-01	8.95E-01	-	-
1370184_at	Cfl1	cofilin 1, non-muscle	29271	Rn.11675	BM389873	8.85	9.02	8.73	8.96	8.63	8.79	1.05	down	5.89E-01	8.95E-01	-	-
1370825_a_at	Cdc42	cell division cycle 42 (GTP binding protein)	64465	Rn.60067	AA925473	8.95	9.69	9.39	9.53	8.86	9.42	1.05	down	8.13E-01	9.40E-01	-	-
1391503_at	Centd3	centaurin, delta 3	361314	---	BF281952	3.33	3.15	3.17	3.22	3.23	2.97	1.05	down	5.05E-01	8.95E-01	-	-
1379847_at	Dysf	dysferlin	312492	Rn.22869	AW141858	2.79	2.72	3.25	3.11	2.71	2.70	1.05	down	7.41E-01	9.17E-01	-	-
1378194_a_at	Rufy3	RUN and FYVE domain containing 3	360921	Rn.203111	BG671338	9.08	9.11	8.52	8.91	8.91	8.66	1.05	down	7.37E-01	9.16E-01	-	-
1380223_at	Cramp1l	Crm, cramped-like (Drosophila)	287127	Rn.163129	AI179452	2.37	2.36	2.37	2.36	2.37	2.59	1.05	up	3.76E-01	8.95E-01	-	-
1375709_at	Sipa1	signal-induced proliferation-associated 1	361710	Rn.24935	BI275966	2.60	2.34	2.38	2.37	2.37	2.36	1.05	down	4.15E-01	8.95E-01	-	-
1391603_at	---	---	---	Rn.52813	AW527410	4.18	4.69	4.26	4.56	4.41	3.92	1.05	down	7.77E-01	9.28E-01	-	-
1386242_at	---	---	---	---	AI179722	2.42	2.59	2.43	2.41	2.42	2.38	1.05	down	2.60E-01	8.95E-01	-	-
1390088_at	Nog	noggin	25495	Rn.10154	BF403302	2.60	2.46	2.53	2.47	2.47	2.43	1.05	down	1.49E-01	8.95E-01	-	-
1372201_at	Cgnbp2	gametogenetin binding protein 2	360584	Rn.48466	AI233698	7.21	7.25	7.75	7.19	7.64	7.61	1.05	up	7.58E-01	9.21E-01	-	-
1371570_at	Scrt1	scratch homolog 1, zinc finger protein (Drosophila)	366951	Rn.220523	AI406286	2.45	2.43	2.66	2.43	2.46	2.42	1.05	down	3.63E-01	8.95E-01	-	-
1391965_at	---	---	---	Rn.65020	BE113310	2.55	2.33	2.33	2.33	2.33	2.32	1.05	down	3.70E-01	8.95E-01	-	-
1391422_at	Dnajb6	DnaJ (Hsp40) homolog, subfamily B, member 6	362293	Rn.129050	BE100486	3.73	4.05	3.77	3.78	3.63	3.92	1.05	down	5.92E-01	8.95E-01	-	-
1385961_at	Klf5	Kruppel-like factor 5	84410	Rn.8954	BM382886	4.13	3.49	2.89	2.67	4.38	3.68	1.05	up	9.08E-01	9.72E-01	-	-
1389423_at	Ddr2	Discoidin domain receptor tyrosine kinase 2	685781	Rn.92730	AI575451	2.33	2.33	2.34	2.32	2.33	2.58	1.05	up	4.22E-01	8.95E-01	-	-
1376816_at	---	---	---	Rn.164344	BF284903	2.51	2.50	2.79	2.49	2.55	2.53	1.05	down	4.78E-01	8.95E-01	-	-
1374165_at	RGD1565457	similar to Rasa4 protein	288589	Rn.1868	AA818264	2.61	2.39	2.40	2.85	2.39	2.38	1.05	up	6.85E-01	9.03E-01	-	-
1370006_at	Ndufs6	NADH dehydrogenase (ubiquinone) Fe-S protein 6	29478	Rn.154403	NM_019223	11.54	11.75	11.74	11.75	11.71	11.78	1.05	up	3.49E-01	8.95E-01	-	-
1392471_at	---	---	---	Rn.17099	BI302750	6.99	7.38	7.25	7.07	6.97	7.80	1.05	up	8.06E-01	9.38E-01	-	-
1382391_at	---	---	---	Rn.21950	BF397532	4.65	4.24	4.97	5.01	4.40	4.66	1.05	up	7.99E-01	9.35E-01	-	-
1393380_at	---	---	---	---	AW917818	5.10	6.36	5.08	5.57	5.78	5.41	1.05	up	8.72E-01	9.61E-01	-	-
1394257_at	Trim16	tripartite motif-containing 16	303214	Rn.171348	AW919209	2.61	2.29	2.30	2.29	2.39	2.29	1.05	down	5.34E-01	8.95E-01	-	-
1390301_at	---	---	---	Rn.15569	AW524414	2.38	2.37	2.96	2.37	2.42	2.69	1.05	down	7.51E-01	9.19E-01	-	-
1377226_at	---	---	---	Rn.146861	BE107326	2.43	2.64	2.44	2.43	2.44	2.43	1.05	down	3.37E-01	8.95E-01	-	-
1377297_at	Ssu72	SSU72 RNA polymerase II CTD phosphatase homolog (S. cerevisiae)	298681	Rn.103950	BE118384	3.94	3.94	3.69	3.14	4.06	4.14	1.05	down	8.33E-01	9.47E-01	-	-
1397244_at	---	---	---	Rn.148070	AI535406	2.60	2.72	2.65	2.59	2.34	2.81	1.05	down	6.17E-01	8.95E-01	-	-
1378571_at	Zfp385b	zinc finger protein 385B	311137	Rn.34063	BF420620	2.57	2.55	2.57	2.56	2.57	2.79	1.05	up	3.77E-01	8.95E-01	-	-
1387099_at	Npr2	natriuretic peptide receptor B/guanylate cyclase B (atrionatriuretic peptide rec	116564	Rn.32984	NM_053838	2.42	2.43	2.44	2.48	2.43	2.60	1.05	up	2.24E-01	8.95E-01	-	-
1367563_at	Sparc	secreted protein, acidic, cysteine-rich (osteonectin)	24791	Rn.98989	D28875	4.58	5.69	3.22	4.38	4.63	4.70	1.05	up	9.22E-01	9.77E-01	-	-
1379571_at	Pkp4	plakophilin 4	295625	Rn.17389	AA819847	4.39	5.04	3.74	3.26	4.65	5.04	1.05	down	9.15E-01	9.75E-01	-	-
1372268_at	---	---	---	Rn.20599	AI071674	6.16	6.59	5.84	5.89	5.83	6.66	1.05	down	8.39E-01	9.50E-01	-	-
1375365_at	LOC685834	Similar to zinc finger protein 740	685834	Rn.144458	BE112020	2.48	2.73	2.57	2.48	2.64	2.89	1.05	up	6.20E-01	8.95E-01	-	-
1369163_at	Grik4	glutamate receptor, ionotropic, kainate 4	24406	Rn.10049	NM_012572	2.63	2.41	2.42	2.42	2.42	2.40	1.05	down	3.66E-01	8.95E-01	-	-
1371440_at	B2m	Beta-2 microglobulin	24223	Rn.1868	AW916647	10.20	10.63	10.54	10.34	10.51	10.28	1.05	down	6.38E-01	8.95E-01	-	-
1396627_at	---	---	---	Rn.172390	BF398496	2.44	2.42	2.50	2.73	2.45	2.41	1.05	up	5.20E-01	8.95E-01	-	-
1374059_at	---	---	---	Rn.164879	AI177428	8.36	8.43	8.24	8.33	8.51	8.41	1.05	up	3.84E-01	8.95E-01	-	-
1371104_at	Srebf1	sterol regulatory element binding transcription factor 1	78968	Rn.221929	AF286470	2.33	2.33	2.35	2.33	2.34	2.57	1.05	up	3.98E-01	8.95E-01	-	-
1369875_at	Il8ra	interleukin 8 receptor, alpha	54258	Rn.138115	NM_019310	2.59	2.36	2.38	2.37	2.37	2.36	1.05	down	3.60E-01	8.95E-01	-	-
1378927_at	---	---	---	---	BE329364	2.69	2.46	2.48	2.47	2.48	2.45	1.05	down	3.76E-01	8.95E-01	-	-
1381728_at	---	---	---	Rn.209350	BF393880	3.89	3.70	4.24	3.89	4.16	3.56	1.05	down	7.67E-01	9.24E-01	-	-
1391044_s_at	Lime1	Lck interacting transmembrane adaptor 1	362289	Rn.28151	BM390051	3.21	2.68	2.56	2.58	2.70	2.95	1.05	down	7.60E-01	9.22E-01	-	-
1378860_at	---	---	---	Rn.26603	AW525986	5.80	8.22	7.84	7.41	6.54	8.13	1.05	up	9.37E-01	9.82E-01	-	-
1385010_at	Krt33a /// Krt33b	keratin 33A /// keratin 33B	303527 /// 450227	Rn.140603	BI288858	2.31	2.31	2.32	2.31	2.55	2.31	1.05	up	3.98E-01	8.95E-01	-	-
1375043_at	Fos	FBJ osteosarcoma oncogene	314322	Rn.103750	BF415939	2.54	2.48	2.77	2.51	2.54	2.51	1.05	down	4.50E-01	8.95E-01	-	-
1385294_at	Etv6	ets variant 6	312777	Rn.147424	BM387000	3.53	3.61	2.96	3.76	3.17	2.95	1.05	down	8.27E-01	9.45E-01	-	-
1391147_at	---	---	---	Rn.199635	BF404398	2.74	2.73	2.77	2.97	2.79	2.69	1.05	up	4.15E-01	8.95E-01	-	-
1381790_at	Map4k4	mitogen-activated protein kinase kinase kinase kinase 4	301363	Rn.101820	BE117850	3.06	2.37	2.38	2.37	2.38	2.84	1.05	down	7.99E-01	9.35E-01	-	-
1396910_at	---	---	---	---	AW535180	2.64	2.43	2.44	2.43	2.46	2.41	1.05	down	5.35E-01	8.95E-01	-	-
1375005_at	---	---	---	Rn.61163	BF403824	2.64	2.64	2.76	2.62	2.64	2.54	1.05	down	2.11E-01	8.95E-01	-	-
1372907_at	Atp6v0e2	ATPase, H+ transporting V0 subunit e2	436582	Rn.11803	BI285242	9.74	9.82	9.49	9.53	9.57	9.73	1.05	down	5.52E-01	8.95E-01	-	-
1372751_at	---	---	---	Rn.120538	BM390320	3.68	4.41	4.34	4.36	4.30	3.99	1.05	up	7.88E-01	9.32E-01	-	-
1395602_at	---	---	---	Rn.211443	BF413296	3.43	3.41	3.33	3.69	3.30	3.41	1.05	up	5.71E-01	8.95E-01	-	-
1390846_at	Col16a1	collagen, type XVI, alpha 1	366474	Rn.74081	BG380309	2.48	2.48	2.71	2.48	2.49	2.48	1.05	down	3.90E-01	8.95E-01	-	-
1368088_at	Cdk5	cyclin-dependent kinase 5	140908	Rn.10749	NM_080885	2.41	4.28	2.43	3.01	3.16	3.17	1.05	up	9.11E-01	9.73E-01	-	-
1383787_at	LOC641520	Popeye domain-containing 3	641520	Rn.195368	AI776912	2.38	2.36	2.56	2.37	2.37	2.34	1.05	down	3.12E-01	8.95E-01	-	-
1386920_x_at	Prl8a4	prolactin family 8, subfamily a, member 4	59088	Rn.203207	NM_021580	2.82	2.75	3.08	2.80	2.99	2.64	1.05	down	6.31E-01	8.95E-01	-	-
1367479_at	Nola3	nucleolar protein family A, member 3	691534	Rn.17615	AI599994	10.55	10.52	10.85	10.58	10.55	10.58	1.05	down	5.18E-01	8.95E-01	-	-
1380046_at	Herc3	Hect domain and RLD 3	362377	Rn.203362	AW524705	2.34	2.34	2.52	2.32	2.35	2.31	1.05	down	2.92E-01	8.95E-01	-	-
1372541_at	Tmem138	transmembrane protein 138	361728	Rn.102785	BG374849	2.55	2.56	2.56	2.55	2.55	2.79	1.05	up	3.82E-01	8.95E-01	-	-
1385314_at	---	---	---	Rn.163656	AA923974	7.36	7.05	7.20	7.47	7.37	6.98	1.05	up	6.92E-01	9.05E-01	-	-
1392727_at	RGD1307365	similar to KIAA1009 protein	300880	Rn.55758	AI235560	2.52	2.60	2.63	2.62	2.77	2.60	1.05	up	2.99E-01	8.95E-01	-	-
1386675_at	---	---	---	Rn.178338	BF543600	2.63	2.63	2.61	2.64	2.75	2.70	1.05	up	9.10E-02	8.95E-01	-	-
1377842_at	Twistnb	TWIST neighbor	362728	Rn.13221	AW533281	8.86	8.24	7.65	8.11	8.33	8.54	1.05	up	8.50E-01	9.53E-01	-	-
1372089_at	---	---	---	Rn.42016	AI171222	4.43	4.54	4.44	4.43	4.45	4.76	1.05	up	5.49E-01	8.95E-01	-	-
1391826_at	Tp53inp1	tumor protein p53 inducible nuclear protein 1	297822	Rn.48267	AA946371	5.61	5.78	4.81	5.69	4.92	5.36	1.05	down	8.51E-01	9.54E-01	-	-
1369248_a_at	Xiap	X-linked inhibitor of apoptosis	63879	Rn.91239	AF304333	6.03	6.13	5.01	6.09	5.95	5.91	1.05	down	3.26E-01	8.95E-01	-	-
1383241_at	C1r	complement component 1, r subcomponent	312705	Rn.70397	BI292425	5.17	5.13	5.75	6.11	5.03	5.14	1.05	up	8.61E-01	9.57E-01	-	-
1388918_at	Hdlbp	High density lipoprotein binding protein (vigilin)	64474	Rn.8515	BG378074	5.64	5.06	5.81	4.89	5.24	6.15	1.05	down	8.74E-01	9.61E-01	-	-
1380334_at	RGD1359713	hypothetical RNA binding protein RGD1359713	305340	Rn.38803	AI555044	8.23	8.38	8.07	8.07	7.94	8.44	1.05	down	6.91E-01	9.05E-01	-	-
1378263_at	---	---	---	Rn.216679	BF403483	8.63	8.68	8.47	8.53	8.71	8.32	1.05	down	6.00E-01	8.95E-01	-	-
1396275_at	---	---	---	Rn.213012	BM390168	2.63	2.45	2.47	2.42	2.47	2.44	1.05	down	2.81E-01	8.95E-01	-	-
1376739_at	Ddx24	DEAD (Asp-Glu-Ala-Asp) box polypeptide 24	373065	Rn.100166	AW252511	7.76	7.78	7.32	7.88	7.76	7.44	1.05	up	7.27E-01	9.13E-01	-	-
1397503_at	---	---	---	Rn.205343	AI555886	2.62	2.60	2.62	2.61	2.86	2.59	1.05	up	4.36E-01	8.95E-01	-	-
1378053_at	---	---	---	Rn.34768	BE120247	2.46	2.41	2.34	2.33	2.34	2.32	1.05	down	9.97E-02	8.95E-01	-	-
1373407_at	---	---	---	Rn.22242	BM386604	4.94	5.17	4.62	4.82	4.82	5.32	1.05	up	7.64E-01	9.23E-01	-	-
1377758_at	Hsd17b13	hydroxysteroid (17-beta) dehydrogenase 13	305150	Rn.25104	BF415386	2.46	2.45	2.47	2.48	2.65	2.47	1.05	up	2.81E-01	8.95E-01	-	-
1391950_at	---	---	---	---	AA944420	3.96	4.47	3.92	4.02	4.24	3.85	1.05	down	7.42E-01	9.17E-01	-	-
1398242_at	Ppp5c	protein phosphatase 5, catalytic subunit	65179	Rn.6107	NM_031729	3.61	5.66	5.31	4.81	5.00	4.54	1.05	down	9.14E-01	9.75E-01	-	-
1377864_at	RGD1305225	similar to RIKEN cDNA C130022K22 gene	297458	Rn.106964	BF393865	2.91	3.24	2.90	2.89	2.90	3.49	1.05	up	7.61E-01	9.22E-01	-	-
1398116_at	---	---	---	---	AI412037	3.45	2.68	2.69	2.68	2.65	3.26	1.05	down	8.30E-01	9.47E-01	-	-
1381084_at	---	---	---	Rn.165297	AA964619	3.22	4.17	3.14	3.46	3.70	3.14	1.05	down	8.51E-01	9.53E-01	-	-
1376043_at	MGC94192	similar to PHD zinc finger containing protein JUNE1	360550	Rn.20080	BI292073	3.44	3.39	3.52	3.44	3.75	3.38	1.05	up	5.74E-01	8.95E-01	-	-
1389417_at	Rbbp5	retinoblastoma binding protein 5	304794	Rn.11729	AA946518	2.47	2.73	2.51	2.50	2.50	2.49	1.05	down	4.25E-01	8.95E-01	-	-
1397949_at	---	---	---	Rn.208519	BE117532	7.38	6.76	7.30	6.63	7.07	7.51	1.05	down	8.29E-01	9.46E-01	-	-
1375979_at	---	---	---	Rn.164800	AA945734	4.69	4.17	3.58	4.61	4.03	4.02	1.05	up	8.53E-01	9.55E-01	-	-
1380514_at	---	---	---	---	AI059926	2.40	2.39	2.61	2.39	2.40	2.38	1.05	down	3.70E-01	8.95E-01	-	-
1375564_at	Mast3	microtubule associated serine/threonine kinase 3	688540	Rn.155444	AI145796	4.66	4.17	4.31	4.31	4.32	4.29	1.05	down	6.39E-01	8.95E-01	-	-
1389122_at	---	---	---	Rn.176859	BI296748	2.34	2.33	2.35	2.34	2.50	2.40	1.05	up	1.72E-01	8.95E-01	-	-
1380288_at	RGD1563821	RGD1563821	500984	Rn.28150	BF286011	2.68	2.61	2.62	2.93	2.59	2.61	1.05	up	5.49E-01	8.95E-01	-	-
1390261_at	Smg5	Smg-5 homolog, nonsense mediated mRNA decay factor (C. elegans)	681012	Rn.203043	AI059850	3.97	3.96	3.97	3.96	4.20	3.96	1.05	up	3.95E-01	8.95E-01	-	-
1389110_at	---	---	---	---	AI639387	7.01	5.97	6.58	6.36	6.82	6.16	1.05	down	8.47E-01	9.52E-01	-	-
1369554_at	Syngr2	synaptogyrin 2	89815	Rn.34912	NM_053553	3.35	3.12	3.19	3.12	3.17	3.60	1.05	up	6.81E-01	9.03E-01	-	-
1380119_at	Tcirg1	T-cell, immune regulator 1, ATPase, H+ transporting, lysosomal V0 subunit A3	293650	Rn.12627	BM392376	3.66	3.69	3.72	3.69	3.71	3.44	1.05	down	4.49E-01	8.95E-01	-	-
1380810_at	Zfp40	zinc finger protein 40	690661	Rn.198487	BE102637	2.58	2.58	2.59	2.58	2.84	2.54	1.05	up	4.71E-01	8.95E-01	-	-
1372421_at	Aga	aspartylglucosaminidase	290923	Rn.104649	AA943766	8.22	9.32	8.73	8.71	8.71	9.07	1.05	up	8.38E-01	9.49E-01	-	-
1390033_at	Rbms2	RNA binding motif, single stranded interacting protein 2	288771	Rn.162925	BG374052	5.49	5.67	4.66	5.38	4.82	5.40	1.05	down	8.49E-01	9.53E-01	-	-
1389943_at	Crocc	ciliary rootlet coiled-coil, rootletin	313663	Rn.41475	BG372724	3.87	3.42	3.50	4.20	2.95	3.42	1.05	down	8.59E-01	9.56E-01	-	-
1368671_at	Srpx	sushi-repeat-containing protein, X-linked	64316	Rn.1489	NM_022524	2.48	2.25	2.26	2.25	2.27	2.24	1.05	down	3.79E-01	8.95E-01	-	-
1383322_at	Rasl11b	RAS-like family 11 member B	305302	Rn.36357	BG375198	2.44	2.43	2.44	2.62	2.49	2.42	1.05	up	2.58E-01	8.95E-01	-	-
1398179_at	---	---	---	---	BF393841	2.35	2.55	2.36	2.35	2.36	2.33	1.05	down	3.25E-01	8.95E-01	-	-
1374318_at	Brcc3	BRCA1/BRCA2-containing complex, subunit 3	316794	Rn.52727	BE328978	7.22	7.19	7.46	6.89	7.45	7.30	1.05	down	7.16E-01	9.10E-01	-	-
1370827_at	Cyb5r4	cytochrome b5 reductase 4	171015	Rn.3334	AF307840	8.12	7.54	7.73	7.74	8.08	7.80	1.05	up	7.32E-01	9.14E-01	-	-
1386996_at	Mrlc2	myosin regulatory light chain MRLC2	80685	Rn.103179	D14688	7.29	7.80	7.77	7.57	7.98	7.52	1.05	up	7.55E-01	9.20E-01	-	-
1374061_at	Cd302	CD302 molecule	295629	Rn.98436	BF282054	7.84	7.66	7.95	8.01	7.80	7.87	1.05	up	5.19E-01	8.95E-01	-	-
1385391_at	Cage1	cancer antigen 1	306872	Rn.128696	AW524879	2.70	2.78	2.74	2.70	2.75	2.56	1.05	down	3.01E-01	8.95E-01	-	-
1376832_at	---	---	---	Rn.6636	AA800763	3.54	2.93	2.59	3.14	3.07	3.07	1.05	up	8.05E-01	9.37E-01	-	-
1388719_at	Ubqln1	Ubiquilin 1	114590	Rn.94884	BI279735	7.57	7.87	7.74	7.77	7.14	8.05	1.05	down	8.07E-01	9.38E-01	-	-
1371302_at

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1372411_at	LOC684755	similar to zinc finger like protein 1	684755	---	BE110638	3.08	3.64	3.51	3.62	3.25	3.57	1.05	up	7.42E-01	9.17E-01	-	-
1395115_at	---	---	---	Rn.176340	BG373926	2.33	2.32	2.33	2.32	2.34	2.53	1.05	up	3.40E-01	8.95E-01	-	-
1391324_at	Dusp27	dual specificity phosphatase 27 (putative)	498267	Rn.206301	BI293812	2.34	2.33	2.35	2.33	2.34	2.56	1.05	up	3.97E-01	8.95E-01	-	-
1375843_at	Ids	iduronate 2-sulfatase	363513	Rn.22226	BM383777	6.22	6.52	6.44	6.11	6.58	6.27	1.05	down	6.80E-01	9.03E-01	-	-
1372029_at	M6prbp1	mannose-6-phosphate receptor binding protein 1	316130	Rn.9506	BI281957	3.11	2.87	2.71	3.04	3.03	2.83	1.05	up	6.18E-01	8.95E-01	-	-
1372854_at	Ttc17	tetratricopeptide repeat domain 17	311224	Rn.207415	AI229046	6.07	6.19	5.73	5.96	5.37	6.44	1.05	down	8.40E-01	9.50E-01	-	-
1380182_at	RGD1563437	similar to KIAA1217	291356	Rn.43612	BF291123	7.30	7.45	6.98	7.18	7.06	7.72	1.05	up	7.83E-01	9.30E-01	-	-
1382256_at	---	---	---	Rn.165709	AI011445	2.51	2.45	2.49	2.73	2.49	2.45	1.05	up	4.51E-01	8.95E-01	-	-
1396105_at	LOC688133	similar to mbt domain containing 1	688133	---	BG671576	4.84	5.46	3.94	5.28	3.48	5.27	1.05	down	9.27E-01	9.79E-01	-	-
1376404_at	---	---	---	Rn.169216	AI639317	2.50	2.49	2.50	2.49	2.72	2.49	1.05	up	4.00E-01	8.95E-01	-	-
1377826_at	---	---	---	Rn.17666	AI176721	2.63	3.02	3.42	2.97	2.95	2.93	1.05	down	7.65E-01	9.23E-01	-	-
1380058_at	Parc	p53-associated parkin-like cytoplasmic protein	316228	Rn.49119	BE113130	2.33	2.32	2.33	2.56	2.32	2.31	1.05	up	4.23E-01	8.95E-01	-	-
1389407_at	Dhrs1	dehydrogenase/reductase (SDR family) member 1	290234	Rn.18628	BE099453	6.18	6.63	5.48	5.76	6.50	6.26	1.05	up	8.65E-01	9.58E-01	-	-
1390099_at	Ube3a	ubiquitin protein ligase E3A	361585	Rn.198497	BE098487	2.27	2.28	2.18	2.17	2.17	2.17	1.05	down	1.01E-01	8.95E-01	-	-
1368124_at	Dusp5	dual specificity phosphatase 5	171109	Rn.10877	NM_133578	3.22	3.99	3.62	3.09	3.56	3.96	1.05	down	8.40E-01	9.50E-01	-	-
1374678_at	Sema4b	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and	293042	Rn.116056	BE109578	5.12	5.35	5.61	5.78	5.55	4.96	1.05	up	8.11E-01	9.39E-01	-	-
1388413_at	Rrbp1	ribosome binding protein 1	311483	Rn.14242	BI282760	8.93	7.97	8.30	9.09	7.53	8.79	1.05	up	9.02E-01	9.70E-01	-	-
1388762_at	Iqgap1	IQ motif containing GTPase activating protein 1	361598	Rn.106939	BF284125	5.28	4.61	3.85	4.93	4.03	4.56	1.05	down	8.90E-01	9.66E-01	-	-
1369123_a_at	Atp7b	ATPase, Cu++ transporting, beta polypeptide	24218	Rn.10025	NM_012511	2.64	2.64	2.66	2.88	2.65	2.63	1.05	up	4.06E-01	8.95E-01	-	-
1389604_at	Hspa12b	heat shock protein 12B	311427	Rn.154616	BI294714	2.66	2.88	2.67	2.66	2.67	2.66	1.05	down	3.69E-01	8.95E-01	-	-
1387006_at	Sult2a1	sulfotransferase family 2A, dehydroepiandrosterone (DHEA)-preferring-like 1	24902	Rn.221887	NM_012695	2.72	2.67	2.93	2.68	2.56	2.56	1.05	down	5.66E-01	8.95E-01	-	-
1384267_at	---	---	---	Rn.166138	BF547003	6.04	6.50	6.33	6.76	6.10	5.80	1.05	down	8.29E-01	9.46E-01	-	-
1395417_at	Pols	polymerase (DNA directed) sigma	306672	Rn.22554	BF547200	2.55	2.34	2.36	2.34	2.35	2.34	1.05	down	3.54E-01	8.95E-01	-	-
1394871_at	---	---	---	Rn.95113	BF394431	5.65	6.12	5.51	5.60	5.52	5.94	1.05	down	7.63E-01	9.22E-01	-	-
1374408_at	Clr	CBF1 interacting corepressor	362149	Rn.99641	AI410173	7.09	6.66	7.47	7.26	6.60	7.57	1.05	up	8.54E-01	9.55E-01	-	-
1372272_at	LOC692032	hypothetical protein LOC692032	692032	Rn.139084	BF394074	3.11	3.11	3.30	3.10	3.12	3.09	1.05	down	3.29E-01	8.95E-01	-	-
1390330_at	---	---	---	Rn.9415	AI236259	2.51	2.48	2.48	2.50	2.69	2.50	1.05	up	3.17E-01	8.95E-01	-	-
1395952_at	---	---	---	Rn.58045	BF393396	2.65	2.45	2.46	2.45	2.46	2.43	1.05	down	3.23E-01	8.95E-01	-	-
1395137_at	---	---	---	Rn.170946	BE105415	2.33	2.32	2.34	2.55	2.36	2.31	1.05	up	3.85E-01	8.95E-01	-	-
1385864_at	Xpo4	exportin 4	290280	Rn.204363	BF542299	2.71	2.51	2.57	2.53	2.55	2.49	1.05	down	3.22E-01	8.95E-01	-	-
1368574_at	Adra1b	adrenergic, alpha-1B-, receptor	24173	Rn.10032	NM_016991	2.85	2.25	2.34	2.46	2.40	2.37	1.05	down	7.23E-01	9.12E-01	-	-
1394880_at	---	---	---	Rn.205842	BE102072	2.42	2.41	2.43	2.67	2.43	2.37	1.05	up	4.76E-01	8.95E-01	-	-
1380276_at	---	---	---	Rn.23205	AA963631	2.55	2.33	2.34	2.34	2.34	2.33	1.05	down	3.66E-01	8.95E-01	-	-
1383300_at	Klhl24	kelch-like 24 (Drosophila)	303803	Rn.163189	BF550390	5.59	5.15	5.26	5.29	5.27	5.66	1.05	up	7.12E-01	9.10E-01	-	-
1393452_at	Car9	carbonic anhydrase 9	313495	Rn.162391	BM391835	2.29	2.28	2.29	2.51	2.29	2.27	1.05	up	3.96E-01	8.95E-01	-	-
1368615_a_at	Slc18a3	solute carrier family 18 (vesicular acetylcholine), member 3	60422	Rn.9987	U09838	2.47	2.47	2.55	2.47	2.47	2.33	1.05	down	2.55E-01	8.95E-01	-	-
1385730_at	Stk36	serine/threonine kinase 36 (fused homolog, Drosophila)	301516	Rn.198846	BE108897	2.50	2.29	2.30	2.29	2.30	2.28	1.05	down	3.50E-01	8.95E-01	-	-
1374139_at	Cdr2	cerebellar degeneration-related 2	308958	Rn.3537	BG671589	4.48	7.58	7.50	5.43	6.36	7.98	1.05	up	9.57E-01	9.88E-01	-	-
1390384_at	H2afx	H2A histone family, member X	500987	Rn.2850	AA875257	4.78	4.78	4.79	4.57	4.79	4.77	1.05	down	3.69E-01	8.95E-01	-	-
1369557_at	Casp7	caspase 7	64026	Rn.53995	NM_022260	2.94	2.89	3.66	2.78	3.08	3.41	1.05	down	8.27E-01	9.45E-01	-	-
1374050_at	Rufy1	RUN and FYVE domain containing 1	360521	Rn.39348	BE100918	2.35	2.81	2.78	2.45	2.94	2.76	1.05	up	7.44E-01	9.17E-01	-	-
1383666_at	Ptrh1	peptidyl-tRNA hydrolase 1 homolog (S. cerevisiae)	362113	---	BG378435	4.08	4.05	4.05	4.10	4.09	4.20	1.05	up	1.21E-01	8.95E-01	-	-
1378614_at	---	---	---	Rn.203780	BI274329	2.54	2.36	2.41	2.37	2.38	2.35	1.05	down	2.52E-01	8.95E-01	-	-
1398518_at	---	---	---	Rn.47498	AW534099	2.54	2.57	2.58	2.31	2.55	2.62	1.05	down	4.92E-01	8.95E-01	-	-
1375614_at	Prdm12	PR domain containing 12	688699	Rn.170582	BE096447	2.89	2.88	3.12	2.89	2.90	2.89	1.05	down	4.02E-01	8.95E-01	-	-
1390907_at	LOC691170	similar to zinc finger protein 84 (HPF2)	691170	Rn.147757	AI145039	3.77	4.69	4.57	4.75	3.98	4.51	1.05	up	8.54E-01	9.55E-01	-	-
1396524_at	---	---	---	Rn.171758	BF410736	2.65	2.46	2.51	2.47	2.47	2.47	1.05	down	2.73E-01	8.95E-01	-	-
1374937_at	RGD1565222	similar to RIKEN cDNA 4931414P19	498514	Rn.19875	BI294726	2.57	2.58	2.57	2.54	2.82	2.85	1.05	up	4.66E-01	8.95E-01	-	-
1370163_at	Odc1	ornithine decarboxylase 1	24609	Rn.874	BF281299	11.32	11.95	11.96	11.68	11.67	12.10	1.05	up	7.91E-01	9.33E-01	-	-
1385384_at	---	---	---	Rn.64418	BF416768	2.98	2.56	2.67	2.66	2.68	2.65	1.05	down	5.97E-01	8.95E-01	-	-
1375450_at	Sdccag1	serologically defined colon cancer antigen 1	289114	Rn.135119	BF403864	3.84	4.05	4.57	4.00	4.06	4.19	1.05	down	7.61E-01	9.22E-01	-	-
1380729_at	---	---	---	---	BG376796	2.31	2.30	2.32	2.54	2.32	2.30	1.05	up	4.03E-01	8.95E-01	-	-
1371052_at	Nog	noggin	25495	Rn.10154	AA859752	2.46	2.44	2.66	2.44	2.47	2.42	1.05	down	3.71E-01	8.95E-01	-	-
1384122_at	---	---	---	Rn.12373	AA996697	3.31	3.87	4.54	4.34	3.09	4.51	1.05	up	9.06E-01	9.71E-01	-	-
1384591_at	Pear1	platelet endothelial aggregation receptor 1	295293	Rn.44763	BG374055	2.35	2.43	2.47	2.34	2.35	2.34	1.05	down	1.15E-01	8.95E-01	-	-
1394830_at	---	---	---	Rn.73828	AI501276	2.54	2.50	3.61	3.40	2.53	2.51	1.05	down	8.85E-01	9.64E-01	-	-
1369635_at	Sord	sorbitol dehydrogenase	24788	Rn.11334	BI285149	8.19	8.19	7.77	8.10	7.80	8.04	1.05	down	6.89E-01	9.04E-01	-	-
1387219_at	Adm	adrenomedullin	25028	Rn.10232	NM_012715	2.69	2.50	2.51	2.50	2.53	2.46	1.05	down	3.38E-01	8.95E-01	-	-
1368969_at	Sost	sclerosteosis	80722	Rn.95369	NM_030584	2.45	2.43	2.63	2.43	2.45	2.41	1.05	down	3.21E-01	8.95E-01	-	-
1379051_at	---	---	---	Rn.124152	AW528292	2.48	2.48	2.53	2.48	2.78	2.44	1.05	up	5.39E-01	8.95E-01	-	-
1379279_at	Stim2	stromal interaction molecule 2	117087	Rn.162277	AI234719	4.53	5.54	4.68	4.61	4.71	5.20	1.05	down	8.53E-01	9.55E-01	-	-
1392983_at	Psmd12	proteasome (prosome, macropain) 26S subunit, non-ATPase, 12	287772	Rn.15873	BE103250	8.87	8.65	8.64	8.68	8.49	8.77	1.05	down	5.47E-01	8.95E-01	-	-
1375297_at	RGD1565289	similar to RIKEN cDNA 0610008C08	363474	Rn.2579	AI168968	6.49	6.40	6.98	6.66	6.84	6.58	1.05	up	7.33E-01	9.15E-01	-	-
1392007_at	Usp6nl	USP6 N-terminal like	291309	Rn.56101	AI044568	3.76	4.28	4.65	5.18	3.46	4.26	1.05	up	9.04E-01	9.71E-01	-	-
1371022_a_at	Tgm4	transglutaminase 4 (prostate)	64679	Rn.9964	M32725	2.98	3.09	2.88	3.01	3.14	3.01	1.05	up	3.89E-01	8.95E-01	-	-
1393324_at	Jam2	junctional adhesion molecule 2	619374	Rn.6473	BF542552	2.86	2.55	2.60	2.62	2.61	2.57	1.05	down	5.11E-01	8.95E-01	-	-
1369386_at	Slc26a2	solute carrier family 26 (sulfate transporter), member 2	117267	Rn.14549	NM_057127	2.58	2.30	2.33	2.32	2.31	2.37	1.05	down	4.73E-01	8.95E-01	-	-
1388172_at	Slc22a25	solute carrier family 22, member 25	192273	Rn.31066	Y09945	7.54	8.10	8.17	8.13	7.84	8.05	1.05	up	7.58E-01	9.21E-01	-	-
1389818_at	---	---	---	Rn.16640	AA997712	8.24	8.73	9.19	9.00	8.32	9.06	1.05	up	8.52E-01	9.54E-01	-	-
1397258_at	---	---	---	Rn.212765	BM383140	2.42	2.36	2.51	2.36	2.36	2.34	1.05	down	1.80E-01	8.95E-01	-	-
1368433_at	Sacm1l	SAC1 suppressor of actin mutations 1-like (yeast)	116482	Rn.161978	NM_053798	8.07	8.63	8.48	8.24	8.27	8.89	1.05	up	8.05E-01	9.37E-01	-	-
1390122_at	---	---	---	Rn.219032	BI275740	2.75	2.95	3.60	2.73	2.95	3.40	1.05	down	8.35E-01	9.48E-01	-	-
1392907_at	---	---	---	Rn.4058	BG668225	2.33	2.33	2.34	2.55	2.33	2.32	1.05	up	3.88E-01	8.95E-01	-	-
1387979_at	Golgb1	golgi autoantigen, golgin subfamily b, macrogolgin 1	192243	Rn.154426	D25543	4.95	4.94	4.95	5.42	4.55	5.10	1.05	up	7.92E-01	9.33E-01	-	-
1372812_at	Dynll2	dynein light chain LC8-type 2	140734	Rn.36362	BG379573	10.69	11.14	10.95	10.83	10.95	11.22	1.05	up	7.03E-01	9.07E-01	-	-
1393815_at	Narg2	NMDA receptor regulated 2	691379	Rn.212908	BM387050	2.54	3.11	3.52	2.58	2.76	4.03	1.05	up	9.00E-01	9.69E-01	-	-
1379459_at	Pnpla8	patatin-like phospholipase domain containing 8	314075	Rn.219239	BI301276	2.96	2.95	2.96	2.95	3.11	3.02	1.05	up	1.93E-01	8.95E-01	-	-
1381150_at	---	---	---	---	BF410638	2.80	2.65	2.86	2.67	3.25	2.60	1.05	up	7.58E-01	9.21E-01	-	-
1383630_at	Dok3	docking protein 3	306760	Rn.19911	BG377464	2.73	2.37	2.39	2.38	2.38	2.52	1.05	down	6.03E-01	8.95E-01	-	-
1395035_at	---	---	---	Rn.48252	BM389765	2.52	2.64	2.56	2.50	2.51	2.50	1.05	down	1.16E-01	8.95E-01	-	-
1373504_at	Glipr1	GLI pathogenesis-related 1	299783	Rn.65764	BF287967	2.39	2.37	2.40	2.38	2.39	2.61	1.05	up	4.05E-01	8.95E-01	-	-
1384381_at	Abca1	ATP-binding cassette, sub-family A (ABC1), member 1	313210	Rn.148916	BF284523	2.60	2.55	2.61	2.58	2.87	2.51	1.05	up	5.54E-01	8.95E-01	-	-
1374516_at	Chtf8	CTF8, chromosome transmission fidelity factor 8 homolog (S. cerevisiae)	364996	Rn.3278	AI008492	7.97	8.77	8.59	9.11	7.75	8.70	1.05	up	8.86E-01	9.65E-01	-	-
1392777_at	---	---	---	Rn.14830	BF287676	5.35	3.44	3.48	4.80	3.54	3.71	1.05	down	9.28E-01	9.80E-01	-	-
1392338_at	---	---	---	Rn.22744	AA892989	2.82	2.88	3.79	3.51	2.88	3.32	1.05	up	8.55E-01	9.55E-01	-	-
1386774_at	Fam5b	family with sequence similarity 5, member B	286895	Rn.22596	BF551863	2.54	2.52	2.72	2.53	2.57	2.46	1.05	down	3.75E-01	8.95E-01	-	-
1389179_at	Cidea	cell death-inducing DNA fragmentation factor, alpha subunit-like effector A	291541	Rn.8171	BF284899	2.75	2.72	3.00	2.75	2.71	2.79	1.05	down	4.89E-01	8.95E-01	-	-
1376287_at	Capn13	calpain 13	362701	Rn.15541	BM389585	2.60	2.40	2.42	2.40	2.41	2.40	1.05	down	3.35E-01	8.95E-01	-	-
1394613_at	---	---	---	Rn.91833	BF288842	2.67	2.38	2.39	2.38	2.47	2.38	1.05	down	5.18E-01	8.95E-01	-	-
1396225_at	Klf16b	kinesin family member 16B	311478	Rn.7029	BF420465	4.01	5.24	5.11	5.67	4.62	4.29	1.05	up	9.06E-01	9.71E-01	-	-
1397882_at	Zbtb8a	zinc finger and BTB domain containing 8a	313049	Rn.82564	BF559709	2.41	2.60	2.43	2.41	2.42	2.39	1.05	down	2.97E-01	8.95E-01	-	-
1384645_at	Toag1	tolerance-associated gene 1	363169	Rn.20696	AI072024	3.14	3.14	3.29	3.01	3.14	3.21	1.05	down	4.08E-01	8.95E-01	-	-
1379269_at	---	---	---	Rn.33933	BM385296	7.87	8.20	7.53	7.35	8.07	8.39	1.05	up	8.55E-01	9.55E-01	-	-
1379417_at	Mdn1	midasin homolog (yeast)	362498	Rn.9052	AA956668	2.58	2.56	2.58	2.56	2.59	2.78	1.05	up	3.67E-01	8.95E-01	-	-
1399005_at	Ppp2r5a	protein phosphatase 2, regulatory subunit B', alpha isoform	312754	Rn.104461	BG673380	8.09	8.36	8.08	8.17	8.19	8.39	1.05	up	5.77E-01	8.95E-01	-	-
1374614_at	Kbtbd4	kelch repeat and BTB (POZ) domain containing 4	311185	Rn.219508	BM385650	3.90	3.64	3.25	3.86	5.20	3.95	1.05	up	9.19E-01	9.76E-01	-	-
1398161_at	---	---	---	Rn.173323	BF405189	2.56	2.36	2.38	2.36	2.37	2.36	1.05	down	3.33E-01	8.95E-01	-	-
1379263_at	Fkrp	fukutin related protein	308390	Rn.7371	AW251362	3.93	3.10	2.91	3.14	3.36	3.22	1.05	down	8.35E-01	9.48E-01	-	-
1392615_at	Sell	selenoprotein I	362713	Rn.64052	AI454224	3.94	4.39	4.43	3.94	4.61	4.00	1.05	down	8.01E-01	9.36E-01	-	-
1391118_at	---	---	---	Rn.199366	BI280337	2.37	2.79	2.42	2.99	2.38	2.42	1.05	up	7.79E-01	9.28E-01	-	-
1393428_at	---	---	---	Rn.164207	BF398638	3.73	5.22	3.59	4.89	3.97	3.89	1.05	up	9.13E-01	9.74E-01	-	-
1387863_at	Csde1	cold shock domain containing E1, RNA binding	117180	Rn.3562	BI289608	8.83	8.64	8.80	8.69	8.19	9.19	1.05	down	8.20E-01	9.42E-01	-	-
1394037_at	Il17d	Interleukin 17D	691799	Rn.17127	AI230670	2.76	2.70	2.86	2.71	2.71	2.69	1.05	down	1.99E-01	8.95E-01	-	-
1374336_at	---	---	---	Rn.104459	AI409666	2.65	4.03	2.82	3.90	2.37	3.44	1.05	up	9.15E-01	9.75E-01	-	-
1389910_at	RGD1307399	similar to chromosome 20 open reading frame 30; HSPC274 protein	681315	Rn.8667	BM390101	4.00	4.00	4.24	4.02	4.07	4.37	1.05	up	6.21E-01	8.95E-01	-	-
1392737_at	---	---	---	Rn.204040	AI044644	2.39	2.37	2.39	2.39	2.63	2.35	1.05	up	4.65E-01	8.95E-01	-	-
1376981_at	---	---	---	Rn.64166	BF400751	2.46	2.43	2.48	2.46	2.70	2.43	1.05	up	4.52E-01	8.95E-01	-	-
1376932_at	RGD1560880	similar to RIKEN cDNA 2310002J15	499747	Rn.15190	BI300388	2.50	2.46	2.80	2.46	2.63	2.45	1.05	down	5.94E-01	8.95E-01	-	-
1387351_at	Fbn1	fibrillin 1	83727	Rn.12759	NM_031825	3.49	3.67	3.51	3.50	3.51	3.45	1.05	down	3.04E-01	8.95E-01	-	-
1394749_at	Atg7	ATG7 autophagy related 7 homolog (S. cerevisiae)	312647	Rn.162765	AW520947	2.64	2.64	2.43	2.42	2.43	2.42	1.05	down	3.89E-01	8.95E-01	-	-
1396592_at	---	---	---	---	BF405096	2.35	2.34	2.36	2.34	2.35	2.56	1.05	up	3.78E-01	8.95E-01	-	-
1369882_at	Pdyn	prodynorphin	29190	Rn.44471	NM_019374	2.50	2.49	2.71	2.49	2.50	2.48	1.05	down	3.82E-01	8.95E-01	-	-
1397072_at	---	---	---	Rn.136266	BF418026	2.89	2.77	2.78	2.78	2.78	2.68	1.05	down	2.33E-01	8.95E-01	-	-
1388910_at	Urg4	up-regulated gene 4	305493	Rn.138962	BI285944	3.11	3.00	3.06	2.66	3.28	3.03	1.05	down	7.18E-01	9.11E-01	-	-
1381346_at	---	---	---	Rn.201940	BE096771	2.73	2.53	2.54	2.53	2.54	2.52	1.05	down	3.46E-01	8.95E-01	-	-
1384551_at	Ranbp6	RAN binding protein 6	309326	Rn.198558	AI578134	6.83	8.00	8.13	7.99	7.22	7.96	1.05	up	8.90E-01	9.66E-01	-	-
1371835_at	Prkacb	protein kinase, cAMP dependent, catalytic, beta	293508	Rn.202491	AI411907	7.57	6.87	7.06	7.13	7.10	7.06	1.05	down	7.50E-01	9.19E-01	-	-
1398425_at	Fam110b	family with sequence similarity 110, member B	500400	Rn.20088	AI101458	3.50	3.39	3.42	3.40	3.42	3.29	1.05	down	2.37E-01	8.95E-01	-	-
1388217_a_at	Calu	calumenin	64366	Rn.1841	AJ001929	6.38	6.35	7.06	6.45	6.38	6.75	1.05	down	7.98E-01	9.35E-01	-	-
1390512_at	---	---	---	Rn.22738	AI170376	2.57	2.55	2.57	2.69	2.56	2.66	1.05	up	1.42E-01	8.95E-01	-	-
1386788_at	---	---	---	Rn.158479	C06771	2.93	2.92	2.94	2.97	2.96	2.65	1.05	down	5.39E-01	8.95E-01	-	-
1373121_at	LOC679330	similar to Mitochondrial 28S ribosomal protein S28 (S28mt) (MRP-S28)	679330	---	BE097240	5.84	6.39	6.45	6.04	5.99	6.86	1.05	up	8.47E-01	9.52E-01	-	-
1376133_at	Mdp-1	magnesium-dependent phosphatase 1	290230	Rn.19870	BF413334	3.38	3.55	3.56	3.55	3.61	3.54	1.05	up	3.16E-01	8.95E-01	-	-
1398495_at	---	---	---	Rn.219415	BE121436	2.61	2.72	3.29	2.73	2.74	3.37	1.05	up	8.25E-01	9.45E-01	-	-
1380257_at	Smc5	structural maintenance of chromosomes 5	293967	Rn.127947	BF419367	2.55	2.77	2.61	2.72	2.58	2.84	1.05	up	5.17E-01	8.95E-01	-	-
1375173_at	P76	mannose-6-phosphate protein p76	246120	Rn.72896	BM392302	6.71	6.94	6.60	6.86	6.61	6.57	1.05	down	6.24E-01	8.95E-01	-	-
1374080_at	Six5	SIX homeobox 5	308406	Rn.129404	AI407118	2.91	2.77	2.43	2.74	2.43	3.16	1.05	up	7.94E-01	9.34E-01	-	-
1376169_at	Phf20l1	PHD finger protein 20-like 1	314964	Rn.22288	BE104290	5.52	4.56	4.23	4.49	4.55	5.48	1.05	up	8.95E-01	9.67E-01	-	-
1367627_at	Gatm	glycine amidinotransferase (L-arginine:glycine amidinotransferase)	81660	Rn.17661	NM_031031	9.44	8.96	10.24	10.30	9.62	8.94	1.05	up	9.02E-01	9.70E-01	-	-
1370425_at	LOC259246	alpha-2u globulin PGCL1	259246	Rn.86422	AB039823	3.22	2.38	2.41	2.49	3.27	2.47	1.05	up	8.61E-01	9.57E-01	-	-
1386247_at	Snx25	sorting nexin 25	306471	Rn.16962	AA859100	5.04	6.07	4.27	4.85	5.19	5.55	1.05	up	9.06E-01	9.71E-01	-	-
1386762_at	Snx18	sorting nexin 18	310097	Rn.8090	BF551439	6.20	8.10	7.60	7.27	7.47	7.37	1.05	up	9.08E-01	9.72E-01	-	-
1385147_at	---	---	---	Rn.212783	BM383929	2.61	2.98	2.70	2.69	2.73	2.66	1.05	down	5.61E-01	8.95E-01	-	-
1398170_at	---	---	---	Rn.173118	BE119687	2.63	2.64	2.65	2.85	2.65	2.64	1.05	up	3.58E-01	8.95E-01	-	-
1381500_at	---	---	---	---	BF386748	2.61	2.44	2.55	2.46	2.52	2.41	1.05	down	3.00E-01	8.95E-01	-	-
1389435_at	Fam114a1	family with sequence similarity 114, member A1	498366	Rn.198969	BE329046	4.78	5.46	4.40	4.81	4.48	5.56	1.05	up	8.82E-01	9.64E-01	-	-
1395210_at	---	---	---	---	BE118557	2.57	2.50	2.76	2.55	2.59	2.47	1.05	down	4.52E-01	8.95E-01	-	-
1384484_at	---	---	---	Rn.163760	AI172598	2.39	2.38	2.40	2.60	2.39	2.38	1.05	up	3.85E-01	8.95E-01	-	-
1381484_at	---	---	---	Rn.170706	BI295208	2.55	2.55	2.56	2.91	2.56	2.41	1.05	up	6.59E-01	8.98E-01	-	-
1377670_at	Pef11	PEF11, cleavage and polyadenylation factor subunit, homolog (S. cerevisiae)	361605	Rn.27595	AW915580	5.36	5.36	5.70	4.77	5.64	5.81	1.05	down	8.46E-01	9.52E-01	-	-
1371730_at	Lonp2	lon peptidase 2, peroxisomal	291922	Rn.103067	BF418786	10.69	10.75	10.48	10.55	10.86	10.71	1.05	up	5.87E-01	8.95E-01	-	-
1388361_at	Ndufb10	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 10	681418	Rn.2867	BI303856	8.58	8.91	8.73	8.90	8.46	8.64	1.05	down	6.78E-01	9.02E-01	-	-

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1396601_at	---	---	---	---	BF404916	2.32	2.29	2.48	2.30	2.30	2.29	1.05	down	2.96E-01	8.95E-01	-	-
1379815_at	LOC683733	similar to Transcription factor 7-like 2 (HMG box transcription factor 4) (T-cell-	683733	---	AI713959	2.65	2.42	2.44	2.42	2.44	2.44	1.05	down	4.04E-01	8.95E-01	-	-
1376611_at	Pola1	Polymerase (DNA directed), alpha 1	85241	Rn.92345	AI103682	2.56	2.57	2.58	2.63	2.51	2.78	1.05	up	4.09E-01	8.95E-01	-	-
1375025_at	Camkk2	calcium/calmodulin-dependent protein kinase kinase 2, beta	83506	Rn.88589	BE099992	2.53	2.37	2.38	2.74	2.38	2.37	1.05	up	6.23E-01	8.95E-01	-	-
1375631_at	Plekhb2	pleckstrin homology domain containing, family B (evectins) member 2	301337	Rn.1410	AI177176	8.75	9.24	9.19	9.17	8.85	9.36	1.05	up	7.63E-01	9.23E-01	-	-
1387909_at	Abi2	abl-interactor 2	286928	Rn.11316	U94904	5.57	5.81	5.92	5.82	5.24	6.04	1.05	down	8.03E-01	9.37E-01	-	-
1368139_s_at	Alpl	alkaline phosphatase, liver/bone/kidney	25586	Rn.82764	Y00714	7.47	7.79	8.35	7.98	8.04	7.80	1.05	up	8.06E-01	9.38E-01	-	-
1397783_at	---	---	---	Rn.146902	AW533493	2.51	2.31	2.32	2.31	2.31	2.30	1.05	down	3.51E-01	8.95E-01	-	-
1379339_at	Isoc1	isochorismatase domain containing 1	364879	Rn.1166	BM390448	8.01	7.93	7.90	7.94	7.84	7.85	1.05	down	2.02E-01	8.95E-01	-	-
1394780_at	---	---	---	Rn.173435	BF284832	2.34	2.34	2.36	2.34	2.57	2.33	1.05	up	4.32E-01	8.95E-01	-	-
1396402_at	---	---	---	Rn.150698	AW534347	2.56	2.52	2.71	2.54	2.59	2.46	1.05	down	3.57E-01	8.95E-01	-	-
1376529_at	---	---	---	Rn.206779	BF390770	2.81	2.40	2.44	2.67	2.38	2.39	1.05	down	6.88E-01	9.04E-01	-	-
1397862_at	---	---	---	Rn.206242	BF414858	2.55	2.54	2.55	2.55	2.81	2.49	1.05	up	5.19E-01	8.95E-01	-	-
1398812_at	Psmb1	proteasome (prosome, macropain) subunit, beta type 1	94198	Rn.6016	NM_053590	8.69	8.99	8.43	8.71	8.72	8.90	1.05	up	7.10E-01	9.09E-01	-	-
1378502_at	---	---	---	Rn.207700	BG381643	2.49	2.59	2.47	2.45	2.47	2.43	1.05	down	1.42E-01	8.95E-01	-	-
1378687_at	---	---	---	Rn.161197	BF393824	2.37	2.59	2.38	2.38	2.39	2.37	1.05	down	3.80E-01	8.95E-01	-	-
1386914_at	Gmpr	guanosine monophosphate reductase	117533	Rn.3862	NM_057188	2.45	2.45	2.45	2.45	2.51	2.59	1.05	up	1.78E-01	8.95E-01	-	-
1382435_at	Fzr1	fizzy/cell division cycle 20 related 1 (Drosophila)	314642	Rn.12924	AA996835	2.39	2.56	2.42	2.39	2.39	2.38	1.05	down	2.56E-01	8.95E-01	-	-
1396115_at	---	---	---	Rn.211324	BF566051	2.47	2.66	2.51	2.50	2.49	2.44	1.05	down	3.02E-01	8.95E-01	-	-
1382703_at	---	---	---	Rn.21696	BE099893	4.79	3.77	4.47	4.32	4.16	4.33	1.05	down	8.32E-01	9.47E-01	-	-
1377561_at	---	---	---	Rn.60593	BF387010	2.64	2.61	2.84	2.62	2.65	2.60	1.05	down	3.94E-01	8.95E-01	-	-
1378257_at	Trex1	three prime repair exonuclease 1	100049583	Rn.98617	BG377140	2.64	2.72	2.60	2.58	2.60	2.57	1.05	down	1.30E-01	8.95E-01	-	-
1375056_at	---	---	---	---	AA943310	8.78	8.72	7.80	8.31	8.52	8.68	1.05	up	8.47E-01	9.52E-01	-	-
1380126_at	---	---	---	Rn.173519	BF409826	2.39	2.39	2.40	2.35	2.40	2.64	1.05	up	4.90E-01	8.95E-01	-	-
1372745_at	---	---	---	---	BE112453	2.69	2.46	2.48	2.46	2.51	2.45	1.05	down	4.11E-01	8.95E-01	-	-
1367897_at	Acadvl	acyl-Coenzyme A dehydrogenase, very long chain	25363	Rn.33319	NM_012891	8.62	8.40	8.39	8.38	8.21	8.60	1.05	down	6.35E-01	8.95E-01	-	-
1380222_at	---	---	---	Rn.206535	AW527973	2.28	2.27	2.29	2.50	2.29	2.27	1.05	up	3.92E-01	8.95E-01	-	-
1382092_at	Phf20l1	PHD finger protein 20-like 1	314964	Rn.22288	AA965250	5.80	5.14	5.33	5.39	5.25	5.83	1.05	up	8.07E-01	9.38E-01	-	-
1381488_at	---	---	---	---	BF419534	2.38	2.59	2.39	2.38	2.39	2.38	1.05	down	3.54E-01	8.95E-01	-	-
1393516_at	---	---	---	Rn.22717	AA892335	6.94	6.31	5.35	4.96	7.25	6.20	1.05	down	9.36E-01	9.82E-01	-	-
1368111_at	Abtb2	ankyrin repeat and BTB (POZ) domain containing 2	171440	Rn.11148	NM_134403	2.59	2.36	2.38	2.37	2.40	2.36	1.05	down	4.10E-01	8.95E-01	-	-
1391767_at	RGD1310495	similar to KIAA1919 protein	309809	Rn.24001	AI548603	2.42	2.42	2.86	2.41	2.43	2.64	1.05	down	6.95E-01	9.06E-01	-	-
1371060_at	Trim23	tripartite motif-containing 23	81002	Rn.6763	L04760	3.31	3.90	4.50	3.48	4.50	3.94	1.05	up	8.86E-01	9.65E-01	-	-
1373451_at	Rnaseh2b	ribonuclease H2, subunit B	361056	Rn.16136	BG380780	6.78	7.15	6.84	6.88	6.93	7.17	1.05	up	6.61E-01	8.98E-01	-	-
1385661_at	Vars	valyl-tRNA synthetase	25009	Rn.12314	BG057536	5.22	4.90	5.73	5.18	5.42	5.03	1.05	down	8.08E-01	9.38E-01	-	-
1375835_at	Prkag2	Protein kinase, AMP-activated, gamma 2 non-catalytic subunit	373545	Rn.51208	BE119806	2.53	2.41	2.52	2.42	2.43	2.41	1.05	down	1.54E-01	8.95E-01	-	-
1375577_at	---	---	---	Rn.209418	BF400031	2.60	2.37	2.38	2.38	2.39	2.38	1.05	down	4.09E-01	8.95E-01	-	-
1392008_at	Pask	PAS domain containing serine/threonine kinase	301617	Rn.66676	BM392331	2.92	2.72	2.74	2.73	2.73	2.72	1.05	down	3.37E-01	8.95E-01	-	-
1372144_at	Dnajb5	DnaJ (Hsp40) homolog, subfamily B, member 5	313811	Rn.92865	BM386741	2.98	2.97	3.00	2.98	2.82	2.95	1.05	down	2.33E-01	8.95E-01	-	-
1375803_at	Ptger1	Prostaglandin E receptor 1 (subtype EP1)	25637	Rn.11423	AI235295	2.46	2.63	2.47	2.45	2.46	2.44	1.05	down	2.80E-01	8.95E-01	-	-
1376836_at	Tgfbr1	transforming growth factor, beta receptor 1	29591	Rn.44402	BE111972	7.64	7.35	7.29	6.66	7.23	8.19	1.05	down	8.88E-01	9.65E-01	-	-
1372032_at	---	---	---	Rn.11271	AA851914	5.60	6.76	7.62	6.36	6.81	7.02	1.05	up	9.16E-01	9.75E-01	-	-
1387089_at	Mobkl3	MOB1, Mps One Binder kinase activator-like 3 (yeast)	171050	Rn.12262	NM_133528	7.87	7.74	7.38	7.39	7.67	7.73	1.05	down	7.22E-01	9.11E-01	-	-
1372387_at	RGD1311874	hypothetical LOC300751	300751	Rn.163007	BF416240	2.84	2.61	2.68	2.68	2.52	2.74	1.05	down	5.08E-01	8.95E-01	-	-
1396149_at	Zdhhc1	zinc finger, DHHC-type containing 1	291987	Rn.41274	AA817682	3.08	2.88	2.89	2.88	2.89	2.87	1.05	down	3.52E-01	8.95E-01	-	-
1386503_at	RGD1310348	similar to Ser/Thr-rich protein T10 in DGCR region	360738	Rn.101776	AA891032	2.36	2.35	2.37	2.58	2.36	2.34	1.05	up	4.08E-01	8.95E-01	-	-
1380096_at	Kitlg	KIT ligand	60427	Rn.44216	AF071204	2.73	2.60	2.73	2.61	2.70	2.54	1.05	down	3.34E-01	8.95E-01	-	-
1374438_at	---	---	---	---	AI103982	8.07	7.98	8.08	8.23	8.03	8.07	1.05	up	3.77E-01	8.95E-01	-	-
1387769_a_at	Id3	inhibitor of DNA binding 3	25585	Rn.2760	AF000942	2.39	3.40	2.57	2.39	3.23	2.54	1.05	down	8.73E-01	9.61E-01	-	-
1385155_at	Lrrfip1	leucine rich repeat (in FLII) interacting protein 1	367314	Rn.153995	BI276243	4.89	4.54	4.16	4.65	4.58	4.57	1.05	up	7.63E-01	9.23E-01	-	-
1371443_at	RGD1304567	similar to RIKEN cDNA A430005L14	362671	Rn.4079	AI409584	7.86	8.09	7.81	7.72	7.76	8.07	1.05	down	6.53E-01	8.97E-01	-	-
1384198_at	Enox2	ecto-NOX disulfide-thiol exchanger 2	302817	Rn.20175	BF288648	2.88	2.94	2.89	2.87	2.81	3.23	1.05	up	6.33E-01	8.95E-01	-	-
1380450_at	Bzrap1	benzodiazapine receptor associated protein 1	287609	Rn.183937	AI044632	2.42	2.41	2.43	2.67	2.42	2.38	1.05	up	4.88E-01	8.95E-01	-	-
1377432_at	---	---	---	---	BF406938	2.46	2.41	2.38	2.33	2.37	2.34	1.05	down	6.72E-02	8.95E-01	-	-
1388737_at	Pbrm1	polybromo 1	306254	Rn.19314	AI410799	6.52	6.53	7.13	6.44	7.42	6.52	1.05	up	8.63E-01	9.57E-01	-	-
1381065_at	LOC499120	hypothetical protein LOC499120	499120	Rn.55566	BG379401	3.06	2.97	2.96	3.05	3.30	2.85	1.05	up	6.39E-01	8.95E-01	-	-
1373225_at	---	---	---	Rn.4067	AI102618	9.49	9.86	10.31	10.13	9.85	9.90	1.05	up	7.98E-01	9.35E-01	-	-
1378572_at	Tollip	toll interacting protein	361677	Rn.13740	BF408962	4.44	3.87	2.52	3.76	3.56	3.72	1.05	up	9.10E-01	9.73E-01	-	-
1391116_at	---	---	---	Rn.163587	BG381692	3.45	3.35	3.40	3.38	3.29	3.33	1.05	down	1.58E-01	8.95E-01	-	-
1398849_at	H3f3b	H3 histone, family 3B	117056	Rn.198918	AI177503	7.68	7.52	7.54	7.58	7.23	7.72	1.05	down	6.77E-01	9.02E-01	-	-
1394938_at	---	---	---	Rn.200322	BI289446	2.52	2.52	2.53	2.52	2.82	2.43	1.05	up	5.89E-01	8.95E-01	-	-
1370576_at	Dync1li1	dynein cytoplasmic 1 light intermediate chain 1	252902	Rn.2064	AF181982	5.13	4.30	4.13	4.31	4.31	5.15	1.05	up	8.77E-01	9.62E-01	-	-
1379876_at	Cog7	component of oligomeric golgi complex 7	293456	Rn.23781	AI407943	4.39	4.03	3.95	4.10	4.01	4.06	1.05	down	6.46E-01	8.95E-01	-	-
1367622_at	Atp5h	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit d	641434	Rn.80	NM_019383	10.00	10.19	10.21	10.20	10.01	10.40	1.05	up	6.26E-01	8.95E-01	-	-
1390800_a_at	Cav2	caveolin 2	363425	Rn.81070	BE346869	2.73	2.60	2.75	2.94	2.82	2.52	1.05	up	6.35E-01	8.95E-01	-	-
1393063_at	---	---	---	Rn.153832	BF409007	2.65	2.45	2.52	2.46	2.50	2.45	1.05	down	3.07E-01	8.95E-01	-	-
1380670_at	---	---	---	Rn.207220	BE095613	2.72	2.59	2.61	2.60	2.60	2.52	1.05	down	2.35E-01	8.95E-01	-	-
1395086_at	Patl1	protein associated with topoisomerase II homolog 1 (yeast)	361736	Rn.162495	BI283086	3.42	2.72	2.78	2.64	3.75	2.73	1.05	up	8.79E-01	9.63E-01	-	-
1382294_at	---	---	---	Rn.203389	AI576111	5.19	4.02	4.35	4.37	5.78	3.62	1.05	up	9.29E-01	9.80E-01	-	-
1384856_at	RGD1563946	similar to mKIAA1623 protein	306340	Rn.141288	AI705077	3.15	3.15	3.07	3.25	3.44	2.89	1.05	up	6.95E-01	9.06E-01	-	-
1395454_at	Ostm1	osteopetrosis associated transmembrane protein 1	499474	Rn.163435	AW920180	7.33	7.15	7.58	7.22	6.86	7.78	1.05	down	8.27E-01	9.45E-01	-	-
1398753_at	Akr1a1	aldo-keto reductase family 1, member A1 (aldehyde reductase)	78959	Rn.835	NM_031000	11.96	11.93	12.00	11.97	11.97	12.16	1.05	up	3.77E-01	8.95E-01	-	-
1372512_at	Stx18	syntaxin 18	360953	Rn.53006	BE113340	7.05	6.01	5.28	6.23	5.55	6.35	1.05	down	9.10E-01	9.73E-01	-	-
1393089_at	LOC690035	similar to Protein KIAA0586	690035	Rn.45864	BI295973	2.46	2.67	2.46	2.46	2.46	2.46	1.05	down	3.80E-01	8.95E-01	-	-
1383785_at	Lef1	Lymphoid enhancer binding factor 1	161452	Rn.21926	BE115061	2.36	2.34	2.36	2.35	2.57	2.35	1.05	up	4.03E-01	8.95E-01	-	-
1393787_at	---	---	---	---	BI278215	2.47	2.45	2.63	2.45	2.46	2.43	1.05	down	3.03E-01	8.95E-01	-	-
1374785_at	Clec2l	C-type lectin domain family 2, member L	296985	Rn.162737	BG380471	2.97	2.87	2.97	2.94	3.02	3.05	1.05	up	2.22E-01	8.95E-01	-	-
1382336_at	Jazf1	JAZF zinc finger 1	685879	Rn.204296	AI236491	2.45	2.43	2.46	2.45	2.46	2.64	1.05	up	3.42E-01	8.95E-01	-	-
1392651_at	---	---	---	Rn.203049	AA858611	2.30	2.29	2.31	2.30	2.32	2.49	1.05	up	3.30E-01	8.95E-01	-	-
1395263_at	---	---	---	Rn.206699	AW529355	2.49	2.47	2.67	2.49	2.50	2.44	1.05	down	3.46E-01	8.95E-01	-	-
1385510_at	Ttll13	tubulin tyrosine ligase-like family, member 13	308762	Rn.186496	BG378965	2.73	2.73	3.04	2.84	2.74	2.73	1.05	down	5.65E-01	8.95E-01	-	-
1397951_at	---	---	---	Rn.172348	BI293109	2.32	2.57	2.64	2.32	2.78	2.78	1.05	up	7.02E-01	9.07E-01	-	-
1383896_at	LOC683504	similar to zinc finger protein 639	683504	Rn.116062	BM387943	5.51	4.85	4.14	4.57	4.98	5.15	1.05	up	8.82E-01	9.64E-01	-	-
1377721_at	Pacrg	Park2 co-regulated	499021	Rn.202340	BE112451	2.87	3.20	2.81	2.81	2.83	3.45	1.05	up	7.91E-01	9.33E-01	-	-
1396615_at	Entpd4	ectonucleoside triphosphate diphosphohydrolase 4	361063	Rn.34634	BF410400	2.66	2.67	2.66	2.65	2.61	2.53	1.05	down	1.12E-01	8.95E-01	-	-
1372616_at	---	---	---	Rn.116146	AI144796	2.39	2.37	2.41	2.60	2.40	2.37	1.05	up	4.18E-01	8.95E-01	-	-
1376380_at	---	---	---	Rn.156241	BF398757	2.66	3.97	4.06	3.63	3.32	3.53	1.05	down	8.90E-01	9.66E-01	-	-
1387034_at	Pah	phenylalanine hydroxylase	24616	Rn.1652	NM_012619	12.33	11.28	11.56	11.77	11.62	11.56	1.05	down	8.42E-01	9.51E-01	-	-
1396064_at	---	---	---	Rn.169405	BF289458	2.53	2.50	2.70	2.53	2.57	2.43	1.05	down	4.20E-01	8.95E-01	-	-
1373071_at	Lin37	lin-37 homolog (C. elegans)	292787	Rn.128023	AI103101	7.56	5.63	5.06	6.45	6.08	5.92	1.05	up	9.34E-01	9.81E-01	-	-
1382328_at	Gimap1 /// Gimap5	GTPase, IMAP family member 1 /// GTPase, IMAP family member 5	246774 /// 312312	Rn.83549	AW918029	2.60	2.57	2.73	2.58	2.62	2.49	1.05	down	3.15E-01	8.95E-01	-	-
1392486_at	Tmem106b	transmembrane protein 106B	312132	Rn.106000	AW433977	2.68	3.01	3.66	2.91	3.14	3.09	1.05	down	8.30E-01	9.46E-01	-	-
1373725_at	---	---	---	Rn.900	BE117010	2.63	2.60	2.82	2.62	2.65	2.58	1.05	down	3.92E-01	8.95E-01	-	-
1388055_at	Cyp4f5	cytochrome P450 4F5	286905	Rn.10171	U39207	2.81	2.51	2.59	2.57	2.62	2.53	1.05	down	5.09E-01	8.95E-01	-	-
1376693_at	RGD1563091	similar to OEF2	500011	Rn.13231	AA998964	2.42	2.60	2.42	2.41	2.42	2.40	1.05	down	3.13E-01	8.95E-01	-	-
1384079_at	Eps8l1	EPS8-like 1	361503	Rn.138370	AI715477	2.57	2.53	2.48	2.46	2.48	2.44	1.05	down	7.71E-02	8.95E-01	-	-
1380976_at	---	---	---	Rn.54356	BF396723	2.31	2.31	2.32	2.59	2.31	2.24	1.05	up	5.58E-01	8.95E-01	-	-
1393633_at	---	---	---	Rn.21998	AI071826	2.62	2.73	2.63	2.56	2.63	3.00	1.05	up	6.88E-01	8.98E-01	-	-
1382341_at	RGD1561878	similar to mKIAA0978 protein	311553	Rn.199307	AI136740	2.53	2.58	2.46	2.46	2.46	2.45	1.05	down	1.21E-01	8.95E-01	-	-
1378299_at	---	---	---	Rn.54309	BF397445	7.47	7.53	6.82	6.80	7.68	7.14	1.05	down	8.53E-01	9.54E-01	-	-
1368024_at	Qsox1	quiescin Q6 sulfhydryl oxidase 1	84491	Rn.44920	AB044285	2.52	2.60	2.32	2.41	2.67	2.56	1.05	up	5.84E-01	8.95E-01	-	-
1374084_at	Nfatc3	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 3	361400	Rn.222025	BG376942	7.83	7.68	7.32	7.38	7.58	7.66	1.05	down	7.12E-01	9.10E-01	-	-
1377184_at	Eaf1	ELL associated factor 1	306261	Rn.34587	AI546231	3.02	3.92	2.98	3.20	3.08	3.84	1.05	up	8.70E-01	9.60E-01	-	-
1371881_at	Znhit2	zinc finger, HIT type 2	309177	Rn.18470	AI229455	7.40	7.66	7.99	7.69	7.51	7.66	1.05	down	7.24E-01	9.12E-01	-	-
1372039_at	Nkiras2	NFKB inhibitor interacting Ras-like 2	287707	Rn.220516	AI406810	2.69	2.68	2.67	2.69	2.69	2.87	1.05	up	3.23E-01	8.95E-01	-	-
1370723_at	Grasp	GRP1 (general receptor for phosphoinositides 1)-associated scaffold protein	192254	Rn.82758	AF374272	2.43	2.42	2.43	2.63	2.43	2.43	1.05	up	3.61E-01	8.95E-01	-	-
1381416_at	---	---	---	Rn.162123	AI029400	2.70	2.72	2.84	2.74	3.07	2.65	1.05	up	6.39E-01	8.95E-01	-	-
1389735_at	Rps6ka6	ribosomal protein S6 kinase polypeptide 6	317203	Rn.51151	BE107296	2.63	2.59	2.79	2.95	2.69	2.58	1.05	up	6.16E-01	8.95E-01	-	-
1389614_at	Hcca2	HCCA2 protein	499288	Rn.11638	AI172472	3.32	3.31	3.33	3.47	3.33	3.36	1.05	up	1.86E-01	8.95E-01	-	-
1382053_at	Pear1	platelet endothelial aggregation receptor 1	295293	Rn.44763	BI289548	2.92	2.62	2.74	2.73	2.62	2.73	1.05	down	5.05E-01	8.95E-01	-	-
1382685_at	Slit2	slit homolog 2 (Drosophila)	360272	Rn.146652	AI101660	5.28	4.85	4.64	4.86	4.86	4.85	1.05	down	7.33E-01	9.15E-01	-	-
1393566_at	LOC687611	similar to transmembrane protein induced by tumor necrosis factor alpha	687611	---	BF409676	2.33	2.33	2.34	2.57	2.33	2.30	1.05	up	4.78E-01	8.95E-01	-	-
1379372_at	---	---	---	---	AA949730	3.50	3.49	3.11	3.44	3.16	3.70	1.05	up	7.53E-01	9.20E-01	-	-
1383501_at	---	---	---	Rn.41665	AI059858	2.92	2.91	2.92	2.85	3.19	2.91	1.05	up	5.49E-01	8.95E-01	-	-
1398536_at	Znf655	zinc finger protein 655	360764	Rn.6640	BI275768	3.42	3.41	3.23	3.45	3.43	3.38	1.05	up	3.58E-01	8.95E-01	-	-
1378653_at	---	---	---	Rn.163715	BE110608	2.79	2.59	2.64	2.62	2.63	2.57	1.05	down	3.53E-01	8.95E-01	-	-
1371912_at	Ndufs7	NADH dehydrogenase (ubiquinone) Fe-S protein 7	362837	Rn.2855	AI231358	9.15	9.17	8.56	9.12	8.74	9.22	1.05	up	7.98E-01	9.35E-01	-	-
1390249_at	RGD1305464	similar to human chromosome 15 open reading frame 39	315702	Rn.59239	BF558075	2.39	2.39	2.40	2.39	2.40	2.60	1.05	up	3.65E-01	8.95E-01	-	-
1369771_at	Irs1	insulin receptor substrate 1	25467	Rn.10476	NM_012969	2.53	2.50	2.53	2.52	2.76	2.48	1.05	up	4.88E-01	8.95E-01	-	-
1386366_at	---	---	---	Rn.204983	AI231610	2.43	2.41	2.45	2.66	2.44	2.40	1.05	up	4.50E-01	8.95E-01	-	-
1377369_at	Cybrd1	cytochrome b reductase 1	295669	Rn.203500	BF419070	2.33	2.32	2.34	2.32	2.54	2.32	1.05	up	4.05E-01	8.95E-01	-	-
1375497_at	---	---	---	Rn.171090	BE107853	2.54	2.53	2.55	2.67	2.63	2.53	1.05	up	1.95E-01	8.95E-01	-	-
1376539_at	---	---	---	---	AW529740	2.64	2.44	2.49	2.44	2.50	2.42	1.05	down	3.67E-01	8.95E-01	-	-
1380899_at	---	---	---	Rn.145055	AW527286	2.34	2.52	2.34	2.33	2.34	2.32	1.05	down	3.04E-01	8.95E-01	-	-
1398080_at	---	---	---	Rn.216896	BF400579	2.71	2.67	2.85	2.69	2.75	2.58	1.05	down	4.12E-01	8.95E-01	-	-
1380028_at	Arl4c	ADP-ribosylation factor-like 4C	367311	Rn.198847	BM384251	2.27	2.26	2.27	2.26	2.29	2.44	1.05	up	2.99E-01	8.95E-01	-	-
1375189_at	Edf1	endothelial differentiation-related factor 1	296570	Rn.17092	BI285635	9.00	9.00	8.75	8.79	8.65	9.10	1.05	down	6.87E-01	9.04E-01	-	-
1380748_at	---	---	---	Rn.209695	AI639385	2.65	2.64	2.69	2.60	2.61	2.56	1.05	down	2.82E-02	8.95E-01	-	-
1398525_at	---	---	---	Rn.148967	AW526095	2.45	2.42	2.49	2.44	2.68	2.43	1.05	up	4.59E-01	8.95E-01	-	-
1382162_at	---	---	---	Rn.23284	BG373568	2.64	2.52	2.66	2.64	2.75	2.63	1.05	up	3.08E-01	8.95E-01	-	-
1387462_at	Chrm3	cholinergic receptor, muscarinic 3	24260	Rn.87735	NM_012527	2.29	2.28	2.29	2.28	2.50	2.28	1.05	up	4.00E-01	8.95E-01	-	-
1388370_at	Ccni	cyclin I	289500	Rn.6670	AA945706	10.82	10.95	10.88	10.81	10.84	10.80	1.05	down	1.63E-01	8.95E-01	-	-
1384003_at	RGD1310230	Similar to RIKEN cDNA 5230400G24	301563	Rn.93479	BF288235	2.38	2.83	2.38	2.38	2.38	3.04	1.05	up	8.12E-01	9.39E-01	-	-
1370533_at	Dlgap3	discs, large (Drosophila) homolog-associated protein 3	289523	Rn.22854	U67139	2.39	2.38	2.61	2.38	2.42	2.37	1.05	down	4.21E-01	8.95E-01	-	-
1374964_at	Dpp8	dipeptidylpeptidase 8	315758	Rn.17532	AI175505	7.09	7.61	6.90	6.90	7.72	7.77	1.05	up	8.51E-01	9.53E-01	-	-
1395017_at	Mrpl15	Mitochondrial ribosomal protein L15	297799	Rn.1122	BG381427	2.46	2.46	2.40	2.57	2.47	2.49	1.05	up	1.54E-01	8.95E-01	-	-
1370891_at	Cd48	CD48 molecule	245962	Rn.3705	X13016	3.05	3.31	2.74	2.92	2.87	3.52	1.05	up	8.11E-01	9.39E-01	-	-
1375125_at	Nudt4	Nudix (nucleoside diphosphate linked moiety X)-type motif 4	94267	Rn.8426	AI602300	2.61	2.43	2.44	2.41	2.44	2.42	1.05	down	3.20E-01	8.95E-01	-	-
1399052_at	Tollip	toll interacting protein	361677	Rn.137040	AA957069	6.35	7.43	7.36	6.75	6.68	7.52	1.05	down	8.85E-01	9.64E-01	-	-
1369840_at	UST4r	integral membrane transport protein UST4r	171397	Rn.81213	NM_134379	2.36	2.34	2.37	2.56	2.36	2.35	1.05	up	3.91E-01	8.95E-01	-	-
1391763_at	---	---	---	Rn.63688	BF420184	2.40	2.39	2.60	2.39	2.41	2.39	1.05	down	3.91E-01	8.95E-01	-	-
1379731_at	Pogk	pogo transposable element with KRAB domain	304941	Rn.18738	BG666613	2.81	2.68	2.73	2.71	2.73	2.98	1.05	up

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1367471_at	Polr2e	polymerase (RNA) II (DNA directed) polypeptide E, 25kDa	690966	Rn.65038	BI279090	9.21	9.97	9.39	9.77	8.79	9.82	1.05	down	8.77E-01	9.62E-01	-	-
1380105_at	RGD1565367	Similar to Solute carrier family 23, member 2 (Sodium-dependent vitamin C tr	312226	Rn.16045	C07059	2.71	2.68	2.75	2.68	2.73	2.54	1.05	down	3.41E-01	8.95E-01	-	-
1394995_at	---	---	---	Rn.212819	BM385139	2.50	2.49	2.51	2.50	2.72	2.48	1.05	up	4.49E-01	8.95E-01	-	-
1371497_at	Asb6	ankyrin repeat and SOCS box-containing 6	296627	Rn.160607	BF393085	3.19	3.26	3.28	3.26	3.10	3.56	1.05	up	6.48E-01	8.96E-01	-	-
1380137_at	---	---	---	Rn.173365	BF406176	5.92	5.72	5.77	5.48	4.65	5.48	1.05	up	9.33E-01	9.81E-01	-	-
1371591_at	Mrps18a	mitochondrial ribosomal protein S18A	301249	Rn.103049	AA858667	7.03	7.67	6.72	7.13	6.87	7.62	1.05	up	8.59E-01	9.56E-01	-	-
1372793_at	Sabp1	single-stranded DNA binding protein 1	54304	Rn.106922	BE108903	10.64	11.08	11.50	11.22	11.13	11.08	1.05	up	8.05E-01	9.37E-01	-	-
1372976_at	Abhd14a	abhydrolase domain containing 14A	300982	Rn.41351	BI294842	9.43	9.43	9.76	9.60	9.43	9.77	1.05	up	6.74E-01	9.01E-01	-	-
1389794_at	---	---	---	Rn.166079	AI044984	7.14	8.06	7.96	7.57	7.59	8.20	1.05	up	8.61E-01	9.57E-01	-	-
1390897_at	RGD1565474	Similar to mKIAA0738 protein	362353	Rn.44698	AI011572	2.58	3.12	2.73	2.97	2.62	3.04	1.05	up	7.65E-01	9.23E-01	-	-
1375246_at	dc72 /// LOC685	cytochrome b-561 domain containing 72 /// hypothetical protein LOC685117	679747 /// 685117	Rn.4334	BG371965	10.59	9.54	9.48	9.76	10.25	9.79	1.05	up	8.74E-01	9.61E-01	-	-
1379734_at	Sypl2	synaptophysin-like 2	362018	Rn.6456	AI502132	2.80	2.76	2.77	2.99	2.79	2.75	1.05	up	4.27E-01	8.95E-01	-	-
1382727_at	---	---	---	Rn.160795	AI071140	2.73	3.10	2.78	2.69	2.75	2.98	1.05	down	6.71E-01	9.00E-01	-	-
1371334_at	Itm2c	integral membrane protein 2C	301575	Rn.8450	BG668228	6.69	5.62	5.53	6.03	6.10	5.91	1.05	up	8.69E-01	9.59E-01	-	-
1381285_at	---	---	---	Rn.148565	BF399879	2.54	2.47	2.56	2.70	2.55	2.53	1.05	up	3.25E-01	8.95E-01	-	-
1372637_at	---	---	---	---	AI169241	2.54	3.95	2.44	2.59	2.66	3.48	1.05	down	9.12E-01	9.74E-01	-	-
1387060_at	Klf6	Kruppel-like factor 6	58954	Rn.163355	NM_031642	3.12	3.05	2.98	3.08	3.20	3.07	1.05	up	3.25E-01	8.95E-01	-	-
1396111_at	---	---	---	Rn.170930	BE104964	2.53	2.51	2.51	2.49	2.56	2.71	1.05	up	3.59E-01	8.95E-01	-	-
1386376_at	---	---	---	Rn.134302	AA892173	8.52	3.39	3.27	4.45	7.44	3.47	1.05	up	9.76E-01	9.93E-01	-	-
1370880_at	Rnh1	ribonuclease/angiogenin inhibitor 1	245964	Rn.3756	X62528	6.95	7.26	6.75	6.72	6.73	7.31	1.05	down	7.99E-01	9.35E-01	-	-
1377295_at	---	---	---	Rn.172720	BF393974	2.35	2.34	2.36	2.56	2.35	2.34	1.05	up	4.12E-01	8.95E-01	-	-
1380479_at	---	---	---	Rn.14574	H31590	4.92	3.96	3.96	3.89	4.62	4.13	1.05	down	8.72E-01	9.60E-01	-	-
1371844_at	Ahcyl1	S-adenosylhomocysteine hydrolase-like 1	362013	Rn.17493	AW144530	8.70	8.62	8.42	8.45	8.40	8.69	1.05	down	6.11E-01	8.95E-01	-	-
1390589_at	Hells	Helicase, lymphoid specific	294071	Rn.18653	AI030995	3.03	3.26	2.93	3.10	3.03	2.88	1.05	down	6.00E-01	8.95E-01	-	-
1392964_at	---	---	---	Rn.91720	BF559822	3.79	3.09	2.60	3.09	3.17	3.02	1.05	down	8.58E-01	9.55E-01	-	-
1388550_at	Rad23b	RAD23 homolog B (S. cerevisiae)	298012	Rn.67042	BI295122	9.70	9.78	9.90	9.84	9.77	9.97	1.05	up	4.53E-01	8.95E-01	-	-
1369496_at	Ptpn12	protein tyrosine phosphatase, non-receptor type 12	117255	Rn.10707	NM_057115	6.09	6.08	6.22	5.88	6.44	5.86	1.05	down	7.54E-01	9.20E-01	-	-
1374231_at	Klf16	Kruppel-like factor 16	690820	Rn.214519	AI103472	3.50	3.32	3.33	3.21	3.19	3.55	1.05	down	6.34E-01	8.95E-01	-	-
1382970_at	LOC363188	similar to ubiquitin protein ligase E3 component n-recognin 2	363188	Rn.67473	AI764733	2.69	3.00	2.69	2.69	2.74	2.76	1.05	down	5.63E-01	8.95E-01	-	-
1376955_at	Col4a4	procollagen, type IV, alpha 4	301562	Rn.22075	AI412936	4.00	4.14	3.90	3.61	4.62	4.01	1.05	up	8.37E-01	9.49E-01	-	-
1395184_at	Clec12a	C-type lectin domain family 12, member A	680338	Rn.158811	AI411699	3.67	4.29	3.51	3.76	4.16	3.75	1.05	up	8.22E-01	9.43E-01	-	-
1370975_at	Kdm3a	lysine (K)-specific demethylase 3A	312440	Rn.10541	AI172079	2.55	2.80	2.68	2.67	2.86	2.69	1.05	up	5.18E-01	8.95E-01	-	-
1373878_at	---	---	---	Rn.203664	AI104213	8.18	8.47	9.24	8.70	8.46	8.93	1.05	up	8.57E-01	9.55E-01	-	-
1387666_at	Gpr85	G protein-coupled receptor 85	64020	Rn.53985	AF2039807	2.58	2.44	2.51	2.41	2.49	2.44	1.05	down	2.21E-01	8.95E-01	-	-
1374129_at	OC690789 /// Oaz	similar to Ornithine decarboxylase antizyme 2 (ODC-Az 2) (AZ2) /// ornithine d	501454 /// 690789	Rn.2946	AI104518	3.77	3.82	3.44	4.02	3.37	3.44	1.05	down	7.95E-01	9.34E-01	-	-
1390378_at	---	---	---	---	AI169241	4.16	4.75	3.80	3.91	4.21	4.79	1.05	up	8.70E-01	9.60E-01	-	-
1381691_at	LOC685179	Similar to SWI/SNF-related matrix-associated actin-dependent regulator of ch	685179	Rn.20004	AW528026	2.57	2.83	2.22	2.48	2.47	2.47	1.05	down	7.28E-01	9.13E-01	-	-
1381268_at	Foxi1	forkhead box I1	287185	Rn.32116	BG377504	3.61	2.95	3.39	3.39	4.13	2.64	1.05	up	8.95E-01	9.67E-01	-	-
1398393_at	Mapk11	mitogen-activated protein kinase 11	689314	Rn.45869	BF414412	2.68	2.78	2.81	2.69	2.76	2.63	1.05	down	2.93E-01	8.95E-01	-	-
1367452_at	Sumo2	SMT3 suppressor of mif two 3 homolog 2 (S. cerevisiae)	690244	Rn.154659	NM_133594	9.56	9.38	9.61	9.32	9.67	9.76	1.05	up	6.80E-01	9.03E-01	-	-
1376159_at	Gzf1	GDNF-inducible zinc finger protein 1	311508	Rn.40179	AI177089	4.87	4.76	4.74	4.50	4.75	4.91	1.05	down	6.25E-01	8.95E-01	-	-
1388315_at	Ndufb11	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 11	299310	Rn.3377	BI282661	7.27	7.73	7.53	7.89	7.35	7.48	1.05	up	7.70E-01	9.25E-01	-	-
1378278_at	Pou2f2	POU class 2 homeobox 2	117058	Rn.155998	BF388807	2.28	2.27	2.62	2.42	2.28	2.27	1.05	down	6.26E-01	8.95E-01	-	-
1382358_at	---	---	---	Rn.203377	AA943771	2.63	2.48	2.50	2.48	2.49	2.43	1.05	down	2.50E-01	8.95E-01	-	-
1376383_at	---	---	---	Rn.209894	BF403938	2.52	2.33	2.35	2.33	2.34	2.32	1.05	down	3.36E-01	8.95E-01	-	-
1383012_at	Rhpn2	rhophilin, Rho GTPase binding protein 2	308516	Rn.16129	BE115155	3.96	4.99	4.32	4.27	4.14	5.06	1.05	up	8.83E-01	9.64E-01	-	-
1383851_at	Ccdc96	coiled-coil domain containing 96	289716	Rn.47243	BF413072	4.69	4.23	3.49	4.23	4.23	3.75	1.05	down	8.73E-01	9.61E-01	-	-
1383086_at	---	---	---	Rn.16489	AA818256	2.40	2.38	2.41	2.42	2.60	2.37	1.05	up	3.97E-01	8.95E-01	-	-
1376034_at	RGD1565474	similar to mKIAA0738 protein	362353	Rn.44698	AW141824	4.88	5.26	5.15	4.58	5.15	5.37	1.05	down	8.13E-01	9.40E-01	-	-
1382049_at	Tmem216	transmembrane protein 216	361727	Rn.854	AW530828	5.53	6.59	5.97	5.98	6.35	5.95	1.05	up	8.54E-01	9.55E-01	-	-
1384558_at	Plac9	placenta-specific 9	361105	Rn.145159	BI276313	2.77	2.75	2.96	2.77	2.74	2.74	1.05	down	3.70E-01	8.95E-01	-	-
1370259_a_at	Pthr1	parathyroid hormone receptor 1	56813	Rn.48025	BE101119	8.62	8.75	9.29	9.23	8.84	8.78	1.05	up	8.06E-01	9.38E-01	-	-
1398801_at	Cdk105	CDK105 protein	171456	Rn.15195	NM_134415	9.22	9.94	10.55	9.88	9.66	10.36	1.05	up	8.88E-01	9.65E-01	-	-
1379533_at	---	---	---	---	BF396653	2.81	2.25	2.75	2.54	2.55	2.51	1.05	down	7.33E-01	9.14E-01	-	-
1395392_at	Ppp1r3d	protein phosphatase 1, regulatory subunit 3D	689995	Rn.93537	D86136	2.45	2.26	2.27	2.26	2.27	2.25	1.05	down	3.40E-01	8.95E-01	-	-
1383212_at	---	---	---	Rn.115473	AA925526	2.54	2.53	2.55	2.54	2.77	2.52	1.05	up	4.59E-01	8.95E-01	-	-
1370436_at	Acsm2	acyl-CoA synthetase medium-chain family member 2	246263	Rn.14875	AF062389	11.32	10.73	11.09	11.25	11.14	10.95	1.05	up	7.52E-01	9.20E-01	-	-
1374936_at	Amdhd2	amidohydrolase domain containing 2	302972	Rn.163127	BI274680	5.83	5.89	5.91	5.89	5.86	6.08	1.05	up	4.06E-01	8.95E-01	-	-
1388153_at	Acsl1	acyl-CoA synthetase long-chain family member 1	25288	Rn.6215	BI277523	6.91	5.65	5.13	6.22	5.68	5.98	1.05	up	9.11E-01	9.73E-01	-	-
1390527_at	RGD1562114	RGD1562114	500795	Rn.9087	BE099470	8.43	8.93	8.86	9.00	8.13	8.88	1.05	down	8.45E-01	9.52E-01	-	-
1385137_at	RGD1307722	similar to hypothetical protein MGC20700	362624	Rn.93047	AA858603	2.42	2.39	2.63	2.42	2.42	2.41	1.05	down	4.25E-01	8.95E-01	-	-
1394290_at	---	---	---	Rn.25146	BG669921	2.44	2.40	2.57	2.40	2.42	2.39	1.05	down	2.73E-01	8.95E-01	-	-
1374730_at	Tyrobp	Tyro protein tyrosine kinase binding protein	361537	Rn.11534	AI102519	2.45	2.43	2.45	2.65	2.44	2.42	1.05	up	4.19E-01	8.95E-01	-	-
1376899_at	Ccdc106	coiled-coil domain containing 106	499071	Rn.93975	BF407154	2.60	2.51	2.54	2.52	2.82	2.50	1.05	up	5.72E-01	8.95E-01	-	-
1391215_at	---	---	---	Rn.172222	BF386303	2.45	2.43	2.61	2.43	2.44	2.41	1.05	down	3.23E-01	8.95E-01	-	-
1388934_at	Vps16	vacuolar protein sorting 16 homolog (S. cerevisiae)	296159	Rn.14968	BI285570	5.16	5.84	6.31	5.82	5.27	6.01	1.05	down	8.78E-01	9.62E-01	-	-
1392899_at	Prc1	protein regulator of cytokinesis 1	308761	Rn.138438	BI284262	2.32	2.92	2.33	2.52	2.32	2.54	1.05	down	7.72E-01	9.26E-01	-	-
1397742_at	---	---	---	Rn.172084	AW920132	2.71	2.69	2.87	2.70	2.78	2.60	1.05	down	4.50E-01	8.95E-01	-	-
1390968_at	RGD1559643	Similar to hypothetical protein A430031N04	498100	Rn.11815	AI706441	2.77	2.77	2.77	2.77	2.86	2.49	1.05	down	5.93E-01	8.95E-01	-	-
1381904_at	G7c	G7c protein	309611	Rn.219144	AW527641	2.59	2.41	2.41	2.41	2.81	2.39	1.05	up	6.87E-01	9.04E-01	-	-
1396654_at	---	---	---	Rn.210908	BF403645	2.41	2.42	2.43	2.64	2.43	2.38	1.05	up	4.53E-01	8.95E-01	-	-
1369611_at	Bcl2l2	Bcl2-like 2	60434	Rn.44228	NM_021850	2.53	2.52	2.54	2.53	2.54	2.71	1.05	up	3.28E-01	8.95E-01	-	-
1386217_at	RGD1310474	similar to KIAA0423	314169	Rn.144424	AI639048	5.65	5.64	5.66	5.57	5.28	5.90	1.05	down	7.34E-01	9.15E-01	-	-
1393749_at	Rbm34	RNA binding motif protein 34	307956	Rn.93968	AI073196	2.59	2.51	2.61	2.52	2.53	2.48	1.05	down	1.34E-01	8.95E-01	-	-
1396380_at	---	---	---	---	BM387013	2.65	2.58	2.69	2.92	2.65	2.55	1.05	up	5.99E-01	8.95E-01	-	-
1371613_at	Elmo2	engulfment and cell motility 2	362271	Rn.2097	BM386781	3.93	3.82	3.99	4.01	3.97	3.96	1.05	up	2.76E-01	8.95E-01	-	-
1379668_at	Alg11	asparagine-linked glycosylation 11, alpha-1,2-mannosyltransferase homolog (	361174	Rn.37199	BI296117	6.33	6.51	6.82	6.40	6.73	6.72	1.05	up	7.35E-01	9.15E-01	-	-
1373983_at	LOC360807	LOC360807	360807	Rn.79033	AI168986	8.31	8.27	8.18	8.39	7.98	8.19	1.05	down	6.23E-01	8.95E-01	-	-
1378632_at	Ptpfia4	Protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interactir	140592	Rn.10593	BI274561	3.87	5.59	4.14	3.59	4.91	5.31	1.05	up	9.34E-01	9.81E-01	-	-
1381334_at	---	---	---	Rn.209506	BF388684	2.49	2.62	2.50	2.49	2.49	2.44	1.05	down	2.14E-01	8.95E-01	-	-
1381216_at	---	---	---	Rn.217105	BI294178	2.77	2.70	2.96	2.74	2.78	2.71	1.05	down	4.72E-01	8.95E-01	-	-
1387886_at	Prelp	proline arginine-rich end leucine-rich repeat protein	84400	Rn.112602	AI011747	2.76	2.56	2.68	2.57	2.69	2.54	1.05	down	4.26E-01	8.95E-01	-	-
1375991_at	Wdr73	WD repeat domain 73	308751	Rn.130371	BE120163	3.92	3.62	3.55	3.40	3.92	3.97	1.05	up	7.77E-01	9.28E-01	-	-
1375513_at	---	---	---	Rn.209108	BG376846	2.43	2.41	2.43	2.64	2.43	2.39	1.05	up	4.46E-01	8.95E-01	-	-
1388334_at	Sec14l1	SEC14-like 1 (S. cerevisiae)	360668	Rn.101656	AI176849	3.66	4.12	4.10	4.07	3.45	4.54	1.05	up	8.62E-01	9.57E-01	-	-
1374264_at	Orc5l	origin recognition complex, subunit 5-like (yeast)	362304	Rn.137519	BM384751	3.34	3.40	3.29	3.35	3.25	3.63	1.05	up	6.06E-01	8.95E-01	-	-
1385463_at	---	---	---	Rn.140811	AI043627	2.56	2.56	2.69	2.55	2.56	2.50	1.05	down	2.42E-01	8.95E-01	-	-
1388410_at	Ugp2	UDP-glucose pyrophosphorylase 2	289827	Rn.3415	AI170679	7.37	7.84	8.23	7.68	7.74	7.83	1.05	down	8.09E-01	9.38E-01	-	-
1368363_at	Klf5	Kruppel-like factor 5	84410	Rn.8954	NM_053394	2.31	2.31	2.33	2.52	2.32	2.30	1.05	up	4.03E-01	8.95E-01	-	-
1377103_at	Midn	midnolin	314623	Rn.45925	AW525765	8.45	7.50	7.81	7.93	7.81	7.81	1.05	down	8.29E-01	9.46E-01	-	-
1390391_at	---	---	---	Rn.25327	BF283381	2.52	2.50	2.53	2.74	2.52	2.48	1.05	up	4.72E-01	8.95E-01	-	-
1385723_at	---	---	---	Rn.34442	BE097133	3.68	3.46	2.93	3.01	3.19	4.06	1.05	up	8.76E-01	9.62E-01	-	-
1377216_at	---	---	---	Rn.33757	BI295997	2.50	2.47	2.51	2.57	2.56	2.54	1.05	up	1.37E-02	8.95E-01	-	-
1376577_at	---	---	---	Rn.13167	AI145247	2.41	2.47	2.45	2.41	2.41	2.70	1.05	up	5.52E-01	8.95E-01	-	-
1398958_at	Narfl	nuclear prelamin A recognition factor-like	360496	Rn.14772	BI278849	3.91	3.79	3.63	4.10	3.64	3.78	1.05	up	6.99E-01	9.07E-01	-	-
1387901_at	Ptprs	protein tyrosine phosphatase, receptor type, S	291202	Rn.91202	L19180	3.14	3.13	3.24	3.13	3.16	3.41	1.05	up	5.30E-01	8.95E-01	-	-
1386070_at	Tbl1xr1	Transducin (beta)-like 1X-linked receptor 1	365755	Rn.140831	AA944938	7.05	6.61	6.32	5.78	6.71	7.29	1.05	down	9.00E-01	9.69E-01	-	-
1373149_at	RGD1564579	similar to yippee-like 3	293491	Rn.138455	BF285344	5.68	6.09	7.23	6.50	6.03	6.27	1.05	down	8.99E-01	9.69E-01	-	-
1389972_at	Atn1	atrophin 1	29515	Rn.11305	NM_017228	5.74	5.90	5.18	5.57	5.79	5.26	1.05	down	8.20E-01	9.42E-01	-	-
1383836_at	---	---	---	Rn.146540	BM384008	2.61	2.53	2.54	2.49	2.54	2.47	1.05	down	1.18E-01	8.95E-01	-	-
1396037_at	---	---	---	Rn.205063	BF544069	2.51	2.48	2.70	2.49	2.54	2.48	1.05	down	4.16E-01	8.95E-01	-	-
1370887_at	Tgfb1i1	transforming growth factor beta 1 induced transcript 1	84574	Rn.103260	BI279862	2.42	2.41	2.43	2.43	2.49	2.54	1.05	up	1.07E-01	8.95E-01	-	-
1373651_at	---	---	---	Rn.169388	BE103440	2.50	2.47	2.48	2.75	2.47	2.43	1.05	up	5.49E-01	8.95E-01	-	-
1370779_x_at	Mup5	major urinary protein 5	298107	Rn.118530	AB039828	2.55	2.51	2.69	2.52	2.54	2.49	1.05	down	3.22E-01	8.95E-01	-	-
1398826_s_at	Nr2f6	nuclear receptor subfamily 2, group F, member 6	245980	Rn.25840	NM_139113	2.64	2.91	2.59	2.68	2.64	2.62	1.05	down	5.59E-01	8.95E-01	-	-
1398538_at	Abhd8	abhydrolase domain containing 8	306338	Rn.22147	AI137533	2.93	2.92	2.94	2.47	3.77	2.74	1.05	up	8.77E-01	9.62E-01	-	-
1381920_at	---	---	---	Rn.131906	AI502118	2.48	2.43	2.59	2.44	2.46	2.40	1.05	down	2.52E-01	8.95E-01	-	-
1398902_at	RGD1307222	similar to mKIAA0664 protein	303300	Rn.92100	BF282978	7.66	8.15	7.64	7.79	8.16	7.70	1.05	up	7.80E-01	9.29E-01	-	-
1384918_at	RGD1307916	LOC362433	362433	Rn.34631	AI511132	2.67	2.48	2.49	2.48	2.49	2.47	1.05	down	3.44E-01	8.95E-01	-	-
1380820_at	---	---	---	Rn.212672	BI295539	2.86	2.63	2.70	2.70	2.68	2.62	1.05	down	4.06E-01	8.95E-01	-	-
1383754_at	---	---	---	Rn.24391	AI548342	2.65	2.60	2.77	2.62	2.65	2.55	1.05	down	3.22E-01	8.95E-01	-	-
1374522_at	LOC683007	similar to melanoma inhibitory activity 3	683007	---	BG670847	9.29	9.30	9.19	9.35	8.77	9.86	1.05	up	8.48E-01	9.53E-01	-	-
1375870_at	Rbms1	RNA binding motif, single stranded interacting protein 1	362138	Rn.98522	BF420140	6.78	5.80	5.05	5.78	5.62	6.02	1.05	down	9.06E-01	9.71E-01	-	-
1369681_at	Isl1	ISL LIM homeobox 1	64444	Rn.202645	NM_017339	2.30	2.29	2.31	2.30	2.51	2.29	1.05	up	4.22E-01	8.95E-01	-	-
1368849_at	Csnk1g3	casein kinase 1, gamma 3	64823	Rn.10084	BE111111	2.75	3.00	2.68	2.86	2.65	2.74	1.05	down	5.98E-01	8.95E-01	-	-
1396497_at	---	---	---	Rn.210724	BE120694	2.46	2.45	2.64	2.45	2.46	2.44	1.05	down	3.68E-01	8.95E-01	-	-
1394022_at	Id4	inhibitor of DNA binding 4	291023	Rn.22987	BE116009	9.47	10.45	10.01	9.63	10.20	10.29	1.05	up	8.63E-01	9.57E-01	-	-
1371106_at	Itgb7	integrin, beta 7	25713	Rn.10767	AF003598	2.41	2.45	2.55	2.40	2.43	2.39	1.05	down	2.23E-01	8.95E-01	-	-
1388417_at	Anapc5	anaphase-promoting complex subunit 5	288671	Rn.101004	BI281876	8.63	8.66	8.77	8.38	8.62	8.87	1.05	down	6.82E-01	9.03E-01	-	-
1377220_at	---	---	---	Rn.150026	BI296738	2.46	2.45	2.52	2.68	2.49	2.45	1.05	up	4.32E-01	8.95E-01	-	-
1376785_at	---	---	---	Rn.216948	AI104799	9.61	10.01	9.86	9.56	9.94	10.18	1.05	up	7.78E-01	9.28E-01	-	-
1398297_at	Mapk12	mitogen-activated protein kinase 12	60352	Rn.162968	NM_021746	2.89	2.77	2.76	2.76	2.75	2.73	1.05	down	2.13E-01	8.95E-01	-	-
1392301_at	Sh3tc1	SH3 domain and tetratricopeptide repeats 1	305441	Rn.66504	AI237897	5.90	6.66	4.97	5.62	5.72	6.01	1.05	down	9.04E-01	9.71E-01	-	-
1384770_at	---	---	---	Rn.147581	AI112057	2.44	2.59	2.46	2.43	2.45	2.41	1.05	down	2.57E-01	8.95E-01	-	-
1391290_at	---	---	---	Rn.171136	BF401802	2.59	2.39	2.41	2.40	2.42	2.38	1.05	down	3.62E-01	8.95E-01	-	-
1388287_at	Hoxb7	homeo box B7	497985	Rn.113631	M37566	4.19	4.37	4.19	4.18	4.19	4.18	1.05	down	3.53E-01	8.95E-01	-	-
1397800_at	---	---	---	Rn.134051	BE106592	2.81	2.67	2.95	2.72	2.90	2.61	1.05	down	6.12E-01	8.95E-01	-	-
1374430_at	Glod4	glyoxalase domain containing 4	363644	Rn.24630	BI274617	9.56	9.34	9.10	9.39	9.46	9.34	1.05	up	6.63E-01	8.99E-01	-	-
1381121_at	---	---	---	Rn.205712	AW533010	2.61	2.79	2.62	2.61	2.62	2.60	1.05	down	3.30E-01	8.95E-01	-	-
1376236_at	---	---	---	Rn.216423	AW534476	2.74	2.65	2.80	2.64	3.05	2.70	1.05	up	6.57E-01	8.98E-01	-	-
1381031_at	---	---	---	Rn.17991	BE108144	2.51	2.31	2.62	2.32	2.33	2.31	1.05	down	3.71E-01	8.95E-01	-	-
1389341_at	Plxnd1	plexin D1	312652	Rn.21111	AI102248	3.08	2.90	2.92	2.91	2.91	2.89	1.05	down	3.29E-01	8.95E-01	-	-
1368875_a_at	Nrxn2	neurexin 2	116595	Rn.11282	BE111779	2.44	2.44	2.53	2.37	2.42	2.82	1.05	up	6.84E-01	9.03E-01	-	-
1395128_at	---	---	---	---	AA899996	2.43	2.42	2.44	2.42	2.44	2.62	1.05	up	3.82E-01	8.95E-01	-	-
1381692_x_at	---	---	---	---	AW532977	2.57	2.57	2.68	2.57	2.57	2.49	1.05	down	2.32E-01	8.95E-01	-	-
1369036_at	Grik2	glutamate receptor, ionotropic, kainate 2	54257	Rn.87696	NM_019309	2.53	2.52	2.72	2.53	2.53	2.51	1.05	down	3.70E-01	8.95E-01	-	-
1373131_at	---	---	---	Rn.12135	AI175544	2.61	2.41	3.00	2.41	2.41	2.81	1.05	down	8.60E-01	9.35E-01	-	-
1397032_at	---	---	---	Rn.211026	BF404482	2.69	2.50	2.57	2.52	2.56	2.49	1.05	down	3.32E-01	8.95E-01	-	-
1380050_at	---	---	---	Rn.149101	AA819428	2.61	2.52	2.57	2.51	2.53	2.46	1.05	down	1.48E-01	8.95E-01	-	-
1386305_at	Araf	v-raf murine sarcoma 3611 viral oncogene homolog	64363	Rn.1714	AI176666	7.27	7.14	7.00	7.55	6.53	7.13	1.05	down	8.44E-01	9.51E-01	-	-
1385818_at	---	---	---	---	AA866435	2.50	2.49	2.55	2.50	2.78	2.46	1.05	up	5.67E-01	8.95E-01	-	-
1386134_at	Ubp1	Upstream binding protein 1 (LBP-1a)	301038	Rn.15705	AA850524	2.90	3.84	2.41	3.64	2.96	2.73	1.05	up	9.04E-01	9.71E

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1398310_at	Akr1d1	aldo-keto reductase family 1, member D1 (delta 4-3-ketosteroid-5-beta-reduc	192242	Rn.25716	D17309	2.75	2.75	2.91	2.73	2.87	2.62	1.05	down	5.25E-01	8.95E-01	-	-
1389964_at	C683884 /// Ndufs	similar to Acyl carrier protein, mitochondrial precursor (ACP) (NADH-ubiquino	293453 /// 683884	Rn.1318	AA944343	9.09	9.34	9.30	9.07	9.20	9.26	1.05	down	5.39E-01	8.95E-01	-	-
1368156_at	Camkk1	calcium/calmodulin-dependent protein kinase kinase 1, alpha	60341	Rn.4851	NM_031682	2.91	2.91	2.73	2.93	2.91	2.96	1.05	up	3.92E-01	8.95E-01	-	-
1391646_at	---	---	---	Rn.23401	AI502092	3.41	3.40	3.36	2.96	3.41	3.61	1.05	down	7.59E-01	9.22E-01	-	-
1381761_at	---	---	---	Rn.199160	AI059890	2.27	2.26	2.47	2.27	2.28	2.26	1.05	down	3.99E-01	8.95E-01	-	-
1384260_at	---	---	---	---	BE095699	3.10	3.10	3.10	3.29	3.11	3.09	1.05	up	3.76E-01	8.95E-01	-	-
1388958_a_at	Slc2a4	solute carrier family 2 (facilitated glucose transporter), member 4	25139	Rn.1314	AA797760	2.51	2.32	2.34	2.33	2.34	2.32	1.05	down	3.39E-01	8.95E-01	-	-
1373843_at	---	---	---	Rn.164946	BE107419	9.45	8.61	9.34	9.18	9.27	9.14	1.05	up	8.22E-01	9.43E-01	-	-
1372328_at	Klc4	kinesin light chain 4	316226	Rn.16800	BM386079	6.79	7.58	6.40	6.85	6.93	6.79	1.05	down	8.65E-01	9.58E-01	-	-
1382016_at	pc5l /// RGD15603	actin related protein 2/3 complex, subunit 5-like /// similar to actin related prot	296710 /// 501132	Rn.110752	AI716661	2.65	2.62	2.41	2.68	2.40	2.40	1.05	down	6.23E-01	8.95E-01	-	-
1392917_at	---	---	---	Rn.166557	BI302971	9.16	8.90	8.86	9.09	9.02	9.01	1.05	up	5.55E-01	8.95E-01	-	-
1383287_at	Fubp1	far upstream element (FUSE) binding protein 1	654496	Rn.219485	BE329232	5.45	5.56	5.64	5.72	5.52	5.60	1.05	up	4.77E-01	8.95E-01	-	-
1387966_at	Asrgl1	asparaginase like 1	246307	Rn.22774	AF329099	9.48	9.77	9.75	9.66	9.29	9.86	1.04	down	7.55E-01	9.20E-01	-	-
1389623_at	Exosc6	Exosome component 6	307850	Rn.163404	BF543142	2.98	2.80	2.81	2.80	2.80	2.79	1.04	down	3.42E-01	8.95E-01	-	-
1396762_at	---	---	---	---	BF400647	2.61	2.41	2.42	2.42	2.42	2.41	1.04	down	3.76E-01	8.95E-01	-	-
1375259_at	Eif4ebp2	eukaryotic translation initiation factor 4E binding protein 2	361845	Rn.24129	BF419161	7.41	8.11	7.72	7.79	7.65	8.00	1.04	up	7.94E-01	9.34E-01	-	-
1375341_at	Tmem189	transmembrane protein 189	362278	Rn.101810	BG664807	3.58	3.89	3.60	3.57	3.72	3.58	1.04	down	6.05E-01	8.95E-01	-	-
1371985_a_at	Balt5	HLA-B associated transcript 5	361796	Rn.203264	BE097389	6.24	7.78	7.62	7.25	7.30	6.91	1.04	down	9.06E-01	9.71E-01	-	-
1395378_at	Srf	serum response factor (c-fos serum response element-binding transcription fa	501099	Rn.1501	BF558969	4.35	4.31	4.54	4.83	4.11	4.45	1.04	up	7.87E-01	9.31E-01	-	-
1381468_at	Lrrc36	leucine rich repeat containing 36	361394	Rn.163400	BM383384	2.38	2.37	2.39	2.38	2.60	2.36	1.04	up	4.51E-01	8.95E-01	-	-
1378273_at	---	---	---	Rn.75290	BF402395	2.55	2.36	2.38	2.36	2.37	2.36	1.04	down	3.47E-01	8.95E-01	-	-
1390097_at	Tspyl4	TSPY-like 4	309828	Rn.161747	BI281738	4.31	4.21	4.50	5.04	3.17	5.00	1.04	up	9.24E-01	9.78E-01	-	-
1393598_at	Ccna1	cyclin A1	295052	Rn.102823	AA964510	2.49	2.31	2.31	2.30	2.31	2.30	1.04	down	3.53E-01	8.95E-01	-	-
1375000_at	---	---	---	Rn.154303	BF415422	2.50	2.55	2.45	2.44	2.45	2.43	1.04	down	9.72E-02	8.95E-01	-	-
1381609_at	Zfp335	zinc finger protein 335	259270	Rn.40737	AI710364	2.32	2.31	2.34	2.32	2.53	2.31	1.04	up	4.37E-01	8.95E-01	-	-
1383941_at	---	---	---	Rn.217082	BF411395	5.70	6.30	5.71	5.78	5.82	6.29	1.04	up	8.18E-01	9.42E-01	-	-
1371250_at	Pf4	platelet factor 4	360918	Rn.6800	AI169104	2.44	2.43	2.45	2.64	2.44	2.43	1.04	up	4.02E-01	8.95E-01	-	-
1396537_at	---	---	---	Rn.208926	BE121110	2.37	2.36	2.55	2.36	2.37	2.35	1.04	down	3.73E-01	8.95E-01	-	-
1399141_at	Clk4	CDC like kinase 4	287269	Rn.23593	BF404428	7.26	6.07	5.88	6.42	6.26	6.33	1.04	down	8.91E-01	9.66E-01	-	-
1394645_at	---	---	---	---	BF287691	2.49	2.65	2.51	2.46	2.50	2.49	1.04	down	2.83E-01	8.95E-01	-	-
1370062_at	Hig1a	HIG1 hypoxia inducible domain family, member 1A	140937	Rn.2084	NM_080902	7.78	8.54	8.47	8.75	8.46	8.78	1.04	up	9.06E-01	9.71E-01	-	-
1375507_at	---	---	---	Rn.208362	BE109700	2.45	2.42	2.58	2.43	2.43	2.40	1.04	down	2.87E-01	8.95E-01	-	-
1373181_at	Afap1l1	actin filament associated protein 1-like 1	291565	Rn.199131	BE101285	2.44	2.43	2.47	2.44	2.46	2.63	1.04	up	3.73E-01	8.95E-01	-	-
1395844_at	---	---	---	---	BF284064	2.32	2.31	2.51	2.32	2.33	2.31	1.04	down	3.85E-01	8.95E-01	-	-
1372154_at	RGD1359616	similar to 2010321M09Rik protein	300782	Rn.9525	AW521019	4.21	4.60	3.42	3.76	3.78	4.88	1.04	up	9.07E-01	9.72E-01	-	-
1367714_at	Eif2b2	eukaryotic translation initiation factor 2B, subunit 2 beta	84005	Rn.5910	NM_032058	6.51	6.17	6.12	6.21	6.05	6.36	1.04	down	6.98E-01	9.07E-01	-	-
1367525_at	Thrap3	thyroid hormone receptor associated protein 3	313591	Rn.25107	AI179833	8.16	8.05	8.10	8.00	7.93	8.19	1.04	down	4.88E-01	8.95E-01	-	-
1379881_at	---	---	---	Rn.45550	BF413190	2.42	2.73	2.44	2.55	2.43	2.42	1.04	down	5.94E-01	8.95E-01	-	-
1382775_at	Ryr2	ryanodine receptor 2, cardiac	689560	Rn.208315	BF418135	2.35	2.34	2.53	2.34	2.35	2.34	1.04	down	3.78E-01	8.95E-01	-	-
1370585_a_at	Prkcb	protein kinase C, beta	25023	Rn.91118	X04440	2.60	2.60	2.61	2.60	2.80	2.59	1.04	up	4.17E-01	8.95E-01	-	-
1382989_at	---	---	---	---	BE116242	2.54	2.56	2.68	2.53	2.54	2.52	1.04	down	2.13E-01	8.95E-01	-	-
1373800_at	---	---	---	---	BF394493	2.48	2.52	2.61	2.48	2.49	2.46	1.04	down	1.71E-01	8.95E-01	-	-
1391872_at	LOC686298	similar to protein phosphatase 2C eta isoform 2	686298	---	AI011509	2.69	2.43	2.48	2.47	2.49	2.45	1.04	down	4.90E-01	8.95E-01	-	-
1383733_at	Ak3	Adenylate kinase 3	26956	Rn.60	BF555825	4.32	5.65	6.56	6.10	4.32	6.29	1.04	up	9.48E-01	9.85E-01	-	-
1386170_at	---	---	---	Rn.205003	AI234526	2.39	2.57	2.40	2.39	2.39	2.38	1.04	down	3.38E-01	8.95E-01	-	-
1376333_at	Btbd1	BTB (POZ) domain containing 1	293060	Rn.162445	BI275800	6.93	7.48	7.37	7.77	6.57	7.25	1.04	down	8.79E-01	9.63E-01	-	-
1386929_at	Hk1	hexokinase 1	25058	Rn.11017	NM_012734	2.52	2.56	2.52	2.52	2.63	2.66	1.04	up	2.30E-01	8.95E-01	-	-
1381738_at	Gpr135	G protein-coupled receptor 135	314213	Rn.56673	BF407796	2.36	2.36	2.36	2.57	2.36	2.34	1.04	up	4.42E-01	8.95E-01	-	-
1377285_at	Znf213	Zinc finger protein 213	287094	Rn.98676	AI578851	2.55	2.77	2.55	2.54	2.60	2.54	1.04	down	4.69E-01	8.95E-01	-	-
1377854_at	Tmem62	transmembrane protein 62	311350	Rn.138047	AI406343	5.44	4.92	4.12	4.92	4.61	5.14	1.04	up	8.86E-01	9.65E-01	-	-
1388329_at	Krt13	keratin 13	287699	Rn.10257	BI280282	2.50	2.49	2.69	2.49	2.50	2.49	1.04	down	4.02E-01	8.95E-01	-	-
1375128_at	Mtdh	Metadherin	170910	Rn.6864	BE110589	3.83	3.30	3.24	3.51	3.53	3.51	1.04	up	7.54E-01	9.20E-01	-	-
1381558_at	---	---	---	---	BG374759	3.52	3.52	3.53	3.52	3.72	3.51	1.04	up	4.18E-01	8.95E-01	-	-
1369767_a_at	Kcnmb1	potassium large conductance calcium-activated channel, subfamily M, beta m	29747	Rn.10820	U40602	2.31	2.27	2.33	2.49	2.31	2.29	1.04	up	3.93E-01	8.95E-01	-	-
1373242_at	Ttc41	TATA box binding protein-like 1	689030	Rn.25148	AW140320	6.20	7.94	6.73	7.26	6.59	7.21	1.04	up	9.16E-01	9.75E-01	-	-
1387582_a_at	Pde7b	phosphodiesterase 7B	140929	Rn.212624	NM_080894	2.33	2.36	2.34	2.33	2.56	2.33	1.04	up	4.74E-01	8.95E-01	-	-
1390504_at	---	---	---	---	AW524470	2.48	2.39	2.39	2.58	2.43	2.45	1.04	up	3.24E-01	8.95E-01	-	-
1398546_at	---	---	---	Rn.208174	BF396217	2.52	2.47	2.51	2.63	2.53	2.54	1.04	up	1.53E-01	8.95E-01	-	-
1373702_at	L3mbtl2	l(3)mbtl-like 2 (Drosophila)	300320	Rn.137566	AI171798	6.90	6.44	4.89	5.99	5.84	6.58	1.04	up	9.28E-01	9.79E-01	-	-
1373018_at	Spryd3	SPRY domain containing 3	315327	Rn.9246	BM390695	2.65	2.75	2.76	2.75	2.87	2.72	1.04	up	3.39E-01	8.95E-01	-	-
1386950_at	Ppp1cb	protein phosphatase 1, catalytic subunit, beta isoform	25594	Rn.128769	NM_013065	8.34	8.23	8.88	8.30	8.69	8.64	1.04	up	8.04E-01	9.37E-01	-	-
1374611_at	---	---	---	Rn.169280	AW535065	6.94	6.92	6.97	6.79	6.99	6.86	1.04	down	8.55E-01	9.50E-01	-	-
1388333_at	Fbxo3	F-box protein 3	690634	Rn.201745	AI407074	5.15	5.15	5.34	4.99	5.16	5.68	1.04	up	7.89E-01	9.32E-01	-	-
1368032_at	Nolc1	nucleolar and coiled-body phosphoprotein 1	64896	Rn.9517	BI290791	5.39	6.11	5.81	5.70	5.78	6.02	1.04	up	8.00E-01	9.35E-01	-	-
1386995_at	Btg2	B-cell translocation gene 2, anti-proliferative	29619	Rn.27923	BI288701	2.84	2.77	2.83	2.96	2.84	2.83	1.04	up	2.32E-01	8.95E-01	-	-
1391139_at	Adamtsl1	ADAMTS-like 1	362539	Rn.105496	BF397925	2.98	2.96	3.00	2.77	3.02	2.96	1.04	down	4.57E-01	8.95E-01	-	-
1389666_at	Rom1	retinal outer segment membrane protein 1	309201	Rn.145021	AA892855	3.06	3.13	3.11	3.07	3.31	3.10	1.04	up	4.66E-01	8.95E-01	-	-
1383152_at	Chid1	chitinase domain containing 1	293628	Rn.162505	BF544427	4.83	3.09	2.98	3.06	3.56	4.10	1.04	down	9.30E-01	9.81E-01	-	-
1389418_at	Bcl9	B-cell CLL/lymphoma 9	310704	Rn.264	BG378875	2.24	2.24	2.24	2.32	2.35	2.24	1.04	up	1.45E-01	8.95E-01	-	-
1396706_at	---	---	---	---	BF398967	2.26	2.26	2.26	2.45	2.26	2.26	1.04	up	3.85E-01	8.95E-01	-	-
1383540_at	---	---	---	Rn.6736	BF551093	3.97	3.22	4.43	3.97	3.26	4.20	1.04	down	8.97E-01	9.68E-01	-	-
1379251_at	---	---	---	Rn.24762	BF398485	4.83	3.02	3.87	4.07	3.97	3.50	1.04	down	9.15E-01	9.75E-01	-	-
1393456_at	---	---	---	Rn.124192	BI281195	2.36	2.45	2.45	2.36	2.37	2.35	1.04	down	1.01E-01	8.95E-01	-	-
1394982_at	Telo2	TEL2, telomere maintenance 2, homolog (S. cerevisiae)	302986	Rn.34729	BM383155	2.57	2.55	2.36	2.54	2.56	2.56	1.04	up	4.08E-01	8.95E-01	-	-
1397310_at	---	---	---	Rn.29226	AI178436	2.43	2.41	2.46	2.42	2.44	2.62	1.04	up	3.95E-01	8.95E-01	-	-
1373347_at	Acbd3	acyl-Coenzyme A binding domain containing 3	289312	Rn.57036	BF419134	4.30	4.29	5.84	3.97	6.30	4.36	1.04	up	9.47E-01	9.85E-01	-	-
1388007_x_at	Amelx	amelogenin X chromosome	29160	Rn.11368	U07054	2.60	2.56	2.77	2.58	2.59	2.57	1.04	down	3.76E-01	8.95E-01	-	-
1387505_at	Gnai1	guanine nucleotide binding protein (G protein), alpha inhibiting 1	25686	Rn.11391	NM_013145	5.85	5.96	5.82	5.36	5.68	6.41	1.04	down	8.52E-01	9.54E-01	-	-
1388784_at	Calf1r	colony stimulating factor 1 receptor	307403	Rn.72599	BI285793	2.39	2.48	2.40	2.37	2.72	2.37	1.04	up	6.37E-01	8.95E-01	-	-
1395819_at	---	---	---	Rn.146532	AW526127	2.84	2.59	2.79	2.71	3.11	2.58	1.04	up	7.43E-01	9.17E-01	-	-
1393644_at	---	---	---	---	BI278967	2.58	2.62	2.66	2.56	2.60	2.50	1.04	down	1.70E-01	8.95E-01	-	-
1391876_at	Hsf2	heat shock factor 2	64441	Rn.163428	AI170412	2.47	2.61	2.49	2.45	2.48	2.45	1.04	down	2.28E-01	8.95E-01	-	-
1383541_at	Nagpa	N-acetylglucosamine-1-phosphodiester alpha-N-acetylglucosaminidase	360476	Rn.27072	BE114815	2.65	2.64	2.65	2.65	2.83	2.65	1.04	up	3.67E-01	8.95E-01	-	-
1390336_at	RGD1307569	similar to Protein C21orf63 homolog precursor	360695	Rn.2895	BF408325	2.44	2.37	2.39	2.37	2.39	2.62	1.04	up	4.98E-01	8.95E-01	-	-
1368101_at	Calm3	calmodulin 3	24244	Rn.2892	NM_012518	10.03	10.13	10.23	10.17	10.00	10.03	1.04	down	4.73E-01	8.95E-01	-	-
1397229_at	---	---	---	Rn.206921	BF565781	2.72	2.58	2.65	2.58	2.64	2.55	1.04	down	2.50E-01	8.95E-01	-	-
1380448_at	Alkbh	alkB, alkylation repair homolog (E. coli)	362766	Rn.107927	AI112926	3.29	3.76	3.36	2.63	4.64	2.95	1.04	down	9.27E-01	9.79E-01	-	-
1371532_at	---	---	---	Rn.173084	BF404505	2.42	2.42	2.60	2.43	2.43	2.38	1.04	down	3.63E-01	8.95E-01	-	-
1380815_at	Scyl1bp1	SCY1-like 1 binding protein 1	304923	Rn.45778	AW523684	4.07	2.72	4.31	3.77	3.79	3.72	1.04	up	9.06E-01	9.71E-01	-	-
1369684_at	Tcfe2a	transcription factor E2a	171046	Rn.10290	NM_133524	2.78	2.81	2.79	2.81	2.95	2.80	1.04	up	2.55E-01	8.95E-01	-	-
1383860_at	Fosl2	Fos-like antigen 2	25446	Rn.163577	BI296947	2.46	2.45	2.47	2.43	2.47	2.66	1.04	up	4.30E-01	8.95E-01	-	-
1380966_at	---	---	---	Rn.16552	BE117653	2.45	2.24	2.46	2.45	2.45	2.44	1.04	up	4.42E-01	8.95E-01	-	-
1390075_at	Olfml2b	olfactomedin-like 2B	304960	Rn.13880	AA859964	2.46	2.59	2.46	2.44	2.43	2.44	1.04	down	2.32E-01	8.95E-01	-	-
1393138_at	Jund	Jun D proto-oncogene	24518	Rn.46225	BE329377	9.91	10.13	10.21	10.14	10.36	9.93	1.04	up	7.07E-01	9.08E-01	-	-
1374580_at	Senp6	SUMO/sentrin specific peptidase 6	300860	Rn.98553	AW535691	7.59	7.64	7.75	7.57	7.47	8.13	1.04	up	7.83E-01	9.30E-01	-	-
1383129_at	Gpr177	G protein-coupled receptor 177	362065	Rn.103639	AI072254	4.05	3.92	5.44	3.51	5.05	5.03	1.04	up	9.34E-01	9.81E-01	-	-
1377943_at	Cd86	CD86 molecule	56822	Rn.6734	BI292219	2.34	2.33	2.34	2.33	2.55	2.32	1.04	up	4.58E-01	8.95E-01	-	-
1382769_at	Ifnar1	interferon (alpha, beta and omega) receptor 1	288264	Rn.105738	AA996880	5.36	5.15	3.32	4.57	4.17	4.90	1.04	down	9.32E-01	9.81E-01	-	-
1372680_at	Leng4	leukocyte receptor cluster (LRC) member 4	308309	Rn.44782	AI406310	3.37	3.37	3.43	3.00	3.38	3.98	1.04	up	8.40E-01	9.50E-01	-	-
1379882_a_at	Ddr2	Discoidin domain receptor tyrosine kinase 2	685781	Rn.92730	BE116018	2.61	2.71	2.62	2.54	2.63	2.58	1.04	down	2.14E-01	8.95E-01	-	-
1391090_at	---	---	---	---	BG380796	2.36	2.35	2.38	2.35	2.58	2.34	1.04	up	4.66E-01	8.95E-01	-	-
1386500_at	RGD1561795	similar to RIKEN cDNA 1700012B09	500945	Rn.219618	BF400284	2.87	2.86	2.91	2.91	2.91	3.01	1.04	up	1.54E-01	8.95E-01	-	-
1379150_at	---	---	---	Rn.210997	BF404462	2.48	2.47	2.51	2.47	2.60	2.58	1.04	up	2.13E-01	8.95E-01	-	-
1384363_at	Sbds	Shwachman-Bodian-Diamond syndrome homolog (human)	288615	Rn.107123	AI070597	2.34	2.35	2.34	2.34	2.34	2.53	1.04	up	3.73E-01	8.95E-01	-	-
1385195_at	---	---	---	Rn.209658	BF390112	2.48	2.45	2.51	2.48	2.66	2.48	1.04	up	3.70E-01	8.95E-01	-	-
1396159_at	Lama5	laminin, alpha 5	140433	Rn.62816	BF414927	2.38	2.37	2.38	2.56	2.39	2.36	1.04	up	3.73E-01	8.95E-01	-	-
1382876_at	---	---	---	Rn.165391	AA892377	2.72	2.43	2.46	2.45	2.54	2.44	1.04	down	5.65E-01	8.95E-01	-	-
1368847_at	Rab10	RAB10, member RAS oncogene family	50993	Rn.65864	NM_017359	7.25	7.69	8.52	7.75	7.34	8.19	1.04	down	8.96E-01	9.67E-01	-	-
1391669_at	Ptprb	protein tyrosine phosphatase, receptor type, B	314843	Rn.198784	BM391921	2.39	2.40	2.36	2.48	2.50	2.35	1.04	up	2.81E-01	8.95E-01	-	-
1383054_at	Zfp91	zinc finger protein 91	246282	Rn.1772	BE116131	6.65	7.13	6.34	6.67	6.99	6.65	1.04	up	8.20E-01	9.42E-01	-	-
1398878_at	Cpsf4	cleavage and polyadenylation specific factor 4	304277	Rn.104788	Y17326	7.42	7.61	7.31	7.16	7.53	7.46	1.04	down	6.86E-01	9.04E-01	-	-
1384344_at	Fkbp7	FK506 binding protein 7	295672	Rn.82775	AI060231	2.45	2.50	2.53	2.73	2.48	2.45	1.04	up	5.37E-01	8.95E-01	-	-
1387537_at	Ptprq	protein tyrosine phosphatase, receptor type, Q	360417	Rn.30011	NM_022925	2.43	2.32	2.43	2.33	2.34	2.32	1.04	down	1.56E-01	8.95E-01	-	-
1374996_at	Nploc4	nuclear protein localization 4 homolog (S. cerevisiae)	140639	Rn.144645	AI172269	7.99	8.59	9.06	9.06	7.94	8.82	1.04	up	8.99E-01	9.69E-01	-	-
1389774_at	Znf23	zinc finger protein 23 (KOX 16)	307839	Rn.6474	AI008371	4.99	5.86	6.17	5.40	5.56	5.87	1.04	down	8.78E-01	9.62E-01	-	-
1383935_at	---	---	---	Rn.1	AW252428	9.44	9.84	9.23	9.06	9.78	9.48	1.04	down	8.32E-01	9.47E-01	-	-
1373295_at	Obfc1	oligonucleotide/oligosaccharide-binding fold containing 1	294025	Rn.15899	BI281889	3.09	4.23	3.44	3.08	3.02	4.84	1.04	up	9.32E-01	9.81E-01	-	-
1395910_at	Dot1l	DOT1-like, histone H3 methyltransferase (S. cerevisiae)	362831	Rn.18027	AI578372	2.43	2.47	2.45	2.67	2.45	2.42	1.04	up	4.70E-01	8.95E-01	-	-
1382668_at	Commd2	COMM domain containing 2	688478	Rn.4168	AI232529	2.41	2.42	2.47	2.44	2.45	2.60	1.04	up	3.28E-01	8.95E-01	-	-
1390736_at	Znf668	zinc finger protein 668	309002	Rn.218024	AW443743	2.53	2.34	2.36	2.35	2.36	2.35	1.04	down	3.55E-01	8.95E-01	-	-
1395341_at	Nek9	NIMA (never in mitosis gene a)- related kinase 9	299204	Rn.102369	BF281916	3.05	3.06	3.20	3.05	3.05	3.03	1.04	down	2.96E-01	8.95E-01	-	-
1380703_at	---	---	---	Rn.177402	BM386391	2.62	2.59	2.62	3.02	2.42	2.58	1.04	up	7.49E-01	9.19E-01	-	-
1376979_at	---	---	---	Rn.93999	BM392214	2.45	2.76	2.46	2.46	2.46	2.56	1.04	down	5.94E-01	8.95E-01	-	-
1369145_a_at	Snd3 /// LOC6841	potassium voltage gated channel, Shal-related family, member 3 /// similar to	65195 /// 684161	Rn.10540	AB003587	3.37	3.31	3.47	3.34	3.80	3.20	1.04	up	7.61E-01	9.22E-01	-	-
1388350_at	Pex19	peroxisomal biogenesis factor 19	289233	Rn.203104	BG377475	6.51	6.60	6.53	6.76	6.31	6.75	1.04	up	7.06E-01	9.08E-01	-	-
1391622_at	LOC681335	hypothetical protein LOC681335	681335	Rn.198835	AI579391	3.89	3.85	3.87	3.87	4.10	3.83	1.04	up	5.05E-01	8.95E-01	-	-
1390906_at	---	---	---	Rn.205564	BE100932	2.75	2.55	2.56	2.55	2.57	2.55	1.04	down	3.92E-01	8.95E-01	-	-
1392604_at	---	---	---	Rn.164194	AA997187	4.73	5.75	5.42	4.75	5.77	5.57	1.04	up	8.93E-01	9.67E-01	-	-
1376559_at	Rpia	Ribose 5-phosphate isomerase A	362383	Rn.12446	AW253884	2.19	2.08	2.19	2.25	2.19	2.21	1.04	up	1.90E-01	8.95E-01	-	-
1391101_at	Arhgap12	Rho GTPase activating protein 12	307016	Rn.34541	AI407134	3.34	2.72	2.67	2.58	2.65	3.69	1.04	up	8.90E-01	9.66E-01	-	-
1396743_at	---	---	---	Rn.154131	BF391580	2.66	3.67	5.21	3.48	3.90	3.98	1.04	down	9.39E-01	9.83E-01	-	-
1382521_at	Gls	glutaminase	24398	Rn.5762	AA925755	5.10	4.75	5.05	5.15	4.97	4.96	1.04	up	6.47E-01	8.95E-01	-	-
1370130_at	Rhoa	ras homolog gene family, member A	117273	Rn.107401	NM_057132	10.59	10.74	10.84	10.91	10.78	10.68	1.04	up	5.71E-01	8.95E-01	-	-
1396941_at	---	---	---	---	AA974470	2.68	2.44	2.42	2.50	2.46	2.39	1.04	down	5.36E-01	8.95E-01	-	-
1377938_at	Fam100a	family with sequence similarity 100, member A	302941	Rn.94991	AA859585	3.88	3.81	3.83	3.81	3.73	3.80	1.04	down	1.13E-01	8.95E-01	-	-
1379986_at	---	---	---	Rn.148495	BM390668	2.79	2.74	2.96	2.77	2.86	2.68	1.04	down	5.10E-01	8.95E-01	-	-
1391705_at	---	---	---	Rn.166998	BI276644	2.48	2.44	2.48	2.56	2.69	2.35	1.04	up	5.71E-01	8.95E-01	-	-
1368764_at	Hist1h2ba	histone cluster 1, H2ba	24829	Rn.10104	NM_022643	2.56	2.53	2.70	2.54	2.55	2.51	1.04	down	3.12E-01	8.95E-01	-	-
1385369_at	Dzip1l	DAZ interacting protein 1-like	315952	Rn.104060	BI290883	6.18	6.34	6.26	6.42	6.77	5.77	1.04	up	8.46E-01	9.52E-01	-	-
1373503_at	Lrch4	leucine-rich repeats and calponin homology (CH) domain containing 4	360779	Rn.24664	AA892504	2.35	2.34	2.36	2.37	2.58	2.30	1.04	up	5.08E-01	8.95E-01	-	-
1374041_at	RGD1561852	similar to Protein C20orf29	499893	Rn.22263	AW528468	2.34	2.34	2.49	2.34	2.34	2.30	1.04	up	3.10E-01	8.95E-01	-	-
1393523_at	---	---	--

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1396415_at	Pigp	Phosphatidylinositol glycan anchor biosynthesis, class P	288238	Rn.53715	BF387862	2.49	2.47	2.53	2.68	2.52	2.47	1.04	up	4.14E-01	8.95E-01	-	-
1380787_at	---	---	---	---	BE109076	2.55	2.50	2.59	2.52	2.57	2.37	1.04	down	3.90E-01	8.95E-01	-	-
1386656_at	---	---	---	---	BF558870	2.54	2.51	2.56	2.53	2.75	2.51	1.04	up	4.77E-01	8.95E-01	-	-
1378682_at	---	---	---	Rn.208964	BF390772	2.61	2.56	2.54	2.51	2.53	2.50	1.04	down	5.88E-02	8.95E-01	-	-
1391248_at	---	---	---	Rn.147677	BF419702	2.71	2.64	2.73	2.68	2.71	2.88	1.04	up	4.17E-01	8.95E-01	-	-
1379289_at	B4galt7	xylosylprotein beta1,4-galactosyltransferase, polypeptide 7 (galactosyltransfe	364675	Rn.41210	BM385124	5.21	5.20	5.21	5.21	5.21	5.39	1.04	up	3.63E-01	8.95E-01	-	-
1371820_at	Mesdc2	mesoderm development candidate 2	308796	Rn.41045	BI282084	8.33	8.79	8.85	8.44	8.52	8.83	1.04	down	7.81E-01	9.29E-01	-	-
1371771_at	LOC313641	Perlecan	313641	Rn.12602	BI274094	3.35	3.37	3.31	3.62	3.40	2.84	1.04	down	8.07E-01	9.38E-01	-	-
1392262_at	---	---	---	Rn.205373	BF402235	2.61	2.45	2.48	2.80	2.47	2.45	1.04	up	6.49E-01	8.96E-01	-	-
1373966_at	Rai1	retinoic acid induced 1	303188	Rn.198857	BF406242	2.36	2.36	2.37	2.36	2.37	2.54	1.04	up	3.70E-01	8.95E-01	-	-
1381729_at	LOC498675	hypothetical LOC498675	498675	Rn.198466	BF394670	3.29	5.96	6.33	5.19	4.43	5.78	1.04	down	9.56E-01	9.87E-01	-	-
1383341_at	Cab39l	calcium binding protein 39-like	290291	Rn.163279	BG662592	5.61	6.27	5.77	6.15	5.57	5.75	1.04	down	8.29E-01	9.46E-01	-	-
1388080_a_at	Hrh3	histamine receptor H3	85268	Rn.7617	AY009337	2.27	2.26	2.45	2.27	2.27	2.26	1.04	down	3.76E-01	8.95E-01	-	-
1372366_at	Kat5	K(lysine) acetyltransferase 5	192218	Rn.6629	BI285597	4.07	4.41	4.38	4.83	3.47	4.37	1.04	down	8.90E-01	9.66E-01	-	-
1378112_at	Myst3	MYST histone acetyltransferase (monocytic leukemia) 3	306571	Rn.33802	BI304019	4.23	4.08	4.29	4.06	4.14	4.22	1.04	down	4.76E-01	8.95E-01	-	-
1374411_at	Mrpl52	mitochondrial ribosomal protein L52	361037	Rn.6660	BF414649	7.63	7.33	6.54	7.09	6.89	7.69	1.04	up	8.88E-01	9.65E-01	-	-
1391421_at	RGD1564209	similar to Acyl-CoA dehydrogenase family member 8, mitochondrial precursor	367046	Rn.8978	AI599819	7.27	6.64	7.28	6.68	7.34	6.98	1.04	down	8.43E-01	9.51E-01	-	-
1385514_at	Zc3h14	zinc finger CCCH type containing 14	192359	Rn.98359	AW524271	2.64	2.61	2.85	2.64	2.67	2.61	1.04	down	4.82E-01	8.95E-01	-	-
1377223_at	Wt1	Wilms tumor 1	24883	Rn.92531	AI599621	2.47	2.43	2.67	2.46	2.52	2.42	1.04	down	4.95E-01	8.95E-01	-	-
1382088_at	---	---	---	Rn.20442	AI548753	2.39	2.37	2.40	2.58	2.41	2.36	1.04	up	4.33E-01	8.95E-01	-	-
1383702_at	---	---	---	Rn.44600	AW534301	3.03	3.48	4.48	3.48	3.50	4.19	1.04	up	9.07E-01	9.72E-01	-	-
1380066_at	Tfr2	transferrin receptor 2	288562	Rn.59926	BF401956	2.41	2.40	2.42	2.53	2.41	2.48	1.04	up	1.56E-01	8.95E-01	-	-
1376058_at	Mtus1	mitochondrial tumor suppressor 1	306487	Rn.95344	AI705731	4.74	5.05	4.26	4.74	4.54	4.60	1.04	down	8.11E-01	9.39E-01	-	-
1389677_at	Syde1	synapse defective 1, Rho GTPase, homolog 1 (C. elegans)	362842	Rn.54315	BE109624	3.24	3.23	3.39	3.27	3.57	3.22	1.04	up	6.41E-01	8.95E-01	-	-
1368013_at	Ddit4l	DNA-damage-inducible transcript 4-like	140582	Rn.19672	NM_080399	2.41	2.40	2.43	2.40	2.41	2.60	1.04	up	4.08E-01	8.95E-01	-	-
1388707_at	---	---	---	---	BF284919	4.61	5.85	5.81	4.47	5.84	6.13	1.04	up	9.31E-01	9.81E-01	-	-
1387554_at	Galnt5	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltrar	83627	Rn.30048	NM_031796	2.35	2.34	2.35	2.54	2.35	2.34	1.04	up	4.03E-01	8.95E-01	-	-
1388173_at	Kcnd1	potassium voltage-gated channel, Shal-related family, member 1	116695	Rn.9458	AA957975	2.31	2.30	2.48	2.30	2.31	2.29	1.04	down	3.74E-01	8.95E-01	-	-
1381226_at	---	---	---	---	BF412152	2.43	2.59	2.44	2.43	2.44	2.42	1.04	down	3.17E-01	8.95E-01	-	-
1377739_at	Gng12	guanine nucleotide binding protein (G protein), gamma 12	114120	Rn.198679	AI576549	9.13	9.03	8.79	9.16	8.41	9.57	1.04	up	8.73E-01	9.61E-01	-	-
1391843_at	---	---	---	Rn.199940	BF393134	2.44	2.57	2.46	2.43	2.46	2.41	1.04	down	2.04E-01	8.95E-01	-	-
1391262_at	RGD1564247 /// Ser	similar to SUMO/sentrin specific protease 5 /// SUMO/sentrin specific proteas	303874 /// 499574	Rn.161817	BE105606	4.25	4.10	3.97	3.76	4.39	4.35	1.04	up	7.97E-01	9.34E-01	-	-
1396244_at	RGD1559545	similar to ATPase inhibitory factor 1	503029	---	AA964859	2.66	2.61	2.90	2.63	2.75	2.61	1.04	down	5.80E-01	8.95E-01	-	-
1394194_x_at	---	---	---	---	AI639126	2.60	2.54	2.81	2.58	2.71	2.49	1.04	down	5.91E-01	8.95E-01	-	-
1370064_at	Psen2	presenilin 2	81751	Rn.11045	AB004454	2.45	2.64	2.47	2.47	2.46	2.45	1.04	down	3.78E-01	8.95E-01	-	-
1389682_at	Chac2	ChaC, cation transport regulator homolog 2 (E. coli)	360994	Rn.207183	BF284967	3.04	3.05	3.16	3.01	3.07	2.99	1.04	down	2.60E-01	8.95E-01	-	-
1382363_at	Mpp5	membrane protein, palmitoylated 5 (MAGUK p55 subfamily member 5)	314259	Rn.8181	AI072027	4.27	5.20	4.15	4.59	4.18	4.67	1.04	down	8.77E-01	9.62E-01	-	-
1393584_at	Tnfrsf21	tumor necrosis factor receptor superfamily, member 21	316256	Rn.98230	AI045201	10.10	9.92	10.14	9.96	9.56	10.46	1.04	down	8.35E-01	9.48E-01	-	-
1383665_at	Lpin2	lipin 2	316737	Rn.203839	BE096055	7.35	8.12	7.71	8.25	7.11	8.00	1.04	up	8.91E-01	9.66E-01	-	-
1372515_at	---	---	---	Rn.9403	BI281177	2.59	2.50	2.73	2.40	2.63	2.97	1.04	up	7.54E-01	9.20E-01	-	-
1397599_at	---	---	---	Rn.209354	BF394205	2.68	2.49	2.53	2.51	2.53	2.48	1.04	down	3.63E-01	8.95E-01	-	-
1389606_at	Anapc1	anaphase promoting complex subunit 1	311412	Rn.8	BI303298	3.61	4.19	5.07	3.68	4.18	4.83	1.04	down	9.17E-01	9.75E-01	-	-
1379413_at	Nmnat1	nicotinamide nucleotide adenylyltransferase 1	298653	Rn.147523	BF285393	3.26	3.12	3.08	3.07	3.20	3.01	1.04	down	4.91E-01	8.95E-01	-	-
1399038_at	Usp19	ubiquitin specific peptidase 19	361190	Rn.13484	AA893224	3.13	3.18	3.16	3.15	3.02	3.13	1.04	down	2.28E-01	8.95E-01	-	-
1390585_at	Maap1	maman-binding lectin serine peptidase 1	84023	Rn.203236	AI169829	2.70	2.69	3.01	3.02	2.51	2.69	1.04	down	7.56E-01	9.21E-01	-	-
1382154_at	Ptpn12	protein tyrosine phosphatase, non-receptor type 12	117255	Rn.10707	BI289625	5.41	5.33	5.12	5.16	4.86	5.65	1.04	down	8.19E-01	9.42E-01	-	-
1386074_at	Mina	myc induced nuclear antigen	266670	Rn.77753	AI710379	2.71	2.77	2.86	2.75	2.73	2.68	1.04	down	2.64E-01	8.95E-01	-	-
1385724_at	LOC682874	hypothetical protein LOC682874	682874	---	BE097295	2.47	2.29	2.31	2.29	2.30	2.29	1.04	down	3.46E-01	8.95E-01	-	-
1392146_at	---	---	---	---	BF418011	2.30	2.44	2.32	2.29	2.31	2.29	1.04	down	2.47E-01	8.95E-01	-	-
1372657_at	Tmem106c	transmembrane protein 106C	315286	Rn.99883	BM391494	4.85	5.66	5.16	5.36	4.64	5.48	1.04	down	8.73E-01	9.61E-01	-	-
1371115_at	Ptpre	protein tyrosine phosphatase, receptor type, E	114767	Rn.107819	D78610	2.41	2.41	2.43	2.41	2.42	2.59	1.04	up	3.74E-01	8.95E-01	-	-
1378541_at	Pus7l	pseudouridylate synthase 7 homolog (S. cerevisiae)-like	315264	---	BE116562	2.37	2.36	2.38	2.37	2.54	2.39	1.04	up	3.42E-01	8.95E-01	-	-
1397900_at	---	---	---	Rn.146314	BG375046	2.71	2.70	2.88	2.71	2.72	2.69	1.04	down	3.64E-01	8.95E-01	-	-
1393160_at	---	---	---	Rn.95167	AA955879	2.56	2.53	2.55	2.53	2.54	2.39	1.04	down	2.99E-01	8.95E-01	-	-
1386594_at	---	---	---	Rn.204157	BF558518	2.67	2.63	2.79	2.63	2.75	2.54	1.04	down	4.77E-01	8.95E-01	-	-
1375874_at	RGD1309759	similar to cDNA sequence BC013529	361448	Rn.145178	AA799680	7.26	7.90	7.79	7.63	7.74	7.76	1.04	up	7.80E-01	9.28E-01	-	-
1371598_at	---	---	---	Rn.199096	BI278598	6.95	6.52	5.72	6.22	6.33	6.47	1.04	down	8.79E-01	9.63E-01	-	-
1389834_at	Nudt8	Nudix (nucleoside diphosphate linked moiety X)-type motif 8	361692	Rn.23628	AI237690	5.59	5.07	4.04	4.88	4.29	5.35	1.04	down	9.18E-01	9.76E-01	-	-
1392730_at	---	---	---	Rn.204638	AI144948	2.57	2.52	2.57	2.55	2.60	2.68	1.04	up	2.37E-01	8.95E-01	-	-
1368469_at	Aqp5	aquaporin 5	25241	Rn.10066	NM_012779	2.35	2.34	2.78	2.35	2.62	2.33	1.04	down	7.42E-01	9.17E-01	-	-
1392443_at	---	---	---	---	BE096522	3.08	2.52	2.85	2.75	2.83	2.69	1.04	down	7.40E-01	9.16E-01	-	-
1367976_at	Tpp2	tripeptidyl peptidase II	81815	Rn.28991	NM_031137	8.23	8.14	8.20	8.12	8.16	8.11	1.04	down	1.20E-01	8.95E-01	-	-
1371718_at	Sra1	steroid receptor RNA activator 1	252891	Rn.29904	BI283124	7.48	7.66	7.81	8.01	7.14	7.61	1.04	down	8.36E-01	9.48E-01	-	-
1376199_at	Ccrk	cell cycle related kinase	364666	Rn.7013	BF419187	5.64	6.12	6.39	6.24	6.36	5.73	1.04	up	8.49E-01	9.53E-01	-	-
1398423_at	---	---	---	---	BF401629	2.50	2.49	2.65	2.48	2.52	2.46	1.04	down	3.47E-01	8.95E-01	-	-
1374599_at	Herc1	hect (homologous to the E6-AP (UBE3A) carboxyl terminus) domain and RCC	315771	Rn.77165	BM386001	4.47	4.72	4.47	4.65	4.33	4.49	1.04	down	6.56E-01	8.98E-01	-	-
1383779_at	Rrp1b	ribosomal RNA processing 1 homolog B (S. cerevisiae)	309673	Rn.54275	BF566806	2.43	2.75	2.44	2.57	2.44	2.43	1.04	down	6.28E-01	8.95E-01	-	-
1385870_at	---	---	---	Rn.22691	AA997980	3.62	3.72	4.39	3.14	4.59	4.18	1.04	up	9.10E-01	9.73E-01	-	-
1393155_at	Plk3	polo-like kinase 3 (Drosophila)	58936	Rn.9284	AA957449	2.69	2.52	2.57	2.51	2.58	2.51	1.04	down	3.38E-01	8.95E-01	-	-
1383233_at	Fam35a	family with sequence similarity 35, member A	364514	Rn.28390	BI289032	3.57	3.40	3.42	3.40	3.41	3.40	1.04	down	3.36E-01	8.95E-01	-	-
1381660_at	Fam65a	family with sequence similarity 65, member A	291974	Rn.105873	AF408426	2.69	2.40	2.46	2.46	2.46	2.45	1.04	down	5.27E-01	8.95E-01	-	-
1368814_at	Aldh6a1	aldehyde dehydrogenase 6 family, member A1	81708	Rn.2098	AI407458	11.74	11.98	11.83	11.67	11.69	12.01	1.04	down	6.65E-01	8.96E-01	-	-
1375483_at	RGD1305680	similar to KIAA0240	301235	Rn.55468	BE109255	3.28	3.27	3.20	3.27	3.28	3.37	1.04	up	2.27E-01	8.95E-01	-	-
1395981_at	Ascc3	activating signal cointegrator 1 complex subunit 3	309887	Rn.24209	AW919934	3.40	3.40	3.79	3.45	3.47	3.48	1.04	down	6.72E-01	9.01E-01	-	-
1393143_at	---	---	---	Rn.200583	AI045856	9.16	8.02	7.86	8.96	8.03	8.23	1.04	up	9.10E-01	9.73E-01	-	-
1389232_at	Wdr5b	WD repeat domain 5B	303907	Rn.162060	BI296464	2.68	2.54	2.77	2.84	2.65	2.68	1.04	up	5.42E-01	8.95E-01	-	-
1394599_at	Zxdc	ZXD family zinc finger C	362399	Rn.144376	AA998165	2.52	2.49	2.42	2.56	2.55	2.50	1.04	up	1.70E-01	8.95E-01	-	-
1368254_a_at	Sphk1	sphingosine kinase 1	170897	Rn.18522	AB049572	2.33	2.32	2.34	2.33	2.33	2.52	1.04	up	3.97E-01	8.95E-01	-	-
1368868_at	Akap12	A kinase (PRKA) anchor protein 12	83425	Rn.122094	BG663107	2.51	2.50	2.63	2.50	2.51	2.44	1.04	down	2.73E-01	8.95E-01	-	-
1396287_at	---	---	---	Rn.53091	BI283465	2.50	2.46	2.49	2.60	2.58	2.45	1.04	up	2.86E-01	8.95E-01	-	-
1396904_at	Iqwd1	IQ motif and WD repeats 1	289181	Rn.3917	BF409502	2.41	2.39	2.41	2.47	2.53	2.39	1.04	up	2.31E-01	8.95E-01	-	-
1376800_at	---	---	---	Rn.163688	AA892496	2.64	3.40	2.62	3.01	2.69	2.79	1.04	down	8.39E-01	9.50E-01	-	-
1378675_at	Tgm3	transglutaminase 3, E polypeptide	366189	Rn.53317	BE119678	2.67	2.66	2.76	2.62	2.67	2.63	1.04	down	1.69E-01	8.95E-01	-	-
1374481_at	Cno	cappuccino homolog (mouse)	364183	Rn.8060	AA946502	4.70	4.93	4.62	5.48	3.17	5.42	1.04	down	9.42E-01	9.83E-01	-	-
1391769_at	---	---	---	Rn.205199	AI502278	2.34	2.46	2.34	2.32	2.33	2.31	1.04	down	2.32E-01	8.95E-01	-	-
1385698_at	Cars	cysteinyl-tRNA synthetase	293638	Rn.14865	AI603068	2.49	2.46	2.71	2.48	2.56	2.44	1.04	down	5.19E-01	8.95E-01	-	-
1398948_at	Tax1bp1	Tax1 (human T-cell leukemia virus type I) binding protein 1	246244	Rn.3474	AI228250	8.51	8.41	8.57	8.42	8.37	8.87	1.04	up	7.36E-01	9.15E-01	-	-
1374301_at	Cog1	component of oligomeric golgi complex 1	303652	Rn.163170	BI294695	6.05	5.94	4.30	5.13	4.80	6.18	1.04	down	9.36E-01	9.82E-01	-	-
1383972_at	---	---	---	---	AW524136	2.54	2.50	2.51	2.74	2.50	2.50	1.04	up	5.01E-01	8.95E-01	-	-
1375430_at	Mmgt2	membrane magnesium transporter 2	303211	Rn.23970	BM389077	2.65	2.63	2.44	2.63	2.64	2.63	1.04	up	4.36E-01	8.95E-01	-	-
1393978_at	Slfa2l3	stefin A2-like 3	498087	Rn.140652	BF415134	2.75	2.68	2.87	2.71	2.84	2.56	1.04	down	5.75E-01	8.95E-01	-	-
1397637_at	---	---	---	Rn.166907	BE121375	3.04	3.34	3.34	2.92	3.33	3.65	1.04	up	8.12E-01	9.39E-01	-	-
1375830_at	---	---	---	---	AW522779	2.37	2.36	2.58	2.40	2.38	2.36	1.04	down	4.57E-01	8.95E-01	-	-
1393226_at	---	---	---	Rn.7774	BI275559	9.80	9.16	9.62	9.55	9.43	9.77	1.04	up	7.96E-01	9.34E-01	-	-
1371899_at	Prkra	protein kinase, interferon inducible double stranded RNA dependent activator	311130	Rn.3217	AI102009	9.07	8.91	8.44	8.91	8.68	9.01	1.04	up	7.92E-01	9.33E-01	-	-
1373546_at	Atp11a	ATPase, class VI, type 11A	306900	Rn.98540	AI409922	10.52	11.16	10.89	10.67	10.62	11.10	1.04	down	8.15E-01	9.40E-01	-	-
1389253_at	Vnn1	vanin 1	29142	Rn.16319	BI289085	5.23	5.43	5.80	5.43	5.26	5.94	1.04	up	8.32E-01	9.47E-01	-	-
1373671_at	LOC681884	similar to CG14483-PA	681884	---	AA944790	5.29	6.03	6.71	5.68	5.67	6.86	1.04	up	9.22E-01	9.77E-01	-	-
1383127_at	---	---	---	Rn.3637	BI295823	6.91	7.59	7.63	6.94	7.23	7.79	1.04	down	8.70E-01	9.60E-01	-	-
1379210_at	Cd68	Cd68 molecule	287435	Rn.12478	AI177761	2.36	2.35	2.31	2.36	2.36	2.48	1.04	up	2.47E-01	8.95E-01	-	-
1397450_at	---	---	---	Rn.148194	BF388728	2.68	2.43	2.48	2.42	2.58	2.40	1.04	down	5.68E-01	8.95E-01	-	-
1370121_at	Add1	adducin 1 (alpha)	24170	Rn.5788	NM_016990	5.78	5.95	4.91	6.48	5.67	4.66	1.04	up	9.28E-01	9.79E-01	-	-
1384732_at	---	---	---	---	AI177301	2.38	2.59	2.38	2.38	2.38	2.77	1.04	up	7.07E-01	9.08E-01	-	-
1395816_at	Fam13c1	family with sequence similarity 13, member C1	294565	Rn.207181	BF393889	2.38	3.11	3.20	2.61	2.69	3.21	1.04	down	8.62E-01	9.57E-01	-	-
1388673_at	Lsp1	lymphocyte-specific protein 1	361680	Rn.101608	AI012109	2.59	2.71	2.62	2.93	2.61	2.56	1.04	up	6.43E-01	8.95E-01	-	-
1392347_at	---	---	---	---	AW527765	2.65	2.75	2.66	2.66	2.69	2.55	1.04	down	3.31E-01	8.95E-01	-	-
1383715_at	Tmem38b	transmembrane protein 38B	362521	Rn.22285	BI284371	6.15	6.60	6.48	5.96	5.92	7.17	1.04	down	8.97E-01	9.68E-01	-	-
1390482_at	---	---	---	Rn.203365	BF285511	2.60	2.55	2.73	2.56	2.63	2.51	1.04	down	4.19E-01	8.95E-01	-	-
1376841_at	Map7d1	MAP7 domain containing 1	681287	Rn.39212	AW253217	2.40	2.39	2.41	2.39	2.61	2.38	1.04	up	4.59E-01	8.95E-01	-	-
1376074_at	Rab11fip4	RAB11 family interacting protein 4 (class II)	303337	Rn.7938	AA942690	2.70	2.71	2.86	3.03	2.72	2.69	1.04	up	6.44E-01	8.95E-01	-	-
1393939_at	---	---	---	Rn.166813	AI137989	3.04	3.03	3.26	2.92	3.21	3.37	1.04	up	7.13E-01	9.10E-01	-	-
1380904_at	---	---	---	Rn.212011	BI300461	2.59	2.52	2.61	2.72	2.62	2.56	1.04	up	3.25E-01	8.95E-01	-	-
1397703_at	RGD1562351	similar to chromosome 7 open reading frame 23	499990	Rn.209094	BF288942	2.59	2.67	2.58	2.57	2.90	2.55	1.04	up	6.38E-01	8.95E-01	-	-
1379967_at	Zfp367	zinc finger protein 367	306695	Rn.35247	AI501039	3.28	3.67	3.02	3.64	3.26	3.25	1.04	up	8.08E-01	9.38E-01	-	-
1395106_at	---	---	---	Rn.171051	BG381322	2.50	2.76	2.51	2.49	2.51	2.58	1.04	down	5.38E-01	8.95E-01	-	-
1367619_at	Pgrmc1	progesterone receptor membrane component 1	291948	Rn.102356	NM_021768	10.04	10.29	10.23	9.71	10.08	10.58	1.04	down	8.31E-01	9.47E-01	-	-
1384190_at	Mapkbp3	mitogen-activated protein kinase 8 interacting protein 3	302983	Rn.16158	BF553848	2.48	2.49	2.55	2.77	2.49	2.43	1.04	up	4.12E-01	8.95E-01	-	-
1373107_at	Alg1	asparagine-linked glycosylation 1, beta-1,4-mannosyltransferase homolog (S.	360475	Rn.8024	BF283792	3.71	3.88	4.25	3.56	3.68	4.42	1.04	down	8.60E-01	9.56E-01	-	-
1375647_at	---	---	---	Rn.164616	BG671943	3.49	4.77	4.48	3.73	4.29	4.91	1.04	up	9.14E-01	9.74E-01	-	-
1375752_at	Bves	Blood vessel epicardial substance	365603	Rn.41396	AI577874	2.44	2.63	2.42	2.49	2.42	2.42	1.04	down	4.37E-01	8.95E-01	-	-
1391875_at	---	---	---	---	AI176106	2.77	2.74	2.76	2.75	2.84	2.85	1.04	up	1.32E-01	8.95E-01	-	-
1393088_at	Rg9mtd1	RNA (guanine-9-) methyltransferase domain containing 1	304012	Rn.13590	BF554013	5.37	5.35	5.38	5.16	5.38	5.38	1.04	down	4.66E-01	8.95E-01	-	-
1379740_at	LOC361346	Similar to chromosome 18 open reading frame 54	361346	Rn.31250	AW521797	2.60	2.58	2.66	2.61	2.82	2.59	1.04	up	4.77E-01	8.95E-01	-	-
1379633_at	Uba7	ubiquitin-like modifier activating enzyme 7	301000	Rn.98275	BE096453	3.04	3.06	3.08	3.25	3.07	3.03	1.04	up	4.34E-01	8.95E-01	-	-
1392120_at	---	---	---	Rn.160913	AW526194	2.70	2.50	2.53	2.51	2.55	2.48	1.04	down	4.19E-01	8.95E-01	-	-
1376228_at	---	---	---	Rn.43445	BF419434	2.49	2.47	2.48	2.47	2.67	2.48	1.04	up	4.01E-01	8.95E-01	-	-
1373991_at	---	---	---	Rn.204426	AI411386	8.34	8.76	8.91	8.89	8.41	8.90	1.04	up	8.14E-01	9.40E-01	-	-
1369231_at	---	---	---	---	NM_017292	2.47	2.47	2.51	2.69	2.48	2.46	1.04	up	4.70E-01	8.95E-01	-	-
1375206_at	Wscd1	WSC domain containing 1	287466	Rn.198297	BI275257	3.00	2.58	2.97	2.65	3.37	2.35	1.04	down	8.67E-01	9.58E-01	-	-
1376217_at	---	---	---	Rn.207071	BI296680	2.86	2.45	2.43	2.42	2.43	2.71	1.04	down	7.48E-01	9.18E-01	-	-
1372362_at	Galk2	galactokinase 2	296117	Rn.2937	BE329241	7.95	8.20	8.55	7.72	8.46	8.34	1.04	down	8.47E-01	9.52E-01	-	-
1373249_at	Ubl4	ubiquitin-like 4	293864	Rn.1138	AA817861	5.59	5.27	5.21	5.43	5.24	5.58	1.04	up	7.19E-01	9.11E-01	-	-
1395905_at	---	---	---	Rn.209057	AW920293	2.45	2.45	2.46	2.66	2.47	2.42	1.04	up	4.62E-01	8.95E-01	-	-
1389029_at	Brd3	Bromodomain containing 3	362092	Rn.16796	BE108923	4.56	3.95	3.67	3.65	3.66	4.69	1.04	down	8.98E-01	9.68E-01	-	-
1370449_at	P2ry14	purinergic receptor P2Y, G-protein coupled, 14	171108	Rn.87082	U76206	2.49	2.29	2.31	2.30	2.32	2.29	1.04	down	4.11E-01	8.95E-01	-	-
1376142_at	Cnnm1	Cyclin M1	309387	Rn.87733	BE120410	2.49	2.49	2.50	2.70	2.47	2.48	1.04	up	4.72E-01	8.95E-01	-	-
1398348_at	---	---	---	Rn.111929	AA945604	11.82	11.72	11.75	11.84	11.58	11.69	1.04	down	5.60E-01	8.95E-01	-	-
1375311_at	---	---	---	Rn.22113	AI575170	2.51	2.30	2.33	2.33	2.33	2.30	1.04	down	4.36E-01	8.95E-01	-	-
1399096_at	Add3	adducin 3 (gamma)	25230	Rn.76589	AA894279	7.60	7.75	7.35	7.85	7.00	7.67	1.04	down	8.45E-01	9.52E-01	-	-
1393175_at	RGD1562094	similar to RIKEN cDNA 2810426N06	499137	Rn.145541	BF523675	6.16	6.10	6.27	5.98	6.22	6.15	1.04	down	5.35E-01	8.95E-01	-	-
1383227_at	LOC688311	similar to ADP-ribosylation factor-like 1	688311	---	BI288882	4.15	2.97	3.05	2.62	3.99	3.38	1.04	down	9.19E-01	9.76E-01	-	-
1367600_at	Des	desmin	64362	Rn.39196	NM_022531	2.45	2.44	2.46	2.62	2.47	2.44	1.04	up	3.52

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1386140_at	---	---	---	---	AI235950	5.61	5.03	5.50	6.95	4.83	4.54	1.04	up	9.44E-01	9.84E-01	-	-
1386042_at	---	---	---	Rn.48405	AW534967	2.66	2.64	2.77	2.28	3.38	2.58	1.04	up	8.69E-01	9.59E-01	-	-
1372122_at	Tsg101	tumor susceptibility gene 101	292925	Rn.7410	AI234654	7.20	7.35	6.50	7.05	6.62	7.20	1.04	down	8.62E-01	9.57E-01	-	-
1377076_at	Siae	sialic acid acetylesterase	363045	Rn.21775	AI716131	4.30	4.29	4.05	4.02	4.42	4.37	1.04	up	7.15E-01	9.10E-01	-	-
1397876_at	---	---	---	Rn.148047	AI549089	2.50	2.32	2.33	2.33	2.32	2.32	1.04	down	3.74E-01	8.95E-01	-	-
1368296_at	Slco2b1	solute carrier organic anion transporter family, member 2b1	140860	Rn.44538	AF169410	2.35	2.52	2.35	2.35	2.36	2.34	1.04	down	3.62E-01	8.95E-01	-	-
1394863_at	---	---	---	Rn.205511	AI547767	2.65	2.62	2.73	2.61	2.68	2.53	1.04	down	3.54E-01	8.95E-01	-	-
1376022_at	Adar	Adenosine deaminase, RNA-specific	81635	Rn.10056	BI292196	2.72	2.74	2.77	2.72	2.90	2.78	1.04	up	3.56E-01	8.95E-01	-	-
1373371_a_at	Fmc1	formation of mitochondrial complexes 1 homolog (S. cerevisiae)	500087	Rn.65180	AA892572	7.41	7.10	6.87	7.44	7.02	7.09	1.04	up	7.90E-01	9.33E-01	-	-
1374690_at	Gle1	GLE1 RNA export mediator homolog (yeast)	362098	Rn.162648	AI599770	7.83	7.30	5.79	6.95	6.44	7.35	1.04	down	9.35E-01	9.82E-01	-	-
1384733_at	Lgi3	leucine-rich repeat LGI family, member 3	306013	Rn.50862	BE106044	2.54	2.64	2.56	2.53	2.54	2.50	1.04	down	1.68E-01	8.95E-01	-	-
1381556_at	Ddx60	DEAD (Asp-Glu-Ala-Asp) box polypeptide 60	306409	Rn.144123	BI303853	2.71	2.59	2.87	2.66	2.80	2.53	1.04	down	6.38E-01	8.95E-01	-	-
1375724_at	RGD1563612	similar to testhymin	500026	Rn.204577	BE108162	2.61	3.01	2.62	2.67	2.68	2.72	1.04	down	6.87E-01	9.04E-01	-	-
1398103_at	---	---	---	---	AI409359	3.16	3.15	3.16	3.15	3.34	3.15	1.04	up	4.02E-01	8.95E-01	-	-
1373719_at	Map4k3	mitogen-activated protein kinase kinase kinase kinase 3	170920	Rn.93345	AA819812	5.73	5.32	5.00	5.32	5.20	5.36	1.04	down	8.02E-01	9.36E-01	-	-
1375857_at	Myof	myoferlin	309499	Rn.73651	AW917760	5.88	5.84	5.91	5.83	6.33	5.64	1.04	up	7.95E-01	9.34E-01	-	-
1391545_at	Ccdc52	colled-coil domain containing 52	288111	Rn.138747	AI409150	2.50	2.84	2.36	2.33	2.49	2.70	1.04	down	7.63E-01	9.22E-01	-	-
1382738_at	---	---	---	---	BF282918	2.43	2.25	2.26	2.26	2.26	2.25	1.04	down	3.74E-01	8.95E-01	-	-
1391860_at	---	---	---	Rn.166113	AI599816	2.58	2.58	2.62	2.77	2.60	2.58	1.04	up	3.92E-01	8.95E-01	-	-
1368782_at	Sstr2	somatostatin receptor 2	54305	Rn.9929	NM_019348	2.37	2.35	2.39	2.36	2.56	2.36	1.04	up	4.42E-01	8.95E-01	-	-
1380795_at	---	---	---	Rn.71580	BM383849	2.49	2.34	2.35	2.34	2.34	2.32	1.04	down	3.04E-01	8.95E-01	-	-
1392446_at	---	---	---	---	AI145435	6.93	7.02	6.65	6.68	6.89	7.20	1.04	up	7.74E-01	9.26E-01	-	-
1382606_at	---	---	---	Rn.209050	BF285438	2.77	2.59	2.61	2.60	2.60	2.59	1.04	down	3.60E-01	8.95E-01	-	-
1381066_at	---	---	---	---	BF403440	2.82	2.79	2.80	2.79	2.80	2.64	1.04	down	3.46E-01	8.95E-01	-	-
1391339_at	---	---	---	Rn.212404	BI304052	2.66	2.66	2.73	2.65	2.71	2.53	1.04	down	3.84E-01	8.95E-01	-	-
1394607_at	Rab11fip2	RAB11 family interacting protein 2 (class I)	308003	Rn.64225	AW523203	2.54	2.53	2.54	2.53	2.54	2.71	1.04	up	3.77E-01	8.95E-01	-	-
1379953_at	Ptpc7	PTC7 protein phosphatase homolog (S. cerevisiae)	304488	Rn.7549	AI712697	4.18	3.34	3.91	3.60	4.15	3.85	1.04	up	8.54E-01	9.55E-01	-	-
1394668_at	Cadm3	cell adhesion molecule 3	360882	Rn.138884	BF409960	2.54	2.37	2.38	2.37	2.38	2.36	1.04	down	3.55E-01	8.95E-01	-	-
1396533_at	---	---	---	Rn.156338	BF405339	2.44	2.45	2.60	2.44	2.45	2.43	1.04	down	3.32E-01	8.95E-01	-	-
1386563_at	Rab39	RAB39, member RAS oncogene family	315668	Rn.156562	AA817920	2.55	2.52	2.67	2.53	2.54	2.49	1.04	down	2.87E-01	8.95E-01	-	-
1391852_at	---	---	---	Rn.20433	BF549454	2.55	2.48	2.55	2.66	2.55	2.54	1.04	up	2.79E-01	8.95E-01	-	-
1390949_at	---	---	---	Rn.87365	BE117624	2.56	2.53	2.56	2.54	2.56	2.72	1.04	up	3.61E-01	8.95E-01	-	-
1392327_s_at	---	---	---	Rn.18294	AW535025	2.49	2.34	2.38	2.34	2.35	2.34	1.04	down	2.63E-01	8.95E-01	-	-
1367589_at	Aco2	aconitase 2, mitochondrial	79250	Rn.43737	NM_024398	9.00	9.26	8.99	9.31	8.80	9.30	1.04	up	7.76E-01	9.27E-01	-	-
1381207_at	---	---	---	Rn.208836	BE120425	2.40	2.54	2.41	2.39	2.41	2.38	1.04	down	2.74E-01	8.95E-01	-	-
1371608_at	Mrps34	mitochondrial ribosomal protein S34	287126	Rn.11777	BI275958	6.11	7.08	6.79	6.73	6.58	6.85	1.04	up	8.56E-01	9.55E-01	-	-
1379924_at	Ptpnm2	phosphatidylinositol transfer protein, membrane-associated 2	304474	Rn.75968	AI178193	2.43	2.42	2.45	2.42	2.45	2.62	1.04	up	4.06E-01	8.95E-01	-	-
1388856_at	Kitlg	KIT ligand	60427	Rn.44216	BG374178	2.51	2.81	2.52	2.61	2.56	2.49	1.04	down	6.10E-01	8.95E-01	-	-
1380416_at	---	---	---	Rn.44991	BF284504	6.94	7.22	8.05	6.50	7.63	7.91	1.04	down	9.21E-01	9.77E-01	-	-
1379799_at	---	---	---	Rn.47821	BF415056	2.27	2.38	2.27	2.27	2.27	2.55	1.04	up	5.98E-01	8.95E-01	-	-
1396055_at	Col6a3	procollagen, type VI, alpha 3	367313	Rn.219672	AW530165	3.68	2.79	2.41	3.07	3.00	2.98	1.04	up	8.86E-01	9.65E-01	-	-
1396804_at	---	---	---	Rn.82552	BM386455	3.07	3.34	2.91	3.88	2.60	2.66	1.04	down	9.01E-01	9.69E-01	-	-
1372618_at	RGD1307615	similar to hypothetical protein FLJ13045	362084	Rn.17709	AI407147	4.30	4.62	3.80	4.23	3.68	4.64	1.04	down	8.83E-01	9.64E-01	-	-
1374818_at	Nxph3	neurexophilin 3	59315	Rn.19736	BM382837	2.45	2.45	2.47	2.62	2.47	2.46	1.04	up	3.54E-01	8.95E-01	-	-
1368518_at	Cd53	CD53 molecule	24251	Rn.31988	NM_012523	2.45	2.45	2.46	2.64	2.46	2.44	1.04	up	4.16E-01	8.95E-01	-	-
1370212_at	Homer3	homer homolog 3 (Drosophila)	29548	Rn.144573	AW253366	2.39	2.37	2.40	2.40	2.55	2.38	1.04	up	3.54E-01	8.95E-01	-	-
1368038_at	Syn2bp	synaptojanin 2 binding protein	64531	Rn.6258	BF284821	6.40	7.02	7.35	6.58	6.75	7.28	1.04	down	8.78E-01	9.62E-01	-	-
1367466_at	Ptpfib	PTPRB pre-mRNA processing factor 8 homolog (S. cerevisiae)	287530	Rn.10642	AI406518	7.15	6.24	4.86	6.19	5.65	6.25	1.04	down	9.38E-01	9.82E-01	-	-
1381931_at	Ablim1	actin-binding LIM protein 1	307989	Rn.40404	AI229552	2.41	3.14	4.65	3.61	3.39	3.37	1.04	up	9.35E-01	9.82E-01	-	-
1373589_at	Mtmr3	myotubularin related protein 3	305482	Rn.8338	BM385209	7.48	7.86	6.94	7.31	7.36	7.44	1.04	down	8.42E-01	9.51E-01	-	-
1396906_at	---	---	---	Rn.208838	BF393816	2.53	2.51	2.54	2.52	2.72	2.50	1.04	up	4.65E-01	8.95E-01	-	-
1397778_at	---	---	---	Rn.205275	AI535458	2.65	2.58	2.77	2.61	2.68	2.54	1.04	down	4.53E-01	8.95E-01	-	-
1370834_at	Hs3st1	heparan sulfate (glucosamine) 3-O-sulfotransferase 1	84406	Rn.17364	AF177430	2.33	2.31	2.33	2.35	2.48	2.31	1.04	up	3.10E-01	8.95E-01	-	-
1396892_at	---	---	---	---	AI548369	2.41	2.41	2.43	2.41	2.61	2.40	1.04	up	4.41E-01	8.95E-01	-	-
1389259_at	---	---	---	Rn.14852	AA894084	2.36	2.35	2.36	2.35	2.36	2.53	1.04	up	3.79E-01	8.95E-01	-	-
1386975_at	Pdk2	pyruvate dehydrogenase kinase, isozyme 2	81530	Rn.88597	AF237719	5.71	5.25	4.96	5.12	5.60	5.03	1.04	down	8.49E-01	9.53E-01	-	-
1396304_at	---	---	---	Rn.170114	AW535090	2.49	2.51	2.52	2.52	2.55	2.61	1.04	up	9.93E-02	8.95E-01	-	-
1397851_at	---	---	---	Rn.207514	BE102226	2.90	2.88	3.07	2.89	2.92	2.87	1.04	down	3.92E-01	8.95E-01	-	-
1370108_a_at	Lin7a	lin-7 homolog a (C. elegans)	85327	Rn.31766	AF090134	2.52	2.69	2.52	2.51	2.52	2.52	1.04	down	3.75E-01	8.95E-01	-	-
1371087_a_at	Map6	microtubule-associated protein 6	29457	Rn.37490	AJ002556	2.60	2.60	2.61	2.83	2.62	2.53	1.04	up	5.52E-01	8.95E-01	-	-
1369448_at	B3galt1	beta-1,3-glucuronyltransferase 1 (glucuronosyltransferase P)	117108	Rn.88274	NM_054003	2.83	2.99	2.84	2.83	2.83	2.82	1.04	down	3.21E-01	8.95E-01	-	-
1382211_at	---	---	---	Rn.107412	AI602542	7.59	8.14	8.12	8.18	8.09	8.40	1.04	down	9.07E-01	9.71E-01	-	-
1380459_at	Btbd14a	BTB (POZ) domain containing 14A	296583	Rn.27698	AI555023	7.94	7.25	8.42	7.55	8.29	7.60	1.04	down	8.97E-01	9.68E-01	-	-
1375108_at	ND3	NADH dehydrogenase subunit 3	26199	---	AI008105	12.72	12.45	12.55	12.46	12.59	12.50	1.04	down	5.51E-01	8.95E-01	-	-
1384635_at	---	---	---	Rn.98687	AA999112	2.53	2.68	2.52	2.53	2.52	2.51	1.04	down	3.42E-01	8.95E-01	-	-
1395173_at	Caprin1	cell cycle associated protein 1	362173	Rn.22572	BF396243	8.94	9.39	9.19	8.93	9.46	9.30	1.04	up	7.92E-01	9.33E-01	-	-
1388658_at	Surf2	surfeit 2	619345	Rn.162644	AA942704	5.74	5.71	5.64	5.76	5.71	5.79	1.04	up	2.22E-01	8.95E-01	-	-
1397124_at	---	---	---	Rn.147857	BE119960	2.28	2.27	2.29	2.28	2.47	2.27	1.04	up	4.29E-01	8.95E-01	-	-
1393474_at	Sult2b1	sulfotransferase family, cytosolic, 2B, member 1	292915	Rn.100005	BF285952	2.34	2.46	2.40	2.35	2.33	2.33	1.04	down	1.60E-01	8.95E-01	-	-
1397170_at	---	---	---	Rn.27435	AI137477	2.36	2.35	2.50	2.35	2.35	2.34	1.04	down	3.22E-01	8.95E-01	-	-
1371139_at	Pls3	plastin 3 (T-isoform)	81748	Rn.32103	X70706	2.56	2.48	2.57	2.61	2.71	2.45	1.04	up	5.13E-01	8.95E-01	-	-
1380956_at	LOC367597	Similar to nidogen 2	367597	Rn.162369	BG672418	2.59	2.65	2.60	2.55	2.65	2.47	1.04	down	3.51E-01	8.95E-01	-	-
1393368_at	Osbpl5	oxysterol binding protein-like 5	361686	Rn.140527	BG372522	8.70	8.23	7.87	7.71	9.74	7.52	1.04	up	9.43E-01	9.84E-01	-	-
1372629_at	Coro2b	coronin, actin binding protein, 2B	300768	Rn.8477	BF285818	2.54	2.47	2.57	2.47	2.47	2.46	1.04	down	1.49E-01	8.95E-01	-	-
1379651_at	Foxp1	Forkhead box P1	297480	Rn.33321	BE109884	4.77	4.65	4.39	4.65	4.54	4.80	1.04	up	6.98E-01	9.07E-01	-	-
1370814_at	Dhrs4	dehydrogenase/reductase (SDR family) member 4	266686	Rn.12783	AB062758	9.19	9.71	9.24	9.25	9.12	9.60	1.04	down	8.07E-01	9.38E-01	-	-
1379264_at	Znrf1	zinc and ring finger 1	362367	Rn.32245	BE109004	8.96	9.46	8.62	8.68	8.84	9.34	1.04	down	8.65E-01	9.58E-01	-	-
1397828_at	Sphkap	SPHK1 interactor, AKAP domain containing	316561	Rn.15453	BF387796	2.47	2.46	2.61	2.46	2.48	2.43	1.04	down	3.21E-01	8.95E-01	-	-
1380914_at	---	---	---	Rn.204846	AI175405	2.99	3.19	2.99	2.80	3.29	3.25	1.04	up	7.54E-01	9.20E-01	-	-
1393432_a_at	Dhx36	DEAH (Asp-Glu-Ala-His) box polypeptide 36	310461	Rn.2744	AA899840	2.88	2.81	3.51	2.63	3.45	2.95	1.04	down	8.70E-01	9.60E-01	-	-
1371201_at	Sstr1	somatostatin receptor 1	25033	Rn.42915	L02915	2.50	2.34	2.34	2.34	2.34	2.33	1.04	down	3.37E-01	8.95E-01	-	-
1382951_at	---	---	---	---	AA957549	2.35	2.35	2.36	2.46	2.44	2.34	1.04	up	2.04E-01	8.95E-01	-	-
1375058_at	Zrsr2	zinc finger (CCCH type), RNA binding motif and serine/arginine rich 2	302670	Rn.26786	BF396164	6.89	7.01	6.53	7.09	7.04	6.46	1.04	up	8.30E-01	9.46E-01	-	-
1370118_at	Ccl17	chemokine (C-C motif) ligand 17	117518	Rn.46679	NM_057151	2.46	2.44	2.46	2.50	2.58	2.44	1.04	up	2.57E-01	8.95E-01	-	-
1371105_at	---	---	---	---	BF564277	3.12	3.10	3.09	3.11	3.12	3.25	1.04	up	2.95E-01	8.95E-01	-	-
1370964_at	Asl1	argininosuccinate synthetase 1	25698	Rn.5078	BF283456	8.76	8.64	8.49	8.65	9.23	8.18	1.04	up	8.64E-01	9.58E-01	-	-
1393154_at	---	---	---	Rn.20196	BM384240	4.65	4.96	4.78	4.62	4.86	5.08	1.04	up	7.40E-01	9.16E-01	-	-
1394569_at	---	---	---	Rn.168787	AI549154	2.41	2.36	2.41	2.40	2.42	2.53	1.04	up	2.65E-01	8.95E-01	-	-
1394482_at	---	---	---	---	AI070736	2.66	2.58	2.77	2.62	2.68	2.54	1.04	down	4.72E-01	8.95E-01	-	-
1392268_at	---	---	---	Rn.152484	AI535076	2.45	2.47	2.48	2.47	2.48	2.63	1.04	up	3.45E-01	8.95E-01	-	-
1391979_at	---	---	---	Rn.6731	AA851345	2.54	2.64	2.69	2.65	2.68	2.73	1.04	up	3.23E-01	8.95E-01	-	-
1377496_at	Cpsf7	cleavage and polyadenylation specific factor 7, 59kDa	365407	Rn.98627	BM391768	4.77	3.60	3.45	4.73	4.07	3.19	1.04	up	9.30E-01	9.81E-01	-	-
1368468_at	Cyp11a1	cytochrome P450, family 11, subfamily a, polypeptide 1	29680	Rn.1401	NM_017286	2.59	2.58	2.55	2.63	2.34	2.58	1.04	down	5.68E-01	8.95E-01	-	-
1373111_at	Capn7	calpain 7	306260	Rn.104104	AI169441	8.85	8.89	9.02	8.57	8.98	9.38	1.04	up	8.25E-01	9.45E-01	-	-
1383976_at	---	---	---	Rn.196108	AW527549	2.39	2.58	3.04	2.39	2.52	2.94	1.04	down	8.36E-01	9.48E-01	-	-
1394227_at	Dnm1l	dynamin 1-like	114114	Rn.216851	AI237251	2.47	2.64	2.47	2.47	2.47	2.47	1.04	down	3.78E-01	8.95E-01	-	-
1387956_s_at	Cklf	chemokine-like factor	245978	Rn.81197	AF253064	2.56	2.58	2.58	2.70	2.57	2.62	1.04	up	2.17E-01	8.95E-01	-	-
1392973_at	---	---	---	Rn.61136	AI073173	7.49	7.87	7.72	7.86	7.52	7.53	1.04	down	7.35E-01	9.15E-01	-	-
1381785_at	---	---	---	Rn.134205	BE099306	2.52	2.51	2.53	2.52	2.70	2.51	1.04	up	4.14E-01	8.95E-01	-	-
1393678_at	RGD1308297	similar to CG10084-PA	306137	Rn.28431	BI275975	4.17	5.10	3.79	5.00	3.95	4.28	1.04	up	9.15E-01	9.75E-01	-	-
1373364_at	Eif4g3	eukaryotic translation initiation factor 4 gamma, 3	298573	Rn.71377	BI294767	7.02	6.98	6.66	7.55	6.10	7.18	1.04	up	9.06E-01	9.71E-01	-	-
1395141_at	---	---	---	Rn.176390	BG376748	2.36	2.34	2.36	2.36	2.53	2.35	1.04	up	3.97E-01	8.95E-01	-	-
1386141_at	Zcwpw1	zinc finger, CW-type with PWWP domain 1	304368	Rn.101750	AI176516	2.49	2.41	2.50	2.48	2.61	2.48	1.04	up	3.35E-01	8.95E-01	-	-
1372835_at	Rhoj	ras homolog gene family, member J	299145	Rn.6890	BM389644	2.55	2.36	2.39	2.38	2.38	2.36	1.04	down	4.10E-01	8.95E-01	-	-
1390050_at	680692 /// LOC68	similar to Golgi phosphoprotein 2 (Golgi membrane protein GP73) /// similar to680692 /// 682869		Rn.203162	BI288898	7.21	6.66	6.99	7.11	6.71	7.21	1.04	up	8.11E-01	9.39E-01	-	-
1369427_at	Mpeg1	macrophage expressed gene 1	64552	Rn.162497	NM_022617	2.75	3.00	2.79	2.77	2.78	2.81	1.04	down	5.09E-01	8.95E-01	-	-
1375304_at	Abhd8	Abhydrolase domain containing 8	306338	Rn.22147	AA998659	2.46	2.32	2.31	2.31	2.31	2.31	1.04	down	3.11E-01	8.95E-01	-	-
1380245_at	---	---	---	Rn.43641	AI411847	4.49	5.55	4.80	5.00	4.91	5.09	1.04	up	8.68E-01	9.59E-01	-	-
1375011_at	---	---	---	Rn.16544	AA818819	6.25	6.30	5.94	5.46	6.42	6.78	1.04	up	8.97E-01	9.68E-01	-	-
1383452_at	---	---	---	Rn.166066	BG670461	6.65	6.58	6.99	6.65	6.66	6.74	1.04	down	6.87E-01	9.04E-01	-	-
1369909_s_at	Tmem150	transmembrane protein 150	245966	Rn.144670	NM_139107	7.10	6.82	6.53	7.65	6.28	6.35	1.04	down	9.11E-01	9.73E-01	-	-
1376280_at	RGD1307284	similar to protein kinase, lysine deficient 1; kinase deficient protein	306811	Rn.204068	AA799789	2.50	2.47	2.66	2.49	2.52	2.46	1.04	down	4.04E-01	8.95E-01	-	-
1381913_at	---	---	---	---	BE113907	2.41	2.25	2.25	2.25	2.24	2.24	1.04	down	3.53E-01	8.95E-01	-	-
1395903_at	---	---	---	Rn.206485	BF565954	2.68	2.65	2.82	2.68	2.74	2.56	1.04	down	4.95E-01	8.95E-01	-	-
1381299_at	---	---	---	---	AI454141	2.69	2.65	2.79	2.66	2.75	2.54	1.04	down	4.95E-01	8.95E-01	-	-
1396777_at	Psmb6	proteasome (prosome, macropain) subunit, beta type 6	29666	Rn.8118	NM_057099	9.19	8.84	9.33	8.85	8.98	9.37	1.04	down	8.06E-01	9.38E-01	-	-
1390839_at	Pqlc3	PQ loop repeat containing 3	298606	Rn.12743	AW915795	2.37	2.51	2.47	2.37	2.41	2.40	1.04	down	2.72E-01	8.95E-01	-	-
1367958_at	Abi1	abl-interactor 1	79249	Rn.43675	NM_024397	6.71	6.78	5.79	5.98	6.91	6.56	1.04	up	8.99E-01	9.69E-01	-	-
1374698_at	LOC687508	similar to Cytochrome c oxidase polypeptide VIIa-heart, mitochondrial precurs	687508	---	AI709531	2.41	2.39	2.91	2.72	2.42	2.40	1.04	down	7.91E-01	9.33E-01	-	-
1386843_at	Cd5l	Cd5 molecule-like	310693	Rn.43804	BF551446	2.86	2.77	3.04	2.81	3.03	2.66	1.04	down	6.97E-01	9.07E-01	-	-
1394942_at	---	---	---	Rn.43421	AI408528	2.51	2.59	2.53	2.49	2.52	2.45	1.04	down	1.47E-01	8.95E-01	-	-
1368787_at	Mutyh	mutY homolog (E. coli)	170841	Rn.44045	NM_133316	2.27	2.26	2.27	2.40	2.31	2.26	1.04	up	2.39E-01	8.95E-01	-	-
1381975_at	---	---	---	Rn.146145	BG371767	2.37	2.36	2.37	2.36	2.37	2.53	1.04	up	3.72E-01	8.95E-01	-	-
1374821_at	---	---	---	Rn.202661	BF399587	2.51	2.70	3.01	2.71	2.52	3.16	1.04	up	8.25E-01	9.45E-01	-	-
1388501_at	MGC125239	hypothetical protein LOC686179	686179	Rn.200952	AW916335	4.69	4.40	3.49	4.51	4.14	4.11	1.04	up	8.90E-01	9.66E-01	-	-
1395337_at	Tjp1	tight junction protein 1	292994	Rn.101871	AW141192	3.40	4.81	4.98	4.37	4.70	4.29	1.04	up	9.18E-01	9.76E-01	-	-
1395468_at	---	---	---	Rn.41186	BF406952	2.40	2.39	2.41	2.58	2.40	2.38	1.04	up	4.21E-01	8.95E-01	-	-
1394343_s_at	Kcne2	Potassium voltage-gated channel, Isk-related subfamily, gene 2	171138	Rn.48691	AW920063	2.42	2.40	2.58	2.41	2.43	2.39	1.04	down	3.82E-01	8.95E-01	-	-
1375473_at	---	---	---	Rn.168250	BI296644	2.52	2.31	2.33	2.32	2.33	2.34	1.04	down	4.40E-01	8.95E-01	-	-
1391685_at	Pnldc1	poly(A)-specific ribonuclease (PARN)-like domain containing 1	361478	Rn.186599	AW521201	2.33	2.34	2.33	2.33	2.52	2.32	1.04	up	4.33E-01	8.95E-01	-	-
1380688_at	Galnti4	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltrar	293181	Rn.212131	BI283107	2.49	2.34	2.36	2.34	2.35	2.33	1.04	down	3.14E-01	8.95E-01	-	-
1385972_at	Kbtbd3	kelch repeat and BTB (POZ) domain containing 3	315394	Rn.98988	AA800770	2.59	2.53	2.82	2.60	2.65	2.53	1.04	down	5.89E-01	8.95E-01	-	-
1374720_at	Exog	endo/exonuclease (5'-3'), endonuclease G-like	301062	Rn.7100	BE109644	2.48	2.65	2.49	2.48	2.48	2.83	1.04	up	6.80E-01	9.03E-01	-	-
1380653_at	Rage	renal tumor antigen	362787	Rn.63172	AI317878	2.98	3.07	3.02	2.97	2.97	2.96	1.04	down	1.11E-01	8.95E-01	-	-
1378474_at	---	---	---	Rn.52203	BF400707	2.73	2.62	2.64	2.60	2.63	2.59	1.04	down	2.16E-01	8.95E-01	-	-
1379191_x_at	---	---	---	Rn.211326	BF410445	2.91	2.78	2.91	2.87	3.14	2.76	1.04	up	6.66E-01	8.99E-01	-	-
1369297_at	Ppp2r2c	protein phosphatase 2 (formerly 2A), regulatory subunit B, gamma isoform	117256	Rn.54550	NM_057116	2.45	2.44	2.58	2.44	2.45	2.42	1.04	down	2.76E-01	8.95E-01	-	-
1396741_at	---	---	---	---	BI291220	2.39	2.39	2.37	2.54	2.39	2.38	1.04	up	3.27E-01	8.95E-01	-	-
1392719_at	Mthfs	5,10-methenyltetrahydrofolate synthetase (5-formyltetrahydrofolate cyclo-ligas	300886	Rn.2215	AA957588	7.88	7.67	7.72	7.62	7.63	7.86	1.04	down	6.07E-01	8.95E-01	-	-
1369758_at	Gpam	glycerol-3-phosphate acyltransferase, mitochondrial	29653	Rn.44456	U36771	2.48	2.61	2.49	2.50	2.46	2.46	1.04	down	2.79E-01	8.95E-01	-	-
1368383_at	Npff	neuropeptide FF-amide peptide precursor	60337	Rn.48705	NM_022586	2.85	2.95	2.94	2.83	2.92	2.82	1.04	down	2.84E-01	8.95E-01	-	-
1385352_at	Slc16a13	Solute carrier family 16, member 13 (monocarboxylic acid transporter 13)	287451	Rn.23260	AW535234	5.20	5.42	4.64	5.45	5.22	4.77	1.04	up	8.64E-01	9.58E-01	-	-
1392

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1382838_at	---	---	---	---	AA799942	3.04	3.02	3.04	3.03	2.91	3.00	1.04	down	1.83E-01	8.95E-01	-	-
1381426_at	---	---	---	---	AI556220	2.51	2.40	2.43	2.41	2.39	2.37	1.04	down	1.92E-01	8.95E-01	-	-
1384746_at	---	---	---	Rn.95544	AA875130	2.54	2.53	2.76	2.54	2.60	2.53	1.04	down	5.13E-01	8.95E-01	-	-
1367908_at	Gcsh	glycine cleavage system protein H (aminomethyl carrier)	171133	Rn.98456	NM_133598	10.35	10.38	10.45	10.33	10.36	10.33	1.04	down	1.57E-01	8.95E-01	-	-
1394482_at	---	---	---	---	AI232686	2.27	2.26	2.28	2.27	2.45	2.26	1.04	up	4.32E-01	8.95E-01	-	-
1370174_at	Ppp1r15a	protein phosphatase 1, regulatory (inhibitor) subunit 15A	171071	Rn.2232	BI284349	2.35	2.34	2.63	2.35	2.35	2.45	1.04	down	6.07E-01	8.95E-01	-	-
1385148_at	P2rx1	purinergic receptor P2X, ligand-gated ion channel, 1	25505	Rn.91178	BM391148	2.56	2.36	2.40	2.38	2.41	2.36	1.04	down	4.30E-01	8.95E-01	-	-
1374639_at	Smg6	Smg-6 homolog, nonsense mediated mRNA decay factor (C. elegans)	287522	Rn.1945	AA800800	3.27	3.26	3.27	2.98	3.51	3.14	1.04	down	7.44E-01	9.17E-01	-	-
1373522_at	---	---	---	Rn.20312	BM385074	2.61	2.60	2.62	2.60	2.62	2.44	1.04	down	3.96E-01	8.95E-01	-	-
1371979_at	RGD1564117	similar to novel protein similar to multidomain presynaptic cytomatrix protein p	317253	Rn.74024	BF413722	2.28	2.40	2.36	2.18	2.36	2.33	1.04	down	4.51E-01	8.95E-01	-	-
1382731_at	---	---	---	Rn.9073	AA818685	2.39	2.53	2.40	2.38	2.40	2.37	1.04	down	2.90E-01	8.95E-01	-	-
1397604_at	LOC681825	similar to Prefoldin subunit 3 (Von Hippel-Lindau-binding protein 1) (VHL-bind	681825	---	BE128641	3.56	4.10	4.15	4.19	3.26	4.52	1.04	up	9.02E-01	9.70E-01	-	-
1371025_at	Masp2	mannan-binding lectin serine peptidase 2	64459	Rn.45144	Y18566	2.48	2.65	2.50	2.49	2.50	2.48	1.04	down	3.76E-01	8.95E-01	-	-
1390532_at	---	---	---	---	AI013778	2.50	2.75	2.53	2.46	2.54	2.61	1.04	down	5.70E-01	8.95E-01	-	-
1390149_at	Tacc2	transforming, acidic coiled-coil containing protein 2	309025	Rn.13989	BI286164	6.82	6.57	6.66	6.65	6.89	6.68	1.04	up	6.30E-01	8.95E-01	-	-
1396896_at	Fst4	follistatin-like 4	303130	Rn.206178	AW524895	2.33	2.32	2.46	2.30	2.33	2.32	1.04	down	3.16E-01	8.95E-01	-	-
1375699_at	---	---	---	Rn.170061	BM389190	3.09	2.62	2.59	2.62	2.69	2.83	1.04	down	7.69E-01	9.24E-01	-	-
1370524_at	Ube2d2	Ubiquitin-conjugating enzyme E2D 2	641452	Rn.7390	AW142720	6.97	6.95	6.52	6.59	6.47	7.22	1.04	down	8.52E-01	9.54E-01	-	-
1370589_at	Zfp709	zinc finger protein 709	266773	Rn.123575	AF277903	2.45	2.43	2.44	2.40	2.44	2.64	1.04	up	5.06E-01	8.95E-01	-	-
1384327_at	Def8	differentially expressed in FDCP 8 homolog (mouse)	307973	Rn.199084	BI291728	10.30	10.31	10.30	10.31	10.26	10.51	1.04	up	5.08E-01	8.95E-01	-	-
1381838_at	---	---	---	Rn.17625	AI548287	6.91	6.95	7.24	6.96	7.08	7.22	1.04	up	6.90E-01	9.05E-01	-	-
1395494_at	---	---	---	---	BF412343	2.58	2.51	2.72	2.56	2.59	2.50	1.04	down	4.48E-01	8.95E-01	-	-
1395331_at	RGD1306508	similar to hypothetical protein CL25084	289874	Rn.102123	BF548263	4.97	6.25	6.74	6.26	5.46	6.08	1.04	down	9.29E-01	9.80E-01	-	-
1367876_at	Ipo13	Importin 13	116458	Rn.14252	NM_053778	3.72	3.73	3.72	3.71	3.91	3.71	1.04	up	4.56E-01	8.95E-01	-	-
1393587_a_at	RGD1309605	similar to RIKEN cDNA 2310047O13	291320	Rn.106046	AI578061	9.90	10.13	9.92	10.10	9.92	10.09	1.04	up	5.91E-01	8.95E-01	-	-
1388030_a_at	Gabbr1	gamma-aminobutyric acid (GABA) B receptor 1	81657	Rn.30059	AF312319	2.32	2.32	2.32	2.32	2.49	2.32	1.04	up	3.98E-01	8.95E-01	-	-
1378459_at	---	---	---	Rn.170845	BE113008	2.43	2.58	2.51	2.45	2.47	2.44	1.04	down	2.79E-01	8.95E-01	-	-
1382965_at	---	---	---	Rn.12347	AA996630	2.32	2.32	2.34	2.32	2.34	2.49	1.04	up	3.63E-01	8.95E-01	-	-
1393662_at	---	---	---	---	BF396974	2.88	3.10	2.92	2.95	2.91	2.86	1.04	down	5.02E-01	8.95E-01	-	-
1394675_at	---	---	---	---	AI178470	2.67	2.79	2.69	2.65	2.68	2.66	1.04	down	2.36E-01	8.95E-01	-	-
1373466_at	Cast	calpastatin	25403	Rn.17481	AA846474	4.68	4.99	4.73	4.22	4.68	5.66	1.04	up	9.06E-01	9.71E-01	-	-
1384595_at	---	---	---	Rn.199241	AI030888	2.78	2.65	2.79	2.66	2.75	2.65	1.04	down	3.82E-01	8.95E-01	-	-
1396538_at	Crtc3	CREB regulated transcription coactivator 3	365297	Rn.153601	BF403765	2.26	2.26	2.27	2.26	2.28	2.42	1.04	up	3.33E-01	8.95E-01	-	-
1374993_at	Rpusd1	RNA pseudouridylate synthase domain containing 1	287148	Rn.98412	BF406627	2.42	2.43	2.53	2.49	2.42	2.42	1.04	up	1.66E-01	8.95E-01	-	-
1398925_at	Fbjd2	FtsJ methyltransferase domain containing 2	309656	Rn.17113	BI274664	3.50	3.78	3.86	3.41	3.69	3.88	1.04	down	7.67E-01	9.24E-01	-	-
1372804_at	RGD1359460	MMR_HSR1 domain containing protein RGD1359460	289562	Rn.13090	AI175555	4.86	5.28	4.31	5.05	4.38	5.18	1.04	up	8.90E-01	9.66E-01	-	-
1397427_at	Ces3	Carboxylesterase 3	113902	Rn.2549	BI302102	2.41	2.40	2.62	2.41	2.46	2.39	1.04	down	5.00E-01	8.95E-01	-	-
1396771_at	---	---	---	Rn.147314	BE107504	2.46	2.44	2.49	2.45	2.69	2.42	1.04	up	5.61E-01	8.95E-01	-	-
1388019_at	Odf2	outer dense fiber of sperm tails 2	29479	Rn.91211	AF162756	2.49	2.48	2.53	2.48	2.71	2.47	1.04	up	5.37E-01	8.95E-01	-	-
1373198_at	Dnajc22	DnaJ (Hsp40) homolog, subfamily C, member 22	362998	Rn.19564	BF283018	7.81	7.39	6.43	7.27	6.91	7.29	1.04	down	9.04E-01	9.71E-01	-	-
1396155_at	---	---	---	---	BF283527	2.58	2.57	2.71	2.58	2.62	2.51	1.04	down	3.68E-01	8.95E-01	-	-
1395514_at	Scyl3	SCY1-like 3 (S. cerevisiae)	360866	Rn.15991	BI281277	2.29	2.28	2.30	2.46	2.29	2.28	1.04	up	3.91E-01	8.95E-01	-	-
1382238_at	Ccar1	cell division cycle and apoptosis regulator 1	361849	Rn.92786	AW534965	7.80	9.00	7.74	8.05	8.07	8.59	1.04	up	9.08E-01	9.72E-01	-	-
1377005_at	Cul4b	Cullin 4B	302502	Rn.21178	BM390962	4.67	4.04	3.53	3.58	3.83	5.00	1.04	up	9.25E-01	9.78E-01	-	-
1387605_at	Casp12	caspase 12	116117	Rn.81078	NM_130422	2.40	2.34	2.36	2.35	2.36	2.56	1.04	up	4.89E-01	8.95E-01	-	-
1383151_at	Akap9	A kinase (PRKA) anchor protein (yotiao) 9	246150	Rn.202416	AI011474	5.32	5.63	5.27	4.83	5.69	5.54	1.04	down	8.58E-01	9.56E-01	-	-
1390739_at	Znf609	zinc finger protein 609	363412	Rn.161077	BE118828	5.32	5.37	5.47	5.61	5.18	5.20	1.04	down	7.28E-01	9.13E-01	-	-
1385897_at	---	---	---	---	AI575697	2.50	2.49	2.50	2.67	2.50	2.49	1.04	up	4.04E-01	8.95E-01	-	-
1387912_at	Ddx46	DEAD (Asp-Glu-Ala-Asp) box polypeptide 46	245957	Rn.3436	U25746	6.53	6.96	6.86	6.68	6.12	7.39	1.04	down	8.95E-01	9.67E-01	-	-
1370156_at	Prnp	prion protein	24686	Rn.3936	BI278802	2.90	2.89	2.90	2.91	2.56	3.06	1.04	down	7.31E-01	9.14E-01	-	-
1390510_at	Mx4a6b	membrane-spanning 4-domains, subfamily A, member 6B	293749	Rn.17885	BI294706	2.42	2.42	2.45	2.45	2.52	2.50	1.04	up	7.87E-02	8.95E-01	-	-
1375275_at	LOC680122	Similar to sin3 associated polypeptide	680122	Rn.4148	AA850745	2.88	2.87	2.88	2.88	3.04	2.87	1.04	up	3.81E-01	8.95E-01	-	-
1384910_at	Lrtm2	leucine-rich repeats and transmembrane domains 2	680883	Rn.34565	AI454016	2.42	2.40	2.55	2.40	2.43	2.38	1.04	down	3.28E-01	8.95E-01	-	-
1375009_at	Nudt14	nudix (nucleoside diphosphate linked moiety X)-type motif 14	299346	Rn.19641	AW254363	7.51	7.41	7.42	7.42	7.35	7.41	1.04	down	2.35E-01	8.95E-01	-	-
1383395_at	Agmat	agmatine ureohydrolase (agmatinase)	298607	Rn.7880	AI028979	10.92	10.76	10.66	10.78	10.62	10.77	1.04	down	5.88E-01	8.95E-01	-	-
1370605_s_at	Lepr	leptin receptor	24536	Rn.9891	U53144	2.54	2.52	2.68	2.52	2.55	2.51	1.04	down	3.41E-01	8.95E-01	-	-
1396393_at	---	---	---	Rn.169550	AW526669	2.71	2.64	2.85	2.67	2.81	2.56	1.04	down	5.95E-01	8.95E-01	-	-
1383670_at	Zfp426	zinc finger protein 426	690895	Rn.204091	BM385134	2.97	3.04	3.04	2.98	3.05	3.19	1.04	up	4.41E-01	8.95E-01	-	-
1377547_at	---	---	---	---	BF419375	2.63	2.58	2.78	2.60	2.65	2.58	1.04	down	4.46E-01	8.95E-01	-	-
1371403_at	Cct3	chaperonin containing Tcp1, subunit 3 (gamma)	295230	Rn.203147	AA799545	10.33	10.27	10.11	10.14	10.18	10.23	1.04	down	4.94E-01	8.95E-01	-	-
1374882_at	RGD1306063	similar to HT021	289928	Rn.16932	AW433860	5.43	5.44	5.28	5.74	5.10	5.15	1.04	down	8.08E-01	9.38E-01	-	-
1393370_at	Dclk2	doublecortin-like kinase 2	310998	Rn.23327	BG380685	2.16	2.53	2.17	2.17	2.34	2.19	1.04	down	6.98E-01	9.07E-01	-	-
1395431_at	---	---	---	Rn.204245	AI112336	2.51	2.44	2.55	2.45	2.46	2.43	1.04	down	1.90E-01	8.95E-01	-	-
1381237_at	---	---	---	Rn.48348	AW534521	5.50	5.24	5.82	5.19	5.83	5.70	1.04	up	8.42E-01	9.51E-01	-	-
1397877_at	Rictor	RPTOR independent companion of MTOR, complex 2	310131	Rn.61013	AI237209	3.32	3.33	3.54	3.34	3.33	3.35	1.04	down	4.77E-01	8.95E-01	-	-
1382069_at	Atp11a	ATPase, class VI, type 11A	306600	Rn.98540	AA946031	9.14	9.82	9.62	9.28	9.46	9.68	1.04	down	8.28E-01	9.46E-01	-	-
1390381_at	Xpc	xeroderma pigmentosum, complementation group C	312560	Rn.22820	BG379358	4.12	4.13	5.13	4.43	4.43	4.68	1.04	up	8.82E-01	9.64E-01	-	-
1380732_at	RGD1560886	similar to sidekick 1	304297	---	BE107085	2.42	2.57	2.43	2.42	2.43	2.41	1.04	down	3.21E-01	8.95E-01	-	-
1379674_at	Ctnbp2l	cortactin-binding factor, runt domain, alpha subunit 2, translocated to, 3 (human)	361431	Rn.128745	BE115481	3.61	2.88	2.75	2.88	2.83	3.70	1.04	up	8.95E-01	9.67E-01	-	-
1377626_at	LOC686634	hypothetical protein LOC686634	686634	---	AA924350	2.38	2.37	2.54	2.38	2.38	2.37	1.04	down	3.83E-01	8.95E-01	-	-
1383841_at	LOC683932	similar to PWWP domain containing 2	683932	---	BF396378	2.99	3.04	3.60	3.00	4.09	2.70	1.04	up	9.13E-01	9.74E-01	-	-
1389252_at	---	---	---	Rn.92325	AI102190	7.92	8.42	8.11	7.77	8.21	8.31	1.04	down	8.17E-01	9.42E-01	-	-
1388734_at	---	---	---	Rn.11542	AA894193	8.78	8.58	9.00	9.00	8.52	8.67	1.04	down	7.85E-01	9.30E-01	-	-
1378009_at	---	---	---	Rn.4116	BF282481	6.98	6.72	7.28	6.70	6.90	7.21	1.04	down	8.17E-01	9.41E-01	-	-
1376563_at	---	---	---	---	BG375165	2.71	2.63	2.87	2.67	2.81	2.57	1.04	down	6.13E-01	8.95E-01	-	-
1396530_at	---	---	---	Rn.143988	BE120509	2.60	2.54	2.57	2.51	2.56	2.47	1.04	down	1.49E-01	8.95E-01	-	-
1379431_at	---	---	---	Rn.8749	AW918368	8.42	8.49	8.60	8.31	8.44	8.61	1.04	down	6.24E-01	8.95E-01	-	-
1374421_at	Baz1b	bromodomain adjacent to zinc finger domain, 1B	368002	Rn.7043	AA850752	7.04	7.65	8.37	7.83	7.66	7.72	1.04	up	8.95E-01	9.67E-01	-	-
1375087_at	---	---	---	Rn.216950	BF398862	2.97	2.81	3.27	2.96	3.15	2.77	1.04	down	7.71E-01	9.25E-01	-	-
1368268_at	Tdg	thymine-DNA glycosylase	114521	Rn.98685	NM_053729	2.79	2.95	2.92	2.91	2.92	3.00	1.04	up	3.84E-01	8.95E-01	-	-
1376492_at	RGD1565247	similar to chromosome 16 open reading frame 28	302987	Rn.129828	AI548527	4.92	5.41	5.93	5.88	5.30	5.24	1.04	up	8.87E-01	9.65E-01	-	-
1388252_at	LOC685283	hypothetical protein LOC685283	685283	Rn.198532	M17960	2.53	2.50	2.53	2.50	2.78	2.44	1.04	up	6.42E-01	8.95E-01	-	-
1379849_at	Thoc3	THO complex 3	290519	Rn.101956	BE098416	5.87	5.97	6.30	5.98	6.42	5.90	1.04	up	8.08E-01	9.38E-01	-	-
1390945_at	Znf292	zinc finger protein 292	50552	Rn.106753	BI294878	2.58	3.42	2.61	3.08	2.73	2.95	1.04	up	8.63E-01	9.57E-01	-	-
1370139_a_at	Trpc6	transient receptor potential cation channel, subfamily C, member 6	89823	Rn.105986	AB051214	2.47	2.44	2.51	2.46	2.69	2.43	1.04	up	5.57E-01	8.95E-01	-	-
1395998_at	Nol5a	nucleolar protein 5A	362214	Rn.145204	BE114011	2.83	2.94	2.95	2.94	3.00	2.95	1.04	up	2.69E-01	8.95E-01	-	-
1391839_at	---	---	---	Rn.9217	AA891521	2.81	2.74	2.97	2.76	2.94	2.98	1.04	up	6.03E-01	8.95E-01	-	-
1378444_at	---	---	---	Rn.28903	AI175473	2.49	2.32	2.64	2.46	2.73	2.43	1.04	up	7.05E-01	9.08E-01	-	-
1392273_at	Letm2	leucine zipper-EF-hand containing transmembrane protein 2	361169	Rn.203805	BF402258	2.47	2.45	2.64	2.46	2.49	2.45	1.04	down	4.11E-01	8.95E-01	-	-
1379351_at	Ccdc90a	coiled-coil domain containing 90A	291034	Rn.162214	BM390871	5.44	5.23	5.26	6.22	4.82	5.06	1.04	up	9.08E-01	9.72E-01	-	-
1380889_at	---	---	---	---	AI009209	2.51	2.36	2.37	2.36	2.37	2.35	1.04	down	3.29E-01	8.95E-01	-	-
1375767_at	Plekhg3	pleckstrin homology domain containing, family G (with RhoGef domain) member	314249	Rn.19912	BI287681	4.99	5.86	6.24	5.62	5.35	5.96	1.04	down	9.02E-01	9.70E-01	-	-
1371617_at	Psmd13	proteasome (prosome, macropain) 26S subunit, non-ATPase, 13	365388	Rn.16918	AI599711	7.60	8.12	7.84	7.90	7.62	7.88	1.04	down	7.73E-01	9.28E-01	-	-
1389076_at	Pkn3	protein kinase N3	296619	Rn.202664	BF282185	2.92	2.81	2.82	2.81	2.81	2.77	1.04	down	2.31E-01	8.95E-01	-	-
1396999_at	---	---	---	Rn.59648	BF400843	2.48	2.34	2.37	2.34	2.36	2.33	1.04	down	2.81E-01	8.95E-01	-	-
1380449_at	---	---	---	Rn.199343	AI112513	4.62	4.56	3.90	4.65	4.36	4.23	1.04	up	8.45E-01	9.52E-01	-	-
1398296_at	Gde1	glycerophosphodiester phosphodiesterase 1	60418	Rn.170542	NM_032615	9.21	8.97	8.60	9.36	8.66	8.92	1.04	up	8.51E-01	9.54E-01	-	-
1373721_at	Hars2l	histidyl-tRNA synthetase 2-like	307491	Rn.139312	BI291360	3.82	3.16	4.10	3.73	3.25	4.27	1.04	up	9.00E-01	9.69E-01	-	-
1384903_at	Gpt2	glutamic pyruvate transaminase (alanine aminotransferase) 2	307759	Rn.205208	AI535168	2.29	2.28	2.46	2.29	2.30	2.28	1.04	down	4.01E-01	8.95E-01	-	-
1369290_at	Ccr5	chemokine (C-C motif) receptor 5	117029	Rn.10736	NM_053960	2.35	2.35	2.36	2.35	2.36	2.52	1.04	up	3.90E-01	8.95E-01	-	-
1376279_at	Pop1	processing of precursor 1, ribonuclease P/MRP subunit (S. cerevisiae)	315045	Rn.22746	BM389467	6.33	6.70	6.48	6.37	6.49	6.81	1.04	up	7.66E-01	9.24E-01	-	-
1387796_at	Alox15	arachidonate 15-lipoxygenase	81639	Rn.11318	NM_031010	2.50	2.36	2.38	2.36	2.36	2.36	1.04	down	3.06E-01	8.95E-01	-	-
1376012_at	RGD1564419	similar to hypothetical gene supported by BC025338	500128	Rn.2617	BI295108	3.66	2.84	2.56	3.18	2.89	2.84	1.04	down	8.84E-01	9.64E-01	-	-
1398195_at	---	---	---	Rn.147516	BF397286	2.60	2.45	2.47	2.46	2.47	2.43	1.04	down	3.21E-01	8.95E-01	-	-
1372292_at	Stk24	Serine/threonine kinase 24 (STE20 homolog, yeast)	361092	Rn.105397	AI009732	7.15	7.46	7.24	7.30	6.83	7.56	1.04	down	8.28E-01	9.46E-01	-	-
1367609_at	Mf1	macrophage migration inhibitory factor	81683	Rn.2661	NM_031051	8.75	8.99	8.42	8.75	8.42	8.83	1.04	down	8.07E-01	9.38E-01	-	-
1389334_at	dufa10 /// Ndufa10	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 10 /// NADH dehydr	316632 /// 678759	Rn.102304	BI277594	10.02	9.79	9.26	9.37	9.91	9.62	1.04	down	8.54E-01	9.55E-01	-	-
1382077_at	---	---	---	Rn.12004	BF388974	2.37	2.35	2.36	2.51	2.37	2.35	1.04	up	3.48E-01	8.95E-01	-	-
1389034_at	Usp18	ubiquitin specific peptidase 18	312688	Rn.161758	BI295179	3.31	2.83	2.85	3.53	2.88	2.75	1.04	up	8.61E-01	9.57E-01	-	-
1384651_at	---	---	---	Rn.34305	AI385295	2.48	2.45	2.62	2.46	2.48	2.44	1.04	down	3.73E-01	8.95E-01	-	-
1394519_at	---	---	---	Rn.156189	AI170569	3.07	3.27	3.10	3.10	3.10	3.09	1.04	down	4.34E-01	8.95E-01	-	-
1386263_at	Nedd4	neural precursor cell expressed, developmentally down-regulated gene 4	25489	Rn.99540	AI227677	4.59	4.66	4.20	4.48	4.64	4.17	1.04	down	7.98E-01	9.35E-01	-	-
1379006_at	LOC691396	similar to Zinc finger protein 551 (Zinc finger protein KOX23)	691396	Rn.38959	AI711098	3.03	3.01	2.96	3.08	3.06	3.03	1.04	up	9.20E-02	8.95E-01	-	-
1382181_at	Pion	pigeon homolog (Drosophila)	311984	Rn.17968	AI555069	3.99	4.22	3.10	3.71	3.42	4.03	1.04	down	8.95E-01	9.67E-01	-	-
1379726_at	Pbx4	pre-B-cell leukemia homeobox 4	361131	Rn.89526	AI412925	2.58	2.57	2.65	2.61	2.59	2.45	1.04	down	3.94E-01	8.95E-01	-	-
1371372_at	Ptges3	prostaglandin E synthase 3 (cytosolic)	362809	Rn.2344	AA944161	8.49	8.71	8.86	8.39	8.54	8.96	1.04	down	8.02E-01	9.36E-01	-	-
1380905_at	---	---	---	Rn.203182	AA893260	9.92	9.16	9.87	9.71	9.69	9.14	1.04	up	8.37E-01	9.49E-01	-	-
1374404_at	Jun	Jun oncogene	24516	Rn.93714	BI288619	9.06	9.81	9.85	9.13	9.67	9.76	1.04	down	8.76E-01	9.61E-01	-	-
1396138_at	---	---	---	Rn.202699	BF544511	2.65	2.51	2.52	2.52	2.53	2.48	1.04	down	2.98E-01	8.95E-01	-	-
1372875_at	---	---	---	Rn.8905	AI408520	2.92	4.04	3.04	2.91	3.54	3.38	1.04	down	9.00E-01	9.69E-01	-	-
1392619_at	---	---	---	---	BE118107	2.60	2.60	2.61	2.77	2.61	2.60	1.04	up	3.98E-01	8.95E-01	-	-
1397948_s_at	RGD1564942	RGD1564942	298409	Rn.92043	BF392047	2.28	3.32	2.32	2.32	2.29	3.17	1.04	down	9.10E-01	9.73E-01	-	-
1396198_at	RGD1310799	Similar to RIKEN cDNA A930008G19	309060	Rn.12282	BF282909	2.69	2.65	2.82	2.67	2.67	2.65	1.04	down	3.63E-01	8.95E-01	-	-
1376523_at	Arid4a	AT rich interactive domain 4A (Rbp1 like)	314205	Rn.106963	BF391127	3.02	3.38	2.65	2.57	2.72	3.60	1.04	down	8.96E-01	9.67E-01	-	-
1395316_at	Mageh1	melanoma antigen, family H, 1	367767	Rn.56595	H32543	7.75	7.57	7.64	6.94	8.01	7.86	1.04	down	8.82E-01	9.64E-01	-	-
1391825_at	---	---	---	Rn.199907	BE120422	2.49	2.67	2.54	2.52	2.50	2.52	1.04	down	3.75E-01	8.95E-01	-	-
1388868_at	Zfand5	zinc finger, AN1-type domain 5	293960	Rn.4050	AI172425	7.41	7.06	7.48	7.75	7.06	7.30	1.04	up	8.36E-01	9.48E-01	-	-
1379003_at	---	---	---	---	BE113169	2.52	2.51	2.67	2.51	2.53	2.50	1.04	down	3.69E-01	8.95E-01	-	-
1397086_at	Gipc3	GIPC PDZ domain containing family, member 3	500789	Rn.141023	BI295629	2.46	2.46	2.75	2.47	2.92	2.45	1.04	up	7.83E-01	9.30E-01	-	-
1389618_at	---	---	---	Rn.161322	AW529588	2.42	2.57	2.57	2.41	2.42	2.40	1.04	down	3.63E-01	8.95E-01	-	-
1368066_at	Bak1	BCL2-antagonist/killer 1	116502	Rn.14598	NM_053812	2.35	2.41	2.39	2.36	2.53	2.42	1.04	up	3.65E-01	8.95E-01	-	-
1386648_at	Dnajc6	DnaJ (Hsp40) homolog, subfamily C, member 6	313409	Rn.23812	AW914996	3.51	3.89	4.58	3.85	4.16	3.82	1.04	down	8.80E-01	9.63E-01	-	-
1397996_at	---	---	---	Rn.199965	BF387766	2.72	2.59	2.67	2.67	2.64	2.51	1.04	down	4.29E-01	8.95E-01	-	-
1374068_at	Cdc26	cell division cycle 2-like 6 (CDK8-like)	309804	Rn.6873	BG376309	4.42	5.90	5.83	5.39	4.44	6.15	1.04	down	9.42E-01	9.84E-01	-	-
1396021_at	Zfp68	Zinc finger protein 68	304337	Rn.144939	AA999128	2.99	2.95	2.99	2.96	2.98	2.83	1.04	down	3.38E-01	8.95E-01	-	-
1394869_at	---	---	---	Rn.146659	BE104854	3.30	3.28	3.33	3.09	3.60	3.38	1.04	up	7.33E-01	9.15E-01	-	-
1395715_at	Cdgap	Cdc42 GTPase-activating protein	288093	Rn.167354	BI288113	3.07	2.68	2.57	2.68	2.80	2.67	1.04	down	7.52E-01	9.20E-01	-	-
1372189_at	Dnajc13	DnaJ (Hsp40) homolog, subfamily C, member 13	363127	Rn.36397	AI411144	7.91	7.99	7.89	8.05	7.62	8.28	1.04	up	7.97E-01	9.35E-01	-	-
1369960_at	Fxyd1	FXYD domain-containing ion transport regulator 1	58971	Rn.3828	NM_031648	2.45	2.29	2.30	2.28	2.33	2.27	1.04	down	3.94E-01	8.95E-01	-	-
1385639_at	Casp8ap2	caspase 8 associated protein 2	313128	Rn.198715	AI058950	3.38	3.51	3.38	3.38	3.38	3.35	1.04	down	2.86E-01	8.95E-01	-	-
1385488_at	Dhrs4	dehydrogenase/reductase (SDR family) member 4	286986	Rn.12783	B

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1379055_x_at	---	---	---	---	BF410240	3.65	3.15	3.76	3.93	3.31	3.17	1.04	down	8.68E-01	9.59E-01	-	-
1390271_at	Plekha6	pleckstrin homology domain containing, family A member 6	360842	Rn.21422	BM392202	3.74	4.15	2.94	4.86	3.00	2.82	1.04	down	9.47E-01	9.85E-01	-	-
1373157_at	Usp47	ubiquitin specific peptidase 47	308896	Rn.101536	AI407830	7.26	8.28	6.24	7.28	6.85	7.81	1.04	up	9.39E-01	9.83E-01	-	-
1370422_at	Ripk3	receptor-interacting serine-threonine kinase 3	246240	Rn.7110	AF036537	2.36	2.35	2.37	2.36	2.36	2.51	1.04	up	3.64E-01	8.95E-01	-	-
1379394_at	---	---	---	Rn.44015	BF289573	2.56	2.57	2.49	2.46	2.48	2.51	1.04	down	1.60E-01	8.95E-01	-	-
1396684_at	Pnpla7	patatin-like phospholipase domain containing 7	246246	Rn.162643	BE120966	2.52	2.51	2.52	2.71	2.54	2.47	1.04	up	5.02E-01	8.95E-01	-	-
1391185_at	---	---	---	Rn.208907	BG377123	2.64	2.43	2.46	2.44	2.51	2.43	1.04	down	4.96E-01	8.95E-01	-	-
1391838_at	Ankrd11	ankyrin repeat domain 11	365023	Rn.23844	BE106639	5.60	5.60	5.43	5.82	5.97	5.00	1.04	up	8.71E-01	9.60E-01	-	-
1386986_at	Oplr	opioid growth factor receptor	83525	Rn.15740	NM_053340	2.77	2.77	2.79	2.77	2.78	2.94	1.04	up	4.03E-01	8.95E-01	-	-
1398353_at	Sar1a	SAR1 homolog A (S. cerevisiae)	361942	Rn.15780	AI236260	8.68	8.40	7.87	8.47	7.81	8.82	1.04	up	8.96E-01	9.67E-01	-	-
1375609_at	Setbp1	SET binding protein 1	291423	Rn.52458	AI137781	2.78	2.77	2.94	2.76	2.94	2.63	1.04	down	6.48E-01	8.96E-01	-	-
1385396_at	---	---	---	Rn.148913	AI044315	2.61	2.61	2.71	2.61	2.62	2.53	1.04	down	2.81E-01	8.95E-01	-	-
1371273_at	Cd247	Cd247 molecule	25300	Rn.9997	J13556	2.74	2.73	2.75	2.74	2.92	2.72	1.04	up	4.62E-01	8.95E-01	-	-
1376953_at	Unc5cl	unc-5 homolog C (C. elegans)-like	301225	Rn.218694	BM389244	6.08	6.27	5.40	6.08	5.76	6.07	1.04	up	8.62E-01	9.57E-01	-	-
1385537_at	---	---	---	Rn.157376	AI412800	2.54	2.62	2.55	2.47	2.56	2.52	1.04	down	2.24E-01	8.95E-01	-	-
1388604_at	Casq1	calsequestrin 1 (fast-twitch, skeletal muscle)	686019	Rn.159963	BI276959	3.51	6.35	4.36	5.13	4.08	5.16	1.04	up	9.57E-01	9.88E-01	-	-
1392094_at	---	---	---	Rn.148966	AW528613	2.49	2.61	2.50	2.49	2.49	2.45	1.04	down	2.57E-01	8.95E-01	-	-
1389486_at	---	---	---	Rn.166955	BE108354	2.48	2.34	2.35	2.34	2.35	2.32	1.04	down	3.08E-01	8.95E-01	-	-
1371682_at	Map1lc3a	microtubule-associated protein 1 light chain 3 alpha	362245	Rn.3135	AI177372	6.35	6.63	6.41	6.31	6.58	6.34	1.04	down	6.87E-01	9.04E-01	-	-
1391192_at	---	---	---	Rn.209145	BF414558	2.54	2.49	2.55	2.54	2.68	2.53	1.04	up	3.69E-01	8.95E-01	-	-
1385554_at	---	---	---	Rn.216768	AI548264	2.40	2.53	2.41	2.39	2.40	2.38	1.04	down	2.95E-01	8.95E-01	-	-
1377322_at	---	---	---	Rn.52812	BE117290	2.38	2.40	2.39	2.38	2.38	2.56	1.04	up	4.18E-01	8.95E-01	-	-
1394683_at	---	---	---	Rn.66798	AW434725	2.51	2.46	2.51	2.48	2.71	2.45	1.04	up	5.63E-01	8.95E-01	-	-
1385028_at	---	---	---	Rn.150572	BE107383	2.45	2.52	2.46	2.43	2.44	2.41	1.04	down	1.05E-01	8.95E-01	-	-
1398754_at	Uba52	ubiquitin A-52 residue ribosomal protein fusion product 1	64156	Rn.110618	NM_031687	11.85	11.61	11.31	11.49	11.27	11.85	1.04	down	8.32E-01	9.47E-01	-	-
1390979_at	LOC499124	mouse zinc finger protein 14-like	499124	Rn.187181	AI409884	2.55	2.57	2.48	2.47	2.48	2.48	1.04	down	1.19E-01	8.95E-01	-	-
1372476_at	Fads3	fatty acid desaturase 3	286922	Rn.35282	AW553321	4.13	3.32	3.50	4.00	3.51	3.59	1.04	up	8.64E-01	9.58E-01	-	-
1397013_at	---	---	---	Rn.209153	BF409867	3.64	2.77	2.75	2.78	3.51	2.72	1.04	down	8.99E-01	9.68E-01	-	-
1386949_a_at	Mta1	metastasis associated 1	64520	Rn.5840	AJ132046	2.69	2.91	2.69	2.74	2.71	2.69	1.04	down	5.23E-01	8.95E-01	-	-
1383465_at	Fbxl14	F-box and leucine-rich repeat protein 14	312675	Rn.18972	AI058747	5.29	6.24	5.58	5.88	5.51	5.88	1.04	up	8.73E-01	9.61E-01	-	-
1382297_x_at	Prr12	proline rich 12	361569	Rn.17162	AI555789	5.02	4.71	3.91	5.34	3.67	4.79	1.04	up	9.34E-01	9.81E-01	-	-
1390835_at	Slc47a1	solute carrier family 47, member 1	360539	Rn.17240	AI013568	11.15	11.37	11.50	11.02	11.30	11.55	1.04	down	7.91E-01	9.33E-01	-	-
1374445_at	Gpr162	G protein-coupled receptor 162	362436	Rn.222068	BM386619	2.38	2.44	2.40	2.38	2.39	2.29	1.04	down	2.15E-01	8.95E-01	-	-
1375396_at	Pum1	pumilio homolog 1 (Drosophila)	362609	Rn.44196	BI282129	7.58	7.54	7.23	7.61	7.30	7.59	1.04	up	7.41E-01	9.16E-01	-	-
1397497_at	---	---	---	Rn.149167	BF391164	2.49	2.47	2.64	2.48	2.51	2.46	1.04	down	3.98E-01	8.95E-01	-	-
1373002_at	Mrps9	mitochondrial ribosomal protein S9	301371	Rn.13913	AI009481	7.70	8.36	8.30	8.05	7.90	8.57	1.04	up	8.66E-01	9.58E-01	-	-
1375065_at	---	---	---	Rn.216894	BI291326	2.45	2.31	2.32	2.31	2.32	2.29	1.04	down	3.20E-01	8.95E-01	-	-
1373017_at	Suclg2	succinate-CoA ligase, GDP-forming, beta subunit	362404	Rn.220383	AI237518	10.41	9.99	10.25	10.19	10.18	10.45	1.04	up	7.44E-01	9.17E-01	-	-
1372897_at	Plod2	procollagen lysine, 2-oxoglutarate 5-dioxygenase 2	300901	Rn.12945	BI279641	3.09	3.08	3.56	3.42	3.09	3.07	1.04	down	8.03E-01	9.37E-01	-	-
1392661_at	---	---	---	Rn.214405	AI228227	2.76	2.59	2.63	2.64	2.63	2.55	1.04	down	4.31E-01	8.95E-01	-	-
1391386_at	Chn1	chimerin (chimaerin) 1	84030	Rn.11168	AI412693	2.50	2.48	2.63	2.49	2.50	2.46	1.04	down	3.32E-01	8.95E-01	-	-
1375947_at	---	---	---	Rn.163661	AI171856	5.26	6.32	5.67	5.89	5.46	6.06	1.04	up	8.90E-01	9.66E-01	-	-
1369571_at	Golph3	golgi phosphoprotein 3 (coat-protein)	78961	Rn.64519	NM_023977	7.90	7.93	7.52	7.38	7.49	8.32	1.04	down	8.80E-01	9.63E-01	-	-
1385687_at	Fam25a	family with sequence similarity 25, member A	684972	Rn.78551	BI285092	4.64	6.75	6.24	6.33	5.34	6.13	1.04	up	9.44E-01	9.84E-01	-	-
1385443_at	Mlx	MAX-like protein X	360631	Rn.16914	AI549299	8.56	8.04	7.81	8.27	8.28	8.01	1.04	up	8.38E-01	9.49E-01	-	-
1383795_at	---	---	---	Rn.220047	BF521753	2.85	3.06	2.86	2.84	2.85	2.91	1.04	down	5.00E-01	8.95E-01	-	-
1391706_at	---	---	---	---	AI715113	2.47	2.47	2.62	2.47	2.48	2.45	1.04	down	3.49E-01	8.95E-01	-	-
1389427_at	Mxra8	matrix-remodelling associated 8	313770	Rn.2457	AA946351	2.32	2.31	2.32	2.43	2.32	2.36	1.04	up	1.79E-01	8.95E-01	-	-
1383734_at	---	---	---	Rn.815	AA859909	3.37	3.37	3.39	3.51	3.38	3.40	1.04	up	2.79E-01	8.95E-01	-	-
1389623_at	Atf1	activating transcription factor 1	315305	Rn.105304	AA849092	7.73	7.87	7.24	7.45	7.45	8.10	1.04	up	8.67E-01	9.58E-01	-	-
1383530_at	Nrip3	nuclear receptor interacting protein 3	361625	Rn.48099	AA925994	2.43	2.43	2.44	2.58	2.45	2.43	1.04	up	3.30E-01	8.95E-01	-	-
1370997_at	Homer1	homer homolog 1 (Drosophila)	29546	Rn.37500	AF030088	2.47	2.52	2.66	2.48	2.50	2.84	1.04	up	7.10E-01	9.09E-01	-	-
1380225_at	---	---	---	Rn.27009	BF396725	2.37	2.36	2.37	2.45	2.44	2.36	1.04	up	1.60E-01	8.95E-01	-	-
1394122_at	Rhoh	ras homolog gene family, member H	305341	Rn.20618	AI012081	2.48	2.32	2.33	2.33	2.33	2.32	1.04	down	3.69E-01	8.95E-01	-	-
1389929_at	RGD1563533	Similar to novel protein	313713	Rn.91524	BE110547	2.45	2.44	2.45	2.45	2.29	2.45	1.04	down	3.83E-01	8.95E-01	-	-
1396648_at	---	---	---	Rn.210980	BF399547	2.32	2.31	2.46	2.31	2.32	2.31	1.04	down	3.40E-01	8.95E-01	-	-
1387744_at	Nppc	natriuretic peptide precursor C	114593	Rn.10637	NM_053750	2.75	2.74	2.77	2.52	2.85	2.74	1.04	down	6.15E-01	8.95E-01	-	-
1385781_at	Ercc6l	excision repair cross-complementing rodent repair deficiency complementatio	317252	---	BF397986	2.51	2.36	2.38	2.36	2.37	2.35	1.04	down	3.36E-01	8.95E-01	-	-
1390400_a_at	---	---	---	Rn.227	BM390922	2.83	2.84	3.01	2.82	3.01	2.70	1.04	down	6.51E-01	8.96E-01	-	-
1383215_at	LOC304558	similar to TPR repeat-containing protein KIAA1043	304558	Rn.137233	BF557467	2.38	2.37	2.39	2.53	2.39	2.37	1.04	up	3.72E-01	8.95E-01	-	-
1367800_at	Plat	plasminogen activator, tissue	25692	Rn.107102	AA849092	7.73	7.87	7.24	7.45	7.45	8.10	1.04	up	8.67E-01	9.58E-01	-	-
1378072_at	Atad5	ATPase family, AAA domain containing 5	303348	Rn.51222	BE115405	2.61	2.60	2.73	2.57	2.62	2.59	1.04	down	2.93E-01	8.95E-01	-	-
1396351_at	---	---	---	---	BF411876	2.51	2.36	2.38	2.37	2.37	2.35	1.04	down	3.49E-01	8.95E-01	-	-
1390616_at	---	---	---	Rn.201976	BI296731	2.27	2.27	2.28	2.44	2.27	2.26	1.04	up	4.03E-01	8.95E-01	-	-
1394689_at	---	---	---	Rn.205975	BE117217	2.84	2.95	2.81	2.74	3.19	2.83	1.04	up	7.37E-01	9.16E-01	-	-
1391999_at	---	---	---	Rn.148540	BI301720	2.56	2.41	2.44	2.73	2.43	2.40	1.04	up	6.72E-01	9.01E-01	-	-
1376455_at	Mfsd3	major facilitator superfamily domain containing 3	500899	Rn.86351	BI296172	3.13	3.13	3.13	3.29	3.13	3.12	1.04	up	3.89E-01	8.95E-01	-	-
1389380_at	Fpgs	folylpolyglutamate synthase	687266	---	AI012181	2.42	2.57	2.42	2.42	2.43	2.41	1.04	down	3.69E-01	8.95E-01	-	-
1375745_at	---	---	---	Rn.203053	BE117491	2.39	3.20	2.93	2.38	3.24	3.05	1.04	up	8.90E-01	9.66E-01	-	-
1382792_at	---	---	---	Rn.208893	BF412158	3.77	3.46	3.48	3.46	3.48	3.61	1.04	down	6.59E-01	8.98E-01	-	-
1384328_at	Tom1	target of myb1 homolog (chicken)	361370	Rn.198076	AW524820	7.10	7.04	6.40	6.19	6.96	7.23	1.04	down	8.99E-01	9.69E-01	-	-
1379892_at	Pax8	paired box 8	81819	Rn.10392	BF564165	8.04	8.10	7.11	8.51	6.79	7.80	1.04	down	9.34E-01	9.81E-01	-	-
1381014_at	Ifi44	interferon-induced protein 44	310969	Rn.43876	BI274623	2.62	2.88	2.66	2.63	2.77	2.60	1.04	down	6.11E-01	8.95E-01	-	-
1374947_at	Bcar3	breast cancer anti-estrogen resistance 3	310838	Rn.7383	BI286041	2.47	2.44	2.49	2.63	2.49	2.43	1.04	up	4.34E-01	8.95E-01	-	-
1385208_at	RGD1305014	similar to RIKEN cDNA 2310057M21	309029	Rn.162476	BF391430	2.59	2.37	2.33	2.38	2.39	2.37	1.04	down	5.64E-01	8.95E-01	-	-
1393700_at	---	---	---	Rn.3424	AA875420	2.32	2.46	2.32	2.31	2.32	2.30	1.04	down	3.25E-01	8.95E-01	-	-
1370721_a_at	Cngb1	cyclic nucleotide gated channel beta 1	83686	Rn.10733	AJ224680	3.81	3.79	3.90	3.80	4.08	3.78	1.04	up	6.41E-01	8.95E-01	-	-
1396196_at	---	---	---	Rn.153658	AI548778	2.79	2.70	2.87	2.78	2.80	2.62	1.04	down	5.17E-01	8.95E-01	-	-
1382237_at	Zfp128	zinc finger protein 128	308363	Rn.214237	AA900012	2.42	2.58	2.43	2.42	2.43	2.43	1.04	down	3.58E-01	8.95E-01	-	-
1389817_at	---	---	---	---	AW536017	2.60	2.48	2.50	2.48	2.48	2.47	1.04	down	2.43E-01	8.95E-01	-	-
1380332_at	---	---	---	Rn.206862	BF411794	2.48	2.60	2.50	2.47	2.50	2.45	1.04	down	2.76E-01	8.95E-01	-	-
1377092_at	---	---	---	Rn.153630	BF389682	2.55	2.55	2.57	2.64	2.56	2.61	1.04	up	9.76E-02	8.95E-01	-	-
1397264_at	---	---	---	Rn.32144	AA859819	2.37	2.36	2.38	2.45	2.47	2.36	1.04	up	1.88E-01	8.95E-01	-	-
1391568_at	---	---	---	---	AI228711	2.41	2.40	2.41	2.39	2.43	2.55	1.04	up	3.47E-01	8.95E-01	-	-
1391373_at	---	---	---	Rn.208173	BF391714	2.45	2.55	2.47	2.43	2.47	2.42	1.04	down	2.26E-01	8.95E-01	-	-
1398157_at	---	---	---	Rn.134745	BF404420	2.59	2.46	2.47	2.46	2.44	2.46	1.04	down	2.76E-01	8.95E-01	-	-
1386519_x_at	---	---	---	---	AI236030	2.23	2.22	2.23	2.23	2.39	2.22	1.04	up	4.05E-01	8.95E-01	-	-
1375741_at	Ccdc88b	coiled-coil domain containing 88B	361715	Rn.22455	AI227953	2.46	2.46	2.48	2.65	2.46	2.44	1.04	up	4.74E-01	8.95E-01	-	-
1377119_at	Pura	purine rich element binding protein A	307498	Rn.41055	AI704675	2.36	2.41	2.42	2.52	2.41	2.41	1.04	up	2.68E-01	8.95E-01	-	-
1377764_at	---	---	---	---	BF411531	2.29	2.28	2.29	2.28	2.45	2.27	1.04	up	4.20E-01	8.95E-01	-	-
1369825_at	Mmp2	matrix metallopeptidase 2	81686	Rn.6422	NM_031054	2.44	2.29	2.30	2.29	2.30	2.28	1.04	down	3.30E-01	8.95E-01	-	-
1384031_at	Efhc1	EF-hand domain (C-terminal) containing 1	301295	Rn.198826	AW532656	2.66	2.65	2.73	2.62	2.72	2.54	1.04	down	4.27E-01	8.95E-01	-	-
1382029_at	RGD1566149	similar to CDNA sequence BC017647	497960	Rn.19152	BE104800	4.19	3.54	3.40	4.26	3.34	3.38	1.04	down	9.00E-01	9.69E-01	-	-
1377833_at	Rif1	RAP1 interacting factor homolog (yeast)	295602	Rn.20916	BF396950	2.65	3.04	2.51	2.55	2.56	2.93	1.04	down	8.11E-01	9.39E-01	-	-
1389335_at	Wdr22	WD repeat domain 22	314273	Rn.47944	BM387479	3.28	2.91	2.82	2.94	2.97	2.95	1.04	down	7.35E-01	9.15E-01	-	-
1397711_at	---	---	---	Rn.205335	AI555694	2.74	2.66	3.18	2.81	2.81	3.13	1.04	up	8.01E-01	9.36E-01	-	-
1389199_at	RGD1309079	similar to Ab2-095	315891	Rn.15757	AI407536	6.48	5.89	5.43	5.91	6.06	5.99	1.04	up	8.74E-01	9.61E-01	-	-
1396982_at	Zscan20	zinc finger and SCAN domain containing 20	500549	Rn.205931	AI410832	2.48	2.34	2.36	2.35	2.33	2.43	1.04	down	2.94E-01	8.95E-01	-	-
1377996_at	---	---	---	Rn.104030	BE103975	5.78	6.22	5.46	6.81	4.97	5.83	1.04	up	9.33E-01	9.81E-01	-	-
1380311_at	---	---	---	Rn.205391	AI535528	2.44	2.43	2.60	2.44	2.45	2.43	1.04	down	3.88E-01	8.95E-01	-	-
1382030_at	Gtf2h2	general transcription factor IIH, polypeptide 2	294693	Rn.144260	BF398500	2.62	2.78	2.65	2.64	2.64	2.62	1.04	down	3.55E-01	8.95E-01	-	-
1385340_at	---	---	---	Rn.212169	BG372105	2.49	2.43	2.54	2.49	2.51	2.61	1.04	up	3.39E-01	8.95E-01	-	-
1380650_at	Trio	TRIO and F-actin binding protein	362656	Rn.119950	AA892317	4.52	4.16	4.18	4.18	4.18	4.35	1.04	down	7.06E-01	9.09E-01	-	-
1393343_at	Cul3	cullin 3	301555	Rn.101949	BE115856	5.68	5.76	3.79	4.72	3.83	6.52	1.04	down	9.62E-01	9.89E-01	-	-
1369809_at	Htr1a	5-hydroxytryptamine (serotonin) receptor 1A	24473	Rn.44486	NM_012585	2.37	2.37	2.53	2.37	2.37	2.37	1.04	down	4.02E-01	8.95E-01	-	-
1385185_at	---	---	---	Rn.149253	BF388679	2.52	2.52	2.56	2.49	2.49	2.46	1.04	down	2.57E-02	8.95E-01	-	-
1381758_at	RGD1565672	similar to MDM2 Binding protein	500870	Rn.34858	AI535566	2.60	2.61	2.67	2.59	2.61	2.51	1.04	down	2.44E-01	8.95E-01	-	-
1390297_at	Zc3h14	zinc finger CCCH type containing 14	192359	Rn.98359	BF395781	2.57	2.42	2.49	2.44	2.45	2.44	1.04	down	2.93E-01	8.95E-01	-	-
1378458_at	---	---	---	Rn.207332	BI281745	2.36	2.35	2.36	2.36	2.52	2.35	1.04	up	4.04E-01	8.95E-01	-	-
1382966_at	---	---	---	Rn.203863	AI017717	2.43	2.41	2.44	2.59	2.44	2.41	1.04	up	4.12E-01	8.95E-01	-	-
1378848_at	LOC361187	similar to ankyrin repeat and SOCs box-containing protein 5	361187	Rn.54639	AI169831	2.54	2.50	2.56	2.51	2.60	2.64	1.04	up	2.95E-01	8.95E-01	-	-
1382240_at	---	---	---	Rn.17234	AI029959	5.44	4.35	4.35	4.43	5.26	4.60	1.04	up	9.13E-01	9.74E-01	-	-
1393840_at	Fam107a	family with sequence similarity 107, member A	361018	Rn.1569	AW530286	2.37	2.36	2.38	2.54	2.37	2.35	1.04	up	4.54E-01	8.95E-01	-	-
1388894_at	---	---	---	Rn.22112	BG664174	2.33	2.32	2.33	2.32	2.33	2.48	1.04	up	3.82E-01	8.95E-01	-	-
1374609_at	---	---	---	Rn.165696	AI011183	4.66	5.00	5.43	5.39	4.72	5.14	1.04	up	8.70E-01	9.60E-01	-	-
1390057_at	---	---	---	Rn.129545	AA875554	5.06	6.42	5.00	5.60	5.38	5.65	1.04	up	9.18E-01	9.76E-01	-	-
1387016_a_at	Nptn	neuroplastin	56064	Rn.37476	NM_019380	8.46	8.92	8.60	8.64	8.63	8.87	1.04	up	7.58E-01	9.21E-01	-	-
1394097_at	---	---	---	Rn.168815	AA849706	2.52	2.97	2.54	3.18	2.54	2.47	1.04	up	8.57E-01	9.55E-01	-	-
1392969_at	---	---	---	Rn.12238	BI282309	11.51	11.49	11.50	11.53	11.28	11.54	1.04	down	5.79E-01	8.95E-01	-	-
1377387_a_at	Ece2	endothelin-converting enzyme 2	408243	Rn.169590	BF414330	5.91	4.42	2.82	3.84	4.88	4.28	1.04	down	9.59E-01	9.89E-01	-	-
1393202_a_at	Igf2bp3	Insulin-like growth factor 2 mRNA binding protein 3	312320	Rn.100446	BF414160	2.36	2.35	2.51	2.36	2.36	2.35	1.04	down	3.90E-01	8.95E-01	-	-
1377579_at	LOC683564	similar to neurexin II	683564	---	AW252555	2.45	2.45	2.45	2.64	2.46	2.41	1.04	up	5.03E-01	8.95E-01	-	-
1393763_at	---	---	---	Rn.172396	BF386083	2.64	2.56	2.75	2.62	2.66	2.52	1.04	down	5.06E-01	8.95E-01	-	-
1384827_at	Polm	polymerase (DNA directed), mu	289757	Rn.16022	AI044758	2.59	2.59	2.74	2.58	2.60	2.58	1.04	down	5.66E-01	8.95E-01	-	-
1378149_at	Vps26b	vacuolar protein sorting 26 homolog B (S. pombe)	300472	Rn.61419	BE097616	2.71	2.44	2.45	2.43	2.59	2.42	1.04	down	6.47E-01	8.95E-01	-	-
1392429_at	---	---	---	Rn.216928	BF387476	2.58	2.57	2.70	2.58	2.62	2.50	1.04	down	3.93E-01	8.95E-01	-	-
1385225_at	386589 /// RGD1559	similar to spermatogenesis and centriole associated 1 /// similar to sphingomy	3150911 /// 686589	Rn.140221	BF386619	2.93	2.80	3.57	2.92	2.90	3.32	1.04	up	8.60E-01	9.57E-01	-	-
1368011_at	Fdxr	ferredoxin reductase	79122	Rn.10860	NM_024153	4.71	4.72	4.72	4.72	4.72	4.86	1.04	up	3.28E-01	8.95E-01	-	-
1379832_at	Polr2d	polymerase (RNA) II (DNA directed) polypeptide D	364834	Rn.128728	BF544977	6.74	7.04	6.73	6.97	6.76	6.94	1.04	up	6.90E-01	9.05E-01	-	-
1387378_at	Fcnb	ficolin B	114091	Rn.48281	NM_053634	2.47	2.32	2.33	2.32	2.33	2.31	1.04	down	3.47E-01	8.95E-01	-	-
1379454_at	---	---	---	Rn.216474	AI072423	2.56	2.41	2.42	2.42	2.42	2.40	1.04	down	3.56E-01	8.95E-01	-	-
1381243_at	---	---	---	Rn.47320	BE102374	2.40	2.44	2.44	2.57	2.47	2.39	1.04	up	4.08E-01	8.95E-01	-	-
1396807_at	---	---	---	Rn.38924	AI577388	2.38	2.37	2.53	2.37	2.39	2.36	1.04	down	3.87E-01	8.95E-01	-	-
1372372_at	Cmbl	carboxymethylenebutenolidase homolog (Pseudomonas)	310201	Rn.64439	BG372437	11.04	10.90	11.35	11.11	10.86	11.07	1.04	down	7.36E-01	9.15E-01	-	-
1374615_at	---	---	---	---	AI175668	7.16	6.87	7.30	7.20	6.90	7.39	1.04	up	8.03E-01	9.36E-01	-	-
1393395_at	Zmym4	zinc finger, MYM-type 4	313598	Rn.3185	BE120797	2.38	2.40	2.71	2.38	2.44	2.52	1.04	down	6.77E-01	9.02E-01	-	-
1371678_at	Umr1	ubiquitin-related modifier 1 homolog (S. cerevisiae)	311840	Rn.6516	BM391872	5.14	5.13	5.10	5.29	5.24	4.99	1.04	up	6.13E-01	8.95E-01	-	-
1398683_at	MGC108974	similar to replication protein-binding trans-activator RBT1	499108	Rn.22759	BF553446	2.48	2.46	2.61	2.47	2.48	2.44	1.04	down	3.45E-01	8.95E-01	-	-
1383353_at	---	---	---	Rn.23346	BF389666	2.40	2.39	2.40	2.39	2.70	2.25	1.04	up	7.19E-01	9.11E-01	-	-
1384414_at	---	---	---	---	AI044483	2.44	2.43	2.59	2.43	2.44	2.42	1.04	down	3.91E-01	8.95E-01	-	-
1374012_at	Sypl2	synaptophysin-like 2	362018	Rn.6456	AI171372	3.31	3.47	3.18	3.23	3.30	3.27	1.04	down	5.77E-01	8.95E-01	-	-
1391672_at	---	---	---	Rn.29773	BF399539	3.37	4.42	4.20	4.33	2.74	4.77	1.04	down	9.45E-01	9.84E-01	-	-
1372236_at	Nod1	nucleotide-binding oligomerization domain containing 1	500133	Rn.53929	BI279079	2.52	2.54	2.38	2.43	2.43	2.42	1.04	down	3.89E-01	8.95E-01	-	-
1379292_at	Txndc16	Thioredoxin domain containing 16	361025	Rn.16701	AI412288	4.54	4.53	4.55	4.55	4.54	4.67	1.04	up	2.86E-01	8.95E-01	-	-
1383272_at	Asb11	ankyrin repeat and SOCS box-containing 11	302666	Rn.6582	BI289784	2.48	2.56	2.50	2.47	2.49	2.43	1.04	down	1.81E-

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1394875_at	---	---	---	Rn.28285	AW919027	2.72	2.67	2.80	2.96	2.75	2.62	1.04	up	6.58E-01	8.98E-01	-	-
1388066_a_at	Grk6	G protein-coupled receptor kinase 6	59076	Rn.10633	AF040750	2.55	2.63	2.57	2.53	2.56	2.51	1.04	down	1.31E-01	8.95E-01	-	-
1397269_at	---	---	---	---	AI017772	2.38	2.37	2.41	2.56	2.39	2.37	1.04	up	4.57E-01	8.95E-01	-	-
1376137_at	Plekhb2	pleckstrin homology domain containing, family B (evectins) member 2	301337	Rn.1410	AW254369	4.09	3.78	3.90	3.90	3.88	3.86	1.04	down	6.07E-01	8.95E-01	-	-
1387526_at	Gpr27	G protein-coupled receptor 27	65275	Rn.54454	NM_023099	2.62	2.38	2.43	2.45	2.42	2.39	1.04	down	5.36E-01	8.95E-01	-	-
1385157_at	Cbx1	chromobox homolog 1 (HP1 beta homolog Drosophila)	360609	Rn.32816	BF389675	2.47	2.65	2.49	2.47	2.48	2.50	1.04	down	4.41E-01	8.95E-01	-	-
1380161_at	---	---	---	Rn.28335	AW916617	2.57	2.61	2.65	2.51	2.57	2.60	1.04	down	2.17E-01	8.95E-01	-	-
1393332_at	Gfod2	glucose-fructose oxidoreductase domain containing 2	307801	Rn.66817	BM390653	2.57	2.52	2.71	2.56	2.59	2.51	1.04	down	4.61E-01	8.95E-01	-	-
1382298_at	---	---	---	Rn.40234	BM385955	6.60	6.57	5.69	6.82	6.40	5.49	1.04	down	9.24E-01	9.78E-01	-	-
1374175_at	Porcn	porcupine homolog (Drosophila)	317368	Rn.63535	BI289635	2.39	2.72	2.39	2.46	2.52	2.37	1.04	down	6.94E-01	9.06E-01	-	-
1390494_at	Rps24	ribosomal protein S24	81776	Rn.979	AI177484	2.63	2.47	2.51	2.49	2.52	2.45	1.04	down	3.82E-01	8.95E-01	-	-
1386470_at	---	---	---	Rn.131034	H33577	2.68	2.68	2.86	2.67	2.69	2.71	1.04	down	4.56E-01	8.95E-01	-	-
1383187_a_at	---	---	---	Rn.24116	AA944136	5.48	4.99	5.30	5.52	5.23	4.86	1.04	down	8.44E-01	9.51E-01	-	-
1395355_at	---	---	---	Rn.38811	AI555210	4.58	4.81	4.92	4.74	4.80	4.92	1.04	up	6.75E-01	9.01E-01	-	-
1397710_at	---	---	---	---	BF284362	2.43	2.28	2.29	2.28	2.28	2.27	1.04	down	3.58E-01	8.95E-01	-	-
1395052_at	---	---	---	Rn.53085	BE118917	2.44	2.46	2.94	2.52	2.66	2.50	1.04	down	7.82E-01	9.29E-01	-	-
1371847_at	Crtap	cartilage associated protein	363158	Rn.98162	BI274357	7.01	6.49	7.41	7.19	7.26	6.61	1.04	up	8.88E-01	9.65E-01	-	-
1378840_at	---	---	---	Rn.147691	BF402541	2.69	2.62	2.65	2.58	2.62	2.61	1.04	down	1.06E-01	8.95E-01	-	-
1369622_at	Prok2	prokineticin 2	192206	Rn.211872	NM_138852	2.73	2.71	2.73	2.72	2.77	2.52	1.04	down	5.44E-01	8.95E-01	-	-
1369519_at	Edn1	endothelin 1	24323	Rn.10918	NM_012548	2.56	2.46	2.46	2.44	2.46	2.43	1.04	down	2.20E-01	8.95E-01	-	-
1397585_at	---	---	---	Rn.160444	BE106241	2.42	2.41	2.57	2.41	2.44	2.40	1.04	down	4.11E-01	8.95E-01	-	-
1378546_at	---	---	---	Rn.147491	AI235245	2.44	2.57	2.44	2.44	2.42	2.42	1.04	down	3.28E-01	8.95E-01	-	-
1387586_at	Csnk1g1	casein kinase 1, gamma 1	64086	Rn.10082	NM_022288	2.43	2.44	2.44	2.45	2.55	2.46	1.04	up	2.03E-01	8.95E-01	-	-
1375160_at	LOC690139	Similar to RNA binding motif protein 24	690139	Rn.199020	AI137180	2.35	2.31	2.31	2.50	2.32	2.30	1.04	up	4.85E-01	8.95E-01	-	-
1375629_at	Lamp1	Lysosomal-associated membrane protein 1	25328	Rn.40177	AI230371	8.48	8.76	9.12	9.37	8.60	8.54	1.04	up	8.85E-01	9.64E-01	-	-
1381742_at	---	---	---	Rn.61918	BF411770	2.45	2.40	2.52	2.41	2.42	2.40	1.04	down	2.22E-01	8.95E-01	-	-
1381052_at	RGD1566141	similar to CG016	288417	Rn.137252	AW534941	2.35	2.70	3.88	3.32	2.39	3.37	1.04	up	9.33E-01	9.81E-01	-	-
1380282_at	Cmip	c-Maf-inducing protein	292051	Rn.220203	BF390568	5.66	6.95	8.11	6.87	7.06	6.95	1.04	up	9.47E-01	9.85E-01	-	-
1367587_at	Prl3d4	prolactin family 3, subfamily d, member 4	24282	Rn.1259	NM_033233	2.45	2.43	2.60	2.44	2.46	2.43	1.04	down	4.17E-01	8.95E-01	-	-
1367945_at	Atox1	ATX1 antioxidant protein 1 homolog (yeast)	84355	Rn.11992	NM_053359	6.44	6.62	6.65	6.57	6.49	6.50	1.04	down	5.18E-01	8.95E-01	-	-
1373823_at	Cks2	CDC28 protein kinase regulatory subunit 2	498709	Rn.6116	AA944180	2.93	2.88	2.87	2.84	2.91	3.08	1.04	up	5.25E-01	8.95E-01	-	-
1375581_at	RGD1563892	similar to MGC15476 protein	499088	Rn.93232	AW251171	2.45	2.33	2.35	2.33	2.32	2.32	1.04	down	2.62E-01	8.95E-01	-	-
1392956_at	RGD1304868	Similar to RIKEN cDNA 2810443J12	296550	Rn.50103	BG373315	4.04	4.03	4.28	4.67	3.89	3.93	1.04	up	8.60E-01	9.57E-01	-	-
1392565_at	LOC691358	hypothetical protein LOC691358	691358	Rn.212569	BI290365	5.36	4.59	4.68	4.82	4.84	4.82	1.04	down	8.47E-01	9.52E-01	-	-
1397723_s_at	Rabep2	rabaptin, RAB GTPase binding effector protein 2	80754	Rn.3228	AA875071	2.79	2.82	2.88	2.76	2.81	2.77	1.04	down	1.91E-01	8.95E-01	-	-
1393035_at	---	---	---	---	AI502529	2.82	2.88	2.83	2.82	2.85	2.70	1.04	down	3.53E-01	8.95E-01	-	-
1371594_at	Fis1	fission 1 (mitochondrial outer membrane) homolog (S. cerevisiae)	288584	Rn.1298	AA892378	6.91	8.00	8.48	7.94	7.62	7.97	1.04	up	9.22E-01	9.77E-01	-	-
1378304_at	---	---	---	Rn.155736	BI276118	2.42	2.42	2.44	2.43	2.46	2.54	1.04	up	2.01E-01	8.95E-01	-	-
1394950_at	---	---	---	Rn.167970	AI502833	2.40	2.40	2.40	2.57	2.41	2.37	1.04	up	4.63E-01	8.95E-01	-	-
1392669_at	RGD1308297	similar to CG10084-PA	306137	Rn.28431	BE117193	5.43	5.69	4.97	5.31	5.43	5.51	1.04	up	8.29E-01	9.46E-01	-	-
1398679_at	---	---	---	Rn.206002	AI639098	2.84	2.58	2.71	2.66	2.70	2.62	1.04	down	5.51E-01	8.95E-01	-	-
1382261_at	RGD1311422	similar to CG8841-PA	287822	Rn.113761	AW534331	2.31	2.30	2.32	2.47	2.32	2.30	1.04	up	4.00E-01	8.95E-01	-	-
1371109_at	C8b	complement component 8, beta polypeptide	313421	Rn.110603	AA819870	2.49	2.36	2.37	2.35	2.36	2.35	1.04	down	3.22E-01	8.95E-01	-	-
1395780_at	---	---	---	Rn.64143	BF563384	2.39	2.38	2.54	2.38	2.40	2.38	1.04	down	4.07E-01	8.95E-01	-	-
1381867_at	---	---	---	---	AI454783	2.25	2.12	2.12	2.12	2.10	2.12	1.04	down	3.15E-01	8.95E-01	-	-
1397833_at	---	---	---	Rn.210623	BF416010	2.48	2.45	2.57	2.45	2.46	2.44	1.04	down	2.56E-01	8.95E-01	-	-
1370940_at	Tjp2	tight junction protein 2	115769	Rn.10965	BG378746	5.34	5.74	6.14	5.70	5.91	5.76	1.04	up	8.46E-01	9.52E-01	-	-
1383002_at	Phf20l1	PHD finger protein 20-like 1	314964	Rn.22288	AA998043	5.16	5.09	5.65	5.15	5.47	5.14	1.04	down	8.21E-01	9.43E-01	-	-
1375773_at	---	---	---	Rn.4018	BG379365	3.08	2.59	2.56	2.69	3.02	2.67	1.04	up	8.18E-01	9.42E-01	-	-
1374259_at	---	---	---	Rn.147583	BG378156	2.51	2.49	2.66	2.50	2.55	2.47	1.04	down	4.36E-01	8.95E-01	-	-
1398079_at	Fam168a	family with sequence similarity 168, member A	361614	Rn.137163	BF390105	2.56	2.50	2.61	2.77	2.57	2.48	1.04	up	6.09E-01	8.95E-01	-	-
1374823_at	Arih1	Ariadne ubiquitin-conjugating enzyme E2 binding protein homolog 1 (Drosoph	300756	Rn.29865	BI291651	4.40	4.02	3.93	4.47	3.61	4.13	1.04	down	8.72E-01	9.60E-01	-	-
1374427_at	---	---	---	Rn.94933	AI144986	2.41	2.30	2.36	2.35	2.39	2.48	1.04	up	3.68E-01	8.95E-01	-	-
1383458_at	---	---	---	Rn.168984	BF403759	8.65	7.44	6.60	7.16	7.56	7.82	1.04	down	9.40E-01	9.83E-01	-	-
1391278_at	Nkx2-4	NK2 transcription factor related, locus 4 (Drosophila)	366213	Rn.91589	BE107754	2.51	2.51	2.64	2.51	2.50	2.50	1.04	down	3.28E-01	8.95E-01	-	-
1389261_at	RGD1305508	similar to hypothetical protein MGC23280	303275	Rn.25006	BI290739	2.82	2.66	2.66	2.65	2.68	2.66	1.04	down	3.90E-01	8.95E-01	-	-
1379094_at	---	---	---	---	BF386909	2.61	2.59	2.63	2.76	2.62	2.61	1.04	up	3.95E-01	8.95E-01	-	-
1382602_at	RGD1565257	similar to zinc finger protein 650	311115	Rn.16154	BE120211	7.40	7.53	7.86	7.85	7.26	7.54	1.04	down	8.32E-01	9.47E-01	-	-
1387763_at	Rab27a	RAB27A, member RAS oncogene family	50645	Rn.37360	NM_017317	2.55	2.40	2.44	2.41	2.43	2.40	1.04	down	3.20E-01	8.95E-01	-	-
1383745_at	---	---	---	Rn.25216	AI548136	2.33	2.33	2.34	2.34	2.34	2.46	1.04	up	3.02E-01	8.95E-01	-	-
1391499_at	---	---	---	Rn.13180	BF551074	2.52	2.50	2.63	2.50	2.51	2.48	1.04	down	2.97E-01	8.95E-01	-	-
1390924_at	---	---	---	Rn.169384	BE109165	3.63	3.79	3.93	3.79	3.67	3.75	1.04	down	6.25E-01	8.95E-01	-	-
1368213_at	Por	P450 (cytochrome) oxidoreductase	29441	Rn.11359	NM_031576	4.77	4.57	5.00	4.74	5.18	4.56	1.04	up	8.33E-01	9.47E-01	-	-
1375537_at	Strn3	striatin, calmodulin binding protein 3	114520	Rn.8394	BE107226	4.82	6.02	5.46	5.61	5.46	5.38	1.04	up	8.95E-01	9.67E-01	-	-
1371821_at	---	---	---	Rn.2220019	BM391330	6.32	5.66	5.57	6.10	5.44	6.16	1.04	up	8.88E-01	9.65E-01	-	-
1376290_at	RGD1561962	similar to ecotropic viral integration site 5-like	304201	Rn.162082	BF412293	3.65	3.50	3.51	3.50	3.51	3.50	1.04	down	3.64E-01	8.95E-01	-	-
1385299_at	Lpar4	lysophosphatidic acid receptor 4	302378	Rn.105026	BI294122	2.55	2.52	2.64	2.53	2.55	2.48	1.03	down	3.12E-01	8.95E-01	-	-
1377975_at	---	---	---	Rn.166950	AI100827	2.63	2.46	2.48	2.46	2.51	2.45	1.03	down	4.40E-01	8.95E-01	-	-
1377258_at	---	---	---	Rn.205464	BE107204	2.75	2.71	2.83	2.72	2.73	2.68	1.03	down	2.80E-01	8.95E-01	-	-
1383114_at	---	---	---	Rn.221958	BI296782	7.16	7.28	8.25	7.81	7.65	7.07	1.03	down	9.10E-01	9.73E-01	-	-
1372572_at	Siat7F	sialyltransferase 7F	407765	Rn.187026	AI009124	2.50	2.50	2.51	2.55	2.61	2.49	1.03	up	2.33E-01	8.95E-01	-	-
1382564_at	---	---	---	Rn.24739	AI233574	2.53	2.53	2.67	2.55	2.58	2.49	1.03	down	3.75E-01	8.95E-01	-	-
1375806_at	Tnfaip2	tumor necrosis factor, alpha-induced protein 2	299339	Rn.34387	BF389535	2.79	2.78	2.82	2.78	3.00	2.76	1.03	up	5.61E-01	8.95E-01	-	-
1386027_at	Rp2h	retinitis pigmentosa 2 homolog (human)	367714	Rn.219400	AI409701	2.94	2.93	2.94	2.94	3.07	2.95	1.03	up	2.91E-01	8.95E-01	-	-
1381510_at	---	---	---	Rn.8759	AI602048	2.52	2.51	2.63	2.48	2.54	2.49	1.03	down	3.11E-01	8.95E-01	-	-
1393898_at	---	---	---	Rn.199238	AA998222	2.72	2.69	2.84	2.68	3.12	2.60	1.03	up	7.81E-01	9.29E-01	-	-
1368678_at	Bdnf	brain derived neurotrophic factor	24225	Rn.11266	X67108	2.45	2.52	2.49	2.44	2.45	2.41	1.03	down	1.12E-01	8.95E-01	-	-
1387817_at	Negr1	neuron specific gene family member 1	25247	Rn.2865	NM_024128	2.37	2.36	2.37	2.52	2.38	2.35	1.03	up	4.08E-01	8.95E-01	-	-
1373664_at	Pigc	phosphatidylinositol glycan anchor biosynthesis, class C	364032	Rn.3171	AI228670	4.90	5.10	4.97	4.86	5.01	5.24	1.03	up	7.12E-01	9.10E-01	-	-
1379209_at	Pkd2	Polycystic kidney disease 2 homolog (human)	498328	Rn.198353	AI548735	2.15	2.15	2.30	2.15	2.15	2.15	1.03	down	3.70E-01	8.95E-01	-	-
1390810_at	---	---	---	Rn.22077	BF281550	2.38	2.38	2.40	2.56	2.39	2.36	1.03	up	4.80E-01	8.95E-01	-	-
1369854_s_at	Ceacam1	carcinoembryonic antigen-related cell adhesion molecule 1 (biliary glycoprote	81613	Rn.91235	NM_031755	3.43	3.88	4.43	3.35	3.43	4.81	1.03	down	9.34E-01	9.81E-01	-	-
1383712_at	---	---	---	Rn.138334	BF524281	6.41	5.52	6.10	5.05	6.63	6.49	1.03	up	9.35E-01	9.82E-01	-	-
1390168_a_at	Dnajc24	DnaJ (Hsp40) homolog, subfamily C, member 24	362184	Rn.15794	BI289564	5.98	4.87	6.52	6.13	4.98	6.11	1.03	down	9.40E-01	9.83E-01	-	-
1378666_at	Arhgap21	Rho GTPase activating protein 21	307178	Rn.162259	BE108537	5.67	4.98	4.13	5.31	5.03	4.59	1.03	up	9.25E-01	9.78E-01	-	-
1393302_at	---	---	---	Rn.118386	BE098538	3.26	2.73	2.59	2.78	3.18	2.48	1.03	down	8.72E-01	9.61E-01	-	-
1372168_s_at	Igfbp6	insulin-like growth factor binding protein 6	25641	Rn.6431	BG673588	2.41	2.40	2.49	2.56	2.46	2.44	1.03	up	3.64E-01	8.95E-01	-	-
1370251_at	Avpi1	arginine vasopressin-induced 1	171386	Rn.13633	BI282724	2.40	2.39	2.54	2.39	2.41	2.38	1.03	down	3.73E-01	8.95E-01	-	-
1384090_at	Pigo	phosphatidylinositol glycan anchor biosynthesis, class O	313341	Rn.123611	AW920561	2.44	2.56	2.52	2.47	2.43	2.47	1.03	down	2.48E-01	8.95E-01	-	-
1390543_at	---	---	---	Rn.8770	BF396416	5.19	5.43	6.55	5.80	5.34	5.89	1.03	down	9.18E-01	9.76E-01	-	-
1395846_at	---	---	---	Rn.149165	BF567901	2.74	2.64	2.73	2.67	2.69	2.60	1.03	down	2.89E-01	8.95E-01	-	-
1387230_at	Slc12a3	solute carrier family 12 (sodium/chloride transporters), member 3	54300	Rn.10467	NM_019345	4.83	2.35	5.64	4.90	5.16	2.61	1.03	down	9.71E-01	9.92E-01	-	-
1380767_at	Gpr180	G protein-coupled receptor 180	306165	Rn.208117	BF416342	2.57	2.57	2.58	2.67	2.51	2.70	1.03	up	4.56E-01	8.95E-01	-	-
1382344_at	---	---	---	Rn.18823	BE112906	2.31	2.31	2.32	2.31	2.48	2.30	1.03	up	4.45E-01	8.95E-01	-	-
1379015_at	Foxj2	forkhead box J2	502886	Rn.63642	BF419783	2.83	2.82	2.72	2.92	2.71	2.89	1.03	up	5.53E-01	8.95E-01	-	-
1378983_at	---	---	---	Rn.146007	AA997020	2.66	2.53	2.66	2.58	2.58	2.54	1.03	down	3.38E-01	8.95E-01	-	-
1398332_at	Ppm1f	protein phosphatase 1F (PP2C domain containing)	287931	Rn.91922	BM386294	4.10	4.47	4.25	4.36	4.37	4.25	1.03	up	6.89E-01	9.04E-01	-	-
1384849_at	---	---	---	Rn.64761	AI230851	2.41	2.54	2.42	2.41	2.41	2.39	1.03	down	3.05E-01	8.95E-01	-	-
1381818_at	---	---	---	---	BF409711	2.59	2.58	2.69	2.57	2.61	2.53	1.03	down	3.14E-01	8.95E-01	-	-
1379414_at	---	---	---	Rn.199545	BI300892	2.40	2.25	2.26	2.26	2.25	2.53	1.03	down	3.73E-01	8.95E-01	-	-
1375129_at	Fgfr2	fibroblast growth factor receptor 2	25022	Rn.12732	AA963213	2.34	2.33	2.34	2.34	2.36	2.45	1.03	up	2.34E-01	8.95E-01	-	-
1391432_at	Wdr75	WD repeat domain 75	314545	Rn.38742	BM385275	6.49	6.76	6.51	6.70	6.35	6.85	1.03	up	7.89E-01	9.32E-01	-	-
1376408_at	83670 /// RGD130	hypothetical protein LOC499339 /// similar to D19Bwg1357e protein /// similar	363682	Rn.127943	BF418111	2.34	2.34	2.36	2.36	2.35	2.48	1.03	up	3.16E-01	8.95E-01	-	-
1372214_at	Mrps33	mitochondrial ribosomal protein S33	296995	Rn.2350	AI104277	8.35	8.77	8.79	8.31	8.75	8.72	1.03	down	8.20E-01	9.42E-01	-	-
1393119_at	---	---	---	Rn.12711	BM388725	2.80	3.00	2.72	2.80	3.25	2.62	1.03	up	8.23E-01	9.43E-01	-	-
1396787_at	---	---	---	Rn.59982	BF404914	2.71	2.70	2.75	2.69	2.76	2.56	1.03	down	4.58E-01	8.95E-01	-	-
1382874_at	Npl	N-acetylneuraminate pyruvate lyase	304860	Rn.114492	BI289407	3.31	3.00	2.91	3.04	3.15	2.88	1.03	down	7.49E-01	9.19E-01	-	-
1385142_at	---	---	---	Rn.138191	BI291176	3.05	3.09	3.06	3.06	3.06	2.92	1.03	down	3.61E-01	8.95E-01	-	-
1371027_at	Cblb	Cas-Br-M (murine) ecotropic retroviral transforming sequence b	171136	Rn.21799	BF556820	2.49	2.57	2.48	2.46	2.46	2.46	1.03	down	1.58E-01	8.95E-01	-	-
1387502_at	Stk17b	serine/threonine kinase 17b	170904	Rn.163004	NM_133392	2.36	2.38	2.34	2.32	2.52	2.38	1.03	up	4.50E-01	8.95E-01	-	-
1390551_at	---	---	---	Rn.165948	AI072285	2.30	2.29	2.44	2.29	2.30	2.29	1.03	down	3.58E-01	8.95E-01	-	-
1375448_at	Opa3	optic atrophy 3 (human)	308409	Rn.146575	BM391628	3.89	3.89	3.91	3.97	3.90	3.96	1.03	up	9.86E-02	8.95E-01	-	-
1393098_at	Lig2	lethal giant larvae homolog 2 (Drosophila)	116904	Rn.198904	BM386610	4.59	6.05	4.45	5.26	4.59	5.10	1.03	down	9.33E-01	9.81E-01	-	-
1391818_at	Tmco4	transmembrane and coiled-coil domains 4	500573	Rn.162838	BI290893	2.76	2.86	2.77	2.74	2.77	2.74	1.03	down	2.16E-01	8.95E-01	-	-
1396646_at	Lca5	Leber congenital amaurosis 5 (human)	300866	Rn.208333	BF400757	2.43	2.60	2.53	2.50	2.51	2.70	1.03	up	5.88E-01	8.95E-01	-	-
1371482_at	Ndufs2	NADH dehydrogenase (ubiquinone) Fe-S protein 2	289218	Rn.99666	AA851675	10.25	10.04	10.17	10.15	9.72	10.44	1.03	down	8.34E-01	9.48E-01	-	-
1383197_at	Jam2	junctional adhesion molecule 2	619374	Rn.6473	AA849471	2.35	2.35	2.51	2.36	2.34	2.39	1.03	down	4.10E-01	8.95E-01	-	-
1384741_at	Pla2g3	phospholipase A2, group III	289733	Rn.148320	BE105438	2.29	2.29	2.44	2.30	2.29	2.30	1.03	down	3.77E-01	8.95E-01	-	-
1368053_at	Pard3	par-3 (partitioning defective 3) homolog (C. elegans)	81918	Rn.31803	NM_031235	2.27	2.27	2.28	2.31	2.39	2.27	1.03	up	2.41E-01	8.95E-01	-	-
1387049_at	Myh6	myosin, heavy chain 6, cardiac muscle, alpha	25556	Rn.54309	BI296041	2.69	2.61	2.75	2.67	2.70	2.53	1.03	down	5.04E-01	8.95E-01	-	-
1377878_at	Fgfbp3	fibroblast growth factor binding protein 3	499349	Rn.166095	AA800782	2.34	3.39	2.72	2.59	2.80	2.91	1.03	down	8.87E-01	9.65E-01	-	-
1368298_at	Adcy5	adenylate cyclase 5	64532	Rn.6278	NM_022600	2.37	2.37	2.38	2.37	2.38	2.52	1.03	up	3.67E-01	8.95E-01	-	-
1387905_at	Dnajc12	DnaJ (Hsp40) homolog, subfamily C, member 12	619393	Rn.9583	AB062135	6.25	6.32	5.50	6.13	6.21	5.88	1.03	up	8.71E-01	9.60E-01	-	-
1371015_at	Mx1	myxovirus (influenza virus) resistance 1	24575	Rn.10373	X52711	2.44	2.43	2.58	2.43	2.46	2.41	1.03	down	3.86E-01	8.95E-01	-	-
1394396_at	---	---	---	Rn.92698	AA997657	2.38	2.48	2.40	2.38	2.39	2.34	1.03	down	2.34E-01	8.95E-01	-	-
1373177_x_at	685817 /// LOC68	hypothetical gene supported by BC082068 /// hypothetical gene supported by	685817 /// 688450	Rn.217851	AI409900	2.88	2.77	2.91	2.80	2.89	2.71	1.03	down	5.14E-01	8.95E-01	-	-
1386334_at	Ubfd1	ubiquitin family domain containing 1	293454	Rn.198517	AI171578	2.48	2.45	2.61	2.46	2.51	2.43	1.03	down	4.07E-01	8.95E-01	-	-
1397163_s_at	---	---	---	Rn.203199	BM392082	2.83	2.65	2.85	2.82	2.86	2.79	1.03	up	5.08E-01	8.95E-01	-	-
1389759_at	Celsr1	cadherin, EGF LAG seven-pass G-type receptor 1 (flamingo homolog, Droso	300128	Rn.166656	AW433901	2.78	3.45	2.84	2.82	2.87	3.52	1.03	up	8.84E-01	9.64E-01	-	-
1396078_at	Krit1	KRIT1, ankyrin repeat containing	362317	Rn.162726	BF388439	2.48	2.51	2.47	2.47	2.48	2.65	1.03	up	4.44E-01	8.95E-01	-	-
1372775_at	Brd3	bromodomain containing 3	362092	Rn.16796	AI172375	2.36	2.39	2.39	2.39	2.43	2.47	1.03	up	1.30E-01	8.95E-01	-	-
1377241_at	Znf503	zinc finger protein 503	305687	Rn.37928	AI600276	2.92	2.91	2.93	2.91	3.08	2.91	1.03	up	4.29E-01	8.95E-01	-	-
1388113_at	Cox8a	cytochrome c oxidase, subunit VIIIa	171335	Rn.2270	BG673321	10.66	10.58	10.76	10.60	10.52	10.74	1.03	down	5.80E-01	8.95E-01	-	-
1396483_at	---	---	---	Rn.161176	AW434740	2.78	2.77	2.80	2.77	2.79	2.93	1.03	up	3.90E-01	8.95E-01	-	-
1378493_at	---	---	---	---	BE117901	2.40	2.39	2.50	2.38	2.39	2.37	1.03	down	2.44E-01	8.95E-01	-	-
1392551_at	LOC503192	zinc finger protein ZFP	503192	Rn.216519	AI104921	6.10	5.48	6.21	6.30	5.40	6.23	1.03	up	9.01E-01	9.69E-01	-	-
1398838_at	Rab7a	RAB7A, member RAS oncogene family	29448	Rn.1425	NM_023950	9.91	9.71	9.38	9.76	9.58	9.80	1.03	up	7.87E-01	9.31E-01	-	-
1382493_at	---	---	---	Rn.41236	BG377427	2.51	2.66	2.51	2.49	2.61	2.44	1.03	down	5.36E-01	8.95E-01	-	-
1371195_at	---	---	---	Rn.129675	M23890	2.48	2.42	2.63	2.46	2.52	2.40	1.03	down	5.33E-01	8.95E-01	-	-
1398240_at	Hspa8	heat shock protein 8	24468	Rn.201298	NM_024351	12.57	12.59	12.51	12.50	12.49	12.54	1.03	down	1.58E-01	8.95E-01	-	-
1393712_at	---	---	---	Rn.155831	BF419515	2.45	2.45	2.55	2.51	2.45	2.51	1.03	up	1.50E-01	8.95E-01	-	-
1393248_at	Nmd3	NMD3 homolog (S. cerevisiae)	310512	Rn.61090	BF407833	5.99	5.82	6.68	5.99	5.93	6.43	1.03	down	8.82E-01	9.64E-01	-	-
1367969_at	Prdx6	peroxiredoxin 6

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1379996_at	---	---	---	Rn.164361	AI411753	8.40	7.84	7.73	7.83	8.07	8.21	1.03	up	8.49E-01	9.53E-01	-	-
1370448_at	Gpc2	glypican 2	171517	Rn.88131	L20468	2.41	2.39	2.44	2.56	2.43	2.41	1.03	up	3.87E-01	8.95E-01	-	-
1384030_at	Txndc17	Thioredoxin domain containing 17	287474	Rn.18447	AI030261	2.33	2.34	2.35	2.34	2.34	2.48	1.03	up	3.72E-01	8.95E-01	-	-
1388471_at	Tcp11l2	t-complex 11 (mouse) like 2	314683	Rn.101085	AA800197	7.39	8.09	7.28	7.72	7.67	7.52	1.03	up	8.63E-01	9.57E-01	-	-
1375498_at	---	---	---	Rn.209120	BF387255	2.51	2.39	2.40	2.39	2.39	2.36	1.03	down	2.98E-01	8.95E-01	-	-
1379844_at	---	---	---	Rn.143804	AW531072	2.50	2.37	2.38	2.37	2.38	2.36	1.03	down	3.13E-01	8.95E-01	-	-
1379949_at	Tfb1m	transcription factor B1, mitochondrial	308140	Rn.62385	AI010265	5.64	3.89	4.11	5.38	3.95	4.17	1.03	down	9.49E-01	9.85E-01	-	-
1388655_at	Ssna1	Sjogren syndrome nuclear autoantigen 1	311802	Rn.145066	AW252465	5.27	5.10	5.40	5.23	5.28	5.40	1.03	up	6.63E-01	8.98E-01	-	-
1386997_at	Eif4e	eukaryotic translation initiation factor 4E	117045	Rn.11275	NM_053974	2.55	2.65	2.59	2.53	2.60	2.50	1.03	down	3.15E-01	8.95E-01	-	-
1369558_at	Inhbc	inhibin beta C	64549	Rn.48697	NM_022614	2.54	2.41	2.44	2.42	2.43	2.40	1.03	down	2.83E-01	8.95E-01	-	-
1393834_at	---	---	---	Rn.198500	BF402667	2.79	2.68	2.95	2.74	2.89	2.64	1.03	down	6.75E-01	9.01E-01	-	-
1371849_at	Nt5dc2	5'-nucleotidase domain containing 2	290558	Rn.2956	BI285551	2.50	2.56	2.47	2.53	2.64	2.51	1.03	up	3.88E-01	8.95E-01	-	-
1383298_at	RGD1310444	LOC363015	363015	Rn.27612	BF546148	2.41	2.41	2.42	2.45	2.47	2.17	1.03	down	6.40E-01	8.95E-01	-	-
1396223_at	---	---	---	---	AW252930	2.68	2.59	2.67	2.69	2.82	2.57	1.03	up	5.68E-01	8.95E-01	-	-
1396786_at	---	---	---	Rn.173097	BF409338	2.66	2.59	2.82	2.62	2.77	2.54	1.03	down	6.33E-01	8.95E-01	-	-
1368407_at	Hpse	heparanase	64537	Rn.6392	NM_022605	2.36	2.36	2.37	2.41	2.47	2.35	1.03	up	2.36E-01	8.95E-01	-	-
1367709_at	Cd63	CD63 molecule	29186	Rn.11068	NM_017125	11.92	12.01	12.01	11.97	12.04	12.08	1.03	up	3.28E-01	8.95E-01	-	-
1383770_at	---	---	---	Rn.171529	BE117323	9.45	9.73	9.63	9.67	9.60	9.69	1.03	up	5.98E-01	8.95E-01	-	-
1367813_at	Ppp1r14a	protein phosphatase 1, regulatory (inhibitor) subunit 14A	114004	Rn.73852	NM_130403	2.38	2.68	2.56	2.66	2.56	2.54	1.03	up	6.41E-01	8.95E-01	-	-
1383367_at	Pole4	polymerase (DNA-directed), epsilon 4 (p12 subunit)	362385	Rn.161846	AI178241	7.56	7.66	7.77	7.63	7.04	8.17	1.03	down	8.93E-01	9.67E-01	-	-
1384646_at	---	---	---	Rn.203435	AA823898	2.51	2.51	2.51	2.68	2.51	2.49	1.03	up	4.69E-01	8.95E-01	-	-
1388324_at	Nit1	nitrilase 1	289222	Rn.64425	BG668463	10.47	10.30	9.90	10.03	10.14	10.36	1.03	down	8.15E-01	9.40E-01	-	-
1397935_at	---	---	---	Rn.153372	BF403843	2.54	2.45	2.47	2.44	2.45	2.42	1.03	down	1.77E-01	8.95E-01	-	-
1397467_at	Zfp329	zinc finger protein 329	308361	Rn.100854	AW524703	2.42	2.41	2.42	2.41	2.45	2.54	1.03	up	2.70E-01	8.95E-01	-	-
1379088_x_at	---	---	---	Rn.210024	BF392858	2.76	2.67	2.84	2.74	2.80	2.58	1.03	down	5.84E-01	8.95E-01	-	-
1376442_at	---	---	---	Rn.62696	BF405719	2.35	2.35	2.50	2.35	2.36	2.35	1.03	down	3.84E-01	8.95E-01	-	-
1387624_at	Usf1	upstream transcription factor 1	83586	Rn.10845	NM_031777	2.50	2.49	2.51	2.49	2.62	2.53	1.03	up	2.65E-01	8.95E-01	-	-
1387384_at	Pld2	phospholipase D2	25097	Rn.9798	NM_033299	2.47	2.38	2.43	2.38	2.39	2.36	1.03	down	1.46E-01	8.95E-01	-	-
1394153_at	---	---	---	Rn.16559	AA858641	2.59	2.43	2.45	2.43	2.46	2.43	1.03	down	4.24E-01	8.95E-01	-	-
1378284_at	---	---	---	Rn.199385	BI292067	5.06	2.40	3.22	3.66	4.17	2.70	1.03	down	9.60E-01	9.89E-01	-	-
1374863_at	Rbp7	retinol binding protein 7, cellular	362662	Rn.13092	BI283223	2.50	2.47	2.64	2.48	2.53	2.45	1.03	down	4.37E-01	8.95E-01	-	-
1387385_at	Cntn1	contactin 1	117258	Rn.21397	NM_057118	2.47	2.34	2.35	2.34	2.35	2.33	1.03	down	3.40E-01	8.95E-01	-	-
1397033_at	Cinp	cyclin-dependent kinase 2-interacting protein	299334	Rn.1799	BI295617	2.39	2.51	2.43	2.40	2.41	2.38	1.03	down	2.55E-01	8.95E-01	-	-
1382462_at	L2hgdh	L-2-hydroxyglutarate dehydrogenase	314196	Rn.22733	BF290937	6.83	6.97	6.00	5.90	7.07	6.98	1.03	up	9.26E-01	9.79E-01	-	-
1399120_at	Trmt5	TRM5 tRNA methyltransferase 5 homolog (S. cerevisiae)	362754	Rn.21018	BF407592	4.29	4.16	3.70	3.70	3.74	4.57	1.03	down	8.94E-01	9.67E-01	-	-
1384445_at	LOC298442	similar to RIKEN cDNA 0610037D15	298442	Rn.204830	BI288489	2.43	2.41	2.43	2.42	2.43	2.56	1.03	up	3.55E-01	8.95E-01	-	-
1396861_at	RGD1566001	similar to DNA segment, Chr 4, Brigham & Womens Genetics 0951 expressed	500527	Rn.59706	BE107967	2.42	2.39	2.54	2.41	2.42	2.39	1.03	down	3.70E-01	8.95E-01	-	-
1389956_a_at	COX1	cytochrome c oxidase subunit 1	26195	---	AI180257	12.36	12.10	12.39	12.19	12.31	12.21	1.03	down	6.58E-01	8.98E-01	-	-
1379306_at	Mrpl48	mitochondrial ribosomal protein L48	293149	Rn.107172	BE111794	5.52	5.51	5.52	5.57	5.52	5.31	1.03	down	5.92E-01	8.95E-01	-	-
1384441_at	Tnfrsf17	tumor necrosis factor receptor superfamily, member 17	287034	Rn.17380	AA963751	2.53	2.41	2.46	2.42	2.44	2.41	1.03	down	2.47E-01	8.95E-01	-	-
1397059_x_at	Prlr8a5	prolactin family 8, subfamily a, member 5	286889	Rn.3757	BI284873	2.64	2.63	2.76	2.62	2.72	2.55	1.03	down	4.96E-01	8.95E-01	-	-
1396004_at	---	---	---	Rn.161227	BF399291	2.77	2.58	3.14	2.73	3.14	2.75	1.03	up	8.34E-01	9.47E-01	-	-
1389201_at	rCG_22919	hypothetical protein LOC100125364	100125364	Rn.203848	BG373545	4.11	4.01	4.03	3.70	4.02	4.29	1.03	down	7.96E-01	9.34E-01	-	-
1393740_at	Cnksr1	connector enhancer of kinase suppressor of Ras 1	298545	Rn.79548	BI294230	2.92	3.28	3.09	2.82	3.52	3.29	1.03	up	8.77E-01	9.62E-01	-	-
1397084_at	---	---	---	Rn.168823	AW530928	2.40	2.52	2.40	2.39	2.40	2.39	1.03	down	3.01E-01	8.95E-01	-	-
1376116_at	Ddx24	DEAD (Asp-Glu-Ala-Asp) box polypeptide 24	373065	Rn.100166	BM389678	5.74	6.28	5.00	5.93	5.01	6.23	1.03	up	9.31E-01	9.81E-01	-	-
1369211_at	Cacna1i	calcium channel, voltage-dependent, T type, alpha 1I subunit	56827	Rn.48680	NM_020084	2.39	2.35	2.37	2.36	2.54	2.36	1.03	up	4.86E-01	8.95E-01	-	-
1381779_s_at	Man2c1	mannosidase, alpha, class 2C, member 1	246136	Rn.11301	BG380027	4.49	4.50	3.77	3.79	4.46	4.37	1.03	down	8.89E-01	9.65E-01	-	-
1372886_at	Tacc3	transforming, acidic coiled-coil containing protein 3	360962	Rn.58838	AI556917	2.35	2.36	2.36	2.36	2.49	2.36	1.03	up	3.36E-01	8.95E-01	-	-
1381537_at	Klc3	kinesin light chain 3	171549	Rn.161815	BF402262	2.33	2.33	2.33	2.34	2.34	2.46	1.03	up	2.97E-01	8.95E-01	-	-
1371213_at	RT1-A3	RT1 class I, A3	309627	---	AJ005023	2.51	2.46	2.60	2.48	2.49	2.46	1.03	down	3.28E-01	8.95E-01	-	-
1372965_at	---	---	---	Rn.212270	BI296595	2.62	2.61	2.78	2.63	2.63	2.61	1.03	down	4.15E-01	8.95E-01	-	-
1385615_at	Ube4a	ubiquitination factor E4A	315608	Rn.102204	BF550268	5.95	5.64	5.72	5.41	5.98	6.06	1.03	up	8.44E-01	9.51E-01	-	-
1384440_at	---	---	---	---	BM385619	2.53	2.52	2.94	2.53	2.57	3.03	1.03	up	8.34E-01	9.47E-01	-	-
1390478_at	Orc4	origin recognition complex, subunit 4	252936	---	BE103826	5.68	5.79	5.88	5.61	5.42	6.18	1.03	down	8.50E-01	9.53E-01	-	-
1377999_at	---	---	---	Rn.26214	BE103242	2.82	2.55	2.60	2.54	2.78	2.80	1.03	up	7.10E-01	9.09E-01	-	-
1390916_at	H13	histocompatibility 13	311545	Rn.12102	AI407187	2.37	2.36	2.38	2.37	2.37	2.51	1.03	up	3.77E-01	8.95E-01	-	-
1384139_at	Gja7	gap junction membrane channel protein alpha 7	266706	Rn.19549	AA956115	2.45	2.44	2.45	2.58	2.49	2.42	1.03	up	3.65E-01	8.95E-01	-	-
1376962_at	Stra6	stimulated by retinoic acid gene 6	363071	Rn.12735	BI284420	2.50	2.36	2.38	2.36	2.38	2.36	1.03	down	3.64E-01	8.95E-01	-	-
1389820_at	Cox7c	cytochrome c oxidase, subunit VIIc	100188937	Rn.105968	BF289041	11.65	11.77	11.95	11.83	11.81	11.87	1.03	up	6.21E-01	8.95E-01	-	-
1373846_at	Btf3l4	basic transcription factor 3-like 4	366434	Rn.3613	BF408064	6.48	7.01	7.34	6.78	6.60	7.31	1.03	down	8.93E-01	9.67E-01	-	-
1379149_at	---	---	---	Rn.62752	BF404318	2.63	2.63	2.69	2.63	2.64	2.54	1.03	down	2.87E-01	8.95E-01	-	-
1398564_at	---	---	---	Rn.166297	BF413246	3.44	3.18	3.39	3.30	3.30	3.27	1.03	down	5.83E-01	8.95E-01	-	-
1387975_at	Ugcg	UDP-glucose ceramide glucosyltransferase	83626	Rn.24091	AF047707	2.42	2.42	2.43	2.47	2.52	2.42	1.03	up	1.82E-01	8.95E-01	-	-
1374033_at	Psmb10	proteasome (prosome, macropain) subunit, beta type 10	291983	Rn.24968	BG373505	3.60	3.34	3.09	3.34	3.35	3.49	1.03	up	7.74E-01	9.28E-01	-	-
1381181_at	---	---	---	Rn.172201	BG377817	2.50	2.46	2.69	2.49	2.53	2.49	1.03	down	5.40E-01	8.95E-01	-	-
1373452_at	Rcl1	RNA terminal phosphate cyclase-like 1	309301	Rn.22496	AI232273	3.42	4.07	3.36	3.64	3.65	3.70	1.03	up	8.47E-01	9.52E-01	-	-
1387085_at	Prps1	phosphoribosyl pyrophosphate synthetase 1	29562	Rn.9761	M29392	7.06	7.37	6.72	7.31	6.89	7.09	1.03	up	8.43E-01	9.51E-01	-	-
1376255_at	Mapk4i	mitogen activated protein kinase kinase kinase kinase 1	292763	Rn.13706	BF284982	2.67	2.67	2.69	2.85	2.67	2.65	1.03	up	4.99E-01	8.95E-01	-	-
1374723_at	---	---	---	Rn.7992	BG380632	2.37	2.94	2.40	2.86	2.30	2.41	1.03	down	8.61E-01	9.57E-01	-	-
1389808_at	LOC688274	hypothetical protein LOC688274	688274	---	BI296177	2.48	2.35	2.36	2.35	2.36	2.34	1.03	down	3.26E-01	8.95E-01	-	-
1378347_at	---	---	---	Rn.196113	AW252020	2.56	2.56	2.69	2.56	2.60	2.51	1.03	down	4.09E-01	8.95E-01	-	-
1379049_a_at	---	---	---	Rn.101964	AW532022	2.60	2.47	2.48	2.47	2.47	2.46	1.03	down	3.12E-01	8.95E-01	-	-
1382694_at	---	---	---	Rn.30113	AA957089	2.55	2.41	2.42	2.41	2.43	2.39	1.03	down	3.72E-01	8.95E-01	-	-
1376246_at	Nrarp	Notch-regulated ankyrin repeat protein	499745	Rn.22790	BE104375	2.75	2.63	2.65	2.62	2.64	2.62	1.03	down	2.68E-01	8.95E-01	-	-
1388236_x_at	RT1-CE12	RT1 class I, CE12	309600	---	M24026	3.43	3.39	3.60	3.43	3.43	3.43	1.03	down	5.09E-01	8.95E-01	-	-
1396523_at	---	---	---	Rn.200115	BF409879	2.53	2.42	2.64	2.42	2.48	2.55	1.03	down	5.64E-01	8.95E-01	-	-
1394412_at	Tmem16c	transmembrane protein 16C	311287	Rn.216624	AI144648	2.61	2.56	2.78	2.59	2.70	2.52	1.03	down	6.05E-01	8.95E-01	-	-
1378559_at	---	---	---	Rn.148220	BF406858	2.50	2.49	2.63	2.51	2.56	2.42	1.03	down	4.70E-01	8.95E-01	-	-
1377098_at	---	---	---	Rn.16632	BF283365	2.58	2.55	2.61	2.59	2.74	2.55	1.03	up	4.81E-01	8.95E-01	-	-
1377416_at	---	---	---	Rn.156150	BG378778	2.60	2.48	2.54	2.49	2.53	2.46	1.03	down	3.08E-01	8.95E-01	-	-
1381518_at	---	---	---	Rn.164858	AF409158	2.74	2.70	2.82	2.72	2.74	2.67	1.03	down	3.36E-01	8.95E-01	-	-
1379899_at	---	---	---	Rn.19126	BI298010	2.65	2.60	2.59	2.54	2.61	2.55	1.03	down	1.89E-01	8.95E-01	-	-
1372281_at	Lypla1	lysophospholipase-like 1	289357	Rn.1612	AA819059	6.66	6.24	6.50	6.34	6.35	6.57	1.03	down	7.57E-01	9.21E-01	-	-
1388836_at	Prkch	protein kinase C, eta	81749	Rn.10398	AA799981	2.45	2.31	2.32	2.32	2.32	2.31	1.03	down	3.62E-01	8.95E-01	-	-
1392116_at	Sike	suppressor of IKK epsilon	362007	Rn.9125	BE102137	2.52	2.65	2.54	2.50	2.55	2.52	1.03	down	3.05E-01	8.95E-01	-	-
1385981_at	Lppr4	plasticity related gene 1	295401	Rn.58355	BF394800	2.48	2.35	2.36	2.35	2.36	2.34	1.03	down	3.20E-01	8.95E-01	-	-
1396284_at	686269 /// LOC69	hypothetical protein LOC686269 /// hypothetical protein LOC690785	686269 /// 690785	Rn.212055	BG376703	2.54	2.50	2.57	2.48	2.56	2.42	1.03	down	3.63E-01	8.95E-01	-	-
1382813_at	RGD1310810	similar to RIKEN cDNA 4930444A02	306549	Rn.39247	BG377386	5.14	5.06	5.22	5.13	5.15	5.28	1.03	up	5.27E-01	8.95E-01	-	-
1385874_at	Usp42	Ubiquitin specific peptidase 42	288482	Rn.25011	AA956418	3.33	3.37	3.99	3.62	3.25	3.68	1.03	down	8.63E-01	9.57E-01	-	-
1397112_at	---	---	---	Rn.171772	BF415784	2.32	2.31	2.46	2.31	2.32	2.31	1.03	down	3.79E-01	8.95E-01	-	-
1368810_a_at	Mbp	myelin basic protein	24547	Rn.63285	NM_017026	2.33	2.32	2.36	2.32	2.51	2.32	1.03	up	4.99E-01	8.95E-01	-	-
1372549_at	Tmem88	transmembrane protein 88	497936	Rn.203394	AI409460	2.37	2.36	2.38	2.37	2.38	2.49	1.03	up	3.09E-01	8.95E-01	-	-
1395420_at	---	---	---	Rn.43962	BF548457	5.49	4.33	4.18	4.99	4.06	5.09	1.03	up	9.33E-01	9.81E-01	-	-
1379449_at	Rb1cc1	RB1-inducible coiled-coil 1	312927	Rn.33137	BG670920	3.38	5.20	4.67	3.88	4.71	4.80	1.03	up	9.43E-01	9.84E-01	-	-
1390976_at	Lynx1	Ly6/neurotoxin 1	300918	Rn.32045	AI385355	2.38	2.43	2.33	2.28	2.33	2.38	1.03	down	2.94E-01	8.95E-01	-	-
1398913_at	Numa1	nuclear mitotic apparatus protein 1	308870	Rn.66392	AI599394	6.19	6.41	6.33	6.16	6.28	6.36	1.03	down	6.19E-01	8.95E-01	-	-
1396459_at	Isl2	ISL LIM homeobox 2	57233	Rn.10026	BE096723	2.67	2.64	2.84	2.65	2.76	2.59	1.03	down	5.83E-01	8.95E-01	-	-
1393496_at	Theg	testicular haploid expressed gene	299599	Rn.49140	BF566173	2.43	2.42	2.43	2.42	2.42	2.57	1.03	up	4.02E-01	8.95E-01	-	-
1377444_at	---	---	---	Rn.171753	BE120680	2.63	2.51	2.64	2.62	2.68	2.61	1.03	up	3.67E-01	8.95E-01	-	-
1388245_a_at	Nrg1	neuregulin 1	112400	Rn.37438	U02315	2.44	3.57	4.99	5.24	2.46	3.45	1.03	up	9.68E-01	9.91E-01	-	-
1374568_at	RGD1309492	similar to mKIAA1737 protein	314330	Rn.19617	BF284775	6.83	7.21	7.63	7.54	6.55	7.44	1.03	down	9.10E-01	9.73E-01	-	-
1398210_at	---	---	---	Rn.210176	BF401765	2.33	2.32	2.34	2.48	2.34	2.31	1.03	up	4.25E-01	8.95E-01	-	-
1382019_at	Alg5	asparagine-linked glycosylation 5, dolichyl-phosphate beta-glucosyltransferas	295051	Rn.155539	AA998062	7.73	7.42	8.17	7.59	7.66	8.21	1.03	up	8.80E-01	9.63E-01	-	-
1387095_at	Gnaz	guanine nucleotide binding protein (G protein), alpha z polypeptide	25740	Rn.10943	J03773	2.40	2.39	2.53	2.39	2.40	2.39	1.03	down	3.79E-01	8.95E-01	-	-
1378780_at	---	---	---	Rn.141582	BF410325	2.48	2.35	2.37	2.36	2.37	2.34	1.03	down	3.23E-01	8.95E-01	-	-
1387276_at	Dclk1	doublecortin-like kinase 1	83825	Rn.80575	NM_021584	2.51	2.45	2.74	2.38	2.53	2.65	1.03	down	7.10E-01	9.09E-01	-	-
1390437_at	Sema5a	sema domain, seven thrombospondin repeats (type 1 and type 1-like), transm	310207	Rn.14619	BE116385	5.39	4.15	5.25	4.40	4.74	5.51	1.03	down	9.32E-01	9.81E-01	-	-
1392790_at	---	---	---	---	BF283033	2.41	2.39	2.52	2.39	2.40	2.38	1.03	down	3.19E-01	8.95E-01	-	-
1385262_at	LOC687333	similar to zinc finger protein 59	687333	---	BF387891	2.64	2.58	2.73	2.59	2.69	2.53	1.03	down	5.13E-01	8.95E-01	-	-
1385005_at	---	---	---	Rn.156626	AW530264	4.24	3.62	3.48	3.97	3.64	3.87	1.03	up	8.64E-01	9.58E-01	-	-
1383939_at	---	---	---	Rn.166642	BG378849	2.37	2.36	2.37	2.35	2.37	2.52	1.03	up	4.30E-01	8.95E-01	-	-
1388353_at	Pa2g4	proliferation-associated 2G4	288778	Rn.9485	BI296168	6.82	7.38	6.83	6.83	7.25	6.92	1.03	down	8.38E-01	9.49E-01	-	-
1393247_at	Zfp26	zinc finger protein 26	367033	Rn.198798	BI298190	2.48	2.49	2.49	2.46	2.46	2.69	1.03	up	5.69E-01	8.95E-01	-	-
1368982_at	Pkia	protein kinase (cAMP-dependent, catalytic) inhibitor alpha	114906	Rn.94808	AA996685	2.32	2.32	2.33	2.47	2.33	2.31	1.03	up	4.23E-01	8.95E-01	-	-
1370143_at	Smo	smoothened homolog (Drosophila)	25273	Rn.44429	NM_012807	2.27	2.39	2.28	2.27	2.27	2.26	1.03	down	3.13E-01	8.95E-01	-	-
1385791_at	Vill	villin-like	301057	Rn.52080	BE112294	8.27	8.35	8.10	8.69	7.99	8.19	1.03	up	8.43E-01	9.51E-01	-	-
1375228_at	Brd2	bromodomain containing 2	294276	Rn.98146	AI172186	2.40	2.31	2.32	2.31	2.55	2.31	1.03	up	6.11E-01	8.95E-01	-	-
1373960_at	Tmem120a	transmembrane protein 120A	288591	Rn.6288	AI235631	2.45	2.44	2.46	2.46	2.44	2.58	1.03	up	3.30E-01	8.95E-01	-	-
1396422_at	---	---	---	Rn.172940	BF397628	2.60	2.57	2.66	2.58	2.66	2.46	1.03	down	5.01E-01	8.95E-01	-	-
1380693_at	---	---	---	Rn.211561	BF415976	2.49	2.37	2.39	2.37	2.38	2.37	1.03	down	2.90E-01	8.95E-01	-	-
1380101_at	Papolg	poly(A) polymerase gamma	305586	Rn.27992	BE109349	3.41	3.12	3.12	3.62	2.44	3.45	1.03	down	9.09E-01	9.72E-01	-	-
1375907_at	Ascc1	activating signal cointegrator 1 complex subunit 1	294512	Rn.16141	BG380458	7.44	6.79	7.55	6.42	8.64	6.59	1.03	down	9.54E-01	9.86E-01	-	-
1389855_at	---	---	---	---	AA859673	2.46	2.43	2.58	2.44	2.47	2.43	1.03	down	3.95E-01	8.95E-01	-	-
1389771_at	LOC683674	similar to Protein C7orf26 homolog	683674	---	AI013885	5.62	5.87	6.63	5.96	6.06	5.97	1.03	down	8.86E-01	9.65E-01	-	-
1374681_at	---	---	---	Rn.7552	AW914967	2.27	2.24	2.25	2.41	2.25	2.24	1.03	up	4.59E-01	8.95E-01	-	-
1368465_at	Accn1	amiloride-sensitive cation channel 1, neuronal	25364	Rn.37523	NM_012892	2.39	2.38	2.52	2.39	2.39	2.38	1.03	down	3.73E-01	8.95E-01	-	-
1379919_at	Cflar	CASP8 and FADD-like apoptosis regulator	117279	Rn.204752	AI575276	2.41	2.62	2.44	2.44	2.40	2.50	1.03	down	5.46E-01	8.95E-01	-	-
1385405_at	Adam23	ADAM metallopeptidase domain 23	301460	Rn.24184	AI535213	2.61	2.61	2.64	2.61	2.62	2.49	1.03	down	3.25E-01	8.95E-01	-	-
1370985_at	Mapk7	mitogen-activated protein kinase 7	114509	Rn.221942	AJ005424	2.43	2.42	2.37	2.37	2.37	2.35	1.03	down	9.34E-02	8.95E-01	-	-
1376688_a_at	OC685020 /// Pllra	similar to paired immunoglobin-like type 2 receptor alpha /// paired immunoglo	288568 /// 685020	Rn.94103	BF288115	2.36	2.34	2.37	2.35	2.36	2.49	1.03	up	3.53E-01	8.95E-01	-	-
1374528_at	---	---	---	---	BF418764	2.52	2.37	2.40	2.38	2.39	2.37	1.03	down	3.57E-01	8.95E-01	-	-
1385241_at	---	---	---	---	AI071210	2.99	2.74	2.75	2.75	2.87	2.73	1.03	down	6.45E-01	8.95E-01	-	-
1375781_at	---	---	---	Rn.63660	BF418844	2.36	2.47	2.37	2.35	2.36	2.34	1.03	down	2.48E-01	8.95E-01	-	-
1376811_a_at	Cpsf6	cleavage and polyadenylation specific factor 6	299811	Rn.164480	BE108383	4.82	4.99	4.64	4.96	4.69	4.66	1.03	down	7.59E-01	9.21E-01	-	-
1379758_at	---	---	---	---	AI229471	2.56	2.54	2.62	2.53	2.59	2.46	1.03	down	3.56E-01	8.95E-01	-	-
1397845_at	---	---	---	Rn.56987	BE106909	2.72	2.68	2.70	2.68	2.70	2.58	1.03	down	3.03E-01	8.95E-01	-	-
1373468_at	---	---	---	Rn.153646	BI295896	2.38	2.37	2.39	2.37	2.55	2.36	1.03	up	4.97E-01	8.95E-01	-	-
1378908_at	Mrps24	mitochondrial ribosomal protein S24	498406	Rn.1914	BF386667	2.60	2.48	2.53	2.49	2.52	2.46	1.03	down	3.10E-01	8.95E-01	-	-
1372783_at	Larp5	La ribonucleoprotein domain family, member 5	307070	Rn.11463	BM387109	8.89	8.87	8.91	8.65	8.92	9.24	1.03	up	7.98E-01	9.35E-01	-	-
1389433_at	Krt19	keratin 19	360626	Rn.9359	BI279605	6.28	6.21	5.74	5.66	6.03	6.42	1.03	down	8.76E-01	9.62E-01	-	-
1369668_x_at	Vps52	vacuolar protein sorting 52 homolog (S. cerevisiae)	25218	Rn.51354	NM_033097	2.64	2.59	2.82	2.71	2.63	2.58	1.03	down	5.98E-01	8.95E-01	-	-
1380511_at	Parvb	Par

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)				REG	MTC
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval		
1378188_at	---	---	---	Rn.37603	BE102810	2.31	2.40	2.34	2.31	2.32	2.29	1.03	down	1.78E-01	8.95E-01	-	-
1385188_at	RGD1309188	similar to hypothetical protein BC011833	315463	Rn.4026	BG379787	2.37	2.36	2.40	2.37	2.37	2.52	1.03	up	4.29E-01	8.95E-01	-	-
1368885_at	Cspg4	chondroitin sulfate proteoglycan 4	81651	Rn.10381	NM_031022	2.53	2.53	2.54	2.53	2.54	2.40	1.03	down	3.77E-01	8.95E-01	-	-
1398915_at	RGD1309735	similar to CG14977-PA	360776	Rn.7295	BI278208	7.96	8.93	7.92	8.06	8.53	8.37	1.03	up	9.04E-01	9.71E-01	-	-
1394674_at	---	---	---	Rn.202644	BG372056	2.69	2.63	2.78	2.65	2.71	2.60	1.03	down	4.38E-01	8.95E-01	-	-
1382741_at	Ube3a	ubiquitin protein ligase E3A	361585	Rn.198497	BI285961	6.12	7.00	6.32	6.50	6.10	6.71	1.03	down	8.94E-01	9.67E-01	-	-
1398595_at	Rbm5	RNA binding motif protein 5	303996	Rn.17033	AI070585	2.51	2.65	2.54	2.58	2.52	2.46	1.03	down	4.54E-01	8.95E-01	-	-
1396512_at	---	---	---	Rn.169783	BF393192	2.56	2.55	2.76	2.90	2.56	2.55	1.03	up	7.50E-01	9.19E-01	-	-
1376655_at	---	---	---	Rn.79583	AA850435	6.17	6.21	6.20	6.06	6.49	6.17	1.03	up	7.39E-01	9.16E-01	-	-
1385083_at	RGD1563056	similar to hypothetical protein	500434	Rn.212089	BG379253	2.54	2.53	2.57	2.55	2.54	2.41	1.03	down	4.08E-01	8.95E-01	-	-
1389155_at	Dos	downstream of Stk11	314622	Rn.91597	AA943139	2.80	2.78	2.81	2.86	2.86	2.81	1.03	up	6.71E-02	8.95E-01	-	-
1374305_at	---	---	---	---	AI408613	2.36	2.53	2.58	2.47	2.42	2.44	1.03	down	5.37E-01	8.95E-01	-	-
1391042_at	Mtf2	metal response element binding transcription factor 2	360905	Rn.20300	BE107750	2.69	2.65	2.88	2.68	2.71	2.69	1.03	down	5.62E-01	8.95E-01	-	-
1371727_at	Glb1	galactosidase, beta 1	316033	Rn.4187	AA893350	8.13	8.41	8.25	9.02	8.11	7.79	1.03	up	9.09E-01	9.73E-01	-	-
1391043_at	Otud7a	OTU domain containing 7A	309252	Rn.207005	BE101732	2.39	2.48	2.40	2.38	2.39	2.36	1.03	down	2.20E-01	8.95E-01	-	-
1396704_at	---	---	---	Rn.130382	BF394808	2.55	2.49	2.57	2.50	2.49	2.48	1.03	down	1.65E-01	8.95E-01	-	-
1370197_a_at	Prkcz	protein kinase C, zeta	25522	Rn.1109	AW533298	4.16	6.59	5.21	6.38	4.43	5.28	1.03	up	9.62E-01	9.89E-01	-	-
1370523_a_at	Ube2d2	ubiquitin-conjugating enzyme E2D 2	641452	Rn.7390	AW142720	10.20	10.61	10.59	10.45	10.52	10.57	1.03	up	7.60E-01	9.22E-01	-	-
1367999_at	Aldh2	aldehyde dehydrogenase 2 family (mitochondrial)	29539	Rn.101781	NM_032416	10.66	10.76	10.64	10.85	10.54	10.54	1.03	down	7.03E-01	9.07E-01	-	-
1377521_at	---	---	---	---	BF415562	2.54	2.52	2.66	2.51	2.56	2.52	1.03	down	3.76E-01	8.95E-01	-	-
1374243_at	---	---	---	Rn.2842	AI102744	6.12	6.09	6.35	6.23	5.83	6.35	1.03	down	8.11E-01	9.39E-01	-	-
1372831_at	---	---	---	Rn.20180	BE349838	2.66	2.75	2.66	2.65	2.38	2.89	1.03	down	7.78E-01	9.28E-01	-	-
1395178_at	---	---	---	Rn.205384	AI556682	2.33	2.33	2.46	2.33	2.34	2.32	1.03	down	3.59E-01	8.95E-01	-	-
1390977_at	Sf3l	suppression of tumorigenicity 7-like	295344	Rn.102337	AW527529	3.05	2.77	2.65	2.77	2.77	2.80	1.03	down	7.20E-01	9.11E-01	-	-
1386886_at	Cd164	CD164 molecule, sialomucin	83689	Rn.3733	NM_031812	10.94	11.34	11.26	10.98	11.21	11.49	1.03	up	8.24E-01	9.44E-01	-	-
1386569_at	---	---	---	Rn.206872	BF563922	3.46	3.37	3.36	3.35	3.36	3.35	1.03	down	2.22E-01	8.95E-01	-	-
1372400_at	RGD1563853	similar to cullin 4A	361181	Rn.1987	AI180403	6.34	5.94	6.55	6.39	6.35	6.23	1.03	up	8.18E-01	9.42E-01	-	-
1393609_at	---	---	---	Rn.203675	AA964480	2.39	2.38	2.52	2.39	2.40	2.37	1.03	down	3.66E-01	8.95E-01	-	-
1377572_at	RGD1562426	similar to UDP-glucose:glycoprotein glucosyltransferase 2	290489	---	AW434912	2.75	2.60	2.77	2.64	2.69	2.65	1.03	down	4.67E-01	8.95E-01	-	-
1376626_at	Mkrn1	makorin ring finger protein 1	296988	Rn.101798	AI145815	7.27	6.96	7.26	7.14	7.56	6.93	1.03	up	8.39E-01	9.50E-01	-	-
1379572_at	Mab21l1	mab-21-like 1 (C. elegans)	688394	Rn.198592	AI406423	2.48	2.46	2.49	2.47	2.63	2.47	1.03	up	4.60E-01	8.95E-01	-	-
1370124_at	Mt3	metallothionein 3	117038	Rn.11325	NM_053968	2.68	2.54	2.57	2.56	2.58	2.52	1.03	down	3.80E-01	8.95E-01	-	-
1392492_at	---	---	---	Rn.165078	AA956982	4.97	5.99	5.88	5.70	5.04	5.96	1.03	down	9.20E-01	9.76E-01	-	-
1396323_at	LOC681383	similar to Protein C10orf11 homolog	681383	Rn.205549	AI709444	5.97	3.99	5.27	5.25	5.22	4.62	1.03	down	9.45E-01	9.84E-01	-	-
1376263_at	Metrn	meteorin, glial cell differentiation regulator	287151	Rn.50391	BG378672	2.49	2.46	2.49	2.57	2.49	2.52	1.03	up	1.42E-01	8.95E-01	-	-
1373634_at	---	---	---	Rn.35353	AI177753	8.78	8.81	8.87	8.58	8.79	9.22	1.03	up	8.22E-01	9.43E-01	-	-
1391898_at	---	---	---	Rn.41955	AW524135	2.60	2.61	2.63	2.63	2.70	2.66	1.03	up	1.31E-01	8.95E-01	-	-
1374370_at	---	---	---	---	BF403383	2.64	2.59	2.66	2.63	2.87	2.53	1.03	up	6.80E-01	9.03E-01	-	-
1390003_at	Zfp57	zinc finger protein 57	361783	Rn.106247	BE103960	2.31	2.30	2.31	2.30	2.31	2.44	1.03	up	3.80E-01	8.95E-01	-	-
1375240_at	Baz1b	Bromodomain adjacent to zinc finger domain, 1B	368002	Rn.7043	AI407473	2.40	2.38	2.50	2.43	2.34	2.38	1.03	down	3.81E-01	8.95E-01	-	-
1389821_at	Tmem158	Transmembrane protein 158	117582	Rn.4294	AA800815	2.36	2.32	2.35	2.35	2.40	2.43	1.03	up	1.70E-01	8.95E-01	-	-
1374329_at	---	---	---	Rn.164921	BI286364	6.61	6.15	5.80	6.23	6.16	6.02	1.03	down	8.61E-01	9.57E-01	-	-
1373819_at	Znf706	zinc finger protein 706	500855	Rn.40403	AI232337	7.52	7.60	7.84	7.23	7.48	8.11	1.03	down	8.79E-01	9.63E-01	-	-
1384944_at	Bcl11b	B-cell CLL/lymphoma 11B (zinc finger protein)	314423	Rn.162897	BE116855	2.52	2.49	2.58	2.50	2.57	2.67	1.03	up	4.50E-01	8.95E-01	-	-
1383317_at	---	---	---	Rn.1940	AA864887	2.35	2.34	2.36	2.34	2.36	2.48	1.03	up	3.50E-01	8.95E-01	-	-
1371267_at	/// RT1-CE15 ///	similar to RT1 class I, CE11 /// RT1 class Ia, locus A1 /// 309627 /// 36	---	Rn.203332	M64795	2.41	2.40	2.53	2.41	2.42	2.38	1.03	down	3.40E-01	8.95E-01	-	-
1397040_at	---	---	---	Rn.146570	BF402347	2.32	2.30	2.33	2.31	2.32	2.46	1.03	up	4.24E-01	8.95E-01	-	-
1386909_a_at	Vdac1	voltage-dependent anion channel 1	83529	Rn.54594	AF268467	11.88	11.91	11.84	11.88	11.58	12.03	1.03	down	7.54E-01	9.20E-01	-	-
1377084_at	---	---	---	Rn.18129	BE106598	2.80	2.59	2.77	2.68	2.68	2.67	1.03	down	5.39E-01	8.95E-01	-	-
1383345_at	---	---	---	---	AI144771	2.54	2.53	2.59	2.52	2.54	2.47	1.03	down	1.96E-01	8.95E-01	-	-
1378491_at	---	---	---	Rn.209749	BF394202	2.60	2.49	2.53	2.49	2.53	2.46	1.03	down	3.05E-01	8.95E-01	-	-
1370739_x_at	Trdn	triadin	59299	Rn.41863	AF220558	2.63	2.61	2.70	2.62	2.66	2.53	1.03	down	3.99E-01	8.95E-01	-	-
1395108_at	---	---	---	Rn.217743	BE104922	2.62	2.50	2.54	2.51	2.56	2.46	1.03	down	3.75E-01	8.95E-01	-	-
1378991_at	---	---	---	---	AI556795	2.58	2.48	2.51	2.49	2.50	2.44	1.03	down	2.40E-01	8.95E-01	-	-
1370060_at	Slc25a11	solute carrier family 25 (mitochondrial carrier; oxoglutarate carrier), member 11	64201	Rn.853	NM_022398	8.66	8.94	8.43	8.72	8.55	8.62	1.03	down	7.83E-01	9.30E-01	-	-
1398194_at	---	---	---	Rn.210932	BF405720	2.47	2.54	2.49	2.47	2.48	2.42	1.03	down	1.81E-01	8.95E-01	-	-
1397371_at	---	---	---	Rn.171571	AI577362	2.48	2.65	2.49	2.54	2.50	2.45	1.03	down	4.99E-01	8.95E-01	-	-
1373961_at	MGC95208	similar to 4930453N24Rik protein	304176	Rn.19101	AI170410	6.73	7.65	7.25	6.74	7.38	7.38	1.03	down	9.00E-01	9.69E-01	-	-
1368784_at	A1cf	APOBEC1 complementation factor	170912	Rn.162520	NM_133400	7.59	7.84	6.88	7.51	7.59	7.07	1.03	down	8.97E-01	9.68E-01	-	-
1382996_at	RGD1566202	similar to RIKEN cDNA 1810007E14	499867	Rn.34033	AI179926	2.48	2.40	2.44	2.39	2.42	2.36	1.03	down	1.87E-01	8.95E-01	-	-
1369847_at	Kcnab1	potassium voltage-gated channel, shaker-related subfamily, beta member 1	29737	Rn.32090	NM_017303	2.54	2.38	2.40	2.41	2.39	2.38	1.03	down	4.35E-01	8.95E-01	-	-
1381900_at	---	---	---	Rn.27138	AI407705	2.55	2.55	2.56	2.55	2.55	2.53	1.03	down	2.45E-01	8.95E-01	-	-
1396777_at	---	---	---	---	BF401331	2.48	2.45	2.60	2.45	2.50	2.45	1.03	down	3.95E-01	8.95E-01	-	-
1388668_at	---	---	---	Rn.878	BM384972	4.95	5.43	5.17	4.60	5.02	6.05	1.03	up	9.25E-01	9.78E-01	-	-
1382192_at	Lyve1	lymphatic vessel endothelial hyaluronan receptor 1	293186	Rn.22111	AI179260	2.52	2.51	2.54	2.52	2.69	2.49	1.03	up	5.14E-01	8.95E-01	-	-
1391084_at	---	---	---	Rn.206365	AW528763	2.67	2.63	2.85	2.65	2.69	2.68	1.03	down	5.30E-01	8.95E-01	-	-
1375590_at	RGD1308290	similar to RIKEN cDNA 5730454B08	360845	Rn.170807	AA894335	3.38	3.98	3.32	3.75	3.58	3.48	1.03	up	8.50E-01	9.53E-01	-	-
1393958_at	Avpr2	arginine vasopressin receptor 2	25108	Rn.209041	AA819795	2.49	2.67	2.50	2.49	2.55	2.49	1.03	down	4.94E-01	8.95E-01	-	-
1369807_at	Cyp4a8	cytochrome P450, family 4, subfamily a, polypeptide 8	266674	Rn.10034	NM_031605	11.61	11.45	11.71	11.65	11.42	11.56	1.03	down	6.80E-01	9.03E-01	-	-
1375762_at	Dnajb5	DnaJ (Hsp40) homolog, subfamily B, member 5	313811	Rn.92865	BF390910	2.72	2.76	2.71	2.74	2.72	2.87	1.03	up	4.16E-01	8.95E-01	-	-
1383798_at	Fam151a	family with sequence similarity 151, member A	313430	Rn.162073	AI411061	8.49	6.68	7.34	8.42	8.01	5.95	1.03	down	9.64E-01	9.90E-01	-	-
1376151_a_at	---	---	---	Rn.113342	AI407953	7.01	6.73	6.23	7.08	5.90	6.86	1.03	down	9.21E-01	9.77E-01	-	-
1394815_at	RGD1559505	Similar to RIKEN cDNA 9030409E16	498953	Rn.137003	BE107436	7.58	6.60	6.57	7.43	6.54	6.91	1.03	up	9.20E-01	9.76E-01	-	-
1380309_at	Vps8	vacuolar protein sorting 8 homolog (S. cerevisiae)	287990	Rn.63502	BI273829	5.03	5.23	5.23	5.06	5.23	5.34	1.03	up	6.87E-01	9.04E-01	-	-
1377312_at	---	---	---	Rn.171259	BF401679	2.84	2.35	2.63	2.93	2.63	2.41	1.03	up	8.37E-01	9.49E-01	-	-
1374207_at	Angpt2	angiopoietin 2	89805	Rn.138360	BI275292	2.39	2.37	2.38	2.52	2.38	2.35	1.03	up	4.79E-01	8.95E-01	-	-
1371602_at	Tspan9	tetraspanin 9	312728	Rn.16430	BI274110	2.58	2.58	2.53	2.67	2.59	2.58	1.03	up	2.49E-01	8.95E-01	-	-
1388159_at	CYTB	cytochrome b	26192	---	AA849795	12.48	12.24	12.60	12.31	12.56	12.32	1.03	down	7.55E-01	9.20E-01	-	-
1395179_at	---	---	---	Rn.159989	BG375582	2.70	2.65	2.78	2.67	2.72	2.60	1.03	down	4.31E-01	8.95E-01	-	-
1396268_at	Sp110	SP110 nuclear body protein	301570	Rn.6459	BF523991	3.15	3.37	3.91	3.21	4.50	2.85	1.03	up	9.39E-01	9.83E-01	-	-
1380399_at	---	---	---	Rn.74895	BF393255	2.42	2.41	2.43	2.60	2.40	2.39	1.03	up	5.50E-01	8.95E-01	-	-
1393480_at	Ppp1r2	protein phosphatase 1, regulatory (inhibitor) subunit 2	192361	Rn.4016	AW919998	7.64	7.63	7.18	7.47	7.36	7.75	1.03	up	8.25E-01	9.45E-01	-	-
1378966_at	---	---	---	Rn.122712	AI406473	2.41	2.40	2.55	2.41	2.42	2.40	1.03	down	4.11E-01	8.95E-01	-	-
1395077_at	---	---	---	Rn.208675	BE119312	2.32	2.30	2.32	2.46	2.31	2.30	1.03	up	4.37E-01	8.95E-01	-	-
1374576_at	---	---	---	---	BF283857	4.53	3.32	3.30	4.05	3.57	3.39	1.03	down	9.26E-01	9.79E-01	-	-
1377569_at	Sav1	Salvador homolog 1 (Drosophila)	299116	Rn.14087	AW534117	2.13	2.13	2.27	2.13	2.13	2.13	1.03	down	3.80E-01	8.95E-01	-	-
1397449_at	---	---	---	Rn.204154	AI059353	2.36	2.37	2.38	2.52	2.38	2.35	1.03	up	4.43E-01	8.95E-01	-	-
1383525_at	---	---	---	Rn.203226	AW918717	2.40	2.53	2.41	2.40	2.41	2.40	1.03	down	3.31E-01	8.95E-01	-	-
1376158_at	---	---	---	---	BG373073	3.93	4.30	4.95	4.53	4.18	4.60	1.03	up	8.96E-01	9.68E-01	-	-
1392649_at	---	---	---	Rn.203964	AI030616	2.69	2.56	2.57	2.56	2.57	2.56	1.03	down	3.50E-01	8.95E-01	-	-
1391350_at	H2afy2	H2A histone family, member Y2	361844	Rn.163432	BI300243	2.65	2.57	2.69	2.79	2.74	2.52	1.03	up	6.48E-01	8.96E-01	-	-
1384564_at	Fam159b	family with sequence similarity 159, member B	499520	Rn.145575	AA925673	2.56	2.55	2.63	2.54	2.57	2.48	1.03	down	2.81E-01	8.95E-01	-	-
1395720_at	---	---	---	Rn.114933	BE098012	2.65	2.65	2.95	2.66	2.71	3.01	1.03	up	7.77E-01	9.28E-01	-	-
1375200_at	Pqcp	polyglutamine-containing protein	314329	Rn.15682	AI169102	2.64	2.76	2.64	2.63	2.64	2.63	1.03	down	3.30E-01	8.95E-01	-	-
1368226_at	RGD620382	Nucleoside 2-deoxyribosyltransferase domain containing protein RGD620382	171047	Rn.6997	NM_133525	2.63	2.62	2.63	2.62	2.78	2.61	1.03	up	4.56E-01	8.95E-01	-	-
1394728_at	---	---	---	---	AI407012	2.67	2.66	2.75	2.70	2.71	2.54	1.03	down	4.98E-01	8.95E-01	-	-
1392803_at	---	---	---	---	AI232150	2.50	3.27	2.55	3.01	2.69	2.49	1.03	down	8.84E-01	9.64E-01	-	-
1394642_at	---	---	---	Rn.1341	AI228209	2.41	2.41	2.41	2.55	2.42	2.39	1.03	up	3.97E-01	8.95E-01	-	-
1394222_at	Znf771	zinc finger protein 771	308992	Rn.32501	AI556398	5.29	8.58	6.77	8.08	5.85	6.57	1.03	down	9.71E-01	9.91E-01	-	-
1380035_at	MGC125002	similar to RIKEN cDNA 5830433M19	500501	Rn.9502	BF523119	3.24	2.92	2.95	2.93	2.94	3.10	1.03	down	7.23E-01	9.12E-01	-	-
1394361_a_at	Wnt2	wingless-type MMTV integration site family member 2	114487	Rn.203764	BF556985	2.47	2.35	2.37	2.35	2.36	2.34	1.03	down	2.99E-01	8.95E-01	-	-
1370810_at	Ccnd2	cyclin D2	64033	Rn.96083	L09752	2.39	2.53	2.41	2.36	2.49	2.35	1.03	down	5.04E-01	8.95E-01	-	-
1380994_at	Otud7b	OTU domain containing 7B	310677	Rn.199225	BG374428	2.93	2.93	2.95	2.92	2.94	3.08	1.03	up	4.29E-01	8.95E-01	-	-
1397227_at	Tmem35	transmembrane protein 35	308134	Rn.45854	BE120895	4.97	5.74	6.36	5.50	5.05	6.39	1.03	down	9.41E-01	9.83E-01	-	-
1376817_at	Iars2	isoleucyl-tRNA synthetase 2, mitochondrial	364070	Rn.163241	AA943165	2.46	2.54	2.46	2.45	2.46	2.41	1.03	down	2.33E-01	8.95E-01	-	-
1397787_at	---	---	---	Rn.156389	BF416511	3.10	2.97	3.01	3.60	2.96	2.65	1.03	up	8.81E-01	9.64E-01	-	-
1381169_at	---	---	---	---	AW253396	2.69	2.54	2.56	2.56	2.56	2.54	1.03	down	3.81E-01	8.95E-01	-	-
1373307_at	Mon1a	MON1 homolog A (yeast)	315999	Rn.25237	BE111711	4.10	4.36	3.96	4.10	4.10	4.09	1.03	down	7.23E-01	9.12E-01	-	-
1367684_at	Crybb2	crystallin, beta B2	25422	Rn.10350	NM_012937	2.37	2.36	2.50	2.37	2.37	2.36	1.03	down	3.65E-01	8.95E-01	-	-
1398226_at	---	---	---	Rn.210144	BF394522	2.54	2.52	2.63	2.54	2.57	2.45	1.03	down	4.09E-01	8.95E-01	-	-
1389343_at	RGD1560187	similar to Hypothetical UPF0327 protein	362641	Rn.14670	H35203	10.97	10.89	10.90	10.82	10.77	11.03	1.03	down	6.24E-01	8.95E-01	-	-
1376349_a_at	Slc29a2	solute carrier family 29 (nucleoside transporters), member 2	65194	Rn.37517	BM391418	3.46	2.79	2.74	3.25	2.80	2.81	1.03	down	8.80E-01	9.63E-01	-	-
1382649_at	Ssb	Sjogren syndrome antigen B	81783	Rn.24494	AI030649	8.98	9.42	9.40	9.46	9.02	9.19	1.03	down	8.30E-01	9.46E-01	-	-
1397378_at	---	---	---	Rn.75045	BE115240	2.57	2.53	2.62	2.54	2.80	2.51	1.03	up	6.69E-01	9.00E-01	-	-
1380526_at	Gcdh	glutaryl-Coenzyme A dehydrogenase	364975	Rn.99039	AI029435	4.76	4.58	4.67	4.59	4.65	4.65	1.03	down	4.72E-01	8.95E-01	-	-
1368670_a_at	Pde4a	phosphodiesterase 4A, cAMP-specific (phosphodiesterase E2 dunce homolog	25638	Rn.91330	L36467	2.66	2.77	2.92	2.71	3.05	2.73	1.03	up	7.56E-01	9.21E-01	-	-
1384226_at	---	---	---	Rn.16010	AI602005	2.39	2.50	2.40	2.38	2.39	2.38	1.03	down	2.84E-01	8.95E-01	-	-
1384415_at	Sox7	SRY (sex determining region Y)-box 7	290317	Rn.17732	AI058292	2.51	2.37	2.40	2.38	2.40	2.37	1.03	down	3.44E-01	8.95E-01	-	-
1387534_at	Cyct	cytochrome c, testis	25310	Rn.88630	NM_012840	2.67	2.65	2.74	2.64	2.70	2.59	1.03	down	3.47E-01	8.95E-01	-	-
1387898_at	Hspb6	heat shock protein, alpha-crystallin-related, B6	192245	Rn.3201	D29860	4.92	4.82	3.58	4.43	4.56	4.21	1.03	down	9.25E-01	9.78E-01	-	-
1390100_s_at	---	---	---	Rn.203200	BG371810	2.53	3.38	2.38	3.42	2.43	2.58	1.03	up	9.24E-01	9.78E-01	-	-
1372036_at	Cd2bp2	Cd2 (cytoplasmic tail) binding protein 2	293505	Rn.14633	BG378032	10.18	10.63	10.49	10.53	10.21	10.68	1.03	up	8.27E-01	9.45E-01	-	-
1377675_at	LOC100302372	hypothetical protein LOC100302372	100302372	---	AI177743	2.40	2.38	2.46	2.54	2.41	2.42	1.03	up	4.12E-01	8.95E-01	-	-
1391113_at	Rhbdl3	rhomboid, veinlet-like 3 (Drosophila)	287556	Rn.20693	BI289575	2.35	2.34	2.35	2.34	2.50	2.33	1.03	up	4.59E-01	8.95E-01	-	-
1395347_at	Arsa	arylsulfatase A	315222	Rn.23323	BF565675	2.63	2.51	2.52	2.51	2.52	2.50	1.03	down	3.13E-01	8.95E-01	-	-
1398784_at	C1qbp	complement component 1, q subcomponent binding protein	29681	Rn.2765	NM_019259	9.90	9.74	10.11	9.63	9.85	10.13	1.03	down	8.18E-01	9.42E-01	-	-
1392549_at	---	---	---	Rn.62243	AA875587	2.47	2.47	2.47	2.60	2.48	2.47	1.03	up	3.49E-01	8.95E-01	-	-
1386892_at	Ptms	parathymosin	83801	Rn.3609	NM_031975	10.83	10.97	10.89	10.93	10.92	10.71	1.03	down	6.14E-01	8.95E-01	-	-
1381482_at	---	---	---	Rn.166635	AI555166	8.70	8.48	7.82	8.17	8.48	8.23	1.03	down	8.83E-01	9.64E-01	-	-
1398069_at	---	---	---	---	BF393848	2.47	2.60	2.60	2.46	2.50	2.44	1.03	down	4.26E-01	8.95E-01	-	-
1367512_at	Chmp5	chromatin modifying protein 5	297995	Rn.9339	AA998435	11.88	11.70	11.77	11.88	11.79	11.82	1.03	up	4.92E-01	8.95E-01	-	-
1372483_at	Zfp469	zinc finger protein 469	304302	Rn.20495	AI230979	5.15	5.34	5.01	5.26	5.08	5.02	1.03	down	7.31E-01	9.14E-01	-	-
1384600_at	---	---	---	Rn.166367	AI070374	2.43	2.42	2.44	2.42	2.62	2.38	1.03	up	5.94E-01	8.95E-01	-	-
1383589_at	---	---	---	---	BE103947	2.50	2.50	2.64	2.46	2.53	2.53	1.03	down	4.29E-01	8.95E-01	-	-
1372931_at	Praf2	PRA1 domain family, member 2	367743	Rn.6226	AI178741	2.71	2.54	2.61	2.51	2.62	2.59	1.03	down	4.88E-01	8.95E-01	-	-
1386259_a_at	RGD1306772	similar to RIKEN cDNA 1110008J03	288683	Rn.20168	AI104152	2.81	2.68	2.68	2.68	2.68	2.67	1.03	down	3.64E-01	8.95E-01	-	-
1397481_at	---	---	---	Rn.33283	BE120751	2.52	2.48	2.62	2.49	2.53	2.46	1.03	down	3.99E-01	8.95E-01	-	-
1383439_at	Npas2	neuronal PAS domain protein 2	316351	Rn.8285	BI278550	2.40	2.38	2.51	2.39	2.40	2.37	1.03	down	3.42E-01	8.95E-01	-	-
1389991_at	Fbf1	Fas (TNFRSF6) binding factor 1	287836	Rn.206391	BI278555	4.25	4.26	4.37	4.21	4.27	4.26	1.03	down	3.55E-01	8.95E-01	-	-
1395057_at	---	---	---	Rn.177644	BM389984	2.28	2.28	2.28	2.28	2.42	2.27	1.03	up	4.18E-01	8.95E-01	-	-
1382802_x_at	---	---	---	---	AW520828	2.42	2.30	2.30	2.30	2.29	2.29	1.03	down	3.43E-01	8.95E-01	-	-
1380456_at	---	---	---	Rn.163414	AI044224	2.52	2.50	2.53	2.67	2.52	2.49	1.03	up	4.65E-01	8.95E-01	-	-
1380301_at	---	---	---	Rn.15116	BM385833	3.99	4.15	5.68	4.16	5.31	4.23	1.03	down	9.49E-01	9.85E-01	-	-
1391924_at	LOC361187	similar to ankyrin repeat and SOCs box-containing protein 5	361187	Rn.54639	AI170760	2.45	2.46	2.62	2.61	2.47	2.46	1.03	down	4.51E-01	8.95E-01	-	-
1394898_at	---	---	---	Rn.164761	BF286853

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1389908_at	---	---	---	Rn.160119	BE107167	9.87	9.87	9.98	9.94	10.11	9.81	1.03	up	6.71E-01	9.00E-01	-	-
1379358_at	Samd4a	Sterile alpha motif domain containing 4A	305826	Rn.32662	BE108208	2.67	2.62	2.59	2.56	2.81	2.64	1.03	up	6.14E-01	8.95E-01	-	-
1381171_at	---	---	---	Rn.211290	BF410222	2.55	2.53	2.65	2.53	2.56	2.51	1.03	down	3.48E-01	8.95E-01	-	-
1376071_at	---	---	---	Rn.3101	BM389326	2.42	2.45	2.39	2.39	2.39	2.35	1.03	down	9.29E-02	8.95E-01	-	-
1391507_at	Znf467	zinc finger protein 467	500110	Rn.27249	BF417765	5.53	6.13	5.73	5.76	5.12	6.39	1.03	down	9.20E-01	9.76E-01	-	-
1398102_at	---	---	---	---	AI511219	2.52	2.58	2.52	2.50	2.52	2.47	1.03	down	1.50E-01	8.95E-01	-	-
1396653_at	RGD1563946	similar to mKIAA1623 protein	306340	Rn.141288	BF399505	2.50	2.53	2.59	2.48	2.53	2.48	1.03	down	2.50E-01	8.95E-01	-	-
1370261_at	Rps6ka1	ribosomal protein S6 kinase polypeptide 1	81771	Rn.34915	BI285433	3.19	2.85	2.93	2.97	2.96	3.16	1.03	up	7.40E-01	9.16E-01	-	-
1373704_at	---	---	---	Rn.205196	BF389325	2.57	3.05	2.72	2.67	2.71	3.09	1.03	up	8.35E-01	9.48E-01	-	-
1375177_at	Klf13	Kruppel-like factor 13	499171	Rn.22229	AI454932	2.29	2.25	2.74	2.40	2.63	2.38	1.03	up	8.18E-01	9.42E-01	-	-
1389310_at	---	---	---	Rn.7568	BF400694	4.14	4.43	6.79	4.41	4.98	5.84	1.03	down	9.65E-01	9.90E-01	-	-
1381578_at	Dusp13	dual specificity phosphatase 13	361002	Rn.137327	BF407867	2.29	2.28	2.43	2.28	2.31	2.28	1.03	down	4.11E-01	8.95E-01	-	-
1397861_at	Vstm2b	V-set and transmembrane domain containing 2B	361560	Rn.65503	BF405195	2.50	2.48	2.52	2.59	2.57	2.48	1.03	up	2.94E-01	8.95E-01	-	-
1392373_at	---	---	---	Rn.210223	BF400637	2.41	2.51	2.42	2.40	2.42	2.39	1.03	down	2.67E-01	8.95E-01	-	-
1387056_at	Axin1	axin 1	79257	Rn.31781	NM_024405	3.63	3.56	3.50	3.55	3.71	3.56	1.03	up	5.48E-01	8.95E-01	-	-
1379700_at	Hs1bp3	HCLS1 binding protein 3	313950	Rn.23111	AA956376	6.94	7.46	6.91	7.25	7.14	7.05	1.03	up	8.29E-01	9.46E-01	-	-
1385270_s_at	lab1b /// Rab1b-ps	RAB1B, member RAS oncogene family /// RAB1B, member RAS oncogene fa	80126191 /// 36177	Rn.105979	AI236576	2.84	2.52	2.58	2.49	2.56	2.76	1.03	down	7.48E-01	9.18E-01	-	-
1395783_at	---	---	---	Rn.167768	AI454003	2.65	2.64	2.65	2.35	2.65	2.81	1.03	down	7.63E-01	9.22E-01	-	-
1390159_at	Rasgrp3	RAS guanyl releasing protein 3 (calcium and DAG-regulated)	313874	Rn.1995	AA819332	2.80	2.63	2.44	2.73	2.54	2.47	1.03	down	7.51E-01	9.19E-01	-	-
1374211_at	RGD1566084	similar to Hypothetical protein LOC73072	501795	Rn.214770	BG380798	2.35	2.36	2.37	2.50	2.37	2.35	1.03	up	4.14E-01	8.95E-01	-	-
1383221_at	RGD1563547	RGD1563547	360478	Rn.137175	BG378440	8.34	9.04	8.89	8.73	8.46	8.96	1.03	down	8.75E-01	9.61E-01	-	-
1398279_at	Trpv5	transient receptor potential cation channel, subfamily V, member 5	116469	Rn.137513	NM_053787	4.20	4.30	4.31	4.36	3.79	4.79	1.03	up	8.89E-01	9.65E-01	-	-
1368480_at	Cdw92	CDW92 antigen	85254	Rn.97686	NM_053492	2.46	2.32	2.33	2.32	2.33	2.32	1.03	down	3.80E-01	8.95E-01	-	-
1388484_at	Ube2c	ubiquitin-conjugating enzyme E2C	296368	Rn.3102	BI296084	2.50	2.52	2.53	2.44	2.51	2.48	1.03	down	1.18E-01	8.95E-01	-	-
1390126_at	---	---	---	---	BE112913	9.24	9.64	8.90	9.07	9.05	9.52	1.03	down	8.76E-01	9.62E-01	-	-
1370993_at	Lamc1	laminin, gamma 1	117036	Rn.7145	AA997129	2.98	2.50	2.51	2.77	2.50	2.84	1.03	up	8.31E-01	9.47E-01	-	-
1394954_at	Slc31a2	solute carrier family 31 (copper transporters), member 2	298091	Rn.15570	BE101666	2.33	2.96	2.34	2.32	2.83	2.61	1.03	up	8.73E-01	9.61E-01	-	-
1381721_at	---	---	---	---	BF388113	2.35	2.35	2.36	2.35	2.50	2.34	1.03	up	4.36E-01	8.95E-01	-	-
1376368_at	Cuedc2	CUE domain containing 2	294009	Rn.19673	BE095878	5.90	7.52	7.09	5.49	7.33	7.57	1.03	down	9.60E-01	9.89E-01	-	-
1393957_at	---	---	---	---	AI548358	2.49	2.48	2.51	2.55	2.49	2.57	1.03	up	1.42E-01	8.95E-01	-	-
1399111_at	Cyb561d2	cytochrome b-561 domain containing 2	363137	Rn.25517	AI102191	4.01	4.54	4.33	4.33	4.38	4.31	1.03	up	7.94E-01	9.34E-01	-	-
1388300_at	Mgst3	microsomal glutathione S-transferase 3	289197	Rn.1916	AA892234	9.41	9.53	8.98	9.54	8.97	9.28	1.03	down	8.63E-01	9.57E-01	-	-
1371722_at	Rrp7a	ribosomal RNA processing 7 homolog A (S. cerevisiae)	362967	Rn.4204	BI274676	5.17	4.72	4.92	4.84	4.96	5.15	1.03	up	7.98E-01	9.35E-01	-	-
1376218_a_at	LOC685152	similar to Probable phospholipid-transporting ATPase ID (ATPase class I type	685152	Rn.164557	BI273855	2.67	2.61	2.66	2.65	2.79	2.62	1.03	up	4.88E-01	8.95E-01	-	-
1391007_s_at	Kcnj11	potassium inwardly rectifying channel, subfamily J, member 11	83535	Rn.3985	BE113377	2.89	2.66	2.67	2.77	2.67	2.65	1.03	down	6.26E-01	8.95E-01	-	-
1398918_at	Zfand3	zinc finger, AN1-type domain 3	361816	Rn.136939	BG380742	5.34	5.70	5.47	5.35	5.39	5.65	1.03	down	7.75E-01	9.27E-01	-	-
1371051_at	Grin1a	glutamate receptor, ionotropic, N-methyl D-aspartate-like 1A	192147	Rn.144666	BG664035	5.76	4.57	4.02	4.47	4.42	5.33	1.03	down	9.45E-01	9.84E-01	-	-
1370740_at	Klra5	killer cell lectin-like receptor, subfamily A, member 5	297666	Rn.37467	U58863	2.67	2.80	3.21	2.82	3.12	2.62	1.03	down	8.51E-01	9.54E-01	-	-
1397132_at	Zfp207	Zinc finger protein 207	303763	Rn.163156	BF390612	3.69	3.56	3.59	3.55	3.93	3.23	1.03	down	8.45E-01	9.52E-01	-	-
1382635_at	Scyl1	SCY1-like 1 (S. cerevisiae)	293684	Rn.143751	BF289119	3.05	3.41	2.90	3.43	2.91	3.14	1.03	up	8.49E-01	9.53E-01	-	-
1380210_at	Gimap1	GTPase, IMAP family member 1	312312	Rn.153907	AI136325	2.48	2.46	2.57	2.46	2.48	2.44	1.03	down	3.03E-01	8.95E-01	-	-
1383865_at	RGD1308759	Similar to KIAA0892 protein	290668	Rn.49215	AA944094	2.25	2.37	2.25	2.25	2.25	2.24	1.03	down	3.26E-01	8.95E-01	-	-
1378761_at	---	---	---	Rn.60851	BF392783	2.36	2.46	2.36	2.35	2.35	2.35	1.03	down	2.52E-01	8.95E-01	-	-
1382790_at	Smc5	structural maintenance of chromosomes 5	293967	Rn.127947	AI639485	2.88	2.73	2.98	2.94	2.44	3.34	1.03	up	8.80E-01	9.63E-01	-	-
1387047_at	Hspb3	heat shock protein 3	78951	Rn.20155	NM_031750	2.48	2.47	2.51	2.48	2.49	2.36	1.03	down	3.73E-01	8.95E-01	-	-
1396899_at	---	---	---	Rn.208297	BE119227	2.72	2.65	2.82	2.69	2.78	2.59	1.03	down	5.99E-01	8.95E-01	-	-
1397781_at	---	---	---	Rn.205785	BF414751	2.53	2.46	2.64	2.50	2.51	2.48	1.03	down	4.51E-01	8.95E-01	-	-
1368971_at	Synj2	synaptojanin 2	84018	Rn.10868	AY034051	2.42	2.41	2.51	2.40	2.43	2.39	1.03	down	2.73E-01	8.95E-01	-	-
1397798_at	---	---	---	---	BE120611	2.53	2.49	2.59	2.51	2.61	2.62	1.03	up	3.87E-01	8.95E-01	-	-
1369177_at	Pik4c2a	phosphatidylinositol 4-kinase type 2 alpha	114554	Rn.162533	NM_053735	2.78	2.78	2.92	2.78	2.79	2.78	1.03	down	4.13E-01	8.95E-01	-	-
1373248_at	RGD1565800	Similar to hypothetical protein FLJ20674	304529	Rn.114291	BI292079	2.58	2.32	3.11	2.41	2.46	3.27	1.03	up	9.11E-01	9.73E-01	-	-
1388240_a_at	Itga7	integrin alpha 7	81008	Rn.54492	X74294	2.58	2.69	2.59	2.58	2.58	2.57	1.03	down	2.81E-01	8.95E-01	-	-
1382513_at	Trem2	triggering receptor expressed on myeloid cells 2	301227	Rn.106975	BF288995	2.37	2.34	2.45	2.34	2.35	2.34	1.03	down	2.45E-01	8.95E-01	-	-
1389736_at	---	---	---	Rn.136777	BM392358	2.58	2.65	2.59	2.56	2.58	2.54	1.03	down	1.60E-01	8.95E-01	-	-
1378344_at	Cyb5	Cytochrome b-245, beta polypeptide	66021	Rn.98457	AI176057	2.50	2.70	2.41	2.75	2.55	2.45	1.03	up	7.40E-01	9.16E-01	-	-
1392527_at	383663 /// RGD156	similar to translocase of the inner mitochondrial membrane 14 isoform a /// sir	502525 /// 683663	Rn.6532	AI137840	9.94	9.85	10.00	9.89	9.86	9.91	1.03	down	4.09E-01	8.95E-01	-	-
1370325_at	Gorasp2	golgi reassembly stacking protein 2	113961	Rn.145137	AF110267	5.20	5.29	5.64	5.45	5.40	5.41	1.03	up	7.69E-01	9.24E-01	-	-
1371857_at	Kctd10	potassium channel tetramerization domain containing 10	294521	Rn.185282	AI010108	3.91	4.19	3.92	3.77	4.00	4.11	1.03	down	7.66E-01	9.24E-01	-	-
1387871_at	89 /// LOC688430	cofilin 1, non-muscle /// similar to Cofilin-1 (Cofilin, non-muscle isoform) /// sim	363176 /// 502589	Rn.11675	BM389673	3.41	3.39	3.29	3.39	3.39	3.43	1.03	up	3.54E-01	8.95E-01	-	-
1395831_at	---	---	---	Rn.172103	BF288661	2.65	2.56	2.63	2.58	2.60	2.53	1.03	down	2.93E-01	8.95E-01	-	-
1385573_at	Homer3	Homer homolog 3 (Drosophila)	29548	Rn.144573	AI070797	2.29	2.39	2.30	2.27	2.29	2.28	1.03	down	2.46E-01	8.95E-01	-	-
1372257_at	---	---	---	Rn.7356	BG862579	6.33	6.16	5.88	5.87	5.79	6.58	1.03	down	8.86E-01	9.65E-01	-	-
1370454_at	Homer1	homer homolog 1 (Drosophila)	29546	Rn.37500	AB003726	3.30	2.99	3.15	3.16	3.28	3.13	1.03	up	6.92E-01	9.05E-01	-	-
1377870_at	LOC301128	similar to jumonji domain containing 2B	301128	Rn.6679	BM392277	2.31	2.30	2.31	2.30	2.31	2.43	1.03	up	3.65E-01	8.95E-01	-	-
1368425_at	Caskin1	CASK interacting protein 1	140722	Rn.48905	NM_080690	2.43	2.32	2.36	2.33	2.34	2.32	1.03	down	2.36E-01	8.95E-01	-	-
1378907_at	RGD1563532	similar to ankyrin repeat domain 25	300439	---	AI454868	2.57	2.36	2.56	2.54	2.56	2.53	1.03	up	5.63E-01	8.95E-01	-	-
1367464_at	Siahbp1	siah binding protein 1; FBP interacting repressor; pyrimidine tract binding splic	84401	Rn.96174	AI598391	8.01	8.00	7.76	8.14	7.52	7.98	1.03	down	8.42E-01	9.51E-01	-	-
1375920_at	Plekho1	pleckstrin homology domain containing, family O member 1	310674	Rn.21037	AI406305	2.69	2.65	2.71	2.89	2.70	2.59	1.03	up	6.58E-01	8.98E-01	-	-
1379266_at	---	---	---	Rn.17750	AI235399	2.68	2.67	2.69	2.82	2.68	2.67	1.03	up	4.15E-01	8.95E-01	-	-
1387076_at	Hif1a	hypoxia-inducible factor 1, alpha subunit (basic helix-loop-helix transcription f	29560	Rn.10852	NM_024359	6.17	6.13	6.17	5.54	6.44	6.36	1.03	down	8.88E-01	9.65E-01	-	-
1385575_at	Tyrp1	tyrosinase-related protein 1	298182	Rn.40774	BG665058	2.57	2.47	2.48	2.47	2.48	2.44	1.03	down	3.08E-01	8.95E-01	-	-
1370611_at	Ahrr	aryl hydrocarbon receptor nuclear translocator 2	25243	Rn.10518	U61405	2.33	2.32	2.33	2.35	2.33	2.42	1.03	up	1.93E-01	8.95E-01	-	-
1385218_at	OC685468 /// Noc	similar to nucleolar complex associated 3 homolog /// nucleolar complex asso	361753 /// 685468	Rn.196322	AI044551	2.87	2.61	2.71	2.62	2.71	2.72	1.03	down	6.25E-01	8.95E-01	-	-
1377286_at	Gimap4	GTPase, IMAP family member 4	286938	Rn.198155	BM389208	3.86	2.46	2.66	3.33	2.80	2.97	1.03	up	9.31E-01	9.81E-01	-	-
1387438_at	Ltc4s	leukotriene C4 synthase	114097	Rn.38594	NM_053639	2.34	2.34	2.34	2.47	2.34	2.34	1.03	up	3.67E-01	8.95E-01	-	-
1389255_at	Cdh5	Cadherin 5	307618	Rn.164510	BE110616	2.91	2.41	2.45	2.80	2.45	2.39	1.03	down	8.45E-01	9.52E-01	-	-
1369055_at	Lpar3	lysophosphatidic acid receptor 3	66025	Rn.64507	NM_023969	2.50	2.48	2.50	2.63	2.50	2.48	1.03	up	4.18E-01	8.95E-01	-	-
1372787_at	Utp3	UTP3, small subunit (SSU) processome component, homolog (S. cerevisiae)	305258	Rn.23516	BE106508	7.49	7.99	8.61	7.58	8.23	8.15	1.03	down	9.17E-01	9.75E-01	-	-
1399099_at	Hnrnpul1	heterogeneous nuclear ribonucleoprotein U-like 1	361522	Rn.95170	BG381219	4.31	5.50	4.27	4.88	4.58	4.74	1.03	up	9.23E-01	9.77E-01	-	-
1377171_at	Lzts1	leucine zipper, putative tumor suppressor 1	266711	Rn.3213	AA875041	2.37	2.35	2.36	2.35	2.36	2.49	1.03	up	3.96E-01	8.95E-01	-	-
1397353_at	---	---	---	---	AW920297	2.48	2.43	2.55	2.46	2.47	2.40	1.03	down	3.27E-01	8.95E-01	-	-
1387827_x_at	Hist1h2bp	histone cluster 1, H2bp	306969	---	NM_022647	2.69	2.60	2.80	2.64	2.77	2.55	1.03	down	6.47E-01	8.95E-01	-	-
1376123_at	Arfgap1	ADP-ribosylation factor GTPase activating protein 1	246310	Rn.11219	BM384190	3.15	2.93	2.95	2.93	2.85	3.12	1.03	down	7.12E-01	9.10E-01	-	-
1381133_at	---	---	---	Rn.201907	BF409213	8.45	7.08	7.12	8.25	8.21	6.06	1.03	down	9.62E-01	9.89E-01	-	-
1394927_at	Dnajc11	DnaJ (Hsp40) homolog, subfamily C, member 11	362666	Rn.66161	BF406642	2.67	2.70	2.68	2.61	2.67	2.65	1.03	down	1.13E-01	8.95E-01	-	-
1397593_at	---	---	---	Rn.63094	BF416553	2.52	2.40	2.41	2.40	2.41	2.39	1.03	down	3.45E-01	8.95E-01	-	-
1373007_at	---	---	---	Rn.63324	BF417885	2.74	2.68	2.85	2.70	2.83	2.61	1.03	down	6.30E-01	8.95E-01	-	-
1376083_at	Memo1	Mediator of cell motility 1	298787	Rn.22312	BE112924	4.43	4.33	4.44	4.43	4.48	4.42	1.03	up	3.39E-01	8.95E-01	-	-
1370374_at	Steap3	STEAP family member 3	170824	Rn.16304	AF335281	2.68	2.67	2.79	2.67	2.68	2.66	1.03	down	3.25E-01	8.95E-01	-	-
1380289_at	LOC691468	similar to Zinc finger protein 84 (Zinc finger protein HPF2)	691468	Rn.35202	AA799834	2.86	2.85	3.48	3.97	2.70	2.66	1.03	up	9.33E-01	9.81E-01	-	-
1381057_at	---	---	---	Rn.199627	AW526130	2.67	2.44	2.40	2.39	2.43	2.56	1.03	down	6.89E-01	9.04E-01	-	-
1380341_at	---	---	---	Rn.146686	BE096469	2.43	2.43	2.44	2.40	2.44	2.59	1.03	up	5.08E-01	8.95E-01	-	-
1392166_at	---	---	---	Rn.90013	BE099838	2.65	2.60	2.76	2.60	2.73	2.55	1.03	down	5.83E-01	8.95E-01	-	-
1384075_at	---	---	---	Rn.147819	BF523960	2.38	2.50	2.39	2.38	2.39	2.38	1.03	down	3.25E-01	8.95E-01	-	-
1394575_at	Gnal	guanine nucleotide binding protein, alpha stimulating, olfactory type	24611	---	BI281656	2.40	2.39	2.50	2.36	2.41	2.38	1.03	down	3.03E-01	8.95E-01	-	-
1390403_at	Fam43a	family with sequence similarity 43, member A	288031	Rn.220114	BE108405	5.56	6.76	4.77	5.80	5.30	5.86	1.03	down	9.48E-01	9.85E-01	-	-
1377942_at	---	---	---	Rn.28084	AI101595	2.55	2.49	2.67	2.51	2.59	2.48	1.03	down	5.32E-01	8.95E-01	-	-
1379711_at	---	---	---	Rn.147218	BE107458	2.56	2.44	2.45	2.44	2.46	2.43	1.03	down	3.56E-01	8.95E-01	-	-
1374772_at	Serp2	stress-associated endoplasmic reticulum protein family member 2	498546	Rn.15872	BE100409	2.47	2.40	2.45	2.40	2.40	2.39	1.03	down	1.21E-01	8.95E-01	-	-
1391708_at	---	---	---	Rn.49187	BE096515	2.52	2.39	2.42	2.41	2.39	2.39	1.03	down	3.42E-01	8.95E-01	-	-
1388645_at	Ola1	Obg-like ATPase 1	296488	Rn.5874	AI175494	8.23	7.79	8.30	7.78	8.03	8.38	1.03	down	8.65E-01	9.58E-01	-	-
1375696_at	Ifnar1	interferon (alpha, beta and omega) receptor 1	288264	Rn.105738	BF420426	2.99	2.45	2.48	2.39	2.37	3.03	1.03	down	8.86E-01	9.65E-01	-	-
1396802_at	---	---	---	---	BE107837	2.46	2.44	2.58	2.45	2.46	2.45	1.03	down	3.75E-01	8.95E-01	-	-
1391372_at	---	---	---	Rn.210919	BF405555	2.64	2.46	2.51	2.49	2.51	2.48	1.03	down	4.84E-01	8.95E-01	-	-
1393690_at	Insig2	insulin induced gene 2	288985	Rn.16736	AA818627	2.55	2.81	2.60	2.65	2.64	2.80	1.03	up	6.75E-01	9.01E-01	-	-
1376509_at	---	---	---	---	AW435117	2.19	2.19	2.20	2.19	2.32	2.19	1.03	up	3.89E-01	8.95E-01	-	-
1397298_at	---	---	---	---	AI011647	2.52	2.53	2.56	2.51	2.53	2.44	1.03	down	2.45E-01	8.95E-01	-	-
1390816_at	LOC685152	similar to Probable phospholipid-transporting ATPase ID (ATPase class I type	685152	Rn.164557	AW529940	2.52	2.47	2.62	2.50	2.50	2.49	1.03	down	3.79E-01	8.95E-01	-	-
1372826_at	---	---	---	Rn.4237	BI285718	6.26	6.25	6.39	6.26	6.26	6.26	1.03	down	3.84E-01	8.95E-01	-	-
1397911_at	---	---	---	---	BF414298	4.94	4.55	3.89	3.50	5.03	4.72	1.03	down	9.43E-01	9.84E-01	-	-
1376960_at	---	---	---	Rn.217702	AA892240	2.71	2.92	2.75	2.74	2.80	2.73	1.03	down	5.68E-01	8.95E-01	-	-
1373389_at	---	---	---	Rn.166888	AI145613	7.45	5.99	6.06	7.09	5.80	6.49	1.03	down	9.48E-01	9.85E-01	-	-
1392127_at	---	---	---	Rn.47529	BF400081	2.55	2.63	2.55	2.55	2.61	2.49	1.03	down	3.52E-01	8.95E-01	-	-
1381624_at	---	---	---	Rn.206240	BF391717	2.59	2.48	2.54	2.49	2.53	2.46	1.03	down	3.35E-01	8.95E-01	-	-
1373999_at	---	---	---	Rn.164900	AI406350	5.63	5.83	5.68	5.21	5.68	6.13	1.03	down	8.85E-01	9.64E-01	-	-
1379672_at	---	---	---	Rn.27953	AI103938	2.46	2.45	2.58	2.45	2.47	2.44	1.03	down	3.75E-01	8.95E-01	-	-
1385196_at	---	---	---	Rn.3089	AA866391	2.47	2.44	2.57	2.45	2.50	2.40	1.03	down	4.12E-01	8.95E-01	-	-
1388605_at	Wfdc3	WAP four-disulfide core domain 3	296366	Rn.161867	BM384938	4.81	5.67	6.09	5.10	6.04	5.30	1.03	down	9.33E-01	9.81E-01	-	-
1376885_at	---	---	---	Rn.24070	BE095660	5.75	6.59	6.15	5.45	6.57	6.60	1.03	up	9.29E-01	9.80E-01	-	-
1374747_at	Pftk1	PFTAIRE protein kinase 1	362316	Rn.12908	BM384279	6.46	5.36	5.67	5.85	5.53	5.98	1.03	down	9.11E-01	9.73E-01	-	-
1376439_at	---	---	---	Rn.101593	BF403552	2.40	2.39	2.40	2.53	2.40	2.39	1.03	up	4.04E-01	8.95E-01	-	-
1381895_at	Nrf1	nuclear respiratory factor 1	312195	Rn.17159	AW435074	3.15	3.15	3.16	3.15	3.32	3.11	1.03	up	5.49E-01	8.95E-01	-	-
1393423_at	Tnks2	tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase 2	309512	Rn.75286	H32233	2.40	2.39	2.42	2.41	2.42	2.52	1.03	up	3.14E-01	8.95E-01	-	-
1379001_at	---	---	---	Rn.203408	AA945695	2.43	2.42	2.51	2.40	2.42	2.43	1.03	down	2.08E-01	8.95E-01	-	-
1376751_at	Stk19	serine/threonine kinase 19	361800	Rn.17283	AI044250	2.38	2.36	2.39	2.51	2.39	2.37	1.03	up	3.80E-01	8.95E-01	-	-
1375603_at	---	---	---	---	AI716154	2.47	2.46	2.59	2.46	2.47	2.46	1.03	down	3.67E-01	8.95E-01	-	-
1387305_s_at	lyp11b1 /// Cyp11b	cytochrome P450, subfamily 11B, polypeptide 1 /// cytochrome P450, subfami	24294 /// 500892	Rn.144549	NM_012539	2.55	2.54	2.60	2.49	2.59	2.48	1.03	down	3.34E-01	8.95E-01	-	-
1388155_at	Krt18	keratin 18	294853	Rn.103924	BI286012	2.63	2.49	2.64	2.62	2.63	2.62	1.03	up	4.37E-01	8.95E-01	-	-
1395012_at	Hero4	hect domain and RLD 4	309758	Rn.18143	BE106727	2.53	2.52	2.53	2.52	2.53	2.66	1.03	up	3.83E-01	8.95E-01	-	-
1371006_at	Jag2	jagged 2	29147	Rn.22459	BI274746	2.70	2.61	2.64	2.49	2.62	2.70	1.03	down	5.58E-01	8.95E-01	-	-
1395870_at	Trmt2a	TRM2 tRNA methyltransferase 2 homolog A (S. cerevisiae)	287953	Rn.60258	BF403357	2.71	2.58	2.61	2.59	2.62	2.57	1.03	down	3.46E-01	8.95E-01	-	-
1395167_at	---	---	---	---	BG672109	3.33	3.32	3.38	3.33	3.59	3.24	1.03	up	7.13E-01	9.10E-01	-	-
1381684_at	---	---	---	Rn.154003	BM391296	2.68	2.53	2.68	2.61	2.63	2.51	1.03	down	5.39E-01	8.95E-01	-	-
1395671_at	Wbscr28	Williams-Beuren syndrome chromosome region 28 (human)	288604	Rn.113318	BF420750	2.47	2.39	2.42	2.37	2.40	2.38	1.03	down	1.35E-01	8.95E-01	-	-
1385771_at	---	---	---	---	BF415532	2.54	2.54	2.61	2.54	2.55	2.48	1.03	down	2.30E-01	8.95E-01	-	-
1381628_at	---	---	---	Rn.199706	AW534812	2.64	2.63	2.72	2.91	2.69	2.52	1.03	up	7.36E-01	9.15E-01	-	-
1393883_at	RGD1306148	similar to KIAA0368	313196	Rn.154631	BF415479	6.12	5.67	4.21	4.95	5.63	5.56	1.03	up	9.49E-01	9.85E-01	-	-
1376244_at	---	---	---	Rn.173052	BF399389	2.36	2.36	2.40	2.36	2.56	2.32	1.03	up	6.14E-01	8.95E-01	-	-
1370039_at	Prm2	protamine 2	25345	Rn.10404	NM_012873	2.46	2.45	2.58	2.46	2.47	2.44	1.03	down	3.65E-01	8.95E-01	-	-
1388314_at	Hmgn1	high-mobility group nucleosome binding domain 1	360754	Rn.4120	BF281179	11.45	11.50	11.52	11.57	11.51	11.52	1.03	up	2.28E-01	8.95E-01	-	-
1385095_at	Rnf222	ring finger protein 222	363827	Rn.161281	BM384473	2.43	2.42	2.55	2.43	2.44	2.42	1.03	down	3.

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1382329_at	---	---	---	---	AW523888	2.57	2.47	2.51	2.48	2.49	2.45	1.03	down	2.53E-01	8.95E-01	-	-
1391617_at	---	---	---	Rn.18667	AI171103	2.34	2.46	2.35	2.34	2.37	2.32	1.03	down	3.63E-01	8.95E-01	-	-
1398585_at	Fbxo21	F-box protein 21	360818	Rn.137498	BE114456	4.24	5.59	4.95	4.91	4.86	5.14	1.03	up	9.22E-01	9.77E-01	-	-
1388003_at	Nfya	nuclear transcription factor-Y alpha	29508	Rn.10747	M34238	2.45	2.57	2.45	2.45	2.36	2.53	1.03	down	5.51E-01	8.95E-01	-	-
1374031_at	Parp6	poly (ADP-ribose) polymerase family, member 6	300759	Rn.137571	BI295824	3.84	4.12	4.30	3.99	4.12	4.27	1.03	up	8.05E-01	9.37E-01	-	-
1394330_at	---	---	---	---	BF544149	5.91	4.98	6.40	5.80	6.15	5.47	1.03	up	9.33E-01	9.81E-01	-	-
1393169_at	---	---	---	Rn.17636	AI578145	2.35	2.34	2.36	2.48	2.36	2.34	1.03	up	3.96E-01	8.95E-01	-	-
1382614_at	Zfyve16	zinc finger, FYVE domain containing 16	499508	Rn.78858	AI029732	4.07	3.31	2.22	4.03	2.65	3.03	1.03	up	9.54E-01	9.87E-01	-	-
1392720_at	Cyp4f17	cytochrome P450, family 4, subfamily f, polypeptide 17	500801	Rn.43212	BG376949	2.52	2.63	2.53	2.52	2.52	2.51	1.03	down	3.03E-01	8.95E-01	-	-
1388391_at	Ndufa1	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 1	363441	Rn.3640	AA996544	12.64	12.69	12.59	12.66	12.63	12.76	1.03	up	4.39E-01	8.95E-01	-	-
1367962_at	Actn3	actinin alpha 3	171009	Rn.17592	NM_133424	2.48	2.35	2.37	2.36	2.37	2.36	1.03	down	3.68E-01	8.95E-01	-	-
1397897_x_at	---	---	---	Rn.136371	BI273954	2.49	2.48	2.57	2.51	2.49	2.42	1.03	down	3.39E-01	8.95E-01	-	-
1381923_at	RGD1564664	similar to LOC387763 protein	499839	Rn.22639	AI454658	4.30	4.11	4.29	4.20	4.18	4.20	1.03	down	5.50E-01	8.95E-01	-	-
1379534_at	---	---	---	Rn.22465	AI104922	2.51	2.50	2.63	2.51	2.52	2.50	1.03	down	3.87E-01	8.95E-01	-	-
1387446_at	C1galt1	core 1 synthase, glycoprotein-N-acetylgalactosamine 3-beta-galactosyltransfe	65044	Rn.37669	NM_022950	5.03	5.36	5.25	4.34	6.34	4.83	1.03	down	9.49E-01	9.85E-01	-	-
1378594_at	---	---	---	Rn.148732	BF402379	2.48	2.35	2.38	2.36	2.37	2.35	1.03	down	3.44E-01	8.95E-01	-	-
1391129_at	---	---	---	Rn.57574	BF394098	2.44	2.43	2.58	2.43	2.46	2.43	1.03	down	4.40E-01	8.95E-01	-	-
1398590_at	---	---	---	Rn.148596	AA965286	2.44	2.43	2.57	2.43	2.45	2.42	1.03	down	4.23E-01	8.95E-01	-	-
1398038_at	---	---	---	Rn.59410	BF399555	2.60	2.60	2.68	2.60	2.61	2.55	1.03	down	2.78E-01	8.95E-01	-	-
1380666_at	Mon1b	MON1 homolog b (yeast)	307868	Rn.63317	BI284181	3.90	5.11	2.29	3.93	3.18	4.32	1.03	up	9.65E-01	9.90E-01	-	-
1370111_at	Kcni2	potassium intermediate/small conductance calcium-activated channel, subfan	54282	Rn.44421	NM_019314	2.50	2.38	2.41	2.39	2.40	2.37	1.03	down	3.29E-01	8.95E-01	-	-
1367882_at	Map1a	microtubule-associated protein 1A	25152	Rn.11402	NM_030995	2.31	2.43	2.32	2.31	2.32	2.31	1.03	down	3.57E-01	8.95E-01	-	-
1367707_at	Fasn	fatty acid synthase	50671	Rn.9486	AI179334	2.57	2.69	4.43	3.06	3.32	3.19	1.03	down	9.49E-01	9.85E-01	-	-
1388585_at	---	---	---	Rn.47344	BF281959	6.29	6.46	6.11	6.69	5.37	6.93	1.03	up	9.38E-01	9.82E-01	-	-
1367802_at	Sgk1	serum/glucocorticoid regulated kinase 1	29517	Rn.4636	NM_019232	9.31	8.23	8.31	9.51	7.32	9.14	1.03	up	9.59E-01	9.89E-01	-	-
1380668_at	MGC72974	Hypothetical LOC316976	316976	Rn.33980	BI275851	2.44	2.74	2.43	2.38	2.85	2.50	1.03	up	8.24E-01	9.44E-01	-	-
1393517_at	---	---	---	Rn.216827	BE097991	2.59	2.55	2.66	2.56	2.57	2.54	1.03	down	2.88E-01	8.95E-01	-	-
1381953_at	St6galnac2	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosami	303692	Rn.53257	AI111705	2.68	2.65	2.73	2.68	2.71	2.55	1.03	down	4.70E-01	8.95E-01	-	-
1392931_at	Atrip	ATR interacting protein	301014	Rn.198820	BM390705	2.71	2.53	2.57	2.55	2.61	2.53	1.03	down	5.26E-01	8.95E-01	-	-
1387303_at	Slc22a2	solute carrier family 22 (organic cation transporter), member 2	29503	Rn.10555	NM_031584	12.00	12.15	11.89	11.89	11.85	12.19	1.03	down	7.68E-01	9.24E-01	-	-
1380986_at	---	---	---	Rn.53234	BF390376	2.43	2.44	2.50	2.41	2.45	2.38	1.03	down	2.41E-01	8.95E-01	-	-
1396987_at	---	---	---	Rn.211136	BF406303	2.34	2.50	2.34	2.34	2.40	2.32	1.03	down	5.08E-01	8.95E-01	-	-
1394841_at	---	---	---	Rn.210243	BF396360	2.59	2.65	2.66	2.72	2.66	2.64	1.03	up	2.71E-01	8.95E-01	-	-
1376880_at	Tbk1	TANK-binding kinase 1	299827	Rn.30683	AI639447	6.60	6.97	6.69	6.74	6.66	6.74	1.03	down	7.40E-01	9.16E-01	-	-
1388460_at	Capg	capping protein (actin filament), gelsolin-like	297339	Rn.8945	BM384693	2.79	4.69	3.08	3.09	3.21	4.38	1.03	up	9.57E-01	9.88E-01	-	-
1382287_at	Rnps1	ribonucleic acid binding protein S1	287113	Rn.7235	BG375343	6.02	6.61	6.14	6.13	6.14	6.38	1.03	down	8.45E-01	9.52E-01	-	-
1398720_at	Kel	Kell blood group, metallo-endopeptidase	297025	Rn.163642	BI289222	2.58	2.55	2.62	2.56	2.58	2.48	1.03	down	3.15E-01	8.95E-01	-	-
1393125_a_at	Sfrs14	splicing factor, arginine/serine-rich 14	361126	Rn.8664	AA855445	4.40	6.40	7.59	5.82	6.63	5.82	1.03	down	9.68E-01	9.91E-01	-	-
1397765_at	---	---	---	Rn.173401	BF406754	4.75	4.44	5.86	4.66	5.55	4.71	1.03	down	9.41E-01	9.83E-01	-	-
1370802_at	Itgb5	integrin, beta 5	257645	Rn.16988	AF336872	2.95	2.70	2.54	2.20	2.63	3.24	1.03	down	9.05E-01	9.71E-01	-	-
1387137_at	Comp	cartilage oligomeric matrix protein	25304	Rn.10343	NM_012834	2.40	2.39	2.40	2.52	2.41	2.39	1.03	up	3.61E-01	8.95E-01	-	-
1379223_x_at	---	---	---	Rn.129744	AW524037	3.00	2.99	3.01	2.99	3.14	2.99	1.03	up	4.51E-01	8.95E-01	-	-
1383568_at	Tube1	tubulin, epsilon 1	361856	Rn.101545	BF523441	2.45	2.44	2.62	2.75	2.45	2.43	1.03	up	7.46E-01	9.18E-01	-	-
1397257_at	---	---	---	Rn.136374	BE108093	2.50	2.53	2.50	2.54	2.58	2.54	1.03	up	8.04E-02	8.95E-01	-	-
1396259_at	Frem3	FRAS1 related extracellular matrix 3	307767	Rn.41880	BE096295	2.46	2.51	2.44	2.43	2.44	2.41	1.03	down	1.38E-01	8.95E-01	-	-
1371454_at	Tmem93	transmembrane protein 93	287477	Rn.258	BI285673	7.45	7.31	7.02	7.30	6.79	7.57	1.03	down	8.83E-01	9.64E-01	-	-
1374792_at	Nol7	nucleolar protein 7	498727	Rn.31940	BM389058	7.41	7.34	7.47	7.54	6.83	7.97	1.03	up	9.09E-01	9.72E-01	-	-
1392228_at	---	---	---	Rn.163715	BI294408	2.92	2.68	3.04	2.91	3.00	2.84	1.03	up	7.44E-01	9.17E-01	-	-
1385067_at	LOC361915	hypothetical protein LOC361915	361915	---	BE117752	2.87	2.84	3.03	2.85	2.95	2.81	1.03	down	6.06E-01	8.95E-01	-	-
1393936_at	Stk22s1	serine/threonine kinase 22 substrate 1	292890	Rn.40908	AI717642	2.46	2.46	2.47	2.45	2.36	2.46	1.03	down	2.56E-01	8.95E-01	-	-
1379891_at	MGC94600	scotin	301013	Rn.102027	AI454858	4.60	4.59	3.89	4.48	3.72	4.76	1.03	down	9.21E-01	9.77E-01	-	-
1392455_at	---	---	---	---	AI105452	2.68	2.60	2.82	2.65	2.78	2.55	1.03	down	6.76E-01	9.02E-01	-	-
1369317_at	Lcn5	lipocalin 5	29552	Rn.10362	NM_024136	2.40	2.38	2.40	2.53	2.41	2.37	1.03	up	4.29E-01	8.95E-01	-	-
1375403_at	---	---	---	Rn.203635	AW251376	2.33	2.44	2.34	2.33	2.33	2.32	1.03	down	3.40E-01	8.95E-01	-	-
1378366_at	---	---	---	Rn.218142	BF386485	2.36	2.35	2.37	2.36	2.50	2.35	1.03	up	4.47E-01	8.95E-01	-	-
1383517_at	---	---	---	Rn.153403	AA998001	2.36	2.47	2.37	2.36	2.37	2.35	1.03	down	3.19E-01	8.95E-01	-	-
1379060_at	---	---	---	Rn.66605	BG378788	2.55	2.46	2.52	2.47	2.49	2.44	1.03	down	2.74E-01	8.95E-01	-	-
1391858_at	Sfrs8	splicing factor, arginine/serine-rich 8	304431	Rn.12338	BM385930	3.77	4.84	5.57	5.10	4.87	4.34	1.03	up	9.46E-01	9.85E-01	-	-
1374864_at	Spry2	sprouty homolog 2 (Drosophila)	306141	Rn.103294	BM390457	2.81	3.10	2.87	2.56	2.85	3.50	1.03	up	8.96E-01	9.67E-01	-	-
1373207_at	---	---	---	Rn.8190	AI235503	6.69	6.80	6.71	6.52	6.52	7.27	1.03	up	8.79E-01	9.63E-01	-	-
1384418_at	---	---	---	Rn.216417	AI556531	2.46	2.58	2.47	2.43	2.48	2.47	1.03	down	3.95E-01	8.95E-01	-	-
1381552_at	---	---	---	Rn.206153	BG380975	2.58	2.57	2.65	2.58	2.61	2.49	1.03	down	3.96E-01	8.95E-01	-	-
1395365_at	---	---	---	---	BF407347	2.40	2.29	2.33	2.30	2.31	2.29	1.03	down	2.64E-01	8.95E-01	-	-
1381044_at	---	---	---	Rn.199773	BI277137	2.37	2.35	2.38	2.36	2.37	2.50	1.03	up	4.10E-01	8.95E-01	-	-
1393328_x_at	RGD1310027	similar to KIAA1582 protein	303774	Rn.156128	BI288201	2.41	2.41	2.43	2.41	2.57	2.40	1.03	up	4.94E-01	8.95E-01	-	-
1375370_at	---	---	---	Rn.171082	BE119626	3.09	3.09	3.10	3.20	2.54	3.42	1.03	down	8.85E-01	9.64E-01	-	-
1382325_at	Gcat	glycine C-acetyltransferase (2-amino-3-ketobutyrate-coenzyme A ligase)	366959	Rn.43940	AW525471	7.70	8.09	8.85	7.85	8.27	8.40	1.03	down	9.19E-01	9.76E-01	-	-
1372575_at	Wbp11	WW domain binding protein 11	297695	Rn.67490	AA892364	4.26	4.25	4.67	4.25	4.16	4.89	1.03	up	8.86E-01	9.65E-01	-	-
1376788_at	Dapk1	death associated protein kinase 1	306722	Rn.23108	AA818353	4.01	5.43	5.10	5.08	4.04	5.29	1.03	down	9.47E-01	9.85E-01	-	-
1393246_at	Zmynd10	zinc finger, MYND-type containing 10	363139	Rn.75726	BG378670	4.64	5.39	5.53	6.22	4.81	4.41	1.03	down	9.50E-01	9.85E-01	-	-
1369935_at	Ccnd3	cyclin D3	25193	Rn.54319	NM_012766	4.64	4.32	4.16	4.39	4.06	4.56	1.03	down	8.51E-01	9.53E-01	-	-
1391426_a_at	Pcnp	PEST proteolytic signal containing nuclear protein	288165	Rn.202642	AI578071	6.88	7.06	6.92	6.27	7.34	7.37	1.03	up	9.17E-01	9.75E-01	-	-
1382656_at	Tlf2	transcription termination factor, RNA polymerase II	295324	Rn.218346	AW521183	2.37	2.37	2.37	2.38	2.50	2.35	1.03	up	4.31E-01	8.95E-01	-	-
1368497_at	Abcc2	ATP-binding cassette, sub-family C (CFTR/MRP), member 2	25303	Rn.10265	NM_012833	3.24	4.18	4.98	4.30	3.52	4.70	1.03	up	9.50E-01	9.85E-01	-	-
1368061_at	Kcnh1	potassium voltage-gated channel, subfamily H (eag-related), member 1	65198	Rn.11071	NM_031742	2.26	2.37	2.26	2.25	2.26	2.25	1.03	down	3.39E-01	8.95E-01	-	-
1379809_at	Plekhf2	pleckstrin homology domain containing, family F (with FYVE domain) membe	362484	Rn.11991	AI535522	3.26	4.90	3.54	4.21	3.16	4.45	1.03	up	9.53E-01	9.86E-01	-	-
1392638_at	---	---	---	Rn.169465	AI599308	2.42	2.31	2.33	2.32	2.32	2.30	1.03	down	3.12E-01	8.95E-01	-	-
1391064_at	Atg16l2	ATG16 autophagy related 16-like 2 (S. cerevisiae)	308865	Rn.104199	BI295177	5.27	3.31	3.30	3.30	5.08	3.64	1.03	up	9.64E-01	9.90E-01	-	-
1380977_at	---	---	---	Rn.160866	BM384974	2.49	2.58	2.49	2.47	2.50	2.46	1.03	down	2.70E-01	8.95E-01	-	-
1393383_at	Arhgdig	Rho GDP dissociation inhibitor (GDI) gamma	360500	Rn.45711	AW521125	2.44	2.43	2.44	2.51	2.51	2.40	1.03	up	3.26E-01	8.95E-01	-	-
1397770_at	---	---	---	Rn.66997	BI296453	2.57	2.54	2.65	2.57	2.57	2.50	1.03	down	3.91E-01	8.95E-01	-	-
1392078_at	---	---	---	Rn.207931	BE108128	2.53	2.52	2.64	2.53	2.53	2.51	1.03	down	3.51E-01	8.95E-01	-	-
1390170_at	---	---	---	---	BI287343	2.47	2.37	2.39	2.37	2.38	2.36	1.03	down	2.68E-01	8.95E-01	-	-
1393803_at	Casp8ap2	caspase 8 associated protein 2	313128	Rn.198715	BF398167	2.54	2.53	2.60	2.53	2.55	2.70	1.03	up	5.15E-01	8.95E-01	-	-
1397611_at	---	---	---	Rn.45049	AW525619	2.32	2.42	2.32	2.31	2.32	2.30	1.03	down	2.85E-01	8.95E-01	-	-
1384108_at	Cdc45l	CDC45 cell division cycle 45-like (S. cerevisiae)	287961	Rn.98535	AI044826	2.36	2.35	2.37	2.36	2.37	2.48	1.03	up	3.83E-01	8.95E-01	-	-
1380694_at	---	---	---	Rn.200315	BM390450	2.42	2.39	2.42	2.41	2.46	2.48	1.03	up	1.67E-01	8.95E-01	-	-
1381156_at	---	---	---	Rn.209288	BF387379	2.55	2.55	2.56	2.55	2.56	2.43	1.03	down	3.77E-01	8.95E-01	-	-
1372394_at	Hedd1	HECT domain containing 1	362736	Rn.36797	AI175474	5.50	6.13	7.27	6.02	6.45	6.30	1.03	down	9.43E-01	9.84E-01	-	-
1369294_at	Bst1	bone marrow stromal cell antigen 1	81506	Rn.10728	NM_030848	2.36	2.53	2.37	2.36	2.43	2.35	1.03	down	5.47E-01	8.95E-01	-	-
1385831_at	Sash3	SAM and SH3 domain containing 3	317578	Rn.15328	AA924459	2.58	2.53	2.69	2.55	2.63	2.50	1.03	down	5.39E-01	8.95E-01	-	-
1392657_at	---	---	---	Rn.172949	BF397806	2.38	2.38	2.38	2.38	2.51	2.37	1.03	up	4.32E-01	8.95E-01	-	-
1394685_at	---	---	---	Rn.204152	AI059337	2.46	2.32	2.46	2.47	2.44	2.43	1.03	up	4.42E-01	8.95E-01	-	-
1380171_at	---	---	---	Rn.219172	BI290076	9.57	10.91	9.90	9.84	9.95	10.71	1.03	up	9.38E-01	9.82E-01	-	-
1398820_at	Mylk2	myosin light chain kinase 2	117558	Rn.81191	NM_057209	2.96	2.88	3.10	3.16	2.97	2.68	1.03	down	8.07E-01	9.38E-01	-	-
1392306_at	---	---	---	Rn.167769	AI454015	2.46	2.45	2.58	2.46	2.46	2.45	1.03	down	3.99E-01	8.95E-01	-	-
1376428_at	---	---	---	Rn.51828	BF412631	2.33	2.33	2.45	2.33	2.34	2.32	1.03	down	3.58E-01	8.95E-01	-	-
1370157_at	Pln	phospholamban	64672	Rn.9740	BI290034	2.49	2.38	2.40	2.38	2.40	2.37	1.03	down	2.98E-01	8.95E-01	-	-
1390316_at	---	---	---	Rn.216789	BF386271	5.14	5.25	5.14	5.20	5.14	5.07	1.03	down	4.74E-01	8.95E-01	-	-
1389612_at	---	---	---	Rn.169064	AI410941	2.77	2.73	2.96	2.74	2.84	3.00	1.03	up	7.15E-01	9.10E-01	-	-
1399070_at	Setd5	SET domain containing 5	297514	Rn.49964	AI180081	2.42	2.41	2.43	2.41	2.31	2.41	1.03	down	2.96E-01	8.95E-01	-	-
1380486_at	LOC687022	similar to SEC22 vesicle trafficking protein-like 3	687022	---	BM383047	2.82	2.56	2.36	2.54	2.21	3.10	1.03	up	8.96E-01	9.67E-01	-	-
1375821_at	---	---	---	---	BF390754	2.57	2.55	2.65	2.56	2.59	2.50	1.03	down	3.77E-01	8.95E-01	-	-
1395568_at	---	---	---	Rn.205092	BF398797	2.53	2.42	2.44	2.43	2.43	2.41	1.03	down	3.10E-01	8.95E-01	-	-
1392539_at	Blvrb	biliverdin reductase B (flavin reductase (NADPH))	292737	Rn.161812	AI009013	6.89	5.93	7.50	6.75	6.83	6.62	1.03	down	9.35E-01	9.82E-01	-	-
1377513_at	---	---	---	Rn.41149	BI287026	2.72	2.70	2.81	2.71	2.74	2.66	1.03	down	3.61E-01	8.95E-01	-	-
1367703_at	Crygd	crystallin, gamma D	24278	Rn.64655	NM_033095	2.43	2.42	2.54	2.42	2.45	2.40	1.03	down	3.78E-01	8.95E-01	-	-
1395573_at	---	---	---	---	BF287254	2.56	2.56	2.65	2.56	2.62	2.47	1.03	down	4.91E-01	8.95E-01	-	-
1391833_at	Crtac1	cartilage acidic protein 1	171438	Rn.198566	AW919289	2.45	2.44	2.51	2.65	2.46	2.41	1.03	up	6.19E-01	8.95E-01	-	-
1379039_at	Cmklr1	chemokine-like receptor 1	80669	Rn.44465	BI276589	2.57	2.56	2.58	2.70	2.57	2.55	1.03	up	4.33E-01	8.95E-01	-	-
1384939_at	Il18r1	Interleukin 18 receptor 1	301365	Rn.149181	BF522954	2.58	2.55	2.65	2.75	2.55	2.60	1.03	up	5.78E-01	8.95E-01	-	-
1381275_at	---	---	---	Rn.24690	AI179171	2.53	2.58	2.55	2.53	2.53	2.47	1.03	down	1.71E-01	8.95E-01	-	-
1369653_at	Tgfbr2	transforming growth factor, beta receptor II	81810	Rn.9954	L09653	2.39	2.44	2.40	2.39	2.40	2.57	1.03	up	5.48E-01	8.95E-01	-	-
1367840_at	Hgs	hepatocyte growth factor-regulated tyrosine kinase substrate	56084	Rn.21	U87863	4.63	6.02	6.47	5.58	5.74	5.67	1.03	down	9.46E-01	9.84E-01	-	-
1371287_at	---	---	---	---	M88356	2.63	2.59	2.71	2.61	2.66	2.55	1.03	down	4.57E-01	8.95E-01	-	-
1377937_at	Mrps14	mitochondrial ribosomal protein S14	289143	Rn.87	AA859719	5.25	5.79	6.25	4.44	5.93	6.79	1.03	down	9.60E-01	9.89E-01	-	-
1399809_at	---	---	---	Rn.147267	AI072048	2.51	2.51	2.52	2.65	2.51	2.49	1.03	up	4.54E-01	8.95E-01	-	-
1383998_at	Smek2	SMEK homolog 2, suppressor of mek1 (Dictyostelium)	360993	Rn.35621	BF545601	6.14	6.10	6.14	6.05	6.19	6.26	1.03	up	5.54E-01	8.95E-01	-	-
1388469_at	---	---	---	Rn.203011	AA945615	2.35	2.35	2.59	2.44	2.37	2.35	1.03	down	6.57E-01	8.98E-01	-	-
1377316_at	---	---	---	Rn.169627	BF397728	2.30	2.49	2.31	2.30	2.30	2.62	1.03	up	7.57E-01	9.21E-01	-	-
1367490_at	LOC681989	similar to defective SPErmatogenesis family member (spe-39)	681989	Rn.190597	AI102046	5.47	4.90	4.91	5.38	5.03	5.00	1.03	up	8.68E-01	9.59E-01	-	-
1383017_at	Ptprm	Protein tyrosine phosphatase, receptor type, M	29616	Rn.205336	AI639001	3.32	3.41	3.34	3.55	3.34	3.30	1.03	up	6.57E-01	8.98E-01	-	-
1384501_at	---	---	---	Rn.149175	BI303932	2.40	2.50	2.43	2.40	2.42	2.39	1.03	down	2.57E-01	8.95E-01	-	-
1369852_at	F10	coagulation factor X	29243	Rn.21393	NM_017143	2.37	2.37	2.38	2.51	2.36	2.37	1.03	up	4.59E-01	8.95E-01	-	-
1397366_at	Asb14	ankyrin repeat and SOCS box-containing 14	680076	Rn.19511	AI410878	2.37	2.36	2.38	2.37	2.51	2.36	1.03	up	4.75E-01	8.95E-01	-	-
1389633_at	---	---	---	---	BI290172	2.74	2.74	2.66	2.74	2.75	2.77	1.03	up	2.33E-01	8.95E-01	-	-
1389422_at	Stap2	signal transducing adaptor family member 2	363334	Rn.19078	BI279446	2.39	2.34	2.35	2.34	2.52	2.33	1.03	up	5.67E-01	8.95E-01	-	-
1374986_x_at	/// Lce1f /// Lce1s	late cornified envelope 1C /// late cornified envelope 1D /// late cornified enve	684 /// 685981 /// 68	Rn.160543	BI281143	2.50	2.50	2.55	2.51	2.53	2.40	1.03	down	3.92E-01	8.95E-01	-	-
1377349_at	---	---	---	Rn.207749	BE106570	2.54	2.51	2.59	2.52	2.55	2.45	1.03	down	3.26E-01	8.95E-01	-	-
1392277_at	---	---	---	Rn.144649	BF390537	2.62	2.59	2.73	2.61	2.66	2.55	1.03	down	4.87E-01	8.95E-01	-	-
1391369_at	Kcnc4	Potassium voltage gated channel, Shaw-related subfamily, member 4	684516	Rn.216718	BE095798	2.36	2.24	2.25	2.24	2.25	2.24	1.03	down	3.53E-01	8.95E-01	-	-
1391378_at	---	---	---	Rn.211524	BF418338	2.55	2.43	2.71	2.56	2.64	2.37	1.03	down	7.46E-01	9.18E-01	-	-
1396101_at	Stc1	stanniocalcin 1	81801	Rn.10647	BF552244	2.48	2.37	2.38	2.37	2.38	2.36	1.03	down	3.48E-01	8.95E-01	-	-
1385911_at	---	---	---	Rn.177572	AI235281	2.57	2.53	2.59	2.58	2.58	2.64	1.03	up	2.08E-01	8.95E-01	-	-
1379871_at	Rfx7	regulatory factor X, 7	315804	Rn.58758	AI408117	2.53	2.52	2.60	2.51	2.55	2.47	1.03	down	3.36E-01	8.95E-01	-	-
1392010_at	Gnl2	guanine nucleotide binding protein-like 2 (nucleolar)	362593	Rn.18964	BF401644	2.65	2.63	2.73	2.54	2.78	2.56	1.03	down	6.56E-01	8.98E-01	-	-
1393661_at	---	---	---	Rn.166280	BG381658	5.58	5.95	5.56	4.97	5.53	6.71	1.03	up	9.43E-01	9.84E-01	-	-
1392124_at	---	---	---	Rn.207913	BE108025	2.36	2.37	2.39	2.38	2.48	2.43	1.03	up	2.92E-01	8.95E-01	-	-
1387726_at	Cdx2	caudal type homeo box 2	66019	Rn.64495	NM_023963	2.46	2.40	2.44	2.41	2.37	2.40	1.03	down	1.26E-01	8.95E-01	-	-
1396017_at	---	---	---	Rn.210079	BF415778	2.66	2.60	2.73	2.64	2.83	2.64	1.03	up	6.10E-01	8.95E-01	-	-
1385303_at	---	---	---	---	BI301855	2.74	2.65	2.91	2.71	2.86	2.62	1.03	down	7.20E-01	9.11E-01	-	-
1394781_at	---	---	---	Rn.32141	AA859755	2.43	2.32	2.34	2.32	2.33	2.31	1.03	down	2.85E-01	8.95E-01	-	-
1385459_at	RGD1306959	similar to C11orf17 protein	361624	Rn.106344	AA799992	2.58	2.57	2.62	2.57	2.59	2.50	1.03	down	2.84E-01	8.95E-01	-	-
1384559_at	Psx1	placenta specific homeobox 1	296535	---	AI072542	2.50	2.42	2.43	2.42	2.41	2.40	1.03	down	2.27E-01	8.95E-01	-	-
1369953_a_at	Cd24	CD24 molecule	25145	Rn.6

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)				REG	MTC
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval		
1370040_at	Ogg1	8-oxoguanine DNA glycosylase	81528	Rn.22623	NM_030870	4.73	4.42	4.09	4.55	4.29	4.28	1.03	down	8.57E-01	9.55E-01	-	-
1398736_at	---	---	---	Rn.209159	BF399976	2.45	2.40	2.41	2.40	2.41	2.34	1.03	down	2.18E-01	8.95E-01	-	-
1380184_at	Fam19a5	family with sequence similarity 19 (chemokine (C-C motif)-like), member A5	500915	Rn.13126	AW521222	2.70	2.44	2.51	2.46	2.51	2.81	1.03	up	7.83E-01	9.30E-01	-	-
1396702_at	---	---	---	Rn.205114	AI501585	2.34	2.34	2.35	2.34	2.47	2.33	1.03	up	4.36E-01	8.95E-01	-	-
1396306_at	---	---	---	Rn.32503	AA943137	2.49	2.59	2.50	2.48	2.51	2.47	1.03	down	3.13E-01	8.95E-01	-	-
1380962_at	---	---	---	Rn.60243	BF386299	2.38	2.37	2.49	2.37	2.38	2.36	1.03	down	3.78E-01	8.95E-01	-	-
1368209_at	Pdzk1ip1	PDZK1 interacting protein 1	81916	Rn.3605	NM_130401	10.08	10.40	9.44	10.07	9.73	10.00	1.03	down	9.03E-01	9.70E-01	-	-
1369105_a_at	Pkib	protein kinase (cAMP-dependent, catalytic) inhibitor beta	24678	Rn.9748	AF413572	2.56	2.53	2.62	2.53	2.56	2.49	1.03	down	3.27E-01	8.95E-01	-	-
1380063_at	Ch25h	cholesterol 25-hydroxylase	309527	Rn.155971	AI169398	2.53	2.66	2.53	2.55	2.53	2.52	1.03	down	4.11E-01	8.95E-01	-	-
1372552_at	Acbd3	acyl-Coenzyme A binding domain containing 3	289312	Rn.57036	AI102275	6.23	6.06	6.08	5.85	5.85	6.79	1.03	up	9.07E-01	9.72E-01	-	-
1376355_at	FAM120C	family with sequence similarity 120C	317423	Rn.41046	BF399639	2.38	2.39	2.38	2.37	2.38	2.51	1.03	up	4.36E-01	8.95E-01	-	-
1375969_at	Tor1aip2	torsin A interacting protein 2	304881	Rn.203174	BI296555	6.38	7.32	7.19	7.12	6.59	7.29	1.03	up	9.19E-01	9.76E-01	-	-
1395516_at	RGD1310061	similar to hypothetical protein FLJ10154	290912	Rn.106829	BG663870	5.99	6.03	5.98	6.28	5.87	5.96	1.03	up	7.69E-01	9.25E-01	-	-
1382852_at	Rnf190	ring finger protein 190	303596	Rn.160625	BG666298	2.50	2.36	2.39	2.36	2.41	2.35	1.03	down	4.45E-01	8.95E-01	-	-
1386598_at	Art1	ADP-ribosyltransferase 1	308873	Rn.6493	BF557807	2.28	2.16	2.17	2.16	2.17	2.16	1.03	down	3.81E-01	8.95E-01	-	-
1392433_at	---	---	---	Rn.57384	BF393447	2.64	2.61	2.71	2.62	2.62	2.61	1.03	down	2.42E-01	8.95E-01	-	-
1379271_at	Socs5	suppressor of cytokine signaling 5	500616	Rn.47568	AA925076	5.24	5.25	4.19	4.95	4.65	4.96	1.03	down	9.20E-01	9.76E-01	-	-
1377417_at	LOC363328	Similar to TICAM-1	363328	Rn.21528	BE099931	2.33	2.32	2.33	2.32	2.46	2.31	1.03	up	4.73E-01	8.95E-01	-	-
1379186_at	Tomm70a	translocase of outer mitochondrial membrane 70 homolog A (S. cerevisiae)	304017	Rn.162009	BF414701	8.39	8.28	8.03	7.91	8.31	8.60	1.03	up	8.71E-01	9.60E-01	-	-
1372060_at	---	---	---	---	AI010668	4.02	5.58	6.56	5.12	5.72	5.43	1.03	up	9.61E-01	9.89E-01	-	-
1384716_at	Syt1	synaptotagmin I	25716	Rn.216272	AI413003	2.31	2.31	2.32	2.31	2.45	2.30	1.03	up	4.67E-01	8.95E-01	-	-
1373631_at	Rap1gap	Rap1 GTPase-activating protein	313644	Rn.18036	BF284067	2.34	2.34	2.34	2.34	2.46	2.33	1.03	up	3.72E-01	8.95E-01	-	-
1369345_at	Inpp4b	inositol polyphosphate-4-phosphatase, type II	116699	Rn.10829	NM_053917	2.39	2.39	2.53	2.39	2.43	2.36	1.03	down	4.87E-01	8.95E-01	-	-
1397616_at	---	---	---	Rn.43415	BI292232	7.86	7.94	7.01	7.67	7.76	7.49	1.03	up	9.05E-01	9.71E-01	-	-
1393304_at	RGD1560475	similar to vesicle transport through interaction with t-SNAREs 1B homolog	366673	---	BF386764	6.73	6.34	6.46	6.53	6.55	6.57	1.03	up	7.45E-01	9.18E-01	-	-
1380639_at	Stx5	syntaxin 5	65134	Rn.5782	BI296446	4.22	3.50	2.76	3.79	3.27	3.29	1.03	down	9.35E-01	9.82E-01	-	-
1378132_at	---	---	---	Rn.160381	AI716098	2.46	2.44	2.55	2.44	2.47	2.43	1.03	down	3.16E-01	8.95E-01	-	-
1391626_at	Mnd1	meiotic nuclear divisions 1 homolog (S. cerevisiae)	295160	Rn.42077	BF288218	2.58	2.54	2.71	2.57	2.63	2.50	1.03	down	5.70E-01	8.95E-01	-	-
1376937_at	RGD1565927	similar to 4631422O05Rik protein	304020	Rn.8383	BM389685	2.54	2.62	2.54	2.52	2.54	2.53	1.03	down	2.43E-01	8.95E-01	-	-
1370677_at	Rin1	Ras and Rab interactor 1	207119	Rn.16006	U80076	2.46	2.45	2.55	2.42	2.46	2.45	1.03	down	2.98E-01	8.95E-01	-	-
1396688_at	---	---	---	Rn.209865	BF393691	2.68	2.66	2.66	2.65	2.66	2.56	1.03	down	2.85E-01	8.95E-01	-	-
1395504_at	Adam19	a disintegrin and metallopeptidase domain 19 (meltrin beta)	303068	Rn.163114	BF408349	2.61	2.54	2.77	2.60	2.61	2.60	1.03	down	5.93E-01	8.95E-01	-	-
1369830_at	Prkch	protein kinase C, eta	81749	Rn.10398	NM_031085	2.40	2.45	2.40	2.37	2.39	2.36	1.03	down	9.70E-02	8.95E-01	-	-
1394644_at	---	---	---	---	BF285817	2.47	2.46	2.51	2.47	2.48	2.38	1.03	down	3.07E-01	8.95E-01	-	-
1373145_at	RGD1560511	similar to Vps41 protein	306991	Rn.6409	BI281884	5.93	6.23	6.64	5.92	6.10	6.90	1.03	up	9.20E-01	9.76E-01	-	-
1390865_at	Cadps2	Ca++-dependent secretion activator 2	312166	Rn.91746	AW524822	5.43	5.60	5.65	5.40	5.40	5.75	1.03	down	7.86E-01	9.31E-01	-	-
1388402_at	Tmem134	transmembrane protein 134	361695	Rn.2950	AI175019	7.17	7.64	7.18	7.19	7.31	7.37	1.03	down	8.22E-01	9.43E-01	-	-
1395279_at	Pxk	PX domain containing serine/threonine kinase	306203	Rn.86175	BI297004	3.89	2.91	2.82	3.59	2.88	3.02	1.03	down	9.28E-01	9.80E-01	-	-
1383122_at	Prkag2	protein kinase, AMP-activated, gamma 2 non-catalytic subunit	373545	Rn.51208	BF415760	5.67	3.89	5.48	5.35	4.99	4.58	1.03	down	9.52E-01	9.86E-01	-	-
1395653_at	---	---	---	---	BG379043	2.49	2.48	2.61	2.49	2.52	2.46	1.03	down	4.25E-01	8.95E-01	-	-
1398658_at	---	---	---	Rn.199074	AI145762	2.51	2.57	2.52	2.49	2.52	2.48	1.03	down	1.65E-01	8.95E-01	-	-
1394576_at	---	---	---	Rn.147300	AA900572	2.45	2.36	2.38	2.37	2.37	2.56	1.03	up	6.01E-01	8.95E-01	-	-
1371421_at	Oxct1	3-oxoacid CoA transferase 1	690163	Rn.98472	BM391873	10.16	10.53	10.71	10.19	10.44	10.66	1.03	down	8.62E-01	9.57E-01	-	-
1376179_at	---	---	---	Rn.203313	BM386051	2.35	2.45	2.34	2.34	2.34	2.57	1.03	up	6.74E-01	9.01E-01	-	-
1379256_at	RGD1565685	similar to RIKEN cDNA 1810030O07	317344	Rn.1298	BF397911	5.31	4.52	4.51	4.88	4.58	4.99	1.03	up	9.06E-01	9.69E-01	-	-
1388396_at	Stk25	serine/threonine kinase 25 (STE20 homolog, yeast)	373542	Rn.67557	BI275932	7.01	6.85	8.04	7.17	7.88	6.98	1.03	up	9.37E-01	9.82E-01	-	-
1397983_at	---	---	---	Rn.156421	BF403330	2.37	2.28	2.29	2.26	2.29	2.28	1.03	down	2.78E-01	8.95E-01	-	-
1375736_at	Rnasen	ribonuclease type III, nuclear	310159	Rn.41113	AW252835	2.37	2.36	2.40	2.37	2.52	2.36	1.03	up	5.22E-01	8.95E-01	-	-
1391766_at	Hs3st5	heparan sulfate (glucosamine) 3-O-sulfotransferase 5	294449	Rn.117403	AI502121	2.51	2.48	2.62	2.47	2.53	2.49	1.03	down	4.44E-01	8.95E-01	-	-
1381760_at	Mical3	microtubule associated monoxygenase, calponin and LIM domain containing	362427	Rn.201751	BF393440	2.59	2.50	2.50	2.48	2.51	2.48	1.03	down	2.92E-01	8.95E-01	-	-
1391694_at	---	---	---	Rn.169287	AW521119	2.50	2.50	2.53	2.66	2.50	2.49	1.03	up	5.14E-01	8.95E-01	-	-
1373377_at	Scnm1	sodium channel modifier 1	310662	Rn.40268	BG376162	9.04	8.59	8.95	8.85	9.15	8.46	1.03	down	8.82E-01	9.64E-01	-	-
1398847_at	Nudt4	nudix (nucleoside diphosphate linked moiety X)-type motif 4	94267	Rn.8426	BG376935	8.82	8.76	8.06	9.03	8.06	8.43	1.03	down	9.23E-01	9.77E-01	-	-
1377884_at	---	---	---	---	BG671879	4.40	5.02	5.12	4.78	5.05	4.82	1.03	up	8.78E-01	9.62E-01	-	-
1397763_at	RGD1359158	Similar to RIKEN cDNA 1110059E24	361740	Rn.105582	BE100891	2.88	3.01	2.96	3.21	2.75	3.01	1.03	up	7.89E-01	9.32E-01	-	-
1378115_at	---	---	---	Rn.204380	AW533316	2.35	2.35	2.37	2.36	2.37	2.47	1.03	up	3.45E-01	8.95E-01	-	-
1396400_at	---	---	---	Rn.199684	BE105443	2.65	2.63	2.68	2.58	2.64	2.63	1.03	down	1.53E-01	8.95E-01	-	-
1385650_at	Rshl2	radial spokehead-like 2	361476	Rn.38258	AI576299	3.05	2.81	2.69	2.82	2.83	2.79	1.03	down	7.38E-01	9.16E-01	-	-
1393073_at	---	---	---	Rn.8011	AI030539	2.27	2.26	2.27	2.40	2.27	2.26	1.03	up	4.31E-01	8.95E-01	-	-
1373771_at	---	---	---	Rn.28058	AI101164	2.63	2.62	2.64	2.63	2.77	2.61	1.03	up	4.94E-01	8.95E-01	-	-
1389851_at	Zfp36l2	zinc finger protein 36, C3H type-like 2	298765	Rn.22055	AA943730	2.34	2.34	2.45	2.34	2.34	2.33	1.03	down	3.74E-01	8.95E-01	-	-
1379236_at	---	---	---	Rn.206648	BF405781	2.51	2.48	2.54	2.48	2.48	2.45	1.03	down	1.30E-01	8.95E-01	-	-
1381695_at	---	---	---	Rn.206501	AW527792	2.24	2.23	2.24	2.23	2.36	2.23	1.03	up	4.03E-01	8.95E-01	-	-
1376403_at	---	---	---	Rn.208029	BE109059	2.29	2.38	2.30	2.28	2.29	2.27	1.03	down	2.42E-01	8.95E-01	-	-
1385563_at	---	---	---	Rn.110415	AA900591	2.39	2.37	2.39	2.37	2.52	2.36	1.03	up	4.96E-01	8.95E-01	-	-
1368792_at	Psen1	presenilin 1	29192	Rn.44440	NM_019163	6.95	8.09	7.67	7.60	7.36	7.86	1.03	up	9.20E-01	9.76E-01	-	-
1387627_at	Cd86	CD86 molecule	56822	Rn.6734	NM_020081	2.34	2.34	2.34	2.35	2.35	2.43	1.03	up	1.97E-01	8.95E-01	-	-
1375952_at	---	---	---	Rn.165523	AI178495	3.68	2.98	2.38	3.13	3.00	3.03	1.03	up	9.23E-01	9.77E-01	-	-
1385414_at	Cd8a	CD8a molecule	24930	Rn.10306	BE117044	2.36	2.36	2.47	2.36	2.37	2.35	1.03	down	3.57E-01	8.95E-01	-	-
1376453_at	---	---	---	Rn.22491	BF419074	2.57	2.77	2.45	2.57	2.61	2.72	1.03	up	7.25E-01	9.13E-01	-	-
1385139_at	LOC500118	similar to RIKEN cDNA D330028D13	500118	Rn.161839	BE109872	2.41	2.40	2.51	2.40	2.41	2.39	1.03	down	3.56E-01	8.95E-01	-	-
1391988_at	---	---	---	Rn.176543	BI296571	2.38	2.37	2.39	2.50	2.38	2.36	1.03	up	4.29E-01	8.95E-01	-	-
1370072_at	Mme	membrane metallo endopeptidase	24590	Rn.33598	NM_012608	10.65	10.71	11.20	11.00	10.67	10.77	1.03	down	8.57E-01	9.55E-01	-	-
1382421_at	---	---	---	---	BI292508	2.35	2.45	2.36	2.34	2.35	2.34	1.03	down	2.67E-01	8.95E-01	-	-
1386331_at	---	---	---	---	AI639137	2.64	2.58	2.74	2.61	2.71	2.53	1.03	down	6.16E-01	8.95E-01	-	-
1396836_at	---	---	---	Rn.35520	AI501570	2.34	2.45	2.34	2.33	2.34	2.33	1.03	down	3.54E-01	8.95E-01	-	-
1386520_at	Irx3	Iroquois homeobox 3	307721	Rn.22133	AI713965	2.29	2.28	2.29	2.28	2.29	2.40	1.03	up	3.65E-01	8.95E-01	-	-
1384028_at	---	---	---	---	AI072042	8.70	9.01	9.05	9.15	8.39	9.11	1.03	down	8.93E-01	9.67E-01	-	-
1377527_at	---	---	---	Rn.209483	BF393186	2.45	2.44	2.57	2.46	2.45	2.43	1.03	down	4.25E-01	8.95E-01	-	-
1388265_x_at	Vcan	versican	114122	Rn.35666	AF084544	2.65	2.64	2.67	2.65	2.67	2.54	1.03	down	3.85E-01	8.95E-01	-	-
1385436_at	Tmc4	transmembrane channel-like 4	308310	Rn.138375	AI556940	2.52	2.49	2.63	2.50	2.55	2.48	1.03	down	4.52E-01	8.95E-01	-	-
1396659_at	---	---	---	Rn.209974	BF393168	2.52	2.51	2.61	2.51	2.51	2.50	1.03	down	2.89E-01	8.95E-01	-	-
1392197_at	---	---	---	---	BF392518	2.39	2.29	2.31	2.28	2.32	2.27	1.03	down	3.10E-01	8.95E-01	-	-
1388401_at	Flnb	filamin, beta	306204	Rn.1761	BI296155	4.91	6.33	4.92	5.27	4.99	6.01	1.03	up	9.48E-01	9.85E-01	-	-
1380724_at	---	---	---	---	BE095844	2.45	2.33	2.35	2.34	2.35	2.33	1.03	down	3.40E-01	8.95E-01	-	-
1392416_at	---	---	---	Rn.169058	AI410749	2.59	2.54	2.68	2.55	2.64	2.51	1.03	down	5.35E-01	8.95E-01	-	-
1374108_at	Lrp12	low density lipoprotein-related protein 12	314941	Rn.17834	BM388942	4.13	3.89	3.96	3.95	3.95	3.95	1.03	down	6.26E-01	8.95E-01	-	-
1385569_at	---	---	---	Rn.23630	BF559640	2.37	2.36	2.38	2.37	2.51	2.35	1.03	up	5.01E-01	8.95E-01	-	-
1373450_at	Usp38	ubiquitin specific peptidase 38	307764	Rn.17881	AI409857	4.77	5.34	5.67	5.12	4.89	5.65	1.03	down	9.17E-01	9.75E-01	-	-
1388505_at	---	---	---	Rn.2378	BE109642	4.69	4.66	5.47	5.24	4.72	4.76	1.03	down	9.09E-01	9.72E-01	-	-
1370213_at	Ybx1	Y box binding protein 1	500538	Rn.194909	BI282111	11.16	11.38	11.24	11.14	11.08	11.44	1.03	down	7.78E-01	9.28E-01	-	-
1377926_at	Tm4sf20	transmembrane 4 L six family member 20	691066	Rn.146111	BM385993	6.18	7.19	8.33	7.33	6.33	8.16	1.03	up	9.65E-01	9.90E-01	-	-
1384815_at	---	---	---	Rn.204683	AI145507	2.44	2.45	2.44	2.43	2.58	2.43	1.03	up	4.62E-01	8.95E-01	-	-
1392503_at	Rbm22	RNA binding motif protein 22	307410	Rn.105130	BE100371	4.39	4.60	4.90	4.44	4.51	5.05	1.03	up	8.82E-01	9.64E-01	-	-
1390471_at	---	---	---	Rn.204747	BM383411	2.25	2.24	2.25	2.24	2.37	2.24	1.03	up	4.13E-01	8.95E-01	-	-
1382382_at	Ermn	ermin, ERM-like protein	295619	Rn.20243	AW524468	2.55	2.55	2.61	2.53	2.58	2.48	1.03	down	3.37E-01	8.95E-01	-	-
1391335_at	---	---	---	Rn.188688	BE113183	2.41	2.40	2.42	2.54	2.41	2.38	1.03	up	4.84E-01	8.95E-01	-	-
1394084_at	---	---	---	---	BF289798	2.52	2.52	2.58	2.52	2.54	2.44	1.03	down	3.54E-01	8.95E-01	-	-
1369047_at	Sult1d1	sulfotransferase family 1D, member 1	60393	Rn.45325	NM_021769	2.63	2.59	2.73	2.60	2.69	2.54	1.03	down	5.61E-01	8.95E-01	-	-
1393602_at	---	---	---	Rn.47209	AW529468	2.72	2.80	2.74	2.70	2.73	2.72	1.03	down	2.27E-01	8.95E-01	-	-
1385037_at	Mga	MAX gene associated	499874	Rn.78917	BF409340	2.44	2.42	2.44	2.43	2.45	2.53	1.03	up	2.68E-01	8.95E-01	-	-
1381775_at	---	---	---	Rn.34703	BF391321	2.44	2.31	2.33	2.32	2.32	2.32	1.03	down	4.00E-01	8.95E-01	-	-
1396550_at	---	---	---	Rn.176800	BG672529	2.71	2.66	2.82	2.68	2.80	2.60	1.03	down	6.35E-01	8.95E-01	-	-
1379322_at	Psmd7	proteasome (prosome, macropain) 26S subunit, non-ATPase, 7	307821	Rn.20659	BI289174	9.13	9.32	9.55	9.18	9.23	9.48	1.03	down	8.15E-01	9.40E-01	-	-
1389562_at	---	---	---	Rn.199571	BF396686	2.87	2.87	2.61	2.88	2.75	2.84	1.03	up	6.99E-01	9.07E-01	-	-
1395956_at	---	---	---	Rn.66166	BG372430	2.35	2.42	2.36	2.34	2.35	2.33	1.03	down	1.75E-01	8.95E-01	-	-
1391497_at	---	---	---	Rn.199232	AA997515	2.43	2.43	2.72	2.43	2.44	2.82	1.03	up	8.25E-01	9.45E-01	-	-
1376775_at	Prr5l	proline rich 5 like	362171	Rn.19060	AI059078	2.41	2.31	2.33	2.31	2.32	2.30	1.03	down	2.91E-01	8.95E-01	-	-
1394471_at	---	---	---	---	BF291036	2.30	2.33	2.31	2.30	2.31	2.45	1.03	up	4.88E-01	8.95E-01	-	-
1371865_at	Tmem111	transmembrane protein 111	312640	Rn.2282	BI283821	6.28	6.46	5.55	6.06	6.52	6.03	1.03	up	9.27E-01	9.79E-01	-	-
1387496_a_at	Cnga3	cyclic nucleotide gated channel alpha 3	85257	Rn.10886	AJ272429	2.43	2.31	2.32	2.31	2.32	2.31	1.03	down	3.57E-01	8.95E-01	-	-
1370438_at	Nos1ap	nitric oxide synthase 1 (neuronal) adaptor protein	192363	Rn.9903	AF037071	2.46	2.36	2.39	2.37	2.38	2.35	1.03	down	2.60E-01	8.95E-01	-	-
1388549_at	---	---	---	---	AI013328	8.88	8.73	8.16	8.35	8.44	8.86	1.03	down	8.94E-01	9.67E-01	-	-
1385616_a_at	Asf1a	ASF1 anti-silencing function 1 homolog A (S. cerevisiae)	294408	Rn.163427	AI137136	7.48	7.63	7.80	6.88	7.94	7.97	1.03	down	9.23E-01	9.77E-01	-	-
1376946_at	---	---	---	Rn.23622	BG380358	2.49	2.39	2.40	2.39	2.40	2.38	1.03	down	2.97E-01	8.95E-01	-	-
1369740_at	Kcnj3	potassium inwardly-rectifying channel, subfamily J, member 3	50599	Rn.9809	NM_031610	2.52	2.35	2.41	2.39	2.40	2.37	1.03	down	4.98E-01	8.95E-01	-	-
1373584_at	RGD1559643	similar to hypothetical protein A430031N04	498100	Rn.11815	BE113205	6.31	5.85	5.73	5.88	6.01	6.07	1.03	down	8.52E-01	9.54E-01	-	-
1394852_at	---	---	---	---	AI175769	2.42	2.42	2.47	2.42	2.43	2.35	1.03	down	2.77E-01	8.95E-01	-	-
1369331_a_at	Unc13b	unc-13 homolog B (C. elegans)	64830	Rn.10127	AF159706	2.35	2.48	2.37	2.36	2.37	2.37	1.03	down	4.09E-01	8.95E-01	-	-
1393477_at	---	---	---	---	AI548924	2.25	2.24	2.25	2.25	2.37	2.24	1.03	up	4.03E-01	8.95E-01	-	-
1393260_at	LOC360228	WDNM1 homolog	360228	Rn.41321	BG661061	2.38	2.25	2.27	2.26	2.28	2.25	1.03	down	3.99E-01	8.95E-01	-	-
1368327_at	Slc12a9	solute carrier family 12 (potassium/chloride transporters), member 9	171443	Rn.176567	NM_134405	3.04	3.03	2.60	3.03	2.39	3.37	1.03	up	9.11E-01	9.73E-01	-	-
1382429_at	---	---	---	---	AI099574	3.53	3.05	2.91	2.89	2.84	3.66	1.03	down	9.12E-01	9.74E-01	-	-
1394393_at	Usp7	ubiquitin specific peptidase 7 (herpes virus-associated)	360471	Rn.72721	BE114562	5.93	8.27	8.15	7.03	7.48	7.72	1.03	down	9.64E-01	9.90E-01	-	-
1381590_at	---	---	---	Rn.209832	BI295719	2.66	2.41	2.43	2.42	2.79	2.40	1.03	up	8.12E-01	9.39E-01	-	-
1371081_at	Rapgef4	Rap guanine nucleotide exchange factor (GEF) 4	252857	Rn.42890	U78517	2.62	2.57	2.72	2.59	2.67	2.53	1.03	down	5.71E-01	8.95E-01	-	-
1377786_at	---	---	---	Rn.147485	BE117884	2.49	2.45	2.53	2.56	2.57	2.46	1.03	up	4.23E-01	8.95E-01	-	-
1371659_at	Rhoc	ras homolog gene family, member C	295342	Rn.162614	AA891940	7.37	6.70	8.17	7.65	7.38	7.09	1.03	down	9.37E-01	9.82E-01	-	-
1390878_at	LOC681309	similar to Thrombospondin-3 precursor	681309	Rn.198600	BI296047	2.46	2.42	2.43	2.42	2.42	2.57	1.03	up	5.02E-01	8.95E-01	-	-
1368645_at	Ptpn1	protein tyrosine phosphatase, non-receptor type 1	24697	Rn.11317	NM_012637	2.62	2.53	2.72	2.42	2.41	2.43	2.41	1.03	down	3.67E-01	8.95E-01	-	-
1378427_at	Bmp6	Bone morphogenetic protein 6	25644	Rn.40476	BF406639	2.61	2.57	2.71	2.59	2.63	2.56	1.03	down	4.55E-01	8.95E-01	-	-
1398134_at	Zfp90	zinc finger protein 90	498945	Rn.38916	BF523421	2.46	2.41	2.47	2.41	2.42	2.39	1.03	down	1.55E-01	8.95E-01	-	-
1375702_at	Arhgef7	Rho guanine nucleotide exchange factor (GEF7)	114559	Rn.146763	BF414089	3.06	2.93	2.97	2.85	2.90	3.10	1.03	down	6.79E-01	9.02E-01	-	-
1385736_at	Blk4	B-cell translocation gene 4	315650	Rn.53419	BE119988	2.51	2.49	2.62	2.50	2.55	2.47	1.03	down	4.62E-01	8.95E-01	-	-
1384342_at	Nisch	nischarin	306255	Rn.96234	AW915747	2.58	2.52	2.53	2.52	2.51	2.48	1.03	down	1.58E-01	8.95E-01	-	-
1388107_at	Ppp2r2d	protein phosphatase 2, regulatory subunit B, delta isoform	246255	Rn.116122	BF282131	7.20	8.15	7.49	7.38	7.95	7.63	1.03	up	9.12E-01	9.74E-01	-	-
1378521_at	LOC690511	hypothetical protein LOC690511	690511	Rn.198787	BF407156	2.53	2.48	2.52	2.48	2.48	2.48	1.03	up	6.11E-01	8.95E-01	-	-
1372674_at	Rybp	RING1 and YY1 binding protein	312603	Rn.33148	BE107155	2.67	2.75	2.77	2.75	2.82	2.74	1.03	up	3.95E-01	8.95E-01	-	-
1395490_at	---	---	---	Rn.209383	BF409918	2.59	2.53	2.72	2.57	2.62	2.55	1.03	down	5.49E-01	8.95E-01	-	-
1398725_at	---	---	---	Rn.216798	BI275478	2.46	2.35	2.37	2.36	2.37	2.35	1.03	down	3.35E-01	8.95E-01	-	-
1381910_at	---	---	---	Rn.176548	BG373774	2.53	2.65	2.51	2.54	2.62	2.53	1.03	up	2.62E-01	8.95E-01	-	-
1382773_at	---	---	---	---	AI235484	2.70	2.65	2.77	2.67	2.70	2.63	1.03	down	4.02E-01	8.95E-01	-	-
1379110_at	---	---	---	Rn.168674	AI763769	2.76	2.66	2.77	2.78	2.77	2.75	1.03	up	3.24E-01	8.95E-01	-	-
1384610_at	Fam63b	family with sequence similarity 63, member B	363089	Rn.15746	AI045985	3.74	3.79	3.69	4.36	5.01	3.73	1.03	down	9.81E-01	9.89E-01	-	-
1398440_at	Sfrs18	splicing factor, arginine/serine-rich 18	297942	Rn.8700	BI292166	4.14	4.65

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1386602_at	Rab40b	Rab40b, member RAS oncogene family	303754	Rn.8397	BF559179	2.59	2.49	2.57	2.53	2.55	2.46	1.03	down	4.12E-01	8.95E-01	-	-
1370225_at	Cited4	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domai	114491	Rn.40380	AI556378	2.81	2.81	2.91	2.81	2.83	2.78	1.03	down	3.41E-01	8.95E-01	-	-
1371011_at	xm2r45 /// Vom2r45	vomeronasal 2 receptor 44 /// vomeronasal 2 receptor, 45 /// vomeronasal 2 re	295090 /// 295091	Rn.111884	AW920487	2.48	2.46	2.48	2.46	2.52	2.55	1.03	up	2.28E-01	8.95E-01	-	-
1376086_at	Ufsp2	UFM1-specific peptidase 2	361151	Rn.14630	AW528625	8.03	7.89	8.10	8.00	7.99	8.14	1.03	up	6.63E-01	8.98E-01	-	-
1389886_at	---	---	---	Rn.203404	AI408942	2.45	2.44	2.49	2.61	2.45	2.44	1.03	up	5.45E-01	8.95E-01	-	-
1370633_at	Cxcl3	chemokine (C-X-C motif) ligand 3	171551	Rn.10525	D87927	2.55	2.52	2.60	2.50	2.59	2.47	1.03	down	4.02E-01	8.95E-01	-	-
1370126_at	Prss2	protease, serine, 2	25052	Rn.1584	NM_012729	2.52	2.45	2.55	2.46	2.50	2.44	1.03	down	3.39E-01	8.95E-01	-	-
1394206_s_at	---	---	---	Rn.43051	AI639084	2.64	2.59	2.75	2.61	2.71	2.54	1.03	down	6.17E-01	8.95E-01	-	-
1377318_at	---	---	---	Rn.173588	BF415648	2.51	2.48	2.59	2.49	2.52	2.46	1.03	down	3.83E-01	8.95E-01	-	-
1395947_at	Rpa1	Replication protein A1	287524	Rn.14841	BE110981	2.41	2.37	2.46	2.37	2.38	2.37	1.03	down	2.23E-01	8.95E-01	-	-
1397146_at	---	---	---	---	AI137437	2.48	2.42	2.45	2.42	2.42	2.40	1.03	down	1.49E-01	8.95E-01	-	-
1382048_at	Atp6v1a	ATPase, H+ transporting, lysosomal V1 subunit A	685232	Rn.1431	BI289589	8.38	8.91	8.09	8.42	8.63	8.22	1.03	down	8.95E-01	9.67E-01	-	-
1394324_at	---	---	---	Rn.41532	BF542337	2.50	2.39	2.40	2.39	2.40	2.38	1.03	down	3.53E-01	8.95E-01	-	-
1370630_a_at	Fgfr2	fibroblast growth factor receptor 2	25022	Rn.1272	L19104	2.68	2.54	2.70	2.72	2.74	2.57	1.03	up	6.33E-01	8.95E-01	-	-
1386059_at	---	---	---	Rn.55181	BF284475	3.45	3.55	2.88	3.48	3.34	3.18	1.03	up	8.76E-01	9.62E-01	-	-
1398643_at	Dicer1	dicer 1, ribonuclease type III	299284	Rn.205881	BF388566	2.45	2.59	2.79	2.63	2.53	2.57	1.03	down	7.32E-01	9.14E-01	-	-
1398892_at	RGD1309104	Similar to RIKEN cDNA 1700025G04 gene	289084	Rn.222036	AI575110	2.42	2.38	2.39	2.39	2.55	2.37	1.03	up	5.44E-01	8.95E-01	-	-
1399002_at	Mrps17	mitochondrial ribosomal protein S17	288621	Rn.3292	BM384239	6.24	6.74	6.64	6.58	6.44	6.70	1.03	up	8.35E-01	9.48E-01	-	-
1396065_at	---	---	---	Rn.205968	AI548204	2.63	2.60	2.59	2.62	2.68	2.63	1.03	up	1.88E-01	8.95E-01	-	-
1370634_x_at	Cxcl3	chemokine (C-X-C motif) ligand 3	171551	Rn.10525	D87927	2.49	2.52	2.50	2.47	2.50	2.44	1.03	down	1.18E-01	8.95E-01	-	-
1389795_at	---	---	---	Rn.20273	BG374972	2.40	2.37	2.52	2.38	2.43	2.38	1.03	down	4.81E-01	8.95E-01	-	-
1395134_at	---	---	---	Rn.148123	AI029710	2.53	2.52	2.60	2.53	2.56	2.46	1.03	down	4.10E-01	8.95E-01	-	-
1382742_at	---	---	---	---	AI176758	2.44	2.38	2.51	2.62	2.44	2.38	1.03	up	6.73E-01	9.01E-01	-	-
1380785_at	---	---	---	Rn.173324	BF465178	2.46	2.45	2.56	2.45	2.46	2.45	1.03	down	3.68E-01	8.95E-01	-	-
1383667_at	Rundc1	RUN domain containing 1	303552	---	AI603411	7.46	7.64	6.00	6.99	6.87	7.36	1.03	up	9.48E-01	9.85E-01	-	-
1381262_at	---	---	---	Rn.207260	BG374101	2.41	2.79	2.41	2.41	2.41	2.68	1.03	down	8.23E-01	9.43E-01	-	-
1374373_at	Shroom1	shroom family member 1	287285	Rn.209227	BF393590	2.87	2.74	3.03	2.83	2.99	2.71	1.03	down	7.69E-01	9.24E-01	-	-
1367756_at	Gfm1	G elongation factor, mitochondrial 1	114017	Rn.10913	NM_053625	7.67	8.72	9.07	8.40	8.45	8.72	1.03	up	9.36E-01	9.82E-01	-	-
1392013_at	---	---	---	Rn.16756	AA819397	2.55	2.48	2.55	2.49	2.53	2.44	1.03	down	3.44E-01	8.95E-01	-	-
1370151_at	Cps1	carbamoyl-phosphate synthetase 1, mitochondrial	497840	Rn.53968	NM_017072	2.31	2.31	2.32	2.31	2.32	2.43	1.03	up	3.80E-01	8.95E-01	-	-
1381374_at	Lgi4	leucine-rich repeat LGI family, member 4	361549	Rn.143830	AI058424	2.38	2.37	2.40	2.38	2.52	2.37	1.03	up	4.96E-01	8.95E-01	-	-
1396368_at	---	---	---	Rn.61512	BF409869	2.43	2.32	2.34	2.32	2.33	2.31	1.03	down	3.25E-01	8.95E-01	-	-
1368504_at	Lamp1	lysosomal-associated membrane protein 1	25328	Rn.40177	BE105853	11.78	11.68	11.74	11.81	11.67	11.62	1.03	down	5.96E-01	8.95E-01	-	-
1371699_at	---	---	---	Rn.8461	BI295739	8.07	8.60	8.70	8.08	8.32	8.85	1.03	down	9.07E-01	9.72E-01	-	-
1381621_at	---	---	---	Rn.209092	BF386153	2.55	2.50	2.59	2.51	2.54	2.47	1.03	down	3.35E-01	8.95E-01	-	-
1383888_at	LOC307495	similar to biliverdin reductase B (flavin reductase (NADPH))	307495	Rn.165482	AA998264	6.46	7.27	4.35	6.46	6.20	5.54	1.03	up	9.69E-01	9.91E-01	-	-
1371378_at	Eif1	eukaryotic translation initiation factor 1	287703	Rn.13799	AI012372	9.11	9.39	9.01	9.06	8.80	9.55	1.03	down	8.88E-01	9.65E-01	-	-
1397165_at	---	---	---	Rn.203779	BF547582	2.31	2.41	2.31	2.30	2.31	2.30	1.03	down	3.09E-01	8.95E-01	-	-
1386751_x_at	Ranbp2	RAN binding protein 2	294429	Rn.101115	BF562032	2.61	2.57	2.67	2.57	2.64	2.53	1.03	down	4.19E-01	8.95E-01	-	-
1385286_at	Elovl3	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 3	309449	Rn.79322	BI292438	2.55	2.51	2.58	2.51	2.57	2.44	1.03	down	4.42E-01	8.95E-01	-	-
1381076_at	Foxk2	forkhead box K2	303753	Rn.44253	BF391525	7.77	6.88	8.16	6.92	7.03	6.75	1.03	down	9.41E-01	9.83E-01	-	-
1392671_at	Thoc3	THO complex 3	290519	Rn.101958	AA999074	4.27	3.74	3.53	4.70	3.25	3.70	1.03	up	9.42E-01	9.84E-01	-	-
1386109_at	---	---	---	Rn.172062	BF287631	4.76	3.79	4.31	4.61	4.27	3.87	1.03	down	9.21E-01	9.77E-01	-	-
1377874_at	---	---	---	Rn.219427	BI290527	2.38	2.37	2.47	2.38	2.38	2.34	1.03	down	3.47E-01	8.95E-01	-	-
1381632_at	---	---	---	---	BF388481	2.43	2.42	2.44	2.42	2.43	2.55	1.03	up	4.27E-01	8.95E-01	-	-
1390893_at	Tmem69	transmembrane protein 69	619582	Rn.146440	BF284878	8.42	8.96	8.93	9.15	7.98	9.29	1.03	up	9.38E-01	9.83E-01	-	-
1398081_at	---	---	---	Rn.172207	BF386129	2.55	2.53	2.64	2.53	2.58	2.49	1.03	down	4.31E-01	8.95E-01	-	-
1379031_at	Gca	grancalcin	295647	Rn.21437	BM390697	2.53	2.56	2.58	2.55	2.52	2.55	1.03	down	1.75E-01	8.95E-01	-	-
1382109_at	Nkap	NFKB activating protein	298342	Rn.12473	BI301006	2.35	2.40	2.36	2.35	2.35	2.30	1.03	down	2.02E-01	8.95E-01	-	-
1374714_at	---	---	---	Rn.9345	BI284781	2.63	2.50	2.52	2.50	2.53	2.50	1.03	down	4.50E-01	8.95E-01	-	-
1380406_at	---	---	---	Rn.156541	BE115630	2.55	3.59	2.52	2.56	2.52	3.47	1.03	down	9.41E-01	9.83E-01	-	-
1392982_at	---	---	---	Rn.70548	AA818059	2.84	3.90	4.36	3.60	3.58	4.03	1.03	up	9.41E-01	9.83E-01	-	-
1393199_at	RGD1560601	similar to Jumonji/ARID domain-containing protein 1C (SmcX protein)	317432	Rn.147997	AA955145	2.43	2.76	2.45	2.42	2.92	2.41	1.03	up	8.62E-01	9.57E-01	-	-
1381112_at	---	---	---	Rn.168136	AI555805	2.36	2.35	2.46	2.35	2.38	2.33	1.03	down	3.73E-01	8.95E-01	-	-
1381198_at	---	---	---	Rn.203807	BF561716	2.50	2.51	2.54	2.52	2.69	2.45	1.03	up	6.33E-01	8.95E-01	-	-
1398930_at	Atp6v0b	ATPase, H+ transporting, lysosomal 21kDa, V0 subunit b	298451	Rn.19803	BI278546	7.91	7.90	7.96	7.97	7.98	7.93	1.03	up	2.02E-01	8.95E-01	-	-
1391011_at	---	---	---	Rn.39284	AW527691	2.45	2.49	2.48	2.44	2.45	2.42	1.03	down	8.55E-02	8.95E-01	-	-
1382667_at	Mfsd10	major facilitator superfamily domain containing 10	305449	Rn.3100	AA866425	2.32	2.32	2.32	2.32	2.44	2.31	1.03	up	4.14E-01	8.95E-01	-	-
1398537_at	Amfr	autocrine motility factor receptor	361367	Rn.107561	BE116658	5.21	5.14	6.33	5.01	5.37	6.41	1.03	up	9.51E-01	9.86E-01	-	-
1394553_at	---	---	---	Rn.216754	AI007661	2.84	3.11	2.80	2.95	2.45	3.25	1.03	down	8.90E-01	9.66E-01	-	-
1396824_at	---	---	---	---	AI385369	2.40	2.38	2.43	2.39	2.55	2.37	1.03	up	5.50E-01	8.95E-01	-	-
1368405_at	Rala	v-ral simian leukemia viral oncogene homolog A (ras related)	81757	Rn.100380	NM_031093	7.04	7.47	8.34	7.52	7.79	7.43	1.03	down	9.31E-01	9.81E-01	-	-
1385359_at	RGD1309534	Similar to RIKEN cDNA 4931406C07	363016	Rn.3085	BF406890	2.27	2.26	2.28	2.38	2.28	2.26	1.03	up	3.89E-01	8.95E-01	-	-
1372824_at	Plekhf2	pleckstrin homology domain containing, family F (with FYVE domain) member	362484	Rn.11991	AI103367	8.80	8.97	9.18	8.85	8.99	9.21	1.03	up	8.19E-01	9.42E-01	-	-
1368591_at	Usf2	upstream transcription factor 2	81817	Rn.44637	NM_031139	3.04	2.72	2.77	2.75	2.84	2.82	1.03	down	7.40E-01	9.16E-01	-	-
1388084_at	Klra22	killer cell lectin-like receptor subfamily A, member 22	24933	Rn.10564	U56822	2.47	2.44	2.44	2.43	2.45	2.36	1.03	down	2.80E-01	8.95E-01	-	-
1372807_at	---	---	---	---	BF402462	2.37	2.64	2.37	2.76	2.37	2.36	1.03	up	8.27E-01	9.45E-01	-	-
1367532_at	Dazap2	DAZ associated protein 2	300235	Rn.107901	AA893186	9.16	9.36	8.79	9.11	9.07	9.02	1.03	down	8.38E-01	9.49E-01	-	-
1387105_at	Zfp422	zinc finger protein 422	360389	Rn.105961	NM_133579	6.73	7.15	6.76	6.99	6.11	7.43	1.03	down	9.33E-01	9.81E-01	-	-
1396397_at	---	---	---	Rn.206628	AW529321	2.61	2.58	2.73	2.83	2.70	2.51	1.03	up	7.38E-01	9.16E-01	-	-
1377507_at	---	---	---	---	AI548219	2.59	2.57	2.67	2.57	2.67	2.47	1.03	down	5.98E-01	8.95E-01	-	-
1373358_at	Usp8	ubiquitin specific peptidase 8	296121	Rn.52174	BG374246	6.54	7.09	6.71	7.01	6.61	6.83	1.03	up	8.62E-01	9.57E-01	-	-
1368789_at	Acpp	acid phosphatase, prostate	56780	Rn.40121	NM_020072	3.64	3.85	3.43	3.68	3.69	3.66	1.03	up	7.81E-01	9.29E-01	-	-
1386963_at	Trip10	thyroid hormone receptor interactor 10	116717	Rn.10814	NM_053920	2.62	2.74	2.63	2.62	2.63	2.63	1.03	down	4.01E-01	8.95E-01	-	-
1392198_at	---	---	---	---	BF398283	2.74	2.67	2.82	2.74	2.82	2.57	1.03	down	6.84E-01	9.03E-01	-	-
1395680_at	Sh3gl1	SH3-domain GRB2-like 1	81922	Rn.8762	BF399925	2.58	2.50	2.59	2.61	2.55	2.41	1.03	down	6.06E-01	8.95E-01	-	-
1391077_at	Clspn	claspin homolog (Xenopus laevis)	298534	Rn.6720	AA851257	2.52	2.51	2.63	2.52	2.52	2.51	1.03	down	3.90E-01	8.95E-01	-	-
1388624_at	RGD1309707	similar to RIKEN cDNA 4930431E10	690516	Rn.13503	BG381291	4.65	4.55	5.00	4.76	4.60	4.72	1.03	down	8.11E-01	9.39E-01	-	-
1381561_at	Camk1	calcium/calmodulin-dependent protein kinase I	171503	Rn.11018	BI283817	2.65	2.78	2.77	2.76	2.74	2.58	1.03	down	6.22E-01	8.95E-01	-	-
1374763_at	Cercam	cerebral endothelial cell adhesion molecule	296616	Rn.93530	BI274117	2.45	2.34	2.35	2.35	2.35	2.34	1.03	down	3.61E-01	8.95E-01	-	-
1394552_at	---	---	---	---	BF287082	2.33	2.41	2.34	2.33	2.33	2.31	1.03	down	2.34E-01	8.95E-01	-	-
1384331_at	Srxn1	sulfiredoxin 1 homolog (S. cerevisiae)	296271	Rn.2835	H31896	2.53	2.50	2.52	2.51	2.49	2.66	1.03	up	5.27E-01	8.95E-01	-	-
1391308_at	---	---	---	Rn.204774	AI101675	2.50	2.42	2.44	2.42	2.43	2.40	1.03	down	2.52E-01	8.95E-01	-	-
1380307_at	---	---	---	Rn.204959	AI556551	2.54	2.52	2.57	2.53	2.54	2.45	1.03	down	3.15E-01	8.95E-01	-	-
1396562_at	---	---	---	Rn.210960	BF409832	2.57	2.56	2.97	2.85	2.69	2.66	1.03	up	8.14E-01	9.40E-01	-	-
1385263_at	Myo7b	myosin VIIb	498834	Rn.212769	BM383209	6.67	5.42	6.64	6.37	6.20	6.05	1.03	down	9.35E-01	9.82E-01	-	-
1368769_at	Abcb11	ATP-binding cassette, sub-family B (MDR/TAP), member 11	83569	Rn.14539	NM_031760	2.36	2.44	2.37	2.35	2.36	2.35	1.03	down	2.44E-01	8.95E-01	-	-
1388890_at	---	---	---	Rn.154332	BM390316	3.16	3.03	3.05	3.04	3.03	3.06	1.03	down	4.01E-01	8.95E-01	-	-
1378889_at	---	---	---	Rn.129590	BF389287	2.61	2.47	2.61	2.60	2.61	2.60	1.03	up	4.81E-01	8.95E-01	-	-
1384153_at	Jakmip2	Janus kinase and microtubule interacting protein 2	307479	Rn.208530	BF415575	2.71	2.65	2.79	2.67	2.74	2.62	1.03	down	5.42E-01	8.95E-01	-	-
1392420_at	---	---	---	Rn.209674	BF409169	2.64	2.54	2.55	2.54	2.54	2.53	1.03	down	3.11E-01	8.95E-01	-	-
1373124_at	Src	V-src sarcoma (Schmidt-Ruppin A-2) viral oncogene homolog (avian)	83805	Rn.112600	BI282912	4.01	3.00	3.14	3.28	3.28	3.48	1.03	down	9.15E-01	9.75E-01	-	-
1371609_at	RGD1303003	homolog of zebrafish ES1	294326	Rn.11498	AI232270	9.06	9.12	9.05	9.03	8.75	9.34	1.03	down	8.42E-01	9.51E-01	-	-
1384297_at	---	---	---	Rn.147301	AI555088	2.66	2.55	2.56	2.55	2.57	2.54	1.03	down	3.77E-01	8.95E-01	-	-
1390080_at	Otud1	OTU domain containing 1	498803	Rn.41363	AI549584	2.38	2.39	2.43	2.50	2.40	2.40	1.03	up	3.67E-01	8.95E-01	-	-
1381239_at	---	---	---	Rn.173170	BF406209	2.28	2.29	2.32	2.32	2.38	2.28	1.03	up	2.76E-01	8.95E-01	-	-
1389067_at	Slco4a1	solute carrier organic anion transporter family, member 4a1	171144	Rn.67081	AI180349	2.35	2.34	2.47	2.35	2.35	2.35	1.03	down	4.23E-01	8.95E-01	-	-
1373308_at	Sgsm3	small G protein signaling modulator 3	362963	Rn.66996	BI296563	2.45	2.35	2.46	2.43	2.45	2.48	1.03	up	3.86E-01	8.95E-01	-	-
1394772_at	---	---	---	Rn.206670	AW521307	2.57	2.57	2.62	2.55	2.58	2.52	1.03	down	2.20E-01	8.95E-01	-	-
1368587_at	Apoc1	apolipoprotein C-I	25292	Rn.8887	NM_012824	2.52	2.42	2.46	2.43	2.44	2.42	1.03	down	2.71E-01	8.95E-01	-	-
1385329_at	Cdadc1	cytidine and dCMP deaminase domain containing 1	361052	Rn.76647	BF401322	4.98	5.01	5.17	5.62	5.12	4.31	1.03	down	9.29E-01	9.80E-01	-	-
1384819_at	---	---	---	Rn.44221	AI070395	2.55	2.54	2.62	2.53	2.56	2.51	1.03	down	2.84E-01	8.95E-01	-	-
1397943_at	---	---	---	Rn.149618	AW530549	2.35	2.34	2.45	2.33	2.37	2.33	1.03	down	3.88E-01	8.95E-01	-	-
1383275_at	---	---	---	Rn.12890	BF523098	2.38	2.37	2.38	2.48	2.39	2.36	1.03	up	3.66E-01	8.95E-01	-	-
1374138_at	---	---	---	Rn.173504	BG378169	2.39	2.38	2.48	2.39	2.39	2.37	1.03	down	3.07E-01	8.95E-01	-	-
1368494_at	S100a8	S100 calcium binding protein A8	116547	Rn.31839	NM_053822	2.58	2.53	2.67	2.55	2.62	2.50	1.03	down	5.42E-01	8.95E-01	-	-
1382195_at	Znf771	Zinc finger protein 771	308992	Rn.32501	AA943021	2.41	2.41	2.42	2.53	2.41	2.40	1.03	up	4.09E-01	8.95E-01	-	-
1383410_at	Srp54a	signal recognition particle 54a	116650	Rn.24880	BI290777	7.36	7.36	7.54	7.57	6.64	7.94	1.03	down	9.30E-01	9.80E-01	-	-
1394601_at	---	---	---	Rn.133923	AW526910	3.29	3.77	3.60	3.37	3.55	3.63	1.03	down	8.29E-01	9.46E-01	-	-
1367937_at	Miox	myo-inositol oxygenase	25899	Rn.19959	AF230096	12.15	11.91	11.76	12.04	11.88	12.00	1.03	up	7.82E-01	9.29E-01	-	-
1371124_a_at	Kng2	kininogen 2	25087	Rn.44576	M11884	2.61	2.55	2.65	2.57	2.62	2.52	1.03	down	4.45E-01	8.95E-01	-	-
1391733_at	---	---	---	Rn.161025	BE116541	4.65	3.95	3.96	3.88	4.45	4.11	1.03	down	9.05E-01	9.71E-01	-	-
1387491_at	Gk	glycerol kinase	79223	Rn.153497	NM_024381	3.46	3.45	3.33	3.34	3.47	3.54	1.03	up	6.37E-01	8.95E-01	-	-
1391728_at	Mab21l2	mab-21-like 2 (C. elegans)	680102	Rn.172813	BE117944	2.50	2.41	2.41	2.42	2.41	2.38	1.03	down	3.20E-01	8.95E-01	-	-
1395689_at	Fam169a	family with sequence similarity 169, member A	310013	Rn.198103	BF409912	2.57	2.55	2.62	2.55	2.62	2.45	1.03	down	5.32E-01	8.95E-01	-	-
1388660_at	Mcts1	malignant T cell amplified sequence 1	302500	Rn.36129	BI285915	7.71	8.82	8.34	8.16	8.26	8.55	1.03	up	9.20E-01	9.76E-01	-	-
1387436_at	07-Sep	septin 7	64551	Rn.222063	NM_022616	7.10	6.61	7.15	7.02	7.10	6.83	1.03	down	8.80E-01	9.63E-01	-	-
1395287_at	---	---	---	---	BE119914	2.46	2.45	2.43	2.40	2.43	2.40	1.03	down	4.88E-02	8.95E-01	-	-
1374593_at	Prkce	protein kinase C, epsilon	29340	Rn.216481	AA799421	2.48	2.75	2.48	2.66	2.49	2.46	1.03	down	7.55E-01	9.20E-01	-	-
1395548_at	---	---	---	Rn.171407	BG666506	7.61	7.56	7.62	7.28	7.83	7.79	1.03	up	8.50E-01	9.53E-01	-	-
1377100_at	Pds5b	PDS5, regulator of cohesion maintenance, homolog B (S. cerevisiae)	304218	Rn.105768	AI172172	2.83	2.48	2.48	2.46	2.53	2.68	1.03	down	7.97E-01	9.35E-01	-	-
1387070_at	Tmpo	thymopoietin	25359	Rn.202955	AI044110	2.46	2.40	2.40	2.35	2.40	2.40	1.03	down	2.24E-01	8.95E-01	-	-
1388199_at	Epcam	epithelial cell adhesion molecule	171527	Rn.106481	BG376410	11.86	11.76	11.90	11.89	11.82	11.92	1.03	up	5.07E-01	8.95E-01	-	-
1380065_at	RGD1565926	RGD1565926	361629	Rn.27126	AI180101	2.44	2.42	2.53	2.42	2.45	2.41	1.03	down	3.87E-01	8.95E-01	-	-
1380935_at	---	---	---	Rn.148477	AI179379	2.45	2.43	2.56	2.44	2.45	2.43	1.03	down	4.11E-01	8.95E-01	-	-
1372015_at	Tacc1	transforming, acidic coiled-coil containing protein 1	306562	Rn.73645	AI008689	2.36	2.35	2.57	2.46	2.36	2.35	1.03	down	6.78E-01	9.02E-01	-	-
1393476_at	RGD1309310	similar to mKIAA0195 protein	303677	Rn.198902	AI717594	2.40	2.39	2.42	2.40	2.54	2.38	1.03	up	5.02E-01	8.95E-01	-	-
1387477_at	Kcnk12	potassium channel, subfamily K, member 12	64119	Rn.64577	NM_022292	2.32	2.31	2.42	2.31	2.32	2.31	1.03	down	3.70E-01	8.95E-01	-	-
1395793_at	---	---	---	Rn.148693	AW534384	2.37	2.46	2.37	2.36	2.37	2.36	1.03	down	2.59E-01	8.95E-01	-	-
1371306_at	Gngt1	guanine nucleotide binding protein (G protein), gamma transducing activity po	680149	Rn.20355	AW533257	2.63	2.58	2.73	2.60	2.68	2.56	1.03	down	5.52E-01	8.95E-01	-	-
1384541_at	Hapln1	hyaluronan and proteoglycan link protein 1	29331	Rn.50531	BM391441	2.61	2.57	2.70	2.59	2.67	2.51	1.03	down	5.75E-01	8.95E-01	-	-
1387499_a_at	Pdcl	phosducin-like	64013	Rn.51153	NM_022247	3.38	3.33	3.40	3.63	3.23	3.37	1.03	up	7.77E-01	9.28E-01	-	-
1380588_at	---	---	---	Rn.34641	AI511180	2.37	2.36	2.38	2.37	2.50	2.35	1.03	up	4.71E-01	8.95E-01	-	-
1379508_at	---	---	---	Rn.14893	AI230386	2.61	2.56	2.60	2.57	2.60	2.49	1.03	down	3.73E-01	8.95E-01	-	-
1373559_at	Nptx2	neuronal pentraxin 2	288475	Rn.162101	AI228623	2.36	2.42	2.38	2.35	2.37	2.33	1.03	down	1.60E-01	8.95E-01	-	-
1374494_at	---	---	---	Rn.199178	AI137375	2.45	2.49	2.44	2.45	2.46	2.58	1.03	up	4.74E-01	8.95E-01	-	-
1375646_at	Efcab2	EF-hand calcium binding domain 2	289280	Rn.12659	BI299709	4.05	3.96	4.24	4.03	4.06	4.04	1.03	down	6.80E-01	9.03E-01	-	-
1368187_at	Gpnmb	glycoprotein (transmembrane) nmb	113955	Rn.13778	NM_133298	2.45	2.40	2.46	2.45	2.45	2.52	1.03	up	2.87E-01	8.95E-01	-	-
1383906_at	Lincr	lung-inducible neuralized-related C3HC4 RING domain protein	316326	Rn.17894	BF416847	6.93	8.01	7.39	7.45	7.46	7.30	1.03	down	9.15E-01	9.75E-01	-	-
1382234_at	Pdhx	Pyruvate dehydrogenase complex, component X	311254	Rn.22801	BI286950	5.77	5.03	4.92	5.92	4.34	5.36	1.03	down	9.49E-01	9.85E-01	-	-
1381272_at	---	---	---	Rn.208810	BE120246	2.55	2.53	2.63	2.54	2.56	2.50	1.03	down	3.52E-01	8.95E-01	-	-
1378550_at	Cblc	Cas-Br-M (murine) ecotropic retroviral transforming sequence c	292699	Rn.20550	BM384014	2.57	2.51	2.60	2.59	2.58	2.39	1.03	down	6.37E-01	8.95E-01	-	-
1374982_at	Ppp1r16a	protein phosphatase 1, regulatory (inhibitor) subunit 16A	362944	Rn.145223	BF412002	4.17	4.16	4.18	4.01	4.17	4.22	1.03	down	6.10E-01	8.95E-01	-

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1385751_at	Thbs2	thrombospondin 2	292406	Rn.165619	BF408413	2.18	2.18	2.19	2.18	2.30	2.18	1.03	up	4.14E-01	8.95E-01	-	-
1392293_at	---	---	---	Rn.52240	BE113790	2.40	2.38	2.40	2.51	2.40	2.38	1.03	up	4.52E-01	8.95E-01	-	-
1395048_at	---	---	---	Rn.205983	BM384985	2.64	2.55	2.57	2.55	2.56	2.54	1.03	down	3.02E-01	8.95E-01	-	-
1395435_at	---	---	---	---	BF285208	2.37	2.27	2.28	2.27	2.28	2.26	1.03	down	3.54E-01	8.95E-01	-	-
1398949_at	RGD1311072	similar to 2410001C21Rik protein	296410	Rn.117476	BM392094	6.78	6.73	6.80	6.77	6.79	6.85	1.03	up	3.09E-01	8.95E-01	-	-
1397197_at	---	---	---	Rn.208807	BE120228	2.51	2.50	2.53	2.67	2.53	2.45	1.03	up	6.08E-01	8.95E-01	-	-
1370781_a_at	Kcnip1	Kv channel-interacting protein 1	65023	Rn.20530	AY082657	2.65	2.62	2.69	2.62	2.70	2.54	1.03	down	5.12E-01	8.95E-01	-	-
1382002_at	---	---	---	Rn.148368	AI230621	2.56	2.52	2.58	2.55	2.69	2.53	1.03	up	5.34E-01	8.95E-01	-	-
1369763_at	Grk4	G protein-coupled receptor kinase 4	59077	Rn.54517	NM_022928	2.59	2.49	2.51	2.49	2.50	2.49	1.02	down	3.24E-01	8.95E-01	-	-
1381091_at	---	---	---	Rn.170782	BE101556	2.83	2.98	2.83	2.82	2.90	2.82	1.02	down	5.57E-01	8.95E-01	-	-
1384759_at	Phf17	PHD finger protein 17	310352	Rn.90858	AW534015	5.80	6.88	6.21	6.25	6.21	6.55	1.02	up	9.20E-01	9.76E-01	-	-
1379600_at	---	---	---	---	BF387498	2.45	2.45	2.51	2.45	2.45	2.40	1.02	down	2.46E-01	8.95E-01	-	-
1368926_at	Sema4f	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and	29745	Rn.42885	NM_019272	2.37	2.36	2.47	2.36	2.37	2.36	1.02	down	3.55E-01	8.95E-01	-	-
1369187_a_at	Ptger3	prostaglandin E receptor 3 (subtype EP3)	24929	Rn.10361	NM_012704	2.31	2.31	2.32	2.33	2.32	2.40	1.02	up	2.33E-01	8.95E-01	-	-
1393650_at	---	---	---	Rn.212549	BI289506	2.34	2.39	2.36	2.33	2.34	2.31	1.02	down	1.10E-01	8.95E-01	-	-
1393775_at	N4bp3	Nedd4 binding protein 3	303112	Rn.35493	BI275777	2.51	2.49	2.53	2.49	2.51	2.41	1.02	down	3.60E-01	8.95E-01	-	-
1392229_at	---	---	---	Rn.206989	AW532790	2.48	2.48	2.49	2.59	2.49	2.48	1.02	up	3.85E-01	8.95E-01	-	-
1393574_at	---	---	---	Rn.167066	AI103347	5.26	4.48	4.82	4.35	4.72	5.60	1.02	up	9.39E-01	9.83E-01	-	-
1369161_at	Abcb4	ATP-binding cassette, sub-family B (MDR/TAP), member 4	24891	Rn.82691	NM_012690	2.49	2.48	2.50	2.49	2.40	2.48	1.02	down	2.88E-01	8.95E-01	-	-
1395848_at	LOC683948	hypothetical protein LOC683948	683948	---	AA998703	2.39	2.38	2.48	2.38	2.39	2.37	1.02	down	3.45E-01	8.95E-01	-	-
1381142_at	---	---	---	Rn.35009	AI408245	2.35	2.34	2.36	2.34	2.35	2.46	1.02	up	4.16E-01	8.95E-01	-	-
1369443_at	Angptl2	angiopoietin-like 2	171100	Rn.162660	NM_133569	2.45	2.39	2.39	2.38	2.38	2.37	1.02	down	1.87E-01	8.95E-01	-	-
1371289_at	---	---	---	---	U16359	2.77	2.68	2.90	2.74	2.86	2.65	1.02	down	7.10E-01	9.09E-01	-	-
1378505_at	---	---	---	---	AI232255	2.66	2.65	2.71	2.66	2.67	2.60	1.02	down	2.74E-01	8.95E-01	-	-
1370738_a_at	Trdn	triadin	59299	Rn.41863	AF220558	2.96	2.79	3.06	2.89	3.00	2.82	1.02	down	7.30E-01	9.14E-01	-	-
1377421_at	---	---	---	Rn.129543	BF562337	2.35	2.33	2.41	2.33	2.34	2.32	1.02	down	2.45E-01	8.95E-01	-	-
1369346_at	Slit2	slit homolog 2 (Drosophila)	360272	Rn.146652	NM_030832	2.45	2.43	2.53	2.44	2.46	2.40	1.02	down	3.68E-01	8.95E-01	-	-
1376367_at	---	---	---	Rn.210686	BF400644	2.40	2.48	2.41	2.39	2.40	2.39	1.02	down	2.63E-01	8.95E-01	-	-
1384698_at	---	---	---	Rn.167033	AI406524	2.56	2.55	2.56	2.65	2.57	2.55	1.02	up	3.02E-01	8.95E-01	-	-
1374847_at	Lztr1	leucine-zipper-like transcription regulator 1	360745	Rn.15759	AI177438	5.38	5.61	4.92	5.14	5.61	5.26	1.02	up	8.92E-01	9.67E-01	-	-
1375908_at	Mpzl2	myelin protein zero-like 2	300679	Rn.8193	BI282616	4.19	5.18	5.70	5.10	5.36	5.72	1.02	up	9.65E-01	9.90E-01	-	-
1389548_at	Adhfe1	alcohol dehydrogenase, iron containing, 1	362474	Rn.17173	BF288683	9.45	9.61	9.20	9.38	9.18	9.61	1.02	down	8.47E-01	9.52E-01	-	-
1372789_at	Zfp637	zinc finger protein 637	362425	Rn.63909	BF397881	3.77	3.71	3.66	3.72	3.24	4.30	1.02	up	9.15E-01	9.75E-01	-	-
1372153_at	Krt15	keratin 15	287700	Rn.153568	BM385502	2.54	2.52	2.63	2.53	2.55	2.49	1.02	down	4.05E-01	8.95E-01	-	-
1386299_at	---	---	---	---	AI639471	2.43	2.35	2.36	2.34	2.36	2.33	1.02	down	2.39E-01	8.95E-01	-	-
1384446_at	---	---	---	Rn.146345	BF402271	2.59	2.55	2.68	2.57	2.60	2.53	1.02	down	4.50E-01	8.95E-01	-	-
1373109_at	Map2k7	mitogen activated protein kinase kinase 7	363855	Rn.162081	BI294813	3.30	3.19	3.20	3.20	3.20	3.19	1.02	down	3.56E-01	8.95E-01	-	-
1369196_at	Ppy	pancreatic polypeptide	24677	Rn.9755	NM_012626	2.49	2.45	2.56	2.47	2.48	2.45	1.02	down	3.68E-01	8.95E-01	-	-
1369926_at	Gpx3	glutathione peroxidase 3	64317	Rn.108074	NM_022525	12.19	11.73	12.26	12.20	12.36	11.74	1.02	up	8.95E-01	9.67E-01	-	-
1386501_at	---	---	---	---	AI639304	2.46	2.40	2.46	2.40	2.42	2.38	1.02	down	2.12E-01	8.95E-01	-	-
1396545_at	---	---	---	Rn.146879	BF403889	2.39	2.37	2.39	2.38	2.51	2.36	1.02	up	5.07E-01	8.95E-01	-	-
1379623_at	RGD1309482	similar to chromosome 10 open reading frame 4; similar to putative acid phos	365458	Rn.23684	AA874896	4.72	4.72	4.82	4.84	4.73	4.58	1.02	down	6.92E-01	9.05E-01	-	-
1369860_a_at	Htr2c	5-hydroxytryptamine (serotonin) receptor 2C	25187	Rn.9935	U35315	2.42	2.30	2.34	2.32	2.35	2.29	1.02	down	4.42E-01	8.95E-01	-	-
1383668_at	Mmp15	matrix metallopeptidase 15	291848	Rn.16543	AA997466	2.45	2.44	2.58	2.45	2.48	2.43	1.02	down	4.86E-01	8.95E-01	-	-
1389613_at	---	---	---	Rn.58294	AI234712	5.16	5.38	4.74	4.68	5.65	4.84	1.02	down	9.71E-01	9.91E-01	-	-
1388269_at	RGD1308470	similar to RIKEN cDNA 4933433P14 gene	362778	Rn.3701	BI285251	2.69	2.67	2.74	2.68	2.54	2.77	1.02	down	6.38E-01	8.95E-01	-	-
1372438_at	Nit2	nitrilase family, member 2	288174	Rn.42859	AI411100	10.13	10.25	10.13	10.07	10.14	10.19	1.02	down	5.48E-01	8.95E-01	-	-
1398578_at	Tyh1	tweety homolog 1 (Drosophila)	292597	Rn.14889	AI102019	2.51	2.49	2.62	2.49	2.53	2.49	1.02	down	4.63E-01	8.95E-01	-	-
1394775_at	---	---	---	Rn.205740	AI547644	2.35	2.33	2.44	2.34	2.35	2.32	1.02	down	3.79E-01	8.95E-01	-	-
1373164_at	---	---	---	Rn.1300	AI012590	5.60	5.54	5.71	5.59	5.53	5.83	1.02	up	7.49E-01	9.19E-01	-	-
1385216_at	Runx1t1	runt-related transcription factor 1; translocated to, 1 (cyclin D-related)	364489	Rn.218117	BI388857	2.83	2.79	2.94	2.81	2.88	2.78	1.02	down	5.48E-01	8.95E-01	-	-
1391125_at	---	---	---	Rn.33461	AI639331	2.65	2.63	2.93	2.65	2.84	2.62	1.02	down	7.81E-01	9.29E-01	-	-
1370604_at	Lepr	leptin receptor	24536	Rn.9891	U53144	2.57	2.49	2.57	2.51	2.55	2.47	1.02	down	3.79E-01	8.95E-01	-	-
1383946_at	Cldn1	claudin 1	65129	Rn.24293	AI137640	2.58	2.54	2.67	2.55	2.63	2.51	1.02	down	5.26E-01	8.95E-01	-	-
1388939_at	Col15a1	collagen, type XV, alpha 1	295669	Rn.31832	AA800298	2.53	2.53	2.47	2.53	2.53	2.57	1.02	up	2.19E-01	8.95E-01	-	-
1373328_at	---	---	---	Rn.39381	AI009678	2.53	2.40	2.42	2.42	2.42	2.41	1.02	down	4.46E-01	8.95E-01	-	-
1398162_at	---	---	---	Rn.210690	BF400617	2.57	2.50	2.54	2.50	2.51	2.49	1.02	down	1.81E-01	8.95E-01	-	-
1372054_at	---	---	---	Rn.220633	BG380399	6.04	6.05	6.81	6.37	5.91	6.52	1.02	down	9.17E-01	9.75E-01	-	-
1387741_at	Htr1b	5-hydroxytryptamine (serotonin) receptor 1B	25075	Rn.138109	NM_022225	2.54	2.47	2.48	2.47	2.49	2.43	1.02	down	2.66E-01	8.95E-01	-	-
1382770_at	RGD1565095	similar to hypothetical protein MGC52110	503252	Rn.3412	BG376622	8.78	8.29	8.56	8.34	8.53	8.65	1.02	down	8.45E-01	9.52E-01	-	-
1381667_at	---	---	---	Rn.147666	AW530329	2.64	2.59	2.68	2.63	2.64	2.52	1.02	down	4.94E-01	8.95E-01	-	-
1368317_at	Aqp7	aquaporin 7	29171	Rn.11111	NM_019157	7.14	8.56	8.54	7.87	8.10	8.17	1.02	down	9.45E-01	9.84E-01	-	-
1397925_at	---	---	---	Rn.147788	BF412309	2.31	2.31	2.41	2.31	2.32	2.30	1.02	down	3.79E-01	8.95E-01	-	-
1368569_at	Akr1b7	aldo-keto reductase family 1, member B7	116463	Rn.32702	NM_053781	2.36	2.35	2.37	2.35	2.37	2.47	1.02	up	3.86E-01	8.95E-01	-	-
1398500_at	---	---	---	Rn.173694	BI295477	5.89	5.70	6.45	5.35	7.72	5.06	1.02	up	9.70E-01	9.91E-01	-	-
1380392_at	Brd4	Bromodomain containing 4	362844	Rn.12110	BF406259	2.50	2.45	2.60	2.50	2.51	2.44	1.02	down	4.99E-01	8.95E-01	-	-
1375308_at	---	---	---	Rn.27282	BM383330	3.16	3.48	3.72	3.63	3.35	3.49	1.02	up	8.57E-01	9.55E-01	-	-
1381610_at	---	---	---	Rn.148878	BF402073	2.50	2.39	2.41	2.40	2.42	2.38	1.02	down	3.63E-01	8.95E-01	-	-
1380156_at	---	---	---	Rn.199523	BF396185	2.46	2.35	2.37	2.36	2.37	2.35	1.02	down	3.60E-01	8.95E-01	-	-
1393408_at	Neurod6	neurogenic differentiation 6	500137	Rn.220502	BF567707	2.35	2.34	2.43	2.34	2.35	2.33	1.02	down	3.27E-01	8.95E-01	-	-
1395955_at	C1qtnf4	C1q and tumor necrosis factor related protein 4	311184	Rn.24378	BF522313	2.26	2.29	2.26	2.41	2.26	2.25	1.02	up	5.50E-01	8.95E-01	-	-
1394773_at	---	---	---	Rn.76781	BG378318	2.43	2.42	2.44	2.54	2.43	2.42	1.02	up	4.22E-01	8.95E-01	-	-
1373193_at	---	---	---	Rn.13584	BE108670	9.03	8.72	8.88	9.00	8.91	8.62	1.02	down	8.21E-01	9.43E-01	-	-
1379984_at	---	---	---	Rn.169642	AI411147	2.36	2.45	2.37	2.36	2.37	2.35	1.02	down	2.74E-01	8.95E-01	-	-
1387682_at	Trhr	thyrotropin releasing hormone receptor	25570	Rn.9962	M90308	2.69	2.64	2.79	2.67	2.71	2.64	1.02	down	5.08E-01	8.95E-01	-	-
1373114_at	---	---	---	Rn.18597	AI408442	2.42	2.42	2.43	2.45	2.43	2.50	1.02	up	1.93E-01	8.95E-01	-	-
1368153_a_at	Nelf	nasal embryonic LHRH factor	117536	Rn.7504	AJ293698	2.47	2.46	2.48	2.46	2.59	2.46	1.02	up	4.58E-01	8.95E-01	-	-
1394346_at	Man1a2	mannosidase, alpha, class 1A, member 2	295319	Rn.218006	BF561763	4.95	4.50	4.35	4.35	4.33	5.01	1.02	down	9.10E-01	9.73E-01	-	-
1381463_at	---	---	---	Rn.200265	BI299627	2.38	2.38	2.40	2.50	2.39	2.37	1.02	up	4.43E-01	8.95E-01	-	-
1396828_at	---	---	---	---	AW524520	2.33	2.32	2.33	2.32	2.33	2.43	1.02	up	3.62E-01	8.95E-01	-	-
1382483_at	---	---	---	Rn.6607	BF288281	2.72	2.69	2.76	2.71	2.70	2.66	1.02	down	2.28E-01	8.95E-01	-	-
1391309_at	C1ql3	complement component 1, q subcomponent-like 3	680404	Rn.13498	AI111970	2.45	2.32	2.34	2.34	2.33	2.32	1.02	down	4.17E-01	8.95E-01	-	-
1376830_at	Exoc3l	exocyst complex component 3-like	291961	Rn.160595	AW520496	2.31	2.31	2.32	2.31	2.32	2.42	1.02	up	3.67E-01	8.95E-01	-	-
1372031_at	---	---	---	Rn.14763	AI407821	10.15	9.88	9.97	10.13	10.19	9.77	1.02	up	8.33E-01	9.47E-01	-	-
1370145_at	Zfp354c	zinc finger protein 354C	78972	Rn.64579	NM_023988	2.69	2.43	2.45	2.61	2.44	2.42	1.02	down	7.55E-01	9.20E-01	-	-
1380554_at	---	---	---	---	AI101463	2.36	2.34	2.50	2.34	2.41	2.42	1.02	down	5.56E-01	8.95E-01	-	-
1392343_at	---	---	---	Rn.165960	AI030867	2.45	2.42	2.47	2.42	2.40	2.42	1.02	down	1.11E-01	8.95E-01	-	-
1376934_x_at	---	---	---	---	BI285801	2.54	2.53	2.64	2.53	2.55	2.52	1.02	down	3.78E-01	8.95E-01	-	-
1395379_at	Zrsr2	zinc finger (CCCH type), RNA binding motif and serine/arginine rich 2	302670	Rn.26786	AW144684	3.17	3.22	3.18	3.17	3.17	3.13	1.02	down	1.42E-01	8.95E-01	-	-
1377023_at	Dusp2	dual specificity phosphatase 2	311406	Rn.136933	AI408580	2.55	2.39	2.40	2.39	2.40	2.44	1.02	down	5.57E-01	8.95E-01	-	-
1377719_a_at	---	---	---	---	AA892765	10.28	9.93	10.55	10.08	10.37	10.21	1.02	down	8.69E-01	9.59E-01	-	-
1373636_at	Spock1	sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) 1	306759	Rn.44057	AI406342	2.39	2.47	2.39	2.38	2.39	2.37	1.02	down	2.96E-01	8.95E-01	-	-
1376995_at	Foxd4 /// Pgm5	forkhead box D4 /// phosphoglucomutase 5	252886 /// 679990	Rn.198192	AI501186	2.34	2.33	2.35	2.46	2.34	2.32	1.02	up	4.75E-01	8.95E-01	-	-
1385440_at	Hcst	hematopoietic cell signal transducer	474146	Rn.145403	BF419129	2.50	2.49	2.46	2.50	2.54	2.52	1.02	up	1.16E-01	8.95E-01	-	-
1398786_at	Psmb2	proteasome (prosome, macropain) subunit, beta type 2	29675	Rn.1981	NM_017284	8.33	8.43	7.90	8.38	7.76	8.41	1.02	down	9.02E-01	9.70E-01	-	-
1382718_at	Nfx1	Nuclear transcription factor, X-box binding 1	313166	Rn.55459	AA900547	7.22	6.04	6.37	6.45	6.35	6.93	1.02	up	9.35E-01	9.82E-01	-	-
1396630_at	---	---	---	Rn.208663	BF393572	2.55	2.56	2.53	2.53	2.53	2.49	1.02	down	7.89E-02	8.95E-01	-	-
1381395_at	Klf15	Kruppel-like factor 15	85497	Rn.22556	AA998067	2.47	2.46	2.57	2.47	2.47	2.45	1.02	down	3.64E-01	8.95E-01	-	-
1389503_at	LOC367994	similar to uroplakin 3B isoform b	367994	Rn.9193	BI286447	2.41	2.40	2.50	2.40	2.41	2.39	1.02	down	3.72E-01	8.95E-01	-	-
1372698_at	aca /// RGD1305	protein kinase, cAMP-dependent, catalytic, alpha /// similar to CG2662-PA	25636 /// 304649	Rn.20	BI275970	3.24	3.22	3.31	3.21	3.46	3.20	1.02	up	7.18E-01	9.11E-01	-	-
1390641_at	Zfp346	Zinc finger protein 346	306765	Rn.17764	BE111799	3.74	3.75	3.96	3.96	3.70	3.69	1.02	down	7.79E-01	9.28E-01	-	-
1392398_at	---	---	---	Rn.160874	BE099964	2.59	2.50	2.53	2.51	2.52	2.48	1.02	down	2.99E-01	8.95E-01	-	-
1395922_at	---	---	---	Rn.50188	BF412539	2.33	2.28	2.34	2.28	2.30	2.27	1.02	down	1.55E-01	8.95E-01	-	-
1374705_at	Col4a5	collagen, type IV, alpha 5	363457	Rn.17094	AA891834	6.71	5.28	4.96	5.75	5.03	6.06	1.02	down	9.58E-01	9.88E-01	-	-
1380107_a_at	Natl8l	N-acetyltransferase 8-like	289727	Rn.76732	BM384521	2.46	2.41	2.46	2.40	2.42	2.41	1.02	down	9.85E-02	8.95E-01	-	-
1389605_at	Jakmip1	janus kinase and microtubule interacting protein 1	305434	Rn.18970	AI101952	2.48	2.47	2.54	2.47	2.50	2.41	1.02	down	3.67E-01	8.95E-01	-	-
1391332_at	Poln	polymerase (DNA directed) nu	498396	Rn.210535	BF403055	2.35	2.33	2.35	2.35	2.47	2.33	1.02	up	4.65E-01	8.95E-01	-	-
1396781_at	---	---	---	Rn.147261	BF387291	2.58	2.54	2.58	2.55	2.57	2.48	1.02	down	3.24E-01	8.95E-01	-	-
1380682_at	Mex3b	mex3 homolog B (C. elegans)	308790	Rn.162433	BF396302	2.51	2.59	2.51	2.50	2.51	2.49	1.02	down	2.76E-01	8.95E-01	-	-
1397192_at	Mycbp2	Myc-binding protein 2	290447	Rn.13538	BF286046	2.55	2.52	2.54	2.54	2.52	2.43	1.02	down	3.82E-01	8.95E-01	-	-
1375902_at	---	---	---	Rn.204980	AI231065	2.43	2.34	2.35	2.35	2.35	2.32	1.02	down	3.10E-01	8.95E-01	-	-
1392571_at	Vps13a	vacuolar protein sorting 13 homolog A (S. cerevisiae)	309243	Rn.16931	AA899216	2.52	2.64	2.58	2.41	2.48	2.74	1.02	down	7.58E-01	9.21E-01	-	-
1379622_at	---	---	---	Rn.204760	BF405145	2.37	2.36	2.38	2.47	2.37	2.36	1.02	up	4.08E-01	8.95E-01	-	-
1381455_at	Als2cr4	amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 4	316412	Rn.98599	AI639359	2.88	2.78	2.93	2.83	2.91	2.75	1.02	down	6.17E-01	8.95E-01	-	-
1392210_at	RGD1307443	similar to mKIAA0319 protein	361244	Rn.139250	BF410487	2.56	2.42	2.44	2.42	2.45	2.45	1.02	down	4.88E-01	8.95E-01	-	-
1390724_at	---	---	---	Rn.40842	AW253006	2.45	2.44	2.53	2.44	2.46	2.42	1.02	down	3.16E-01	8.95E-01	-	-
1383600_at	Slc13a5	solute carrier family 13 (sodium-dependent citrate transporter), member 5	266998	Rn.107582	BG381311	2.44	2.44	2.44	2.44	2.54	2.42	1.02	up	3.73E-01	8.95E-01	-	-
1386472_at	---	---	---	Rn.125044	H33301	2.59	2.67	2.60	2.58	2.59	2.58	1.02	down	2.75E-01	8.95E-01	-	-
1389092_at	Il2rg	interleukin 2 receptor, gamma	140924	Rn.14508	AI178808	2.41	2.34	2.34	2.33	2.34	2.32	1.02	down	2.48E-01	8.95E-01	-	-
1384046_at	---	---	---	---	BF543195	4.94	5.81	6.19	5.44	5.51	5.88	1.02	down	9.35E-01	9.82E-01	-	-
1390152_at	Tmed7	transmembrane emp24 protein transport domain containing 7	252889	Rn.67055	BE095882	2.14	2.13	2.14	2.14	2.24	2.24	1.02	up	3.70E-01	8.95E-01	-	-
1370550_at	Lsamp	limbic system-associated membrane protein	29561	Rn.10176	U31554	2.35	2.42	2.36	2.34	2.35	2.33	1.02	down	2.27E-01	8.95E-01	-	-
1375682_at	Pura	Purine rich element binding protein A	307498	Rn.41055	BM382879	3.99	3.46	3.77	3.88	3.49	3.74	1.02	down	8.66E-01	9.58E-01	-	-
1374028_at	LOC500974	similar to cDNA sequence BC024479	500974	Rn.96035	AI412685	2.74	2.75	2.75	2.85	2.80	2.69	1.02	up	5.09E-01	8.95E-01	-	-
1380177_at	Mat2a	Methionine adenosyltransferase II, alpha	171347	Rn.144658	BE097659	2.42	2.51	2.43	2.42	2.42	2.41	1.02	down	2.74E-01	8.95E-01	-	-
1390748_at	---	---	---	---	BF405352	2.40	2.38	2.46	2.40	2.41	2.34	1.02	down	3.29E-01	8.95E-01	-	-
1382787_at	Kif5a	kinesin family member 5A	314906	Rn.161936	BF408705	2.50	2.48	2.53	2.48	2.50	2.44	1.02	down	2.09E-01	8.95E-01	-	-
1391761_at	Chit1	chitinase 1 (chitotriosidase)	289032	Rn.47819	AW531798	2.38	2.37	2.38	2.37	2.38	2.47	1.02	up	3.57E-01	8.95E-01	-	-
1381774_at	---	---	---	Rn.204406	BE095849	2.54	2.64	2.54	2.52	2.57	2.52	1.02	down	3.93E-01	8.95E-01	-	-
1392115_at	---	---	---	Rn.210783	BF401730	2.53	2.50	2.68	2.53	2.62	2.47	1.02	down	6.57E-01	8.98E-01	-	-
1382302_at	---	---	---	---	AI044633	2.34	2.32	2.33	2.44	2.34	2.31	1.02	up	4.44E-01	8.95E-01	-	-
1392375_at	---	---	---	Rn.210840	BF405872	2.40	2.37	2.45	2.38	2.39	2.36	1.02	down	2.36E-01	8.95E-01	-	-
1384240_at	Agtr1a	angiotensin II receptor, type 1a	24180	Rn.214849	BI290306	4.66	3.85	4.79	5.00	3.66	4.74	1.02	up	9.49E-01	9.85E-01	-	-
1368141_at	Cnbp	CCHC-type zinc finger, nucleic acid binding protein	64530	Rn.6187	AF242650	10.76	10.79	11.19	10.80	10.95	10.88	1.02	down	8.24E-01	9.44E-01	-	-
1375019_at	Hnrnph3	heterogeneous nuclear ribonucleoprotein H3 (2H9)	361838	Rn.60652	AI101886	7.29	8.46	8.67	7.91	7.91	8.01	1.02	down	9.46E-01	9.84E-01	-	-
1371451_at	Rnaseh2a	ribonuclease H2, subunit A	364974	Rn.3693	AI010940	7.24	7.00	5.83	6.50	6.49	7.17	1.02	up	9.48E-01	9.85E-01	-	-
1395207_at	---	---	---	Rn.168333	AW527787	2.53	2.45	2.46	2.45	2.45	2.44	1.02	down	2.65E-01	8.95E-01	-	-
1375040_at	Nfe2	nuclear factor, erythroid derived 2	366998	Rn.137607	AW252129	2.48	2.46	2.59	2.47	2.50	2.46	1.02	down	4.56E-01	8.95E-01	-	-
1389938_at	Etv6	Ets variant 6	312777	Rn.147424	AW253265	2.75	3.48	2.40	3.44	2.55	2.75	1.02	up	9.39E-01	9.83E-01	-	-
1374597_at	---	---	---	---	BI275770	7.59	7.96	7.54	7.48	7.88	7.83	1.02	up	8.61E-01	9.57E-01	-	-
1389464_at	Lnx1	ligand of numb-protein X 1	360926	Rn.25032	BE120953	2.42	2.49	2.41	2.41	2.43	2.39	1.02	down	2.95E-01	8.95E-01	-	-
1392372_at	---	---	---	Rn.117883	BF396089	2.33	2.41	2.33	2.32	2.33	2.31	1.02	down	2.70E-01	8.95E-01	-	-
1396793_at	Ppfia2	protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interactin	362876	Rn.208769	BE121129	2.53	2.51	2.60	2.53	2.72	2.50	1.02	up	6.65E-01	8.99E-01	-	-
1381550_at	---	---	---	Rn.207236	BE095969	2.60	2.59	2.82	2.63	2.70	2.59	1.02	down	7.00E-01	9.07E-01	-	-
1386783_at	Chsy3	chondroitin s

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1384365_at	Cdyl	chromodomain protein, Y chromosome-like	361237	Rn.146844	BF557607	2.38	2.31	2.34	2.31	2.32	2.30	1.02	down	2.22E-01	8.95E-01	-	-
1380793_at	Plk3ip1	Phosphoinositide-3-kinase interacting protein 1	305472	Rn.138969	BM387766	2.33	2.27	2.32	2.28	2.29	2.26	1.02	down	1.70E-01	8.95E-01	-	-
1380941_at	---	---	---	Rn.21201	AI501031	2.62	2.51	2.68	2.57	2.57	2.56	1.02	down	5.36E-01	8.95E-01	-	-
1385081_s_at	Vps33a	vacuolar protein sorting 33 homolog A (S. cerevisiae)	65081	Rn.217659	BM386498	3.52	3.53	3.65	3.61	3.69	3.51	1.02	up	6.40E-01	8.95E-01	-	-
1399088_at	Tlk2	tousled-like kinase 2	303592	Rn.23125	AA819648	6.89	6.98	6.46	6.74	6.36	7.12	1.02	down	9.08E-01	9.72E-01	-	-
1383646_at	---	---	---	Rn.7606	AI072798	2.45	2.42	2.52	2.43	2.45	2.40	1.02	down	3.79E-01	8.95E-01	-	-
1374435_at	---	---	---	Rn.13041	AA896970	5.88	5.47	6.34	5.84	5.59	6.15	1.02	down	9.16E-01	9.75E-01	-	-
1390849_at	---	---	---	Rn.20519	AW520584	2.45	2.42	2.46	2.55	2.45	2.44	1.02	up	4.47E-01	8.95E-01	-	-
1396872_at	Magi1	membrane associated guanylate kinase, WW and PDZ domain containing 1	500261	Rn.95239	AI555260	2.28	2.27	2.28	2.38	2.28	2.27	1.02	up	3.95E-01	8.95E-01	-	-
1381377_at	---	---	---	Rn.199413	AI178302	2.48	2.56	2.43	2.42	2.43	2.52	1.02	down	5.19E-01	8.95E-01	-	-
1380099_at	---	---	---	Rn.146732	BM391357	2.42	2.38	2.78	2.66	2.42	2.39	1.02	down	8.37E-01	9.49E-01	-	-
1382801_at	---	---	---	Rn.21668	AI043667	2.50	2.48	2.58	2.49	2.50	2.48	1.02	down	3.49E-01	8.95E-01	-	-
1386205_at	Flvcr2	feline leukemia virus subgroup C cellular receptor family, member 2	314323	Rn.92663	AA956782	2.26	2.26	2.27	2.37	2.27	2.25	1.02	up	4.19E-01	8.95E-01	-	-
1379357_at	---	---	---	---	AI408767	2.55	2.45	2.51	2.46	2.51	2.43	1.02	down	3.97E-01	8.95E-01	-	-
1367799_at	Eef1a2	eukaryotic translation elongation factor 1 alpha 2	24799	Rn.9764	NM_012660	2.44	2.40	2.45	2.50	2.44	2.45	1.02	up	2.32E-01	8.95E-01	-	-
1379265_at	---	---	---	Rn.7380	BF398764	6.33	5.52	5.79	5.85	5.92	5.76	1.02	down	8.98E-01	9.68E-01	-	-
1373488_at	---	---	---	Rn.41289	BF288154	9.72	8.67	7.52	9.05	8.48	8.28	1.02	down	9.63E-01	9.89E-01	-	-
1379361_at	Pex11a	peroxisomal biogenesis factor 11 alpha	85249	Rn.14519	BI273703	7.21	7.78	8.17	7.74	7.46	8.06	1.02	up	9.23E-01	9.78E-01	-	-
1379942_at	Sox2	SRY (sex determining region Y)-box 2	499593	Rn.219221	AA858564	2.55	2.50	2.61	2.52	2.54	2.49	1.02	down	3.93E-01	8.95E-01	-	-
1377132_at	---	---	---	Rn.169648	AW527797	2.75	2.72	2.81	2.66	2.77	2.75	1.02	down	4.75E-01	8.95E-01	-	-
1388356_at	S100a16	S100 calcium binding protein A16	361991	Rn.1053	AI406499	3.59	3.13	3.21	3.29	3.33	3.21	1.02	down	8.30E-01	9.46E-01	-	-
1395815_at	---	---	---	---	BF291198	2.97	2.94	3.00	2.85	3.01	2.95	1.02	down	5.29E-01	8.95E-01	-	-
1397749_at	---	---	---	Rn.205553	AI715712	2.59	2.59	2.68	2.91	2.53	2.52	1.02	up	8.12E-01	9.39E-01	-	-
1388869_at	Sspn	sarcospan	500364	Rn.22364	AA799392	2.26	2.25	2.26	2.36	2.26	2.25	1.02	up	4.14E-01	8.95E-01	-	-
1392042_at	Znf213	zinc finger protein 213	287094	Rn.98676	AI146029	2.47	2.43	2.46	2.43	2.62	2.40	1.02	up	6.50E-01	8.96E-01	-	-
1391317_at	RGD1310784	similar to RIKEN cDNA 2810433K01	291441	Rn.106906	BE109802	2.48	2.46	2.48	2.46	2.61	2.44	1.02	up	5.74E-01	8.95E-01	-	-
1378121_at	---	---	---	---	AI600165	2.54	2.63	2.54	2.56	2.60	2.45	1.02	down	5.52E-01	8.95E-01	-	-
1373835_at	Fbxo8	F-box protein 8	306436	Rn.91689	AI009785	3.99	5.74	5.76	5.00	4.63	5.76	1.02	down	9.63E-01	9.89E-01	-	-
1381143_at	---	---	---	Rn.203934	AI029836	2.52	2.46	2.49	2.46	2.49	2.43	1.02	down	2.15E-01	8.95E-01	-	-
1383580_at	---	---	---	---	AA859643	2.27	2.26	2.28	2.38	2.27	2.26	1.02	up	4.17E-01	8.95E-01	-	-
1377537_at	RGD1559980	RGD1559980	499158	Rn.52198	BE121268	2.32	2.32	2.42	2.31	2.34	2.32	1.02	down	3.84E-01	8.95E-01	-	-
1392608_at	---	---	---	Rn.18419	AI030154	2.56	2.49	2.56	2.50	2.54	2.47	1.02	down	3.43E-01	8.95E-01	-	-
1372439_at	Col4a1	collagen, type IV, alpha 1	290905	Rn.53801	AI176393	4.35	5.13	4.60	5.44	4.15	4.38	1.02	down	9.45E-01	9.84E-01	-	-
1372342_at	Marveld1	MARVEL domain containing 1	309375	Rn. 1215	AI176583	2.89	2.38	2.42	2.44	2.73	2.42	1.02	down	8.69E-01	9.59E-01	-	-
1380866_at	LOC365985	similar to adenylate kinase 5 isoform 1	365985	Rn.16387	AA817746	2.41	2.47	2.40	2.40	2.41	2.38	1.02	down	2.30E-01	8.95E-01	-	-
1384963_at	---	---	---	Rn.200300	BI277632	2.47	2.46	2.58	2.47	2.48	2.46	1.02	down	4.31E-01	8.95E-01	-	-
1394532_at	---	---	---	---	BE107163	2.48	2.38	2.39	2.38	2.38	2.38	1.02	down	3.60E-01	8.95E-01	-	-
1382842_at	---	---	---	Rn.203988	BE107996	2.50	2.63	2.49	2.48	2.52	2.72	1.02	up	7.18E-01	9.11E-01	-	-
1381599_at	---	---	---	Rn.211312	BF414434	2.63	2.52	2.71	2.60	2.82	2.54	1.02	up	7.52E-01	9.20E-01	-	-
1377290_at	Tnrc6a	trinucleotide repeat containing 6a	308971	Rn.6839	BF389113	2.60	2.65	2.61	2.60	2.61	2.55	1.02	down	2.10E-01	8.95E-01	-	-
1384211_at	Col11a1	collagen, type XI, alpha 1	25654	Rn.260	BM388456	2.62	2.56	2.70	2.58	2.66	2.54	1.02	down	5.67E-01	8.95E-01	-	-
1385727_at	Fgfr1op2	FGFR1 oncogene partner 2	362463	Rn.68658	BE107623	5.62	7.13	5.81	6.35	6.15	6.16	1.02	up	9.48E-01	9.85E-01	-	-
1394877_at	---	---	---	Rn.147503	AI137678	2.52	2.51	2.53	2.52	2.52	2.62	1.02	up	3.82E-01	8.95E-01	-	-
1384696_at	389479 /// MGC11	similar to Discs large homolog 5 (Placenta and prostate DLG) (Discs large pro	367620 /// 689479	Rn.155021	BE113106	2.49	2.48	2.62	2.50	2.52	2.47	1.02	down	5.04E-01	8.95E-01	-	-
1390072_at	---	---	---	Rn.210008	BF401531	2.52	2.51	2.52	2.51	2.63	2.51	1.02	up	4.67E-01	8.95E-01	-	-
1383696_at	Ptpla	protein tyrosine phosphatase-like (proline instead of catalytic arginine), membr	680115	Rn.38334	AW525428	2.96	3.57	7.09	5.74	4.07	3.72	1.02	down	9.83E-01	9.95E-01	-	-
1383507_at	---	---	---	Rn.165784	AI045091	2.43	2.49	2.45	2.42	2.44	2.41	1.02	down	1.36E-01	8.95E-01	-	-
1389590_at	---	---	---	Rn.3844	AA925513	7.73	7.41	7.67	7.37	7.21	8.13	1.02	down	9.17E-01	9.75E-01	-	-
1381876_at	Fras1	Fraser syndrome 1 homolog (human)	289486	Rn.23357	AI008494	2.98	2.74	2.78	3.12	2.76	2.72	1.02	up	8.32E-01	9.47E-01	-	-
1385465_at	Siglec5	sialic acid binding Ig-like lectin 5	292843	Rn.161194	BG379188	2.58	2.57	2.66	2.56	2.62	2.52	1.02	down	4.88E-01	8.95E-01	-	-
1382436_at	RGD1566265	similar to RIKEN cDNA 2610002M06	363487	Rn.8881	BM386497	2.61	2.55	2.77	2.59	2.59	2.85	1.02	up	7.76E-01	9.27E-01	-	-
1388796_at	Gosr1	Golgi SNAP receptor complex member 1	94189	Rn.8228	AI169291	6.87	6.62	7.37	6.89	6.76	7.31	1.02	up	9.10E-01	9.73E-01	-	-
1378185_at	Nxt2	nuclear transport factor 2-like export factor 2	315352	Rn.30120	AW528873	4.15	4.33	4.53	3.72	4.42	4.75	1.02	down	9.23E-01	9.77E-01	-	-
1391141_at	---	---	---	Rn.123494	BF413254	2.64	3.03	2.80	2.79	2.80	2.79	1.02	down	7.83E-01	9.30E-01	-	-
1377936_at	---	---	---	---	AI008241	2.46	2.36	2.38	2.37	2.37	2.36	1.02	down	3.10E-01	8.95E-01	-	-
1390756_at	Fam155a	family with sequence similarity 155, member A	498667	Rn.45013	BF401379	2.61	2.53	2.56	2.53	2.55	2.52	1.02	down	2.86E-01	8.95E-01	-	-
1384554_at	---	---	---	---	AI058725	2.41	2.39	2.52	2.41	2.42	2.40	1.02	down	4.59E-01	8.95E-01	-	-
1375248_at	Klf2	Kruppel-like factor 2 (lung)	306330	Rn.92853	BI294916	3.45	3.44	3.54	3.44	3.45	3.44	1.02	down	3.71E-01	8.95E-01	-	-
1371340_at	29 /// LOC498555	hypothetical gene supported by X15098 /// similar to 60S acidic ribosomal prot	2 /// 363929 /// 49	Rn.976	AW919054	12.44	12.45	12.47	12.53	12.47	12.46	1.02	up	2.20E-01	8.95E-01	-	-
1384992_at	Hdac10	histone deacetylase 10	362981	Rn.107028	AI236142	2.47	2.46	2.50	2.58	2.48	2.46	1.02	up	4.51E-01	8.95E-01	-	-
1397937_at	---	---	---	Rn.211282	BF409772	2.62	2.60	2.69	2.61	2.66	2.53	1.02	down	5.03E-01	8.95E-01	-	-
1392051_at	Tmem87b	transmembrane protein 87B	362212	Rn.28728	BE106315	7.80	7.93	6.83	6.91	6.76	7.99	1.02	up	9.68E-01	9.91E-01	-	-
1393684_at	Hells	helicase, lymphoid specific	294071	Rn.18653	BF389489	2.54	2.54	2.55	2.52	2.55	2.46	1.02	down	2.66E-01	8.95E-01	-	-
1387021_at	Zmat3	zinc finger, matrin type 3	64394	Rn.2925	NM_022548	2.73	2.59	2.60	2.60	2.64	2.59	1.02	down	5.19E-01	8.95E-01	-	-
1392507_at	---	---	---	Rn.17797	AI385280	4.88	5.20	5.19	5.15	5.17	5.04	1.02	up	7.84E-01	9.30E-01	-	-
1380143_at	---	---	---	Rn.165884	AI029786	10.96	11.18	11.23	11.30	11.22	10.95	1.02	up	8.18E-01	9.42E-01	-	-
1373326_at	---	---	---	Rn.15193	AI716512	2.54	2.54	2.60	2.54	2.57	2.47	1.02	down	4.04E-01	8.95E-01	-	-
1378933_at	Isy1	ISY1 splicing factor homolog (S. cerevisiae)	362394	Rn.25170	AA817909	2.49	2.73	2.48	2.50	2.82	2.49	1.02	up	8.19E-01	9.42E-01	-	-
1391808_at	---	---	---	Rn.14854	AI535140	2.51	2.51	2.52	2.51	2.52	2.61	1.02	up	3.75E-01	8.95E-01	-	-
1391453_at	Ebi3	Epstein-Barr virus induced 3	680609	Rn.14957	BF390736	2.60	2.45	2.48	2.46	2.48	2.50	1.02	down	5.22E-01	8.95E-01	-	-
1398903_at	Esd	esterase D/formylglutathione hydrolase	290401	Rn.3682	AI411425	10.78	11.04	10.66	10.85	10.89	11.03	1.02	up	8.44E-01	9.51E-01	-	-
1389628_at	Plcd3	phospholipase C, delta 3	287745	Rn.95716	BG371532	2.44	2.43	2.44	2.43	2.55	2.43	1.02	up	4.64E-01	8.95E-01	-	-
1393470_at	---	---	---	Rn.207313	BE097303	2.51	2.43	2.46	2.43	2.45	2.42	1.02	down	2.36E-01	8.95E-01	-	-
1368917_at	Nudt1	nudix (nucleoside diphosphate linked moiety X)-type motif 1	117260	Rn.10669	NM_057120	3.62	3.62	3.71	3.62	3.63	3.61	1.02	down	3.36E-01	8.95E-01	-	-
1393708_at	Bhlhe22	basic helix-loop-helix family, member e22	365748	Rn.161818	BE115766	2.58	2.49	2.51	2.49	2.50	2.49	1.02	down	2.88E-01	8.95E-01	-	-
1398409_at	---	---	---	Rn.163705	AA850428	8.30	8.04	8.16	8.24	7.66	8.50	1.02	down	9.04E-01	9.71E-01	-	-
1386458_x_at	Agap3	ArfGAP with GTPase domain, ankyrin repeat and PH domain 3	362300	Rn.98623	AA899458	2.64	2.59	2.72	2.61	2.71	2.53	1.02	down	6.43E-01	8.95E-01	-	-
1370462_at	Hmmr	hyaluronan mediated motility receptor (RHAMM)	25460	Rn.92304	AI171185	2.26	2.26	2.36	2.26	2.26	2.26	1.02	down	3.65E-01	8.95E-01	-	-
1376544_at	---	---	---	Rn.211016	BF414624	2.56	2.53	2.61	2.56	2.56	2.48	1.02	down	4.27E-01	8.95E-01	-	-
1387165_at	Maf	v-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian)	54267	Rn.10726	NM_019318	8.20	7.07	8.82	8.76	8.51	6.72	1.02	down	9.70E-01	9.91E-01	-	-
1371223_a_at	Lepr	leptin receptor	24536	Rn.9891	AF304191	2.55	2.54	2.56	2.54	2.77	2.44	1.02	up	7.51E-01	9.19E-01	-	-
1377545_at	---	---	---	---	BF406286	2.51	2.50	2.54	2.49	2.52	2.45	1.02	down	2.54E-01	8.95E-01	-	-
1389158_at	---	---	---	Rn.204649	BE329196	2.48	2.52	2.72	2.63	2.56	2.42	1.02	down	7.47E-01	9.18E-01	-	-
1396362_at	---	---	---	Rn.160288	BF398806	2.67	2.72	2.72	2.67	2.70	2.65	1.02	down	1.83E-01	8.95E-01	-	-
1397285_at	---	---	---	Rn.56052	BM385916	2.49	2.48	2.55	2.49	2.50	2.44	1.02	down	3.27E-01	8.95E-01	-	-
1386707_at	---	---	---	---	BF553488	2.59	2.57	2.64	2.58	2.62	2.50	1.02	down	4.52E-01	8.95E-01	-	-
1379302_at	Rbpj	recombination signal binding protein for immunoglobulin kappa J region	679028	Rn.58803	AA848916	2.72	2.81	2.73	2.75	2.73	2.69	1.02	down	3.72E-01	8.95E-01	-	-
1378967_at	Hnrpdl	heterogeneous nuclear ribonucleoprotein D-like	305178	Rn.102146	BF420350	2.53	2.49	2.53	2.62	2.53	2.51	1.02	up	4.38E-01	8.95E-01	-	-
1392980_at	Tiam1	T-cell lymphoma invasion and metastasis 1	304109	Rn.204561	AI716456	2.31	2.30	2.32	2.31	2.46	2.28	1.02	up	5.86E-01	8.95E-01	-	-
1373205_at	U2af1l4	U2 small nuclear RNA auxiliary factor 1-like 4	361542	Rn.145185	BM391897	4.87	6.19	5.83	5.89	4.59	6.51	1.02	up	9.64E-01	9.90E-01	-	-
1373615_at	Frzb	frizzled-related protein	295691	Rn.12034	BM391538	2.64	2.99	2.40	2.85	2.65	2.63	1.02	up	8.67E-01	9.59E-01	-	-
1384245_at	---	---	---	Rn.12701	AA897442	2.76	2.70	2.83	2.75	2.79	2.65	1.02	down	5.96E-01	8.95E-01	-	-
1396256_at	Itsn2	intersectin 2	313934	Rn.37673	AI045614	10.55	10.10	9.82	10.45	10.24	9.88	1.02	up	9.09E-01	9.72E-01	-	-
1374711_at	Cpsf3	cleavage and polyadenylation specificity factor 3	298916	Rn.100522	BF283512	8.13	7.79	7.69	7.84	8.21	7.66	1.02	up	8.84E-01	9.64E-01	-	-
1380831_at	---	---	---	Rn.168089	AI237035	2.64	2.61	2.64	2.59	2.63	2.58	1.02	down	1.25E-01	8.95E-01	-	-
1389544_at	Tomm7	translocase of outer mitochondrial membrane 7 homolog (yeast)	685620	Rn.160555	BG869998	11.01	11.08	11.07	11.10	11.00	11.16	1.02	up	5.60E-01	8.95E-01	-	-
1369336_at	Hr	hairless	60563	Rn.41543	NM_024364	2.44	2.36	2.37	2.36	2.36	2.34	1.02	down	2.73E-01	8.95E-01	-	-
1377396_at	---	---	---	Rn.209687	BF413101	2.50	2.41	2.44	2.43	2.43	2.39	1.02	down	3.48E-01	8.95E-01	-	-
1372304_at	Commd4	COMM domain containing 4	363068	Rn.17650	BG378042	4.73	5.54	5.65	5.25	5.00	5.78	1.02	up	9.33E-01	9.81E-01	-	-
1389514_at	Lingo1	leucine rich repeat and Ig domain containing 1	315691	Rn.20269	AI711152	2.45	2.42	2.57	2.44	2.47	2.44	1.02	down	2.04E-01	8.95E-01	-	-
1386913_at	Pdpn	podoplanin	54320	Rn.794	NM_019358	2.39	2.44	2.40	2.38	2.39	2.36	1.02	down	1.58E-01	8.95E-01	-	-
1398986_at	Serinc3	serine incorporator 3	296350	Rn.3775	AA944455	8.23	8.83	8.74	8.48	8.70	8.52	1.02	down	8.77E-01	9.62E-01	-	-
1393331_at	Heca	headcase homolog (Drosophila)	308624	Rn.8167	AI576856	2.78	2.71	2.63	2.70	2.63	2.89	1.02	up	7.28E-01	9.13E-01	-	-
1369527_at	Cx3cr1	chemokine (C-X3-C motif) receptor 1	171056	Rn.10482	NM_133534	2.32	2.40	2.33	2.32	2.32	2.31	1.02	down	2.95E-01	8.95E-01	-	-
1380011_at	---	---	---	Rn.147426	BM383573	2.69	2.48	2.57	2.57	2.54	2.54	1.02	down	6.27E-01	8.95E-01	-	-
1381435_at	LOC691770	similar to Ankyrin repeat domain-containing protein 28	691770	Rn.27640	AI705793	2.92	2.89	2.88	3.12	2.90	2.76	1.02	up	7.73E-01	9.28E-01	-	-
1384739_at	RGD1306195	similar to RAN protein	313163	Rn.107841	BE102257	2.63	2.62	2.72	2.62	2.63	2.61	1.02	down	3.50E-01	8.95E-01	-	-
1396993_at	---	---	---	Rn.132366	BM390929	4.47	4.31	4.06	3.95	4.06	4.74	1.02	down	9.11E-01	9.73E-01	-	-
1382182_at	Hoxc6	homeo box C6	252885	Rn.91646	AI501494	2.64	2.61	2.63	2.68	2.70	2.60	1.02	up	3.58E-01	8.95E-01	-	-
1385033_at	---	---	---	Rn.199746	BE097270	2.73	2.72	2.75	2.82	2.75	2.73	1.02	up	3.25E-01	8.95E-01	-	-
1387264_at	Kcnk6	potassium inwardly-rectifying channel, subfamily K, member 6	116491	Rn.43365	NM_053806	2.44	2.43	2.44	2.54	2.44	2.42	1.02	up	4.35E-01	8.95E-01	-	-
1384055_at	---	---	---	Rn.162112	BF288144	2.52	2.50	2.61	2.51	2.53	2.49	1.02	down	4.29E-01	8.95E-01	-	-
1391693_at	Atp8b1	ATPase, Class I, type 8B, member 1	291555	Rn.6957	BM384161	2.48	2.34	2.36	2.38	2.36	2.34	1.02	down	4.97E-01	8.95E-01	-	-
1375855_at	Epdr1	ependymin related protein 1 (zebrafish)	291180	Rn.2881	AI171799	2.32	2.31	2.41	2.31	2.32	2.30	1.02	down	3.79E-01	8.95E-01	-	-
1396542_at	---	---	---	Rn.171154	BF393011	2.60	2.56	2.62	2.57	2.60	2.50	1.02	down	4.04E-01	8.95E-01	-	-
1369188_at	Fbxo32	F-box protein 32	171043	Rn.72619	NM_133521	2.55	2.54	2.55	2.55	2.55	2.65	1.02	up	3.63E-01	8.95E-01	-	-
1391241_at	---	---	---	Rn.12421	BF394755	2.58	2.49	2.59	2.57	2.62	2.56	1.02	up	4.06E-01	8.95E-01	-	-
1373726_at	---	---	---	Rn.66273	AI072251	2.37	2.36	2.38	2.47	2.37	2.36	1.02	up	3.88E-01	8.95E-01	-	-
1381732_at	---	---	---	Rn.206760	BF398558	2.48	2.43	2.56	2.45	2.49	2.43	1.02	down	4.76E-01	8.95E-01	-	-
1384175_at	Efna4	ephrin A4	310943	Rn.18531	AI030569	2.58	2.57	2.58	2.64	2.58	2.60	1.02	up	1.64E-01	8.95E-01	-	-
1392384_s_at	Akr1d1	aldo-keto reductase family 1, member D1 (delta 4-3-ketosteroid-5-beta-reduct	192242	Rn.25716	AI028867	2.58	2.53	2.66	2.55	2.62	2.50	1.02	down	5.67E-01	8.95E-01	-	-
1374725_at	Mov10	Moloney leukemia virus 10	310756	Rn.3508	AW252811	4.40	3.52	3.57	2.77	5.10	3.52	1.02	down	9.67E-01	9.90E-01	-	-
1397891_at	---	---	---	Rn.177436	BM387048	2.58	2.48	2.59	2.60	2.59	2.57	1.02	up	4.05E-01	8.95E-01	-	-
1384847_at	---	---	---	Rn.101910	AA924641	2.37	2.36	2.39	2.37	2.38	2.48	1.02	up	4.04E-01	8.95E-01	-	-
1373010_at	Krt12	keratin 12	360625	Rn.94852	BG372059	2.33	2.32	2.41	2.32	2.34	2.30	1.02	down	3.60E-01	8.95E-01	-	-
1396039_at	---	---	---	Rn.210044	BI289224	2.35	2.34	2.36	2.48	2.35	2.32	1.02	up	5.43E-01	8.95E-01	-	-
1392360_at	---	---	---	Rn.206730	BE116503	2.70	2.60	2.78	2.69	2.76	2.53	1.02	down	7.19E-01	9.11E-01	-	-
1376208_at	---	---	---	---	BF419406	2.57	2.57	2.61	2.57	2.59	2.50	1.02	down	3.55E-01	8.95E-01	-	-
1375960_at	Gmcl1	germ cell-less homolog 1 (Drosophila)	312516	Rn.22813	BF281879	4.29	3.88	3.49	3.63	3.79	4.15	1.02	down	9.12E-01	9.73E-01	-	-
1384752_at	LOC689770	similar to osteoclast inhibitory lectin	689770	Rn.61078	BF407755	2.50	2.48	2.57	2.49	2.49	2.47	1.02	down	3.10E-01	8.95E-01	-	-
1381214_at	---	---	---	Rn.161262	BF391527	2.64	2.58	2.69	2.61	2.67	2.55	1.02	down	5.17E-01	8.95E-01	-	-
1393697_at	Gdf11	growth differentiation factor 11	29454	Rn.51292	BE107795	2.41	2.40	2.42	2.50	2.43	2.40	1.02	up	3.61E-01	8.95E-01	-	-
1375710_at	siat7D	Alpha-2,6-sialyltransferase ST6GalNAc IV	407764	Rn.195322	AI602428	3.07	3.06	3.97	2.48	4.10	3.43	1.02	down	9.56E-01	9.88E-01	-	-
1384491_at	Aox4	aldehyde oxidase 4	316424	Rn.198845	BI283592	2.64	2.59	2.72	2.61	2.69	2.55	1.02	down	5.86E-01	8.95E-01	-	-
1377153_a_at	Klhl6	kelch-like 6 (Drosophila)	287974	Rn.137232	AI178384	2.49	2.41	2.43	2.41	2.42	2.40	1.02	down	2.54E-01	8.95E-01	-	-
1399059_at	Ezh1	enhancer of zeste homolog 1 (Drosophila)	303547	Rn.154549	BI283868	5.27	5.51	4.47	5.14	5.39	4.63	1.02	down	9.37E-01	9.82E-01	-	-
1368302_at	Msx1	msh homeobox 1	81710	Rn.18617	NM_031059	2.47	2.47	2.56	2.47	2.49	2.45	1.02	down	3.54E-01	8.95E-01	-	-
1386521_at	---	---	---	Rn.205793	AI511291	8.19	7.09	6.75	6.63	7.43	8.07	1.02	up	9.60E-01	9.89E-01	-	-
1381408_at	---	---	---	Rn.204703	BI275477	2.59	2.57	2.55	2.58	2.67	2.55	1.02	up	4.28E-01	8.95E-01	-	-
1374137_at	---	---	---	Rn.98640	AA818055	3.12	3.23	3.87	2.78	3.80	3.55	1.02	down	9.37E-01	9.82E-01	-	-
1389426_at	Ccdc92	coiled-coil domain containing 92	100036765	Rn.32270	AW528806	4.49	3.63	5.53	4.38	5.58	3.61	1.02	down	9.69E-01	9.91E-01	-	-
1375842_at	LOC688972	similar to Glycophorin	688972	Rn.6717	AI177505	2.39	2.37	2.47	2.38	2.39	2.36	1.02	down	3.86E-01	8.95E-01	-	-
1394870_at	---	---	---	Rn.168551	BE115332	3.28	2.65	2.65	3.30	2.63	2.56	1.02	down	9.23E-01	9.77E-01	-	-
1383746_at	Ptpn14	protein tyrosine phosphatase, non-receptor type 14	305064	Rn.61069	BE100981	2.44	2.49	2.44	2.43	2.46	2.38

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1371275_at	---	---	---	---	X77818	2.48	2.46	2.50	2.44	2.48	2.43	1.02	down	1.76E-01	8.95E-01	-	-
1380606_at	---	---	---	Rn.210395	BF404346	2.87	2.70	2.62	2.73	2.76	2.59	1.02	down	7.47E-01	9.18E-01	-	-
1381831_at	---	---	---	Rn.204455	AI112536	2.40	2.39	2.49	2.39	2.40	2.38	1.02	down	3.68E-01	8.95E-01	-	-
1381813_at	---	---	---	---	BI294535	2.32	2.30	2.40	2.31	2.31	2.30	1.02	down	3.82E-01	8.95E-01	-	-
1380231_at	---	---	---	---	AI013485	2.54	2.48	2.58	2.50	2.54	2.47	1.02	down	4.16E-01	8.95E-01	-	-
1369265_at	Senp2	SUMO1/sentrin/SMT3 specific peptidase 2	78973	Rn.9367	NM_023989	3.11	3.27	3.37	2.99	3.21	3.65	1.02	up	8.86E-01	9.65E-01	-	-
1391883_at	Wwox	WW domain-containing oxidoreductase	292041	Rn.158117	BI295082	3.78	3.77	3.79	3.78	3.79	3.87	1.02	up	3.56E-01	8.95E-01	-	-
1370840_at	Stxbp1	syntaxin binding protein 1	25558	Rn.80843	U21116	2.54	2.53	2.55	2.53	2.54	2.46	1.02	down	2.93E-01	8.95E-01	-	-
1383755_at	Fkbp15	FK506 binding protein 15	362528	Rn.162820	AW918485	2.34	2.40	2.35	2.33	2.34	2.33	1.02	down	1.81E-01	8.95E-01	-	-
1389109_at	Pip4k2a	phosphatidylinositol-5-phosphate 4-kinase, type II, alpha	116723	Rn.24177	AI407351	8.06	8.31	8.10	8.12	7.76	8.50	1.02	down	8.96E-01	9.67E-01	-	-
1378381_x_at	---	---	---	Rn.156506	BF552442	2.94	2.93	3.03	2.93	2.94	2.93	1.02	down	3.77E-01	8.95E-01	-	-
1388083_a_at	Casp9	caspase 9, apoptosis-related cysteine peptidase	58918	Rn.32199	AY008275	2.51	2.39	2.45	2.43	2.43	2.40	1.02	down	4.27E-01	8.95E-01	-	-
1388144_at	Bfsp1	beaded filament structural protein 1, filensin	25394	Rn.9795	AI715339	2.39	2.29	2.30	2.29	2.30	2.29	1.02	down	3.79E-01	8.95E-01	-	-
1380883_at	---	---	---	Rn.14588	BF386294	2.78	2.46	2.50	2.45	2.50	2.70	1.02	down	8.14E-01	9.40E-01	-	-
1372047_at	RGD1563136	similar to Cystatin-related protein 2 precursor (Prostatic 22 kDa glycoprotein F	296230	Rn.198654	BI285146	2.58	2.54	2.66	2.56	2.61	2.50	1.02	down	5.42E-01	8.95E-01	-	-
1394421_at	---	---	---	Rn.213362	BF282980	2.26	2.26	2.27	2.36	2.27	2.26	1.02	up	4.01E-01	8.95E-01	-	-
1370471_at	Prl6a1	prolactin family 6, subfamily a, member 1	24657	Rn.54428	M31155	2.37	2.36	2.45	2.36	2.38	2.34	1.02	down	3.49E-01	8.95E-01	-	-
1379812_at	Nnmt	nicotinamide N-methyltransferase	300691	Rn.15755	AI171727	2.49	2.40	2.44	2.41	2.43	2.39	1.02	down	3.32E-01	8.95E-01	-	-
1377530_at	---	---	---	Rn.209663	BF392268	2.42	2.41	2.44	2.42	2.54	2.41	1.02	up	4.88E-01	8.95E-01	-	-
1378738_at	Kcnab1	potassium voltage-gated channel, shaker-related subfamily, beta member 1	29737	Rn.32690	BE097574	2.47	2.46	2.63	2.47	2.49	2.50	1.02	down	5.84E-01	8.95E-01	-	-
1369020_at	Slc5a5	solute carrier family 5 (sodium iodide symporter), member 5	114613	Rn.10505	NM_052983	2.37	2.29	2.30	2.29	2.29	2.28	1.02	down	3.04E-01	8.95E-01	-	-
1375795_at	---	---	---	Rn.73068	BI301062	2.54	2.47	2.49	2.48	2.48	2.63	1.02	up	5.97E-01	8.95E-01	-	-
1372235_at	---	---	---	---	BE104709	2.38	2.35	2.42	2.35	2.36	2.35	1.02	down	2.15E-01	8.95E-01	-	-
1389235_at	Icam2	intercellular adhesion molecule 2	360647	Rn.162206	AI410467	2.48	2.47	2.49	2.48	2.59	2.45	1.02	up	4.92E-01	8.95E-01	-	-
1387585_at	Slc29a2	solute carrier family 29 (nucleoside transporters), member 2	65194	Rn.37517	NM_031738	2.27	2.25	2.27	2.27	2.27	2.35	1.02	up	3.23E-01	8.95E-01	-	-
1370493_a_at	OC690948 /// LOC	leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domai	91 /// 683446 /// 69	Rn.198480	AF169637	2.56	2.54	2.61	2.55	2.57	2.49	1.02	down	3.72E-01	8.95E-01	-	-
1382095_at	---	---	---	Rn.203953	AW916106	2.51	2.50	2.54	2.64	2.52	2.48	1.02	up	5.53E-01	8.95E-01	-	-
1396964_at	---	---	---	Rn.148750	BE109227	2.38	2.41	2.38	2.39	2.51	2.37	1.02	up	5.34E-01	8.95E-01	-	-
1371073_at	B4galt1	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 1	24390	Rn.17157	BI286141	2.60	2.54	2.56	2.56	2.55	2.68	1.02	up	5.14E-01	8.95E-01	-	-
1374901_at	---	---	---	Rn.176534	BI296416	2.37	2.37	2.42	2.52	2.38	2.36	1.02	up	5.73E-01	8.95E-01	-	-
1377455_at	---	---	---	Rn.164721	BE106526	2.66	2.64	2.65	2.65	2.69	2.70	1.02	up	9.59E-02	8.95E-01	-	-
1373388_at	Sppl3	signal peptide peptidase 3	360822	Rn.5977	BI279290	5.81	6.28	6.48	5.94	6.56	6.17	1.02	up	9.13E-01	9.74E-01	-	-
1383213_at	Eps8	epidermal growth factor receptor pathway substrate 8	312812	Rn.123609	BF393611	7.29	7.81	7.88	8.00	7.42	7.66	1.02	up	9.06E-01	9.71E-01	-	-
1383475_at	---	---	---	Rn.204952	AW521250	2.62	2.64	2.73	2.61	2.65	2.63	1.02	down	4.04E-01	8.95E-01	-	-
1396381_at	MGC116202	hypothetical protein LOC688736	688736	Rn.72979	BE097451	2.67	2.64	2.74	2.65	2.69	2.62	1.02	down	4.23E-01	8.95E-01	-	-
1368697_at	Fabp6	fatty acid binding protein 6, ileal	25440	Rn.10008	NM_017098	2.56	2.54	2.63	2.54	2.58	2.51	1.02	down	4.10E-01	8.95E-01	-	-
1398728_at	---	---	---	Rn.17109	BI296458	2.50	2.49	2.57	2.49	2.51	2.46	1.02	down	3.71E-01	8.95E-01	-	-
1384629_at	Siva1	SIVA1, apoptosis-inducing factor	362791	Rn.23804	AI071533	2.38	2.37	2.38	2.38	2.39	2.46	1.02	up	2.61E-01	8.95E-01	-	-
1387593_at	Hdgfl1	hepatoma derived growth factor-like 1	171074	Rn.81074	NM_133549	2.28	2.27	2.32	2.41	2.28	2.26	1.02	up	5.59E-01	8.95E-01	-	-
1369412_a_at	Slc19a1	solute carrier family 19 (folate transporter), member 1	29723	Rn.9042	NM_017299	7.67	7.30	7.56	7.52	7.01	7.90	1.02	down	9.16E-01	9.75E-01	-	-
1391998_at	Phf20l1	PHD finger protein 20-like 1	314964	Rn.22288	BE107625	2.44	2.35	2.37	2.36	2.37	2.34	1.02	down	3.36E-01	8.95E-01	-	-
1371751_at	---	---	---	Rn.63071	BF409807	2.40	2.46	2.40	2.38	2.40	2.38	1.02	down	1.91E-01	8.95E-01	-	-
1388606_at	---	---	---	Rn.60868	BI300748	2.56	2.48	2.55	2.54	2.61	2.53	1.02	up	4.30E-01	8.95E-01	-	-
1381308_at	---	---	---	Rn.33864	AI172180	2.44	2.41	2.45	2.41	2.58	2.40	1.02	up	6.24E-01	8.95E-01	-	-
1380409_at	---	---	---	Rn.172759	BF413455	2.52	2.51	2.56	2.52	2.52	2.45	1.02	down	3.05E-01	8.95E-01	-	-
1392011_at	---	---	---	Rn.63125	BM384514	2.47	2.48	2.52	2.63	2.45	2.49	1.02	up	6.03E-01	8.95E-01	-	-
1395592_at	---	---	---	Rn.55334	AA957981	2.57	2.51	2.59	2.57	2.58	2.52	1.02	up	3.36E-01	8.95E-01	-	-
1384360_at	Nckap1l	NCK associated protein 1 like	316348	Rn.149002	BM388989	2.56	2.54	2.56	2.55	2.67	2.54	1.02	up	4.89E-01	8.95E-01	-	-
1389332_at	---	---	---	Rn.13202	BF283404	3.62	4.24	3.24	3.80	3.58	3.63	1.02	down	9.22E-01	9.77E-01	-	-
1378711_x_at	---	---	---	---	BF414888	2.91	2.81	2.81	2.81	2.81	2.81	1.02	down	3.82E-01	8.95E-01	-	-
1369798_at	Atp1b2	ATPase, Na+/K+ transporting, beta 2 polypeptide	24214	Rn.10624	U45946	2.41	2.39	2.49	2.40	2.41	2.38	1.02	down	3.56E-01	8.95E-01	-	-
1381248_at	---	---	---	Rn.168678	AI763874	2.97	3.69	3.44	3.35	3.38	3.47	1.02	up	8.91E-01	9.66E-01	-	-
1379038_at	---	---	---	Rn.147340	AW525506	2.42	2.41	2.49	2.40	2.43	2.39	1.02	down	2.84E-01	8.95E-01	-	-
1394710_at	Azi2	5-azacytidine induced 2	316051	Rn.161972	AI045510	3.96	3.94	3.56	3.98	3.56	3.82	1.02	down	8.69E-01	9.59E-01	-	-
1382713_at	Lrig3	leucine-rich repeats and immunoglobulin-like domains 3	299830	Rn.204519	AI235654	2.41	2.40	2.49	2.41	2.41	2.38	1.02	down	3.62E-01	8.95E-01	-	-
1398554_at	Atp6v0b	ATPase, H+ transporting, lysosomal 21kDa, V0 subunit b	298451	Rn.19803	BE097687	2.35	2.35	2.68	2.35	2.59	2.35	1.02	down	8.29E-01	9.46E-01	-	-
1396685_at	---	---	---	Rn.208965	BE121368	2.37	2.36	2.46	2.37	2.38	2.35	1.02	down	3.72E-01	8.95E-01	-	-
1380833_at	Gpld1	glycosylphosphatidylinositol specific phospholipase D1	291132	Rn.18350	AI045802	2.93	3.41	2.76	2.82	2.95	3.23	1.02	down	8.98E-01	9.68E-01	-	-
1381361_at	---	---	---	Rn.147946	BE119364	2.43	2.42	2.46	2.43	2.58	2.40	1.02	up	6.13E-01	8.95E-01	-	-
1376659_at	Nubpl	nucleotide binding protein-like	299008	Rn.13455	BF282469	6.07	6.50	5.26	5.22	6.35	6.16	1.02	down	9.53E-01	9.86E-01	-	-
1392205_at	---	---	---	Rn.208737	BF412070	2.46	2.43	2.50	2.43	2.44	2.42	1.02	down	2.41E-01	8.95E-01	-	-
1379176_at	---	---	---	Rn.154348	BF389083	2.58	2.52	2.69	2.55	2.65	2.49	1.02	down	6.69E-01	9.00E-01	-	-
1373905_at	Hnrnpr	heterogeneous nuclear ribonucleoprotein R	319110	Rn.195396	AI178441	6.11	6.80	6.19	6.34	6.42	6.43	1.02	up	8.93E-01	9.67E-01	-	-
1384894_at	Rp1h	retinitis pigmentosa 1 homolog (human)	681377	Rn.102494	AI577591	2.50	2.47	2.59	2.48	2.53	2.45	1.02	down	5.14E-01	8.95E-01	-	-
1368081_at	Abca2	ATP-binding cassette, sub-family A (ABC1), member 2	79248	Rn.13115	NM_024396	3.07	2.83	3.45	3.06	3.17	3.03	1.02	down	8.75E-01	9.61E-01	-	-
1377440_at	---	---	---	---	BG375500	2.57	2.53	2.64	2.53	2.62	2.50	1.02	down	5.58E-01	8.95E-01	-	-
1371740_at	Sike	suppressor of IKK epsilon	362007	Rn.9125	AI178732	2.48	2.68	2.49	2.47	2.49	2.59	1.02	down	6.97E-01	9.07E-01	-	-
1397043_at	---	---	---	Rn.159844	BF404441	2.41	2.38	2.46	2.39	2.39	2.37	1.02	down	2.67E-01	8.95E-01	-	-
1386178_at	---	---	---	Rn.153871	AA799690	2.52	2.50	2.53	2.61	2.54	2.49	1.02	up	4.35E-01	8.95E-01	-	-
1386313_x_at	Als2cr4	amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 4	316412	Rn.98599	AI227882	2.72	2.63	2.87	2.68	2.87	2.57	1.02	down	7.89E-01	9.32E-01	-	-
1377117_at	---	---	---	---	BF387780	5.41	7.42	5.90	6.27	5.52	6.84	1.02	down	9.67E-01	9.90E-01	-	-
1386430_at	---	---	---	---	AI639183	2.58	2.53	2.66	2.55	2.63	2.50	1.02	down	5.87E-01	8.95E-01	-	-
1395418_at	Zfp131	zinc finger protein 131	310375	Rn.92641	BE110637	4.01	3.96	3.94	3.93	3.93	3.96	1.02	down	2.40E-01	8.95E-01	-	-
1382190_at	Mrgprf	MAS-related GPR, member F	266762	Rn.9848	BF405725	2.31	2.30	2.32	2.42	2.32	2.30	1.02	up	4.68E-01	8.95E-01	-	-
1396895_at	---	---	---	Rn.146848	BF392459	2.46	2.44	2.59	2.46	2.47	2.46	1.02	down	5.61E-01	8.95E-01	-	-
1379608_at	RGD1560010	RGD1560010	310537	Rn.151465	AA899113	2.54	2.53	2.56	2.52	2.65	2.55	1.02	up	5.03E-01	8.95E-01	-	-
1378733_at	---	---	---	Rn.62411	BF403401	2.42	2.41	2.50	2.42	2.43	2.40	1.02	down	3.44E-01	8.95E-01	-	-
1384657_at	Mfhas1	malignant fibrous histiocytoma amplified sequence 1	306508	Rn.106316	AI071532	2.44	2.33	2.34	2.33	2.34	2.34	1.02	down	4.12E-01	8.95E-01	-	-
1369094_a_at	Ptprs	protein tyrosine phosphatase, receptor type, S	25229	Rn.91202	NM_019140	4.11	3.92	4.06	3.95	4.06	3.98	1.02	down	6.60E-01	8.98E-01	-	-
1374613_at	---	---	---	Rn.13909	BE100609	5.48	7.28	7.06	6.57	6.31	7.03	1.02	up	9.61E-01	9.89E-01	-	-
1381939_at	RGD1310507	similar to RIKEN cDNA 1300017J02	315963	Rn.202677	BM388141	2.81	2.53	2.62	2.59	2.70	2.58	1.02	down	7.45E-01	9.17E-01	-	-
1373663_at	Dmkn	dermokine	361548	Rn.12825	AI102482	2.41	2.36	2.35	2.34	2.35	2.33	1.02	down	1.58E-01	8.95E-01	-	-
1391267_at	Iqce	IQ motif containing E	304318	Rn.62392	BF413580	2.27	2.27	2.27	2.27	2.27	2.36	1.02	up	3.56E-01	8.95E-01	-	-
1389731_at	---	---	---	---	BF405946	2.33	2.32	2.43	2.34	2.33	2.31	1.02	down	4.29E-01	8.95E-01	-	-
1391862_at	---	---	---	Rn.174576	BG377635	3.57	3.52	3.53	3.48	3.53	3.52	1.02	down	2.04E-01	8.95E-01	-	-
1398200_at	Myl2	myosin, light polypeptide 2, regulatory, cardiac, slow	363925	Rn.37176	BF410695	2.39	2.38	2.44	2.38	2.39	2.34	1.02	down	2.79E-01	8.95E-01	-	-
1382586_at	---	---	---	Rn.199947	AW919926	2.61	2.43	2.49	2.45	2.56	2.43	1.02	down	6.74E-01	9.01E-01	-	-
1368719_at	Pfkfb4	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 4	54283	Rn.90092	NM_019333	2.94	2.76	2.73	3.04	2.72	2.74	1.02	up	8.11E-01	9.39E-01	-	-
1368147_at	Dusp1	dual specificity phosphatase 1	114856	Rn.98260	BE110108	2.54	2.49	2.62	2.50	2.59	2.46	1.02	down	5.93E-01	8.95E-01	-	-
1393394_at	---	---	---	Rn.204319	AI071827	2.52	2.50	2.61	2.52	2.54	2.48	1.02	down	4.73E-01	8.95E-01	-	-
1386838_at	RGD1311251	similar to RIKEN cDNA 4930550C14	315665	Rn.209981	BF521886	2.66	2.59	2.77	2.61	2.73	2.58	1.02	down	6.82E-01	9.03E-01	-	-
1397463_at	Rab14	RAB14, member RAS oncogene family	94197	Rn.6008	BE105818	2.53	2.50	2.60	2.51	2.56	2.47	1.02	down	4.83E-01	8.95E-01	-	-
1382851_at	---	---	---	Rn.52051	BE112084	2.38	2.38	2.49	2.39	2.39	2.36	1.02	up	4.80E-01	8.95E-01	-	-
1385718_at	RGD1308031	coiled-coil domain-containing-like	300442	Rn.47411	AW530248	4.34	4.38	3.56	4.24	3.30	4.65	1.02	down	9.52E-01	9.86E-01	-	-
1395125_at	RGD1309095	Similar to hypothetical protein BC015148	301381	Rn.40282	BI301937	2.81	2.75	2.98	2.76	2.94	2.75	1.02	down	7.55E-01	9.20E-01	-	-
1380995_at	---	---	---	Rn.131122	BF412118	2.43	2.41	2.53	2.42	2.45	2.40	1.02	down	4.96E-01	8.95E-01	-	-
1396366_at	---	---	---	Rn.148646	BF409020	2.53	2.50	2.57	2.50	2.55	2.46	1.02	down	4.02E-01	8.95E-01	-	-
1389773_at	S100a7a	S100 calcium binding protein A7A	685479	Rn.15117	BI300498	2.38	2.46	2.39	2.39	2.39	2.37	1.02	down	2.83E-01	8.95E-01	-	-
1381531_at	---	---	---	Rn.220607	BE100194	2.49	2.54	2.47	2.47	2.47	2.47	1.02	down	2.08E-01	8.95E-01	-	-
1377599_at	Lpin1	lipin 1	313977	Rn.214286	BM385286	2.65	2.64	2.65	2.64	2.76	2.64	1.02	up	4.77E-01	8.95E-01	-	-
1368170_at	Slc6a1	solute carrier family 6 (neurotransmitter transporter, GABA), member 1	79212	Rn.10035	NM_024371	2.61	2.55	2.59	2.54	2.59	2.54	1.02	down	2.86E-01	8.95E-01	-	-
1396245_at	Np	nucleoside phosphorylase	290029	Rn.2738	AI711265	3.60	3.56	3.66	3.75	3.62	3.36	1.02	down	8.05E-01	9.37E-01	-	-
1393552_x_at	Phf14	PHD finger protein 14	500030	Rn.117647	AI717644	2.45	2.48	2.46	2.45	2.45	2.39	1.02	down	2.41E-01	8.95E-01	-	-
1380600_at	LOC685269	similar to Integrin alpha-IIb precursor (Platelet membrane glycoprotein IIb) (G	685269	Rn.128177	AA893733	5.79	6.39	5.89	6.09	6.12	5.94	1.02	up	8.80E-01	9.63E-01	-	-
1380256_at	Polr3c	polymerase (RNA) III (DNA directed) polypeptide C (62kD)	310685	Rn.35251	BE103946	6.47	5.52	6.76	5.95	6.70	6.20	1.02	up	9.47E-01	9.85E-01	-	-
1387107_at	Znfr7a	zinc finger and BTB domain containing 7a	117107	Rn.162908	NM_054002	2.67	2.40	2.44	2.50	2.43	2.49	1.02	down	7.43E-01	9.17E-01	-	-
1396614_at	Sfrp2	secreted frizzled-related protein 2	310552	Rn.102416	BF396545	2.32	2.31	2.41	2.32	2.33	2.31	1.02	down	3.78E-01	8.95E-01	-	-
1388923_at	Ny-sar-48	sarcoma antigen NY-SAR-48	290626	Rn.106450	BG381657	4.97	3.40	2.96	4.62	3.11	3.51	1.02	down	9.69E-01	9.91E-01	-	-
1394291_at	---	---	---	---	AI639055	2.38	2.36	2.41	2.37	2.38	2.31	1.02	down	2.67E-01	8.95E-01	-	-
1371986_at	---	---	---	Rn.144053	AI576652	5.89	5.62	5.73	4.92	6.59	5.63	1.02	down	9.53E-01	9.86E-01	-	-
1391959_at	---	---	---	Rn.211707	BM387121	2.25	2.25	2.34	2.25	2.26	2.24	1.02	down	3.88E-01	8.95E-01	-	-
1393318_at	---	---	---	Rn.63937	BG379074	2.39	2.44	2.39	2.37	2.39	2.36	1.02	down	1.56E-01	8.95E-01	-	-
1384151_at	---	---	---	---	AI578392	2.70	2.70	2.70	2.70	2.70	2.79	1.02	up	3.68E-01	8.95E-01	-	-
1397438_at	Magi1	membrane associated guanylate kinase, WW and PDZ domain containing 1	500261	Rn.95239	BF402906	2.30	2.29	2.30	2.29	2.40	2.28	1.02	up	4.73E-01	8.95E-01	-	-
1397619_at	---	---	---	Rn.160375	BG381732	2.45	2.70	2.47	2.45	2.66	2.42	1.02	down	7.94E-01	9.34E-01	-	-
1376924_a_at	Palmd	palmdelphin	310811	Rn.24602	AI176360	2.41	2.39	2.42	2.51	2.42	2.39	1.02	up	4.36E-01	8.95E-01	-	-
1381247_at	---	---	---	Rn.168676	BE096812	2.75	2.66	2.71	2.64	2.89	2.87	1.02	up	7.00E-01	9.07E-01	-	-
1386846_at	Rprd1a	regulation of nuclear pre-mRNA domain containing 1A	291736	Rn.162287	BG672730	2.30	2.30	2.44	2.33	2.33	2.48	1.02	up	6.82E-01	9.03E-01	-	-
1385623_at	Tulp2	tubby-like protein 2	361576	Rn.45038	BF566948	2.40	2.47	2.41	2.40	2.40	2.39	1.02	down	2.37E-01	8.95E-01	-	-
1397491_at	Agpat3 /// Rrp1	1-acylglycerol-3-phosphate O-acyltransferase 3 /// ribosomal RNA processing	294324 /// 309674	Rn.100251	BF396472	2.42	2.41	2.41	2.53	2.40	2.41	1.02	up	5.11E-01	8.95E-01	-	-
1378280_at	RGD1306148	similar to KIAA0368	313196	Rn.154631	AI712832	2.24	2.23	2.32	2.24	2.24	2.22	1.02	down	3.54E-01	8.95E-01	-	-
1396661_at	Ddx19a	DEAD (Asp-Glu-Ala-Asp) box polypeptide 19a	292022	Rn.199065	BE108555	2.86	2.55	2.48	2.56	2.88	2.54	1.02	up	8.57E-01	9.55E-01	-	-
1397303_at	---	---	---	---	AI178467	2.59	2.55	2.64	2.58	2.61	2.50	1.02	down	4.99E-01	8.95E-01	-	-
1383526_at	---	---	---	Rn.146377	AA857027	7.09	7.07	7.10	7.09	7.09	7.17	1.02	up	3.25E-01	8.95E-01	-	-
1379069_at	LOC100192314	Hypothetical protein LOC100192314	100192314	Rn.217950	AI145821	4.99	4.99	5.00	5.22	4.69	4.98	1.02	down	8.48E-01	9.53E-01	-	-
1386887_at	Cox5b	cytochrome c oxidase subunit Vb	94194	Rn.6686	NM_053586	11.25	11.08	11.18	11.21	11.09	11.31	1.02	up	7.23E-01	9.12E-01	-	-
1382127_at	---	---	---	Rn.25033	AI176708	8.35	9.49	8.47	8.74	8.44	9.04	1.02	down	9.43E-01	9.84E-01	-	-
1391273_at	Naglt1	Na+ dependent glucose transporter 1	337920	Rn.22741	AA892404	9.81	10.16	10.40	10.07	9.74	10.48	1.02	down	9.16E-01	9.75E-01	-	-
1392815_at	Arap2	ArfGAP with RhoGAP domain, ankyrin repeat and PH domain 2	305367	Rn.106446	BE114489	2.32	2.38	2.65	2.34	2.33	2.59	1.02	down	8.29E-01	9.46E-01	-	-
1375981_at	Dstn	destrin	502674	Rn.102412	AI170442	9.26	9.38	9.18	9.10	9.25	9.56	1.02	up	8.46E-01	9.52E-01	-	-
1396081_at	Spire1	spire homolog 1 (Drosophila)	307348	Rn.98481	BM387505	2.35	2.34	2.61	2.35	2.36	2.68	1.02	up	8.37E-01	9.49E-01	-	-
1368856_at	Jak2	Janus kinase 2	24514	Rn.18909	NM_031514	2.63	2.76	2.48	2.63	2.63	2.70	1.02	up	7.30E-01	9.14E-01	-	-
1394997_at	---	---	---	Rn.171011	AI409919	2.59	2.57	2.57	2.58	2.67	2.57	1.02	up	4.17E-01	8.95E-01	-	-
1373498_at	Vps11	vacuolar protein sorting 11 homolog (S. cerevisiae)	315600	Rn.2637	BI295924	7.42	5.99	4.48	5.77	5.85	6.17	1.02	down	9.73E-01	9.92E-01	-	-
1397248_at	---	---	---	Rn.34726	AI547500	2.38	2.51	2.39	2.37	2.40	2.42	1.02	down	5.20E-01	8.95E-01	-	-
1375037_at	---	---	---	Rn.136567	AI176244	7.30	7.51	7.45	7.69	7.41	7.25	1.02	up	8.40E-01	9.50E-01	-	-
1392346_at	---	---	---	Rn.209842	BF391214	2.49	2.50	2.54	2.48	2.50	2.46	1.02	down	1.51E-01	8.95E-01	-	-
1371235_at	Grm6	glutamate receptor, metabotropic 6	24419	Rn.44615	AJ245718	2.35	2.33	2.43	2.34	2.34	2.33	1.02	down	3.64E-01	8.95E-01	-	-
1379499_at	Ltb	lymphotoxin beta (TNF superfamily, member 3)	361795	Rn.203016	BF282228	2.41	2.40	2.52	2.41	2.43	2.39	1.02	down	4.89E-01	8.95E-01	-	-
1385154_at	Otub2	OTU domain, ubiquitin aldehyde binding 2	314405	Rn.18862	BE121382	2.39	2.38	2.40	2.50	2.39	2.37	1.02	up	5.15E-01	8.95E-01	-	-
1387908_at	Rasd1	RAS, dexamethasone-induced 1	64455	Rn.54720	AF239157	2.59	2.54	2.59	2.61	2.54	2.67	1.02	up	4.96E-01	8.95E-01	-	-
1392925_at	ST7	suppression of tumorigenicity 7	296911	Rn.24435	BI132374	6.77	5.30	4.24	5.28	5.31	5.62	1.02	down	9.69E-01	9.91E-01	-	-
1375823_at	---

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1397505_at	Kif1a	kinesin family member 1A	363288	---	BE115743	2.49	2.47	2.62	2.54	2.49	2.46	1.02	down	6.09E-01	8.95E-01	-	-
1373641_at	---	---	---	Rn.17848	BI301187	2.32	2.32	2.40	2.32	2.33	2.31	1.02	down	3.40E-01	8.95E-01	-	-
1397614_at	Gabra2	gamma-aminobutyric acid (GABA-A) receptor, subunit alpha 2	289606	Rn.48180	BF404116	2.50	2.48	2.56	2.48	2.51	2.44	1.02	down	3.99E-01	8.95E-01	-	-
1396457_at	---	---	---	Rn.205879	AW920931	2.53	2.51	2.68	2.52	2.61	2.49	1.02	down	6.66E-01	8.99E-01	-	-
1392926_at	Lama1	laminin, alpha 1	316758	Rn.2807	BI281952	2.48	2.47	2.48	2.48	2.58	2.46	1.02	up	4.80E-01	8.95E-01	-	-
1390821_at	Pcdha3 /// Pcdha4 /// Pcdha5 /// Pcdha6 /// Pcdha7 /// Pcdha8 /// Pcdha9 /// Pcdha10 /// Pcdha11 /// Pcdha12 /// Pcdhac1 /// Pcdhac2	protocadherin alpha 1 /// protocadherin alpha 10 /// protocadherin alpha 11 /// protocadherin alpha 12 /// protocadherin alpha 2 /// protocadherin alpha 3 /// protocadherin alpha 4 /// protocadherin alpha 5 /// protocadherin alpha 6 /// protocadherin alpha 7 /// protocadherin alpha 8 /// protocadherin alpha 9 /// protocadherin alpha c1 /// protocadherin alpha c2	393086 /// 393087 /// 393088 /// 393089 /// 393090 /// 393091 /// 393092 /// 393093 /// 393094 /// 393095 /// 393096 /// 393097 /// 393098 /// 393099 /// 393100 /// 393101 /// 393102 /// 393103 /// 393104 /// 393105 ///

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1398322_at	Igf2	insulin-like growth factor 2	24483	Rn.118681	M17960	2.49	2.54	2.50	2.49	2.49	2.46	1.02	down	2.12E-01	8.95E-01	-	-
1367566_at	Scgb1a1	secretoglobin, family 1A, member 1 (uteroglobin)	25575	Rn.2206	NM_013051	2.43	2.43	2.50	2.43	2.44	2.40	1.02	down	3.24E-01	8.95E-01	-	-
1397096_at	---	---	---	Rn.211427	BF413218	2.31	2.30	2.32	2.31	2.42	2.30	1.02	up	4.98E-01	8.95E-01	-	-
1371692_at	Mllt11	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila);	295264	Rn.144837	AI009661	2.68	2.67	2.70	2.62	2.68	2.67	1.02	down	2.27E-01	8.95E-01	-	-
1395796_at	Iffo2	intermediate filament family orphan 2	641315	Rn.222020	AI103143	2.48	2.42	2.48	2.43	2.46	2.41	1.02	down	2.85E-01	8.95E-01	-	-
1391283_at	---	---	---	Rn.203490	AI713146	2.72	2.66	2.69	2.69	2.83	2.64	1.02	up	6.55E-01	8.97E-01	-	-
1398263_at	Syne1	spectrin repeat containing, nuclear envelope 1	499010	Rn.89150	NM_019355	2.38	2.36	2.44	2.37	2.38	2.36	1.02	down	3.14E-01	8.95E-01	-	-
1387427_at	Rad50	RAD50 homolog (S. cerevisiae)	64012	Rn.51136	NM_022246	3.52	3.86	3.36	3.70	3.73	3.40	1.02	up	8.83E-01	9.64E-01	-	-
1382089_at	---	---	---	Rn.199570	AI070489	2.48	2.39	2.42	2.41	2.41	2.38	1.02	down	3.42E-01	8.95E-01	-	-
1384362_at	Zbtb24	zinc finger and BTB domain containing 24	365590	Rn.43308	BF392187	2.59	2.85	2.61	2.57	2.60	2.80	1.02	down	8.07E-01	9.38E-01	-	-
1398239_at	---	---	---	Rn.156277	BF390399	2.44	2.43	2.51	2.43	2.45	2.41	1.02	down	3.96E-01	8.95E-01	-	-
1398735_at	---	---	---	---	BF559001	2.58	2.58	2.67	2.58	2.59	2.57	1.02	down	4.12E-01	8.95E-01	-	-
1398710_at	Cyp2u1	cytochrome P450, family 2, subfamily u, polypeptide 1	310848	Rn.161862	BF392959	3.65	2.91	4.51	3.99	2.83	4.15	1.02	down	9.65E-01	9.90E-01	-	-
1381340_at	RGD1311893	hypothetical LOC288478	288478	Rn.72071	BE119655	2.42	2.41	2.52	2.41	2.44	2.41	1.02	down	4.89E-01	8.95E-01	-	-
1392107_at	Sbno2	strawberry notch homolog 2 (Drosophila)	314619	Rn.67287	BI302669	2.50	2.41	2.44	2.42	2.44	2.41	1.02	down	3.41E-01	8.95E-01	-	-
1396312_at	---	---	---	Rn.171338	BF388765	2.34	2.33	2.35	2.43	2.35	2.33	1.02	up	4.10E-01	8.95E-01	-	-
1387235_at	Chga	chromogranin A	24258	Rn.41024	NM_021655	2.44	2.42	2.49	2.43	2.44	2.40	1.02	down	3.03E-01	8.95E-01	-	-
1388485_at	Cxcl14	chemokine (C-X-C motif) ligand 14	306748	Rn.3130	BG380414	2.36	2.36	2.37	2.46	2.37	2.36	1.02	up	4.39E-01	8.95E-01	-	-
1374647_at	Rsbn1	round spermatid basic protein 1	310749	Rn.38954	BI299718	2.77	2.75	2.80	2.88	2.78	2.75	1.02	up	5.16E-01	8.95E-01	-	-
1376826_at	Cox11	COX11 homolog, cytochrome c oxidase assembly protein (yeast)	690300	Rn.19469	AI071535	2.39	2.38	2.39	2.47	2.40	2.38	1.02	up	3.50E-01	8.95E-01	-	-
1390554_at	Zfp385b	zinc finger protein 385B	311137	Rn.34063	AA818377	2.38	2.36	2.39	2.47	2.39	2.35	1.02	up	4.48E-01	8.95E-01	-	-
1382351_at	Gem	GTP binding protein (gene overexpressed in skeletal muscle)	297902	Rn.40436	AI069972	2.51	2.51	2.54	2.53	2.44	2.42	1.02	down	3.61E-01	8.95E-01	-	-
1379582_a_at	Ccna2	cyclin A2	114494	Rn.13094	AA998516	2.54	2.51	2.68	2.53	2.62	2.49	1.02	down	6.80E-01	9.03E-01	-	-
1376670_at	Yipf2	Yip1 domain family, member 2	363027	Rn.94869	AW434026	3.60	3.48	3.51	3.45	3.56	3.50	1.02	down	5.97E-01	8.95E-01	-	-
1384546_at	---	---	---	Rn.23057	AA924204	2.44	2.42	2.51	2.43	2.45	2.41	1.02	down	3.79E-01	8.95E-01	-	-
1380945_at	---	---	---	Rn.43273	BE099407	2.43	2.43	2.48	2.42	2.44	2.40	1.02	down	2.04E-01	8.95E-01	-	-
1370415_at	Rassf5	Ras association (RalGDS/AF-6) domain family member 5	54355	Rn.36106	AF002251	2.87	2.48	2.09	2.45	2.46	2.45	1.02	down	9.06E-01	9.71E-01	-	-
1397997_at	Odz2	odz, odd Oz/ten-m homolog 2 (Drosophila)	117242	Rn.205610	BF402505	2.51	2.51	2.57	2.50	2.54	2.46	1.02	down	4.05E-01	8.95E-01	-	-
1397123_at	---	---	---	Rn.146237	BE106480	2.49	2.47	2.52	2.49	2.62	2.46	1.02	up	6.09E-01	8.95E-01	-	-
1387724_at	Omp	olfactory marker protein	24612	Rn.9720	NM_012616	2.34	2.33	2.35	2.34	2.44	2.32	1.02	up	5.03E-01	8.95E-01	-	-
1395695_at	Aebp1	AE binding protein 1	305494	Rn.37157	BE126420	4.89	4.33	3.82	4.51	3.87	4.58	1.02	down	9.44E-01	9.84E-01	-	-
1392867_at	---	---	---	Rn.164994	AA956057	2.38	2.34	2.40	2.37	2.50	2.33	1.02	up	6.22E-01	8.95E-01	-	-
1378624_at	---	---	---	Rn.50650	BE107074	2.48	2.44	2.49	2.47	2.49	2.52	1.02	up	2.59E-01	8.95E-01	-	-
1384971_at	Depdc7	DEP domain containing 7	295971	Rn.97407	BI289108	6.57	7.13	7.51	6.89	6.92	7.48	1.02	up	9.36E-01	9.82E-01	-	-
1380224_at	Eftud2	Elongation factor Tu GTP binding domain containing 2	287739	Rn.62495	AI103321	2.36	2.35	2.47	2.36	2.39	2.34	1.02	down	5.04E-01	8.95E-01	-	-
1380648_at	---	---	---	Rn.204742	AI101352	2.44	2.38	2.43	2.39	2.39	2.37	1.02	down	1.75E-01	8.95E-01	-	-
1373487_at	---	---	---	Rn.203249	AI030552	2.70	3.27	2.70	3.03	2.81	2.74	1.02	down	8.98E-01	9.68E-01	-	-
1370521_at	Vps33b	vacuolar protein sorting 33 homolog B (yeast)	64060	Rn.10661	U35245	2.61	2.67	2.47	2.48	2.47	2.71	1.02	down	7.86E-01	9.30E-01	-	-
1368838_at	Tpm4	tropomyosin 4	24852	Rn.108199	NM_012678	8.55	8.35	9.13	8.67	8.45	8.81	1.02	down	9.17E-01	9.75E-01	-	-
1375570_at	Notch4	Notch homolog 4 (Drosophila)	406162	Rn.12967	AI559986	2.42	2.42	2.43	2.42	2.52	2.42	1.02	up	4.19E-01	8.95E-01	-	-
1370805_at	Cites1	Cbp/p300-interacting transactivator with Glu/Asp-rich carboxy-terminal domai	64466	Rn.8163	AF104399	2.80	2.78	2.80	2.78	2.74	2.77	1.02	down	1.16E-01	8.95E-01	-	-
1394700_at	---	---	---	Rn.169574	AW526895	2.39	2.42	2.41	2.38	2.40	2.36	1.02	down	1.21E-01	8.95E-01	-	-
1384569_at	---	---	---	Rn.12254	BF548417	2.35	2.42	2.37	2.35	2.37	2.34	1.02	down	3.03E-01	8.95E-01	-	-
1393255_at	Krtap14l	keratin associated protein 14 like	363739	---	AI136435	2.33	2.32	2.34	2.32	2.43	2.31	1.02	up	5.10E-01	8.95E-01	-	-
1375274_at	Hipk3	Homeodomain interacting protein kinase 3	83617	Rn.8099	BF281898	2.50	2.53	2.51	2.47	2.50	2.48	1.02	down	9.07E-02	8.95E-01	-	-
1386327_at	RGD1561057	similar to ceramide kinase-like	502640	---	AI639450	2.55	2.52	2.65	2.52	2.58	2.53	1.02	down	5.58E-01	8.95E-01	-	-
1392278_at	---	---	---	Rn.211531	BF418109	2.56	2.53	2.62	2.54	2.61	2.49	1.02	down	5.60E-01	8.95E-01	-	-
1370851_a_at	Kalrn	kalirin, RhoGEF kinase	84009	Rn.87882	AI639313	2.82	2.57	2.62	2.72	2.62	2.59	1.02	down	7.54E-01	9.20E-01	-	-
1379122_at	---	---	---	Rn.216941	BF390811	2.40	2.38	2.39	2.38	2.39	2.32	1.02	down	3.00E-01	8.95E-01	-	-
1395257_at	---	---	---	Rn.212537	BI288688	2.40	2.29	2.29	2.29	2.32	2.28	1.02	down	4.96E-01	8.95E-01	-	-
1383470_at	---	---	---	Rn.44126	AI548857	3.76	4.34	3.97	3.74	3.93	4.32	1.02	down	9.12E-01	9.73E-01	-	-
1380691_at	---	---	---	Rn.156448	BM392272	2.45	2.40	2.42	2.41	2.41	2.37	1.02	down	2.47E-01	8.95E-01	-	-
1377636_at	---	---	---	Rn.48646	BE109363	2.46	2.47	2.55	2.46	2.47	2.47	1.02	down	3.79E-01	8.95E-01	-	-
1395456_at	---	---	---	---	AW919228	2.55	2.47	2.48	2.47	2.48	2.46	1.02	down	3.53E-01	8.95E-01	-	-
1395430_at	---	---	---	Rn.169347	BG375551	2.35	2.34	2.43	2.35	2.36	2.33	1.02	down	4.01E-01	8.95E-01	-	-
1388013_at	Cd80	Cd80 molecule	25408	Rn.10138	AF010465	2.41	2.36	2.36	2.35	2.37	2.33	1.02	down	2.56E-01	8.95E-01	-	-
1394937_at	---	---	---	Rn.208200	BE112859	2.53	2.49	2.58	2.52	2.53	2.47	1.02	down	4.29E-01	8.95E-01	-	-
1378276_at	---	---	---	---	AI058679	2.38	2.37	2.47	2.38	2.39	2.37	1.02	down	4.04E-01	8.95E-01	-	-
1396730_at	---	---	---	Rn.209123	BF391440	2.43	2.41	2.64	2.42	2.56	2.42	1.02	down	7.60E-01	9.22E-01	-	-
1392572_at	Msi2	Musashi homolog 2 (Drosophila)	360596	Rn.43808	BI282339	8.18	8.06	8.08	8.07	8.09	8.07	1.02	down	4.80E-01	8.95E-01	-	-
1394272_at	Slc24a4	solute carrier family 24 (sodium/potassium/calcium exchanger), member 4	314396	Rn.198754	BF546274	2.33	2.40	2.34	2.33	2.34	2.32	1.02	down	2.56E-01	8.95E-01	-	-
1396496_at	---	---	---	Rn.171671	BE121412	2.41	2.47	2.43	2.40	2.42	2.40	1.02	down	1.55E-01	8.95E-01	-	-
1389853_at	B9d2	B9 protein domain 2	308443	Rn.22197	AI227900	2.34	2.25	2.26	2.25	2.26	2.25	1.02	down	3.62E-01	8.95E-01	-	-
1376197_at	Tcf7	transcription factor 7, T-cell specific	363595	Rn.106335	AW251860	2.53	2.51	2.58	2.49	2.54	2.50	1.02	down	3.38E-01	8.95E-01	-	-
1368763_at	Il3	interleukin 3	24495	Rn.10652	NM_031513	2.46	2.44	2.45	2.57	2.47	2.41	1.02	up	5.82E-01	8.95E-01	-	-
1390611_at	Gbf1	golgi-specific brefeldin A resistant guanine nucleotide exchange factor 1	309451	Rn.61235	BF406297	2.45	2.52	2.46	2.45	2.45	2.45	1.02	down	2.87E-01	8.95E-01	-	-
1376201_at	Mettl10d	methyltransferase 10 domain containing	360568	Rn.203131	AI070397	4.26	5.26	4.22	4.26	4.17	5.22	1.02	down	9.56E-01	9.87E-01	-	-
1394252_at	Spock3	sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) 3	306404	Rn.76519	BG668794	2.58	2.53	2.61	2.54	2.60	2.50	1.02	down	4.99E-01	8.95E-01	-	-
1390281_a_at	Coq10a	coenzyme Q10 homolog A (S. cerevisiae)	360570	Rn.25373	AI407062	6.19	5.96	5.92	6.87	5.54	5.58	1.02	down	9.53E-01	9.86E-01	-	-
1377482_at	---	---	---	---	AA899068	2.44	2.34	2.36	2.34	2.35	2.36	1.02	down	4.28E-01	8.95E-01	-	-
1392089_at	Hcfc2	host cell factor C2	314704	Rn.90662	AW435314	2.68	4.22	3.26	3.24	2.99	3.85	1.02	down	9.59E-01	9.89E-01	-	-
1389781_at	Elmod1	ELMO/CED-12 domain containing 1	315670	Rn.13823	AI412625	2.57	2.55	2.67	2.56	2.60	2.54	1.02	down	5.38E-01	8.95E-01	-	-
1381633_at	---	---	---	Rn.208439	BE116563	2.66	2.61	2.66	2.64	2.70	2.50	1.02	down	6.64E-01	8.99E-01	-	-
1395109_at	---	---	---	Rn.152129	BE117709	2.48	2.46	2.53	2.45	2.50	2.42	1.02	down	4.12E-01	8.95E-01	-	-
1368255_at	Ntm	neurotrimin	50864	Rn.10075	NM_017354	2.37	2.44	2.39	2.38	2.38	2.36	1.02	down	2.51E-01	8.95E-01	-	-
1380312_at	---	---	---	Rn.146443	AA900436	2.58	2.53	2.64	2.54	2.62	2.50	1.02	down	5.85E-01	8.95E-01	-	-
1387507_at	Il1rap	interleukin 1 receptor accessory protein	25466	Rn.10511	NM_012968	2.58	2.41	2.51	2.51	2.51	2.57	1.02	up	6.34E-01	8.95E-01	-	-
1395656_at	---	---	---	Rn.161409	BI298185	2.64	2.61	2.69	2.62	2.71	2.52	1.02	down	6.62E-01	8.98E-01	-	-
1384560_x_at	Psx1	placenta specific homeobox 1	296535	---	AI072542	2.40	2.44	2.40	2.39	2.40	2.37	1.02	down	1.58E-01	8.95E-01	-	-
1380468_a_at	---	---	---	Rn.114311	AI012603	2.53	2.48	2.61	2.51	2.56	2.47	1.02	down	5.65E-01	8.95E-01	-	-
1391059_at	Npw	neuropeptide W	259224	Rn.14575	AW530225	2.25	2.24	2.33	2.24	2.25	2.24	1.02	down	3.64E-01	8.95E-01	-	-
1382834_at	---	---	---	---	AI070996	2.86	2.84	2.95	2.85	2.86	2.85	1.02	down	4.46E-01	8.95E-01	-	-
1368590_at	Mmp16	matrix metallopeptidase 16	65205	Rn.208361	NM_080776	2.44	2.36	2.38	2.36	2.38	2.35	1.02	down	3.52E-01	8.95E-01	-	-
1383257_at	A2bp1	ataxin 2 binding protein 1	302920	Rn.92540	BE099787	2.55	2.51	2.63	2.53	2.60	2.48	1.02	down	5.94E-01	8.95E-01	-	-
1368266_at	Arg1	arginase, liver	29221	Rn.9857	NM_017134	2.39	2.44	2.39	2.38	2.39	2.37	1.02	down	1.64E-01	8.95E-01	-	-
1373137_at	RGD1308154	similar to CGI1388-PA	363799	Rn.17212	BI284380	2.58	3.87	4.71	3.96	3.67	3.61	1.02	up	9.67E-01	9.90E-01	-	-
1385826_at	---	---	---	Rn.895	AA860047	2.52	2.46	2.52	2.47	2.50	2.45	1.02	down	3.36E-01	8.95E-01	-	-
1379042_at	---	---	---	Rn.146339	BF419814	2.44	2.36	2.39	2.36	2.38	2.35	1.02	down	3.15E-01	8.95E-01	-	-
1388327_at	Cisd1	CDGSH iron sulfur domain 1	294362	Rn.1164	AI232357	12.32	12.48	12.37	12.50	12.27	12.31	1.02	down	7.54E-01	9.20E-01	-	-
1375207_at	Scarf2	scavenger receptor class F, member 2	287949	Rn.22134	AI072682	2.97	2.91	2.91	2.91	2.92	2.88	1.02	down	2.98E-01	8.95E-01	-	-
1368765_at	Clcnka	chloride channel Ka	79425	Rn.88871	NM_053327	2.46	2.39	2.42	2.40	2.41	2.38	1.02	down	2.49E-01	8.95E-01	-	-
1373380_at	Zc3h15	zinc finger CCCH-type containing 15	362154	Rn.129005	AI169085	7.20	7.70	8.23	7.71	7.79	7.72	1.02	up	9.30E-01	9.80E-01	-	-
1372494_a_at	Hmg20b	high mobility group 20 B	362825	Rn.162912	BM384171	7.24	5.92	5.96	5.64	6.03	6.02	1.02	down	9.78E-01	9.93E-01	-	-
1384673_at	---	---	---	---	BF562000	2.54	2.52	2.56	2.52	2.54	2.48	1.02	down	2.77E-01	8.95E-01	-	-
1373229_at	Lsm12	LSM12 homolog (S. cerevisiae)	287731	Rn.130804	AI407946	6.06	6.19	6.23	5.94	6.19	6.27	1.02	down	8.18E-01	9.42E-01	-	-
1386097_at	Ankrd12	ankyrin repeat domain 12	316775	Rn.94994	AW527230	6.15	7.29	7.00	6.60	7.09	6.83	1.02	up	9.44E-01	9.84E-01	-	-
1371507_at	---	---	---	Rn.17118	BM384151	9.25	9.77	9.53	9.68	9.18	9.78	1.02	up	9.12E-01	9.74E-01	-	-
1397047_at	---	---	---	---	BI288855	2.50	2.50	2.60	2.50	2.52	2.49	1.02	down	4.55E-01	8.95E-01	-	-
1390037_at	Nkain4	Na+/K+ transporting ATPase interacting 4	296469	Rn.7222	AI102026	2.42	2.34	2.37	2.35	2.36	2.34	1.02	down	2.96E-01	8.95E-01	-	-
1397700_x_at	---	---	---	200086 /// Rn.201	BG670822	2.55	2.53	2.64	2.54	2.59	2.51	1.02	down	5.50E-01	8.95E-01	-	-
1383516_at	Fgl2	fibrinogen-like 2	84586	Rn.64635	BG663284	2.66	2.60	2.74	2.62	2.71	2.58	1.02	down	6.45E-01	8.95E-01	-	-
1395992_at	---	---	---	Rn.172400	BF403041	2.53	2.49	2.59	2.50	2.56	2.48	1.02	down	5.00E-01	8.95E-01	-	-
1394038_at	Ift81	intraflagellar transport 81 homolog (Chlamydomonas)	373066	Rn.47911	BG371654	3.76	4.96	5.42	3.65	4.95	5.63	1.02	up	9.72E-01	9.92E-01	-	-
1380527_at	---	---	---	Rn.153615	AI454790	2.50	2.44	2.45	2.44	2.45	2.41	1.02	down	2.54E-01	8.95E-01	-	-
1378515_at	---	---	---	Rn.204398	BE116005	2.38	2.34	2.37	2.46	2.36	2.34	1.02	up	5.06E-01	8.95E-01	-	-
1398461_at	---	---	---	---	BF393839	2.52	2.50	2.54	2.50	2.52	2.45	1.02	down	3.34E-01	8.95E-01	-	-
1388017_at	Mamdc4	MAM domain containing 4	252882	Rn.10059	L37380	2.72	2.49	2.50	2.71	2.42	2.50	1.02	down	8.18E-01	9.42E-01	-	-
1398625_at	LOC679126	similar to SMAD-interacting zinc finger protein 2	679126	---	BG673169	2.53	2.51	2.57	2.51	2.54	2.47	1.02	down	3.72E-01	8.95E-01	-	-
1372936_at	Pcp2	Purkinje cell protein 2	304195	Rn.162078	BF395833	2.48	2.46	2.53	2.46	2.47	2.46	1.02	down	2.84E-01	8.95E-01	-	-
1398463_at	---	---	---	Rn.13470	BG375937	4.55	2.85	4.31	4.12	4.50	3.19	1.02	up	9.68E-01	9.91E-01	-	-
1373957_at	Reln	reelin	24718	Rn.98353	BF281544	2.38	2.46	2.39	2.38	2.39	2.37	1.02	down	3.26E-01	8.95E-01	-	-
1396317_at	Ccpg1	cell cycle progression 1	363098	Rn.43385	AI764350	7.85	7.14	5.25	6.82	6.82	6.69	1.02	up	9.73E-01	9.92E-01	-	-
1395933_at	---	---	---	Rn.147700	BI289822	2.53	2.50	2.63	2.53	2.58	2.47	1.02	down	6.05E-01	8.95E-01	-	-
1367608_at	Cryba4	crystallin, beta A4	64348	Rn.10802	NM_031689	2.37	2.35	2.38	2.36	2.47	2.34	1.02	up	5.43E-01	8.95E-01	-	-
1384534_at	---	---	---	---	BF412469	2.51	2.53	2.55	2.50	2.54	2.63	1.02	up	5.28E-01	8.95E-01	-	-
1378862_at	---	---	---	Rn.146426	BF391842	2.32	2.31	2.38	2.31	2.32	2.30	1.02	down	3.06E-01	8.95E-01	-	-
1373176_at	---	---	---	Rn.45023	AA943208	6.33	6.09	5.72	5.68	5.99	6.55	1.02	up	9.33E-01	9.81E-01	-	-
1384666_at	---	---	---	Rn.20094	AI072397	2.43	2.42	2.51	2.43	2.45	2.40	1.02	down	4.05E-01	8.95E-01	-	-
1381520_at	---	---	---	Rn.204089	BE105072	2.40	2.35	2.43	2.37	2.38	2.35	1.02	down	2.85E-01	8.95E-01	-	-
1369459_at	Gdf10	growth differentiation factor 10	79216	Rn.8707	NM_024375	2.41	2.40	2.43	2.40	2.52	2.40	1.02	up	5.40E-01	8.95E-01	-	-
1378044_at	---	---	---	Rn.211897	AA864294	2.43	2.36	2.38	2.36	2.37	2.35	1.02	down	2.49E-01	8.95E-01	-	-
1368831_at	Mark3	MAP/microtubule affinity-regulating kinase 3	170577	Rn.23232	NM_130749	7.30	8.36	8.47	7.84	7.95	8.43	1.02	up	9.49E-01	9.85E-01	-	-
1375711_at	---	---	---	Rn.204052	BG373688	3.22	3.17	3.25	3.50	3.41	2.81	1.02	up	9.05E-01	9.71E-01	-	-
1389941_at	Arl2bp	ADP-ribosylation factor-like 2 binding protein	498910	Rn.985	BE109130	10.19	10.97	10.80	10.51	10.50	11.03	1.02	up	9.29E-01	9.80E-01	-	-
1368726_a_at	Zfp347	zinc finger protein 347	170902	Rn.127808	AB047638	2.84	3.12	2.85	2.82	2.94	2.98	1.02	down	8.04E-01	9.37E-01	-	-
1377031_at	LOC366225	similar to UTP11-like, U3 small nucleolar ribonucleoprotein	366225	Rn.66959	BG372809	2.59	2.55	2.74	2.57	2.68	2.54	1.02	down	7.13E-01	9.10E-01	-	-
1395897_at	---	---	---	---	AI044421	2.52	2.48	2.53	2.49	2.51	2.44	1.02	down	3.43E-01	8.95E-01	-	-
1398696_at	---	---	---	---	AI178692	2.76	2.72	2.80	2.73	2.76	2.71	1.02	down	3.42E-01	8.95E-01	-	-
1384216_at	---	---	---	---	AW534148	2.45	2.49	2.45	2.43	2.46	2.41	1.02	down	2.00E-01	8.95E-01	-	-
1395760_at	---	---	---	Rn.27222	AI367272	2.34	2.25	2.27	2.27	2.26	2.25	1.02	down	4.03E-01	8.95E-01	-	-
1393121_at	Agr2	anterior gradient homolog 2 (Xenopus laevis)	298961	Rn.98889	BI292233	2.44	2.43	2.46	2.44	2.55	2.43	1.02	up	5.18E-01	8.95E-01	-	-
1375833_at	Ptpn4	Protein tyrosine phosphatase, non-receptor type 4	246116	Rn.41717	AA923975	2.70	2.71	2.89	2.78	2.72	2.71	1.02	down	6.91E-01	9.05E-01	-	-
1374420_at	RGD1308874	similar to RIKEN cDNA 2310001A20	366227	Rn.2352	BE117936	11.37	11.58	11.58	11.45	11.40	11.76	1.02	up	8.43E-01	9.51E-01	-	-
1386871_at	Gpx4	glutathione peroxidase 4	25328	Rn.3647	NM_017165	9.63	9.79	9.43	9.59	9.72	9.62	1.02	up	8.16E-01	9.41E-01	-	-
1391216_at	Znf509	zinc finger protein 509	305428	Rn.38580	BE114482	2.44	2.40	2.51	2.41	2.42	2.43	1.02	down	4.49E-01	8.95E-01	-	-
1374735_at	Arhgap4	Rho GTPase activating protein 4	246249	Rn.163458	BE111827	2.39	2.62	2.51	2.49	2.49	2.46	1.02	down	7.01E-01	9.07E-01	-	-
1376927_at	RGD1564978	similar to LOC432779 protein	502225	Rn.140570	BI284849	2.42	2.36	2.37	2.36	2.37	2.34	1.02	down	2.51E-01	8.95E-01	-	-
1398781_at	Atp6v1f	ATPase, H transporting, lysosomal V1 subunit F	116664	Rn.6167	NM_053884	9.43	9.13	8.59	9.09	9.10	9.05	1.02	up	9.16E-01	9.75E-01	-	-
1381222_at	Ttll7	tubulin tyrosine ligase-like family, member 7	310982	Rn.158385	BF387913	2.40	2.38	2.42	2.40	2.53	2.36	1.02	up	6.34E-01	8.95E-01	-	-
1391071_at	---	---	---	Rn.167995	AI556612	2.43	2.42	2.50	2.43	2.45	2.40	1.02	down	3.83E-01	8.95E-01	-	-
1381178_at	---	---	---	Rn.28094	BE120314	2.61	2.54	2.86	2.75	2.67	2.51	1.02	down	8.28E-01	9.45E-01	-	-
1375753_at	Tars2	threonyl-tRNA synthetase 2, mitochondrial (putative)	310672	Rn.44110	AW251612	2.36	2.36	2.37	2.36	2.36	2.45	1.02	up	4.31E-01	8.95E-01	-	-
1393434_at	---	---	---	Rn.49063	AI145492	2.56	2.52	2.70	2.53	2.65	2.51	1.02	down	7.17E-01	9.10E-01	-	-
1382285_at	Naga	N-acetyl galactosaminidase, alpha	315165	Rn.55746	BM388851	2.87	3.62	2.97	2.96	2.89	3.53	1.02	down	9.34E-01	9.81E-01	-	-
1398058_at	---	---	---	---	BE120039

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)				REG	MTC
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval		
1381278_at	---	---	---	Rn.134210	BI286227	2.61	2.56	2.59	2.58	2.71	2.56	1.02	up	6.15E-01	8.95E-01	-	-
1384144_at	Nxn	Nucleoredoxin	360577	Rn.105982	AI058824	2.46	2.45	2.49	2.46	2.58	2.45	1.02	up	5.64E-01	8.95E-01	-	-
1390136_at	---	---	---	Rn.167512	BE109274	3.39	4.17	3.89	3.68	3.50	4.18	1.02	down	9.33E-01	9.81E-01	-	-
1374454_at	Pcmtd2	protein-L-isoaspartate (D-aspartate) O-methyltransferase domain containing 2	311726	Rn.96446	BM388557	6.74	6.02	6.82	6.15	6.84	6.67	1.02	up	9.38E-01	9.83E-01	-	-
1391128_at	Bcl9l	B-cell CLL/lymphoma 9-like	300673	Rn.32447	BE109129	3.07	3.03	3.04	3.02	3.04	3.00	1.02	down	1.69E-01	8.95E-01	-	-
1373839_at	Nope	neighbor of Punc E11	363081	Rn.164673	BG372386	2.34	2.26	2.27	2.26	2.27	2.26	1.02	down	3.27E-01	8.95E-01	-	-
1370846_at	P22x15	cystatin related protein 2	296229	Rn.43503	BI285266	2.59	2.54	2.66	2.56	2.65	2.50	1.02	down	6.52E-01	8.97E-01	-	-
1397663_at	---	---	---	Rn.147518	BF394561	2.34	2.32	2.35	2.43	2.34	2.32	1.02	up	4.59E-01	8.95E-01	-	-
1380686_at	---	---	---	Rn.153617	BM385607	2.33	2.32	2.39	2.32	2.33	2.31	1.02	down	2.69E-01	8.95E-01	-	-
1380983_at	---	---	---	Rn.206259	AW524497	2.43	2.42	2.53	2.42	2.46	2.41	1.02	down	5.32E-01	8.95E-01	-	-
1391627_at	---	---	---	Rn.168191	AI237138	2.43	2.34	2.35	2.30	2.40	2.34	1.02	down	5.31E-01	8.95E-01	-	-
1368172_a_at	Lox	lysyl oxidase	24914	Rn.11372	BI304009	2.44	2.42	2.51	2.42	2.44	2.42	1.02	down	3.71E-01	8.95E-01	-	-
1398659_at	Vwc2	von Willebrand factor C domain containing 2	501231	Rn.121577	AW528611	2.56	2.53	2.64	2.55	2.61	2.49	1.02	down	6.12E-01	8.95E-01	-	-
1368891_at	Gnpat	glyceronephosphate O-acyltransferase	84470	Rn.1739	AI014001	3.60	3.82	3.57	3.72	3.20	4.16	1.02	up	9.30E-01	9.80E-01	-	-
1392370_at	Tube1	tubulin, epsilon 1	361856	Rn.101545	BF392339	2.37	2.40	2.38	2.36	2.36	2.35	1.02	down	7.17E-02	8.95E-01	-	-
1391555_at	---	---	---	---	BI276668	2.97	3.14	2.98	2.97	2.97	3.06	1.02	down	6.87E-01	9.04E-01	-	-
1396918_at	---	---	---	Rn.60656	BF405582	2.37	2.37	2.45	2.37	2.38	2.35	1.02	down	3.74E-01	8.95E-01	-	-
1397029_at	---	---	---	Rn.173102	BF399100	2.45	2.44	2.46	2.52	2.50	2.41	1.02	up	4.47E-01	8.95E-01	-	-
1398183_at	---	---	---	---	BE101139	5.15	5.10	5.20	5.51	5.04	4.98	1.02	up	8.81E-01	9.64E-01	-	-
1397260_at	---	---	---	---	AA850079	2.57	2.54	2.58	2.55	2.57	2.49	1.02	down	3.53E-01	8.95E-01	-	-
1377512_at	---	---	---	Rn.211998	BI291272	2.63	2.53	2.63	2.59	2.61	2.51	1.02	down	5.61E-01	8.95E-01	-	-
1380689_at	---	---	---	---	BM389555	2.49	2.47	2.53	2.48	2.48	2.44	1.02	down	2.60E-01	8.95E-01	-	-
1387096_at	Hps1	Hermansky-Pudlak syndrome 1 homolog (human)	114638	Rn.17691	NM_040669	3.60	3.58	3.89	3.58	3.51	3.89	1.02	down	8.89E-01	9.59E-01	-	-
1380027_at	---	---	---	Rn.203603	AW523502	2.37	2.41	2.38	2.50	2.38	2.36	1.02	up	5.87E-01	8.95E-01	-	-
1390964_at	RGD1561115	similar to Gene model 1568	500686	Rn.141508	BE095730	2.39	2.37	2.46	2.38	2.39	2.36	1.02	down	3.84E-01	8.95E-01	-	-
1398522_at	Ankle2	ankyrin repeat and LEM domain containing 2	360829	Rn.202689	BM386512	3.38	3.87	4.18	3.49	3.71	4.16	1.02	down	9.34E-01	9.81E-01	-	-
1370616_at	Nrg1	neuregulin 1	112400	Rn.37438	U02324	2.36	2.29	2.30	2.29	2.30	2.29	1.02	down	2.58E-01	8.95E-01	-	-
1369034_at	Kcnj6	potassium inwardly-rectifying channel, subfamily J, member 6	25743	Rn.10185	NM_013192	2.30	2.36	2.30	2.29	2.30	2.29	1.02	down	2.80E-01	8.95E-01	-	-
1373576_at	---	---	---	---	BE107337	5.89	5.55	5.47	5.12	5.63	6.06	1.02	down	9.33E-01	9.81E-01	-	-
1388121_at	Aplp2	amyloid beta (A4) precursor-like protein 2	64312	Rn.1423	M31322	8.39	8.56	8.07	8.79	8.34	7.96	1.02	up	9.29E-01	9.80E-01	-	-
1394058_at	Lgals12	lectin, galactoside-binding, soluble, 12	293710	Rn.28915	AI175573	2.44	2.40	2.51	2.42	2.44	2.40	1.02	down	4.79E-01	8.95E-01	-	-
1393544_at	---	---	---	Rn.40565	AA859687	2.46	2.42	2.44	2.42	2.44	2.39	1.02	down	2.03E-01	8.95E-01	-	-
1387681_at	Ucp3	uncoupling protein 3 (mitochondrial, proton carrier)	25708	Rn.9902	U92069	2.26	2.25	2.36	2.26	2.29	2.25	1.02	down	5.14E-01	8.95E-01	-	-
1375069_at	Fam116b	family with sequence similarity 116, member B	362983	Rn.48823	BG380530	2.43	2.50	2.44	2.43	2.43	2.43	1.02	down	3.04E-01	8.95E-01	-	-
1372735_at	Eif3k	eukaryotic translation initiation factor 3, subunit K	292762	Rn.1706	BI283109	9.64	9.38	9.36	9.55	9.22	9.53	1.02	down	8.58E-01	9.56E-01	-	-
1369102_at	Mapk10	mitogen activated protein kinase 10	25272	Rn.9911	NM_012806	2.41	2.40	2.49	2.40	2.42	2.40	1.02	down	4.22E-01	8.95E-01	-	-
1388201_at	Bmp6	bone morphogenetic protein 6	25644	Rn.40476	AW141680	2.43	2.36	2.38	2.36	2.37	2.35	1.02	down	3.01E-01	8.95E-01	-	-
1391025_at	---	---	---	Rn.47994	BI291162	2.52	2.51	2.54	2.51	2.53	2.45	1.02	down	3.77E-01	8.95E-01	-	-
1378855_a_at	74 /// LOC680282	similar to transcription elongation factor A (SII)-like 3 /// hypothetical protein LOC	680282 /// 679974 /// 68	Rn.181498	BE097672	2.72	2.64	2.74	2.67	2.72	2.63	1.02	down	5.34E-01	8.95E-01	-	-
1384225_at	---	---	---	Rn.54031	BI289963	2.37	2.36	2.42	2.35	2.38	2.50	1.02	up	6.26E-01	8.95E-01	-	-
1377536_at	Zzef1	zinc finger, ZZ-type with EF hand domain 1	287476	Rn.24218	BE115737	2.34	2.33	2.39	2.33	2.34	2.32	1.02	down	2.41E-01	8.95E-01	-	-
1383312_at	---	---	---	Rn.12292	BF396751	2.49	2.48	2.52	2.49	2.60	2.48	1.02	up	5.34E-01	8.95E-01	-	-
1395860_at	---	---	---	Rn.169753	BF403320	2.47	2.37	2.41	2.39	2.40	2.38	1.02	down	4.30E-01	8.95E-01	-	-
1384232_at	---	---	---	Rn.16540	AI709768	2.77	2.73	2.82	2.74	2.75	2.74	1.02	down	3.71E-01	8.95E-01	-	-
1373062_at	---	---	---	Rn.20864	BM388650	2.39	2.33	2.36	2.33	2.34	2.32	1.02	down	1.83E-01	8.95E-01	-	-
1380117_at	---	---	---	Rn.172952	BF397842	2.39	2.31	2.31	2.31	2.31	2.47	1.02	up	6.70E-01	9.00E-01	-	-
1396090_at	Rnf150	ring finger protein 150	364983	Rn.205888	BF564059	2.36	2.41	2.37	2.36	2.37	2.34	1.02	down	2.11E-01	8.95E-01	-	-
1371793_at	---	---	---	Rn.216478	AI008697	3.86	4.16	3.96	3.96	4.14	3.97	1.02	up	8.15E-01	9.40E-01	-	-
1398614_at	Ptch1	patched homolog 1 (Drosophila)	89830	Rn.102312	BE109565	2.51	2.49	2.53	2.50	2.61	2.51	1.02	up	5.05E-01	8.95E-01	-	-
1375573_at	---	---	---	Rn.204937	BE120038	2.45	2.43	2.44	2.41	2.43	2.40	1.02	down	5.76E-02	8.95E-01	-	-
1391441_at	---	---	---	Rn.8955	AA899943	6.93	6.57	7.05	6.92	5.84	7.87	1.02	up	9.67E-01	9.90E-01	-	-
1395805_at	Prickle1	prickle homolog 1 (Drosophila)	315259	Rn.141040	BF552903	2.57	2.56	2.60	2.53	2.74	2.53	1.02	up	7.28E-01	9.13E-01	-	-
1392359_at	---	---	---	Rn.206465	BE120205	2.49	2.48	2.53	2.47	2.51	2.44	1.02	down	3.40E-01	8.95E-01	-	-
1393030_at	---	---	---	---	BE115641	2.53	2.52	2.56	2.49	2.53	2.51	1.02	down	1.75E-01	8.95E-01	-	-
1370912_at	Hspa1b	heat shock 70kD protein 1B (mapped)	294254	---	BI278231	2.56	2.64	2.56	2.75	2.57	2.53	1.02	up	7.32E-01	9.14E-01	-	-
1398653_at	LOC683514	hypothetical protein LOC683514	683514	Rn.65190	BF386227	2.55	2.54	2.57	2.52	2.68	2.54	1.02	up	6.26E-01	8.95E-01	-	-
1386368_at	---	---	---	---	AI639036	2.66	2.63	2.79	2.63	2.75	2.63	1.02	down	7.00E-01	9.07E-01	-	-
1379391_at	---	---	---	---	AI103389	2.33	2.32	2.34	2.42	2.33	2.31	1.02	up	4.87E-01	8.95E-01	-	-
1376933_at	---	---	---	Rn.23214	AI170377	2.47	3.14	2.70	3.00	2.58	2.65	1.02	down	9.15E-01	9.75E-01	-	-
1381917_at	Dpm1	dolichyl-phosphate mannosyltransferase polypeptide 1, catalytic subunit	296394	Rn.7840	AI578081	2.47	2.45	2.56	2.46	2.48	2.46	1.02	down	4.78E-01	8.95E-01	-	-
1394385_s_at	Drd4	dopamine receptor D4	25432	Rn.10159	BI284462	2.37	2.36	2.45	2.37	2.38	2.36	1.02	down	3.68E-01	8.95E-01	-	-
1389659_at	Ctla2a	cytotoxic T lymphocyte-associated protein 2 alpha	498690	Rn.7778	AI230591	2.57	2.73	2.58	2.56	2.58	2.81	1.02	up	7.95E-01	9.34E-01	-	-
1392014_at	---	---	---	Rn.210536	BF416257	2.36	2.42	2.36	2.35	2.36	2.34	1.02	down	2.44E-01	8.95E-01	-	-
1391996_a_at	---	---	---	Rn.54114	BI284367	2.47	2.45	2.53	2.45	2.48	2.44	1.02	down	3.84E-01	8.95E-01	-	-
1373351_at	Ank2	ankyrin 2, neuronal	362036	Rn.10131	BI286775	2.73	2.69	2.86	2.71	2.84	2.66	1.02	down	7.38E-01	9.16E-01	-	-
1384637_at	---	---	---	---	AW535033	2.59	2.53	2.69	2.57	2.65	2.51	1.02	down	6.89E-01	9.04E-01	-	-
1392408_at	---	---	---	Rn.212008	BI297463	2.44	2.41	2.46	2.41	2.44	2.37	1.02	down	3.23E-01	8.95E-01	-	-
1381368_at	---	---	---	Rn.209773	BF416738	2.61	2.60	2.65	2.59	2.77	2.58	1.02	up	6.89E-01	9.05E-01	-	-
1398512_at	Nfx1	nuclear transcription factor, X-box binding 1	313166	Rn.55459	BM389434	2.31	2.39	2.31	2.31	2.32	2.31	1.02	down	3.68E-01	8.95E-01	-	-
1391962_at	---	---	---	Rn.208981	BF402644	2.46	2.39	2.41	2.40	2.40	2.38	1.02	down	3.13E-01	8.95E-01	-	-
1368975_at	Cd38	CD38 molecule	25668	Rn.11414	D30795	2.43	2.43	2.44	2.52	2.44	2.43	1.02	up	4.17E-01	8.95E-01	-	-
1381451_at	Mmp23	matrix metallopeptidase 23	94339	Rn.22582	AI548892	2.42	2.34	2.37	2.36	2.37	2.34	1.02	down	3.41E-01	8.95E-01	-	-
1380287_at	RGD1566107	similar to cAMP responsive element binding protein 5	500131	Rn.210235	BF396289	2.43	2.36	2.38	2.37	2.37	2.35	1.02	down	3.07E-01	8.95E-01	-	-
1390614_at	---	---	---	Rn.52143	BE112987	2.44	2.37	2.37	2.51	2.37	2.38	1.02	up	6.36E-01	8.95E-01	-	-
1392999_at	Neto2	neuropilin (NRP) and tolloid (TLL)-like 2	307757	Rn.147067	AA819279	2.64	2.60	2.97	2.95	2.65	2.53	1.02	down	8.84E-01	9.64E-01	-	-
1380299_at	---	---	---	Rn.206581	BF411579	2.66	2.60	2.84	2.63	2.75	2.63	1.02	down	7.63E-01	9.22E-01	-	-
1370452_at	Cacna1c	calcium channel, voltage-dependent, L type, alpha 1C subunit	24239	Rn.9827	M59786	2.44	2.42	2.44	2.52	2.45	2.42	1.02	up	4.09E-01	8.95E-01	-	-
1394993_at	---	---	---	Rn.169908	AW531339	2.61	4.00	4.13	3.84	2.84	3.97	1.02	down	9.67E-01	9.90E-01	-	-
1374212_at	---	---	---	Rn.14344	AI012753	3.09	2.73	2.72	3.01	2.83	2.62	1.02	down	8.79E-01	9.63E-01	-	-
1389721_at	---	---	---	Rn.167362	BI285940	2.37	2.37	2.43	2.36	2.38	2.35	1.02	down	2.92E-01	8.95E-01	-	-
1370693_a_at	Cnp	2',3'-cyclic nucleotide 3' phosphodiesterase	25275	Rn.31762	M18630	2.39	2.38	3.05	2.97	2.39	2.38	1.02	down	9.32E-01	9.81E-01	-	-
1391399_at	---	---	---	Rn.129744	AW524037	2.70	2.64	2.73	2.77	2.71	2.67	1.02	up	5.37E-01	8.95E-01	-	-
1369936_at	Calm1	calmodulin 1	24242	Rn.4166	NM_031969	10.69	11.02	10.56	10.65	10.67	11.04	1.02	up	8.93E-01	9.67E-01	-	-
1374757_at	Pag29	pregnancy-specific glycoprotein 29	292666	Rn.154014	BI285954	2.37	2.29	2.31	2.30	2.31	2.29	1.02	down	3.54E-01	8.95E-01	-	-
1376583_at	RGD1304884	similar to RIKEN cDNA 6430548M08	307907	Rn.199301	BE095847	2.34	2.42	2.34	2.51	2.34	2.33	1.02	up	6.91E-01	9.05E-01	-	-
1381836_at	Rab20	RAB20, member RAS oncogene family	689377	Rn.140755	BF403394	2.34	2.39	2.34	2.33	2.34	2.32	1.02	down	2.42E-01	8.95E-01	-	-
1395912_at	---	---	---	Rn.27708	BF419537	2.40	2.37	2.48	2.39	2.41	2.38	1.02	down	4.64E-01	8.95E-01	-	-
1375602_at	Rin2	Ras and Rab interactor 2	311494	Rn.34193	BG378103	2.40	2.41	2.40	2.50	2.40	2.39	1.02	up	5.22E-01	8.95E-01	-	-
1390708_at	---	---	---	Rn.156274	AI012518	2.69	2.61	2.79	2.62	2.75	2.64	1.02	down	7.12E-01	9.10E-01	-	-
1382043_at	Unc93b1	unc-93 homolog B1 (C. elegans)	361689	Rn.204473	AI234533	2.54	2.58	2.55	2.54	2.55	2.67	1.02	up	5.69E-01	8.95E-01	-	-
1381697_at	---	---	---	Rn.129683	AW530378	2.91	2.81	2.97	2.88	2.88	2.84	1.02	down	6.15E-01	8.95E-01	-	-
1394921_at	Prkaa1	protein kinase, AMP-activated, alpha 1 catalytic subunit	65248	Rn.87789	BF290064	2.40	2.39	2.46	2.40	2.41	2.37	1.02	down	3.41E-01	8.95E-01	-	-
1376199_at	Pik3c2	phosphoinositide-3-kinase, regulatory subunit 2 (beta)	25741	Rn.22497	AI103391	2.40	2.58	2.42	2.41	2.42	2.49	1.02	down	6.94E-01	9.05E-01	-	-
1395216_at	---	---	---	Rn.167269	AI176768	2.47	2.45	2.51	2.46	2.47	2.42	1.02	down	3.10E-01	8.95E-01	-	-
1371230_x_at	Atp1f1	ATPase inhibitory factor 1	25392	Rn.1658	M35300	2.90	2.87	2.91	2.89	3.00	2.87	1.02	up	5.77E-01	8.95E-01	-	-
1378089_at	Tmem100	Transmembrane protein 100	497979	Rn.18850	AI715411	2.33	2.32	2.37	2.33	2.46	2.32	1.02	up	6.03E-01	8.95E-01	-	-
1398843_at	Vapa	VAMP (vesicle-associated membrane protein)-associated protein A	58857	Rn.162275	AI411103	9.34	9.26	9.46	9.45	9.25	9.29	1.02	down	7.71E-01	9.25E-01	-	-
1381786_at	---	---	---	---	BE114356	2.59	2.57	2.68	2.58	2.61	2.57	1.02	down	4.88E-01	8.95E-01	-	-
1396691_at	---	---	---	Rn.153649	BF391972	2.39	2.37	2.41	2.39	2.39	2.32	1.02	down	3.48E-01	8.95E-01	-	-
1390667_at	Lrrc51	leucine rich repeat containing 51	293156	Rn.162471	AF406542	2.85	2.75	2.78	2.79	2.77	2.74	1.02	down	4.65E-01	8.95E-01	-	-
1370751_at	LOC257642	rRNA promoter binding protein	257642	---	U77931	13.81	13.48	13.65	13.78	13.76	13.32	1.02	down	8.87E-01	9.65E-01	-	-
1395329_at	Gmppb	GDP-mannose pyrophosphorylase B	363145	Rn.102187	AW141715	2.34	2.32	2.34	2.41	2.35	2.34	1.02	up	3.01E-01	8.95E-01	-	-
1378694_at	Plxnb1	plexin B1	316009	Rn.26773	BI294858	2.71	2.78	2.85	2.74	2.81	2.72	1.02	down	6.36E-01	8.95E-01	-	-
1374806_at	Stfn	stratifin	313017	Rn.145079	BI286166	3.01	3.01	3.01	3.01	2.99	3.11	1.02	up	5.20E-01	8.95E-01	-	-
1389045_at	---	---	---	Rn.41482	AW251869	2.30	2.22	2.23	2.23	2.23	2.22	1.02	down	3.58E-01	8.95E-01	-	-
1383597_at	Dclre1c	DNA cross-link repair 1C, PSO2 homolog (S. cerevisiae)	259171	Rn.204346	AI072301	2.44	2.44	2.45	2.52	2.47	2.42	1.02	up	4.03E-01	8.95E-01	-	-
1377448_at	Tmem38a	transmembrane protein 38a	306327	Rn.162265	BG374556	2.50	2.51	2.50	2.48	2.49	2.45	1.02	down	1.19E-01	8.95E-01	-	-
1378350_at	---	---	---	Rn.156510	AA859902	2.59	2.55	2.63	2.59	2.61	2.49	1.02	down	5.72E-01	8.95E-01	-	-
1377825_at	---	---	---	Rn.121336	AI411841	5.82	5.82	5.77	5.77	5.85	5.87	1.02	up	4.75E-01	8.95E-01	-	-
1384636_at	---	---	---	---	AI136316	7.48	7.84	7.93	7.94	8.07	7.17	1.02	down	9.36E-01	9.82E-01	-	-
1368119_at	Inpp5j	inositol polyphosphate-5-phosphatase J	171088	Rn.23872	NM_133562	3.02	2.44	2.38	2.32	3.29	2.31	1.02	up	9.48E-01	9.85E-01	-	-
1383693_at	Ephb2	Eph receptor B2	313633	Rn.27233	AI070837	2.27	2.26	2.28	2.34	2.28	2.26	1.02	up	3.22E-01	8.95E-01	-	-
1391074_at	Crabp1	cellular retinoic acid binding protein 1	25061	Rn.3207	BF387793	2.26	2.25	2.26	2.24	2.36	2.24	1.02	up	5.58E-01	8.95E-01	-	-
1393868_at	Pcdh10	Protocadherin 10	361943	Rn.207128	AW535602	2.60	2.55	2.66	2.56	2.65	2.51	1.02	down	6.55E-01	8.98E-01	-	-
1384572_at	---	---	---	Rn.21291	AI716028	2.33	2.37	2.35	2.33	2.32	2.32	1.02	down	1.19E-01	8.95E-01	-	-
1377294_at	---	---	---	Rn.173152	BF401588	2.58	2.56	2.59	2.55	2.58	2.52	1.02	down	2.91E-01	8.95E-01	-	-
1385986_at	---	---	---	Rn.173399	BF391203	2.41	2.35	2.38	2.36	2.36	2.35	1.02	down	2.10E-01	8.95E-01	-	-
1398782_at	Napa	N-ethylmaleimide-sensitive factor attachment protein, alpha	140673	Rn.31745	NM_080585	5.72	6.56	6.48	6.57	5.72	6.55	1.02	up	9.49E-01	9.85E-01	-	-
1391425_at	Nckipsd	NCK interacting protein with SH3 domain	301009	Rn.90103	AW528585	2.90	2.50	2.58	2.69	2.62	2.58	1.02	down	8.46E-01	9.52E-01	-	-
1387794_at	Fcn1	ficolin (collagen/fibrinogen domain containing) 1	83517	Rn.20051	NM_031348	2.36	2.35	2.37	2.36	2.46	2.35	1.02	up	4.99E-01	8.95E-01	-	-
1384398_at	---	---	---	---	BM383680	2.35	2.39	2.35	2.33	2.36	2.31	1.02	down	2.63E-01	8.95E-01	-	-
1386937_at	Atp1b1	ATPase, Na+/K+ transporting, beta 1 polypeptide	25650	Rn.8925	AI232036	12.13	12.11	12.13	12.04	12.16	12.25	1.02	up	6.90E-01	9.05E-01	-	-
1390668_at	Smc3	structural maintenance of chromosomes 3	29486	Rn.11074	BG378312	2.56	2.50	2.59	2.51	2.57	2.49	1.02	down	5.04E-01	8.95E-01	-	-
1369514_at	Insrr	insulin receptor-related receptor	60663	Rn.44446	NM_022212	2.32	2.25	2.26	2.25	2.26	2.25	1.02	down	3.08E-01	8.95E-01	-	-
1369212_s_at	Epb4.1l1	erythrocyte protein band 4.1-like 1	59317	Rn.20361	NM_021681	4.51	4.42	4.62	4.27	4.57	4.80	1.02	up	8.82E-01	9.64E-01	-	-
1380901_at	Syt16	synaptotagmin XVI	299142	Rn.42973	AW527298	2.41	2.39	2.51	2.40	2.46	2.37	1.02	down	5.84E-01	8.95E-01	-	-
1374469_at	---	---	---	Rn.22305	BG372375	2.47	2.43	2.47	2.46	2.47	2.52	1.02	up	2.86E-01	8.95E-01	-	-
1399051_at	Patl1	protein associated with topoisomerase II homolog 1 (yeast)	361736	Rn.162495	BE104409	2.99	3.30	2.83	3.08	3.07	3.05	1.02	up	8.58E-01	9.56E-01	-	-
1371290_a_at	Htr7	5-hydroxytryptamine (serotonin) receptor 7	65032	Rn.87132	U68491	2.44	2.42	2.50	2.42	2.44	2.41	1.02	down	3.69E-01	8.95E-01	-	-
1383574_at	Man1a1	mannosidase, alpha, class 1A, member 1	294410	Rn.3576	AI502956	4.70	4.38	4.69	3.96	5.05	4.83	1.02	up	9.44E-01	9.84E-01	-	-
1386292_at	---	---	---	Rn.131614	AI639358	2.54	2.50	2.60	2.51	2.58	2.48	1.02	down	5.63E-01	8.95E-01	-	-
1396870_at	---	---	---	Rn.161957	BF419761	2.53	2.49	2.58	2.51	2.54	2.48	1.02	down	4.43E-01	8.95E-01	-	-
1386342_at	---	---	---	---	BG057568	2.39	2.39	2.41	2.39	2.50	2.38	1.02	up	5.34E-01	8.95E-01	-	-
1389044_at	Gbf1	golgi-specific brefeldin A resistant guanine nucleotide exchange factor 1	309451	Rn.61235	BF283388	2.61	2.60	2.60	2.60	2.60	2.53	1.02	down	3.15E-01	8.95E-01	-	-
1398651_at	---	---	---	Rn.16128	AI045148	2.58	2.58	2.65	2.56	2.62	2.55	1.02	down	4.42E-01	8.95E-01	-	-
1389739_at	Neurl2	neuralized-like 2 (Drosophila)	311633	Rn.98792	AA800025	3.99	3.96	4.00	3.97	4.05	4.01	1.02	up	3.42E-01	8.95E-01	-	-
1393152_at	Mut	methylmalonyl-Coenzyme A mutase	688517	Rn.54738	AI007821	7.38	6.84	6.40	6.77	6.45	7.32	1.02	down	9.48E-01	9.85E-01	-	-
1396917_at	---	---	---	Rn.205270	AI535209	2.68	3.20	2.60	3.13	2.68	2.59	1.02	down	9.21E-01	9.77E-01	-	-
1370575_a_at	Azin1	antizyme inhibitor 1	58961	Rn.6290	D50734	5.37	5.44	5.65	5.36	5.57	5.45	1.02	down	8.11E-01	9.39E-01	-	-
1389876_at	Camk2n1	Calcium/calmodulin-dependent protein kinase II inhibitor 1	287005	Rn.12600	BE111167	9.48	9.36	9.88	9.55	9.96	9.28	1.02	up	9.22E-01	9.77E-01	-	-
1383673_at	Nap1l2	nucleosome assembly protein 1-like 2	317247	Rn.43670	BI288925	2.55	2.48	2.60	2.51	2.56	2.47	1.02	down	5.78E-01	8.95E-01	-	-
1396595_at	---	---	---	Rn.60800	BF405078	2.37	2.36	2.36	2.36	2.38	2.45	1.02	up	3.76E-01	8.95E-01	-	-
1377074_at	---	---	---	---	AW251840	2.39	2.38	2.46	2.39	2.40	2.37	1.02	down	3.94E-01	8.95E-01	-	-
1373475_at	Ccdc58	coiled-coil domain containing 58	288065	Rn.162059	BM390469	8.92	8.91	9.24	9.07	8.80	9.13	1.02	down	8.68E-01	9.59E-01	-	-
1369573_at	Mcpt4	mast cell protease 4	54270

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1368023_at	Qsox1	quiescin Q6 sulfhydryl oxidase 1	84491	Rn.44920	AB044285	2.44	2.44	2.48	2.53	2.48	2.44	1.02	up	4.24E-01	8.95E-01	-	-
1373456_at	Rnf111	ring finger protein 111	300813	Rn.82537	BI300764	6.38	7.04	6.71	6.06	7.20	6.79	1.02	down	9.50E-01	9.85E-01	-	-
1368869_at	Akap12	A kinase (PRKA) anchor protein 12	83425	Rn.122094	BG663107	2.52	2.53	2.57	2.52	2.52	2.49	1.02	down	2.58E-01	8.95E-01	-	-
1396548_at	---	---	---	Rn.161438	BF388530	2.47	2.44	2.46	2.43	2.45	2.41	1.02	down	1.75E-01	8.95E-01	-	-
1396863_at	---	---	---	Rn.48417	AW535061	2.46	2.45	2.53	2.45	2.46	2.45	1.02	down	3.82E-01	8.95E-01	-	-
1384624_at	---	---	---	---	AI233317	2.39	2.37	2.47	2.38	2.40	2.37	1.02	down	4.49E-01	8.95E-01	-	-
1369579_at	Stc2	stanniocalcin 2	63878	Rn.44823	NM_022230	2.37	2.39	2.39	2.36	2.37	2.34	1.02	down	7.43E-02	8.95E-01	-	-
1387907_at	Itpr1	inositol 1,4,5-trifhosphate receptor, type 1	25262	Rn.2135	J05510	5.50	6.34	6.58	5.84	6.35	6.15	1.02	down	9.46E-01	9.85E-01	-	-
1387788_at	Junb	jun B proto-oncogene	24517	Rn.15806	NM_021836	2.66	2.58	2.59	2.59	2.59	2.58	1.02	down	3.56E-01	8.95E-01	-	-
1388280_a_at	Lepr	leptin receptor	24536	Rn.9851	AF001818	2.40	2.45	2.40	2.38	2.42	2.38	1.02	down	3.11E-01	8.95E-01	-	-
1396638_at	---	---	---	Rn.170847	BM382854	2.41	2.40	2.48	2.41	2.41	2.40	1.02	down	3.63E-01	8.95E-01	-	-
1390194_at	---	---	---	Rn.58133	BI296401	2.48	2.49	2.60	2.49	2.70	2.46	1.02	up	7.75E-01	9.27E-01	-	-
1395480_at	---	---	---	Rn.10358	BI303370	2.62	2.59	2.64	2.60	2.75	2.58	1.02	up	6.58E-01	8.98E-01	-	-
1393716_at	Slc35f1	solute carrier family 35, member F1	502421	Rn.85970	BE104555	2.41	4.23	2.41	2.41	3.59	2.97	1.02	down	9.72E-01	9.92E-01	-	-
1387670_at	Gpd2	glycerol-3-phosphate dehydrogenase 2, mitochondrial	25062	Rn.89705	U08027	4.55	6.61	4.80	5.18	5.08	5.63	1.02	down	9.71E-01	9.92E-01	-	-
1375901_at	Ddx21	DEAD (Asp-Glu-Ala-Asp) box polypeptide 21	317399	Rn.162310	AI178527	6.13	6.44	7.19	6.08	6.94	6.66	1.02	down	9.52E-01	9.86E-01	-	-
1385179_at	RGD1307537	similar to RIKEN cDNA 4933417A18	291077	Rn.194901	BF408798	2.34	2.33	2.35	2.33	2.43	2.32	1.02	up	5.14E-01	8.95E-01	-	-
1393677_at	---	---	---	Rn.212704	BI275079	4.02	3.85	3.83	3.85	3.86	3.92	1.02	down	6.95E-01	9.06E-01	-	-
1387574_at	Chrna2	cholinergic receptor, nicotinic, alpha 2 (neuronal)	170945	Rn.9713	NM_133420	2.42	2.44	2.45	2.42	2.40	2.41	1.02	down	6.57E-02	8.95E-01	-	-
1376306_at	---	---	---	---	BE112643	2.82	2.79	2.83	2.82	2.94	2.77	1.02	up	6.46E-01	8.95E-01	-	-
1369532_at	Prokr2	prokineticin receptor 2	192649	Rn.82760	NM_138978	2.43	2.36	2.38	2.36	2.38	2.35	1.02	down	3.13E-01	8.95E-01	-	-
1373762_a_at	---	---	---	---	BF410953	2.46	2.46	2.52	2.46	2.50	2.40	1.02	down	5.11E-01	8.95E-01	-	-
1375966_at	Mmrn2	multimerin 2	306288	Rn.219773	BE098266	2.43	2.41	2.52	2.42	2.46	2.41	1.02	down	5.05E-01	8.95E-01	-	-
1369232_at	Kcnk10	potassium channel, subfamily K, member 10	65272	Rn.53999	AF196865	2.40	2.38	2.45	2.39	2.39	2.37	1.02	down	3.11E-01	8.95E-01	-	-
1388556_at	Stx6	syntaxin 6	60562	Rn.100217	BG381589	4.89	4.79	4.60	4.81	4.42	4.97	1.02	down	8.95E-01	9.67E-01	-	-
1372104_at	---	---	---	Rn.163637	BF289002	7.13	7.29	7.57	7.09	6.89	7.94	1.02	down	9.45E-01	9.84E-01	-	-
1384772_at	Prkacb	protein kinase, cAMP dependent, catalytic, beta	293508	Rn.202491	BF400907	5.13	4.98	6.13	4.90	5.25	6.02	1.02	down	9.61E-01	9.89E-01	-	-
1383453_at	Olfml1	olfactomedin-like 1	361621	Rn.22729	AA946156	9.83	9.49	9.92	9.85	9.46	9.85	1.02	down	8.96E-01	9.67E-01	-	-
1396089_at	LOC683522	similar to Transcriptional enhancer factor TEF-3 (TEA domain family member	683522	---	BF398376	2.32	2.31	2.37	2.31	2.32	2.28	1.02	down	2.98E-01	8.95E-01	-	-
1398502_at	---	---	---	Rn.166081	AI556780	2.51	2.49	2.55	2.50	2.49	2.48	1.02	down	1.96E-01	8.95E-01	-	-
1387035_a_at	Arhgap17	Rho GTPase activating protein 17	63994	Rn.64581	NM_022244	8.49	7.86	7.13	7.62	7.82	7.96	1.02	down	9.53E-01	9.86E-01	-	-
1381642_at	---	---	---	---	AW533436	2.46	2.45	2.57	2.47	2.51	2.43	1.02	down	6.06E-01	8.95E-01	-	-
1382579_at	Tox3	TOX high mobility group box family member 3	291908	Rn.41060	BE107165	2.37	2.35	2.42	2.35	2.37	2.35	1.02	down	3.25E-01	8.95E-01	-	-
1376460_at	RGD1560070	similar to ataxin 2-binding protein 1 isoform 2	287847	Rn.143966	BI286710	2.31	2.31	2.32	2.32	2.38	2.32	1.02	up	3.19E-01	8.95E-01	-	-
1371971_at	RGD1560212	similar to DNA segment, Chr 18, Wayne State University 98, expressed	498890	Rn.98561	AI599676	5.83	6.39	6.90	6.92	5.94	6.34	1.02	up	9.55E-01	9.87E-01	-	-
1391301_at	t h2bm /// LOC680	histone cluster 1, H2bm /// similar to H2B histone family, member T	361247 /// 680312	Rn.165244	AA997499	2.63	2.57	2.73	2.60	2.69	2.56	1.02	down	6.89E-01	9.04E-01	-	-
1368714_at	Pri8a2	prolactin family 8, subfamily a, member 2	24315	Rn.10114	NM_022846	2.60	2.58	2.67	2.58	2.68	2.51	1.02	down	6.70E-01	9.00E-01	-	-
1385045_at	---	---	---	---	BI301747	2.50	2.46	2.52	2.47	2.48	2.46	1.02	down	2.10E-01	8.95E-01	-	-
1394456_at	---	---	---	Rn.168623	AW525722	8.61	9.08	8.79	8.90	8.76	8.90	1.02	up	8.70E-01	9.60E-01	-	-
1379214_at	---	---	---	Rn.45543	AW523029	2.58	2.54	2.65	2.56	2.62	2.50	1.02	down	6.20E-01	8.95E-01	-	-
1376209_at	J87237 /// RGD13	similar to CG17680-PA /// similar to hypothetical protein supported by AL4492315166 /// 687237		Rn.205491	BG669208	10.33	10.59	10.44	10.26	10.50	10.67	1.02	up	8.65E-01	9.58E-01	-	-
1380068_at	---	---	---	Rn.11869	AA964641	2.79	2.77	3.01	2.78	2.78	3.08	1.02	up	8.46E-01	9.52E-01	-	-
1386160_at	Tchh	Trichohyalin	310588	Rn.42981	AI639401	2.46	2.45	2.49	2.45	2.46	2.41	1.02	down	2.69E-01	8.95E-01	-	-
1376700_at	---	---	---	Rn.43951	AI179472	3.27	3.19	3.20	3.19	3.36	3.19	1.02	up	7.01E-01	9.07E-01	-	-
1396246_at	---	---	---	Rn.161746	AA955093	4.60	4.34	3.73	4.68	3.15	4.91	1.02	up	9.69E-01	9.91E-01	-	-
1398704_at	---	---	---	Rn.57442	BF391251	2.43	2.43	2.46	2.43	2.43	2.38	1.02	down	2.62E-01	8.95E-01	-	-
1382290_at	Mettl10	methyltransferase like 10	361664	Rn.21246	AI717186	3.65	4.03	3.82	3.34	3.94	4.15	1.02	down	9.28E-01	9.80E-01	-	-
1398623_at	Chrnb4	cholinergic receptor, nicotinic, beta 4	25103	Rn.9695	AI454607	2.57	2.53	2.62	2.55	2.58	2.51	1.02	down	4.82E-01	8.95E-01	-	-
1370412_at	Tnnt1	troponin T type 1 (skeletal, slow)	171409	Rn.13846	AF399874	2.42	2.41	2.49	2.41	2.43	2.39	1.02	down	3.98E-01	8.95E-01	-	-
1375924_at	---	---	---	---	AA892778	5.20	4.82	5.24	4.34	5.83	5.18	1.02	up	9.58E-01	9.88E-01	-	-
1369534_at	Il11	interleukin 11	171040	Rn.198483	NM_133519	2.52	2.51	2.58	2.51	2.52	2.49	1.02	down	3.28E-01	8.95E-01	-	-
1388711_at	Il13ra1	interleukin 13 receptor, alpha 1	252963	Rn.81210	BF282650	5.63	5.56	6.29	5.72	5.76	5.92	1.02	down	9.20E-01	9.76E-01	-	-
1392270_at	---	---	---	Rn.207643	BE104334	2.53	2.53	2.56	2.52	2.55	2.47	1.02	down	3.83E-01	8.95E-01	-	-
1392759_at	Trem2	triggering receptor expressed on myeloid cells 2	301227	Rn.106975	AI176732	2.31	2.30	2.32	2.30	2.39	2.30	1.02	up	4.46E-01	8.95E-01	-	-
1370359_at	Amy1a	amylase, alpha 1A (salivary)	24203	Rn.116361	AB057450	2.56	2.53	2.57	2.54	2.71	2.49	1.02	up	7.35E-01	9.15E-01	-	-
1397715_at	---	---	---	Rn.205650	AI716475	2.38	2.37	2.43	2.38	2.39	2.34	1.02	down	3.17E-01	8.95E-01	-	-
1394247_x_at	---	---	---	Rn.105740	AA799816	4.08	3.55	4.50	4.07	4.16	3.82	1.02	down	9.35E-01	9.82E-01	-	-
1393723_at	Plk5p	polo-like kinase 5 pseudogene	314627	Rn.65962	AW520114	2.51	2.51	2.65	2.52	2.58	2.50	1.02	down	6.47E-01	8.95E-01	-	-
1378037_at	Rnf215	ring finger protein 215	305478	Rn.41695	BM390078	7.04	6.46	6.36	6.56	6.29	6.94	1.02	down	9.33E-01	9.81E-01	-	-
1375905_at	Ttyh1	tweety homolog 1 (Drosophila)	292597	Rn.14889	AI412746	2.44	2.43	2.51	2.44	2.44	2.43	1.02	down	3.66E-01	8.95E-01	-	-
1385477_at	RGD1563155	similar to RIKEN cDNA 1700054O13	367734	Rn.112507	BE102379	2.74	2.74	2.76	2.72	2.75	2.69	1.02	down	2.12E-01	8.95E-01	-	-
1397674_at	Eif3c	eukaryotic translation initiation factor 3, subunit C	293484	Rn.4207	AI502930	11.02	10.87	11.21	11.02	10.88	11.14	1.02	down	8.47E-01	9.52E-01	-	-
1382870_at	---	---	---	Rn.165544	AI103536	2.45	2.44	2.51	2.44	2.45	2.43	1.02	down	3.57E-01	8.95E-01	-	-
1379007_at	---	---	---	Rn.198945	AI712659	2.56	2.55	2.62	2.55	2.58	2.53	1.02	down	3.93E-01	8.95E-01	-	-
1387856_at	Cnn3	calponin 3, acidic	54321	Rn.57635	BI274457	9.97	9.85	9.67	9.87	9.63	10.07	1.02	up	8.77E-01	9.62E-01	-	-
1368521_at	Napsa	napsin A aspartic peptidase	60575	Rn.17097	NM_031670	9.65	10.05	10.07	9.91	9.89	9.90	1.02	down	8.62E-01	9.57E-01	-	-
1395650_at	---	---	---	Rn.205969	BF543766	2.53	2.50	2.60	2.51	2.58	2.47	1.02	down	5.88E-01	8.95E-01	-	-
1382733_at	---	---	---	Rn.164521	AW915163	2.64	2.59	2.61	2.61	2.60	2.56	1.02	down	3.22E-01	8.95E-01	-	-
1396161_at	---	---	---	Rn.167664	BI285362	2.41	2.44	2.42	2.40	2.41	2.38	1.02	down	1.28E-01	8.95E-01	-	-
1374314_at	---	---	---	Rn.210166	BF394728	2.64	2.61	2.78	2.62	2.75	2.59	1.02	down	7.39E-01	9.16E-01	-	-
1370180_at	Nudt4	nudix (nucleoside diphosphate linked moiety X)-type motif 4	94267	Rn.8426	BG376935	8.14	7.81	7.57	7.66	8.29	7.50	1.02	down	9.35E-01	9.82E-01	-	-
1385764_at	Slc25a41	solute carrier family 25, member 41	301114	Rn.140434	BF405897	2.28	2.27	2.28	2.32	2.28	2.30	1.02	up	1.28E-01	8.95E-01	-	-
1375146_at	LOC691504	similar to Zinc finger protein ZFPM1 (Zinc finger protein multitype 1) (Friend c	691504	Rn.160024	AW252880	2.31	2.31	2.31	2.31	2.39	2.31	1.02	up	3.90E-01	8.95E-01	-	-
1381655_at	---	---	---	Rn.207493	BE102083	2.49	2.47	2.55	2.48	2.52	2.45	1.02	down	4.84E-01	8.95E-01	-	-
1376160_at	Sfrs16	splicing factor, arginine/serine-rich 16	499390	Rn.17553	BF408850	2.27	2.26	2.28	2.27	2.27	2.34	1.02	up	3.67E-01	8.95E-01	-	-
1371164_at	Mcpt10	mast cell protease 10	54269	Rn.48655	X68657	2.54	2.52	2.58	2.53	2.56	2.48	1.02	down	4.26E-01	8.95E-01	-	-
1371851_at	Psmd6	proteasome (prosome, macropain) 26S subunit, non-ATPase, 6	289924	Rn.103875	BM383811	7.56	8.28	7.84	7.98	7.43	8.19	1.02	down	9.39E-01	9.83E-01	-	-
1386703_at	---	---	---	Rn.216910	BE566738	2.55	2.51	2.60	2.51	2.57	2.49	1.02	down	5.05E-01	8.95E-01	-	-
1368734_at	Chrnd	cholinergic receptor, nicotinic, delta	54240	Rn.41489	NM_019298	2.33	2.34	2.35	2.33	2.43	2.34	1.02	up	4.75E-01	8.95E-01	-	-
1394125_at	/// LOC685392 ///	hypothetical protein LOC682990 /// hypothetical protein LOC683021 /// hypoth	21 /// 685110 /// 68	Rn.130206	AI639140	2.36	2.40	2.37	2.35	2.36	2.33	1.02	down	1.72E-01	8.95E-01	-	-
1368241_a_at	Flot1	flotillin 1	64665	Rn.9567	NM_022701	5.88	4.38	5.39	4.85	5.76	5.12	1.02	up	9.64E-01	9.90E-01	-	-
1372821_at	Ccny	cyclin Y	361261	Rn.17533	AI236621	8.30	8.88	8.77	8.08	9.02	8.92	1.02	up	9.45E-01	9.84E-01	-	-
1384596_at	---	---	---	Rn.204378	AI073013	2.50	2.42	2.50	2.49	2.52	2.49	1.02	up	4.03E-01	8.95E-01	-	-
1379486_at	---	---	---	Rn.27421	AA860029	2.41	2.39	2.42	2.40	2.51	2.39	1.02	up	5.57E-01	8.95E-01	-	-
1368695_at	C4bpb	complement component 4 binding protein, beta	24236	Rn.11151	NM_016995	2.36	2.35	2.41	2.35	2.36	2.34	1.02	down	2.94E-01	8.95E-01	-	-
1384707_at	Scara5	scavenger receptor class A, member 5 (putative)	305974	Rn.163284	AI600020	2.34	2.33	2.41	2.34	2.34	2.33	1.02	down	3.81E-01	8.95E-01	-	-
1396868_at	---	---	---	Rn.204509	AI555860	2.46	2.45	2.48	2.43	2.47	2.40	1.02	down	3.10E-01	8.95E-01	-	-
1373420_at	Ecsit	ECSIT homolog (Drosophila)	300447	Rn.8455	AI175479	7.06	7.55	7.15	7.15	6.84	7.70	1.02	down	9.35E-01	9.82E-01	-	-
1383342_at	Lrrc14	leucine rich repeat containing 14	500900	Rn.138067	BE098779	4.71	4.70	5.04	5.06	4.72	4.74	1.02	up	8.80E-01	9.63E-01	-	-
1394121_at	---	---	---	---	AI639332	2.51	2.49	2.56	2.49	2.53	2.46	1.02	down	4.76E-01	8.95E-01	-	-
1382901_at	Gfi1b	growth factor independent 1B transcription repressor	311832	Rn.47963	AW532478	2.45	2.39	2.40	2.39	2.40	2.38	1.02	down	3.04E-01	8.95E-01	-	-
1374244_at	---	---	---	---	AI411141	8.03	8.02	8.36	8.07	8.02	8.38	1.02	up	8.82E-01	9.64E-01	-	-
1392699_at	Zfp346	zinc finger protein 346	306765	Rn.17764	BF411888	3.18	3.52	3.07	3.04	3.18	3.47	1.02	down	8.96E-01	9.69E-01	-	-
1376631_at	---	---	---	Rn.18550	BF283675	2.41	2.33	2.34	2.33	2.34	2.32	1.02	down	3.85E-01	8.95E-01	-	-
1387721_at	Adora1	adenosine A1 receptor	29290	Rn.32078	NM_017155	2.57	2.44	2.47	2.45	2.47	2.49	1.02	down	5.51E-01	8.95E-01	-	-
1376699_at	LOC679158	similar to SRY (sex determining region Y)-box 3	679158	---	AW916994	2.31	2.30	2.31	2.30	2.40	2.29	1.02	up	5.24E-01	8.95E-01	-	-
1393944_at	Znf521	zinc finger protein 521	307579	Rn.102276	AI764505	2.48	2.40	2.43	2.40	2.43	2.39	1.02	down	3.88E-01	8.95E-01	-	-
1392018_at	---	---	---	Rn.106765	BE120031	2.48	2.46	2.50	2.45	2.49	2.43	1.02	down	2.96E-01	8.95E-01	-	-
1385159_at	Nbeal2	neurobeachin-like 2	316014	Rn.73847	AI509986	2.51	2.48	2.51	2.57	2.51	2.50	1.02	up	3.95E-01	8.95E-01	-	-
1380576_at	---	---	---	Rn.168202	AI556894	2.56	2.55	2.64	2.55	2.59	2.54	1.02	down	4.67E-01	8.95E-01	-	-
1379244_at	---	---	---	Rn.13581	AW522926	4.82	6.27	5.62	4.80	5.85	6.14	1.02	up	9.68E-01	9.91E-01	-	-
1384069_at	Lrp11	low density lipoprotein receptor-related protein 11	292462	Rn.40930	BG670059	6.47	6.55	7.01	6.50	7.01	6.44	1.02	down	9.24E-01	9.78E-01	-	-
1367657_at	Big1	B-cell translocation gene 1, anti-proliferative	29618	Rn.1000	NM_017258	8.19	8.60	8.84	8.35	8.86	8.35	1.02	down	9.27E-01	9.79E-01	-	-
1387680_at	Pde1b	phosphodiesterase 1B, calmodulin-dependent	29691	Rn.53489	AF327906	2.46	2.48	2.48	2.45	2.46	2.44	1.02	down	7.48E-02	8.95E-01	-	-
1381735_at	---	---	---	Rn.173178	BF387525	2.53	2.48	2.59	2.53	2.54	2.46	1.02	down	5.63E-01	8.95E-01	-	-
1381907_at	---	---	---	Rn.164988	AA955915	2.52	2.50	2.56	2.50	2.53	2.47	1.02	down	3.53E-01	8.95E-01	-	-
1381486_at	---	---	---	Rn.206572	BF386108	2.55	2.52	2.59	2.52	2.56	2.50	1.02	down	4.27E-01	8.95E-01	-	-
1397953_at	LOC687696	similar to AMSH-family protein	687696	Rn.216616	AI113261	2.67	2.61	2.83	2.62	3.08	2.49	1.02	up	9.02E-01	9.70E-01	-	-
1376033_at	Rfx1	regulatory factor X, 1 (influences HLA class II expression)	288906	Rn.154447	BF415398	2.44	2.42	2.49	2.43	2.44	2.41	1.02	down	3.30E-01	8.95E-01	-	-
1373253_at	Anln	anillin, actin binding protein	307056	Rn.163364	AI229404	2.44	2.42	2.49	2.43	2.45	2.41	1.02	down	3.50E-01	8.95E-01	-	-
1391792_at	---	---	---	Rn.210520	BF398762	2.47	2.47	2.53	2.46	2.49	2.44	1.02	down	3.69E-01	8.95E-01	-	-
1395784_at	---	---	---	Rn.204900	BF287979	2.52	2.44	2.46	2.45	2.46	2.44	1.02	down	3.87E-01	8.95E-01	-	-
1370917_at	Hsf1	heat shock transcription factor 1	79245	Rn.20418	AI172496	2.39	2.42	2.39	2.38	2.51	2.38	1.02	up	5.98E-01	8.95E-01	-	-
1376787_at	RGD1310773	similar to hypothetical protein FLJ31810	313156	Rn.16996	BE097267	2.38	2.37	2.39	2.38	2.48	2.37	1.02	up	5.36E-01	8.95E-01	-	-
1396865_at	---	---	---	Rn.206030	AW253045	2.41	2.40	2.42	2.49	2.42	2.40	1.02	up	4.09E-01	8.95E-01	-	-
1385162_at	---	---	---	Rn.150733	AW523702	2.33	2.31	2.36	2.31	2.33	2.30	1.02	down	2.41E-01	8.95E-01	-	-
1384730_at	---	---	---	Rn.196107	AA996877	2.40	2.33	2.35	2.33	2.34	2.32	1.02	down	3.00E-01	8.95E-01	-	-
1393628_at	Tagа13	testis specific, 13	688848	Rn.198673	AI453910	2.49	2.46	2.51	2.47	2.50	2.42	1.02	down	4.08E-01	8.95E-01	-	-
1388536_at	Bat2	HLA-B associated transcript 2	294250	Rn.34262	BM391608	3.72	3.70	3.68	3.72	3.71	3.75	1.02	up	1.70E-01	8.95E-01	-	-
1380895_at	---	---	---	Rn.203919	BE103215	2.36	2.40	2.37	2.35	2.36	2.34	1.02	down	1.46E-01	8.95E-01	-	-
1380885_at	---	---	---	Rn.207324	BE107574	2.40	2.34	2.36	2.34	2.36	2.32	1.02	down	3.10E-01	8.95E-01	-	-
1393379_a_at	Blk	B lymphoid tyrosine kinase	364403	Rn.20030	AI385291	2.24	2.37	2.44	2.37	2.38	2.37	1.02	up	6.94E-01	9.05E-01	-	-
1380408_at	---	---	---	Rn.148869	BI290397	2.51	2.50	2.53	2.50	2.53	2.44	1.02	down	4.28E-01	8.95E-01	-	-
1397012_at	---	---	---	---	AI411908	2.48	2.46	2.60	2.47	2.57	2.43	1.02	down	7.00E-01	9.07E-01	-	-
1392589_at	Rfc5	replication factor C (activator 1) 5	304528	Rn.105670	AA866296	2.95	2.88	2.70	2.14	3.34	3.12	1.02	up	9.50E-01	9.85E-01	-	-
1398638_at	Fign1	fidgetin-like 1	289777	Rn.211783	AI045011	2.40	2.39	2.47	2.39	2.41	2.38	1.02	down	3.70E-01	8.95E-01	-	-
1394981_at	---	---	---	Rn.206319	BI282102	2.36	2.35	2.36	2.35	2.37	2.33	1.02	down	3.39E-01	8.95E-01	-	-
1379928_at	Cops3	COP9 constitutive photomorphogenic homolog subunit 3 (Arabidopsis)	287367	Rn.3963	AW529192	2.60	2.66	2.60	2.60	2.60	2.59	1.02	down	3.21E-01	8.95E-01	-	-
1387249_at	Blk	BCL2-interacting killer (apoptosis-inducing)	114496	Rn.38487	NM_053704	2.45	2.42	2.47	2.43	2.57	2.41	1.02	up	6.46E-01	8.95E-01	-	-
1397930_at	---	---	---	Rn.156665	BE104754	2.49	2.48	2.53	2.49	2.51	2.43	1.02	down	4.24E-01	8.95E-01	-	-
1386308_at	---	---	---	Rn.135779	AI639292	2.65	2.56	2.63	2.59	2.63	2.55	1.02	down	5.33E-01	8.95E-01	-	-
1374463_at	---	---	---	Rn.220384	AI172068	6.80	6.22	6.61	5.97	6.92	6.83	1.02	up	9.47E-01	9.85E-01	-	-
1394582_at	---	---	---	Rn.160936	AW531299	2.61	2.56	2.73	2.57	2.69	2.55	1.02	down	7.26E-01	9.13E-01	-	-
1388106_x_at	P22k15	cystatin related protein 2	296229	Rn.43503	BI285286	2.58	2.54	2.67	2.56	2.64	2.53	1.02	down	6.50E-01	8.96E-01	-	-
1376170_at	Col14a1	collagen, type XIV, alpha 1	314981	Rn.99441	BI290821	2.31	2.38	2.32	2.31	2.32	2.31	1.02	down	3.02E-01	8.95E-01	-	-
1381166_at	---	---	---	Rn.203402	AA944650	2.57	2.57	2.60	2.57	2.59	2.50	1.02	down	4.35E-01	8.95E-01	-	-
1395681_at	---	---	---	Rn.216927	BF410168	3.05	2.83	3.45	3.04	3.17	3.04	1.02	down	9.01E-01	9.69E-01	-	-
1380181_at	Lhx4	LIM homeobox 4	360858	Rn.48080	AI236017	2.42	2.35	2.38	2.36	2.37	2.35	1.02	down	3.12E-01	8.95E-01	-	-
1392336_at	---	---	---	---	AI712387	3.35	3.30	3.37	3.43	3.38	3.29	1.02	up	6.24E-01	8.95E-01	-	-
1381320_at	---	---	---	Rn.170855	BF386936	2.42	2.37	2.40	2.37	2.38	2.36	1.02	down	2.19E-01	8.95E-01	-	-
1369586_at	Mcpt8	mast cell protease 8	29269	Rn.55163	NM_021598	2.52	2.51	2.58	2.51	2.53	2.49	1.02	down	3.96E-01	8.95E-01	-	-
1392153_at	---	---	---	Rn.204302	BE107755	2.49	2.47	2.54	2.49	2.50	2.44	1.02	down	4.32E-01	8.95E-01	-	-
1378911_at	---	---	---	Rn.62552	BF404615	2.43	2.55	2.43	2.43	2.45	2.47	1.02	down	5.96E-01	8.95E-01	-	-
1384718_at	---	---	---	Rn.203909	AI030198	2.38	2.37	2.45	2.38	2.39	2.36	1.02	down	4.12E-01	8.95E-01	-	-
1380984_at	---	---	---	Rn.200101	BF401369	2.52	2

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1391859_at	---	---	---	---	BI291444	2.47	2.46	2.50	2.46	2.47	2.43	1.02	down	2.64E-01	8.95E-01	-	-
1375046_at	Nacad	NAC alpha domain containing	289786	Rn.11849	AA964581	2.47	2.46	2.55	2.47	2.49	2.46	1.02	down	4.67E-01	8.95E-01	-	-
1380280_at	---	---	---	Rn.172048	BE118420	2.56	2.76	2.72	2.61	2.64	2.72	1.02	down	7.50E-01	9.19E-01	-	-
1373070_at	---	---	---	Rn.165363	AI406379	6.63	6.65	6.66	7.04	5.67	7.30	1.02	up	9.64E-01	9.90E-01	-	-
1395489_at	Ankrd13d	ankyrin repeat domain 13 family, member D	361699	Rn.15704	BF387055	2.28	2.27	2.35	2.28	2.28	2.27	1.02	down	3.81E-01	8.95E-01	-	-
1391138_at	---	---	---	Rn.160266	BF410536	2.41	2.40	2.43	2.38	2.49	2.43	1.02	up	5.06E-01	8.95E-01	-	-
1374275_at	Car11	carbonic anhydrase 11	308588	Rn.44281	AW252112	2.49	2.49	2.49	2.59	2.49	2.48	1.02	up	5.34E-01	8.95E-01	-	-
1395194_at	---	---	---	Rn.211457	BF413525	2.54	2.50	2.56	2.52	2.55	2.47	1.02	down	4.35E-01	8.95E-01	-	-
1386777_at	LOC500054	similar to POT1-like telomere end-binding protein	500054	Rn.138054	BF557764	2.62	2.66	2.65	2.61	2.64	2.60	1.02	down	2.66E-01	8.95E-01	-	-
1397550_at	---	---	---	---	BF413110	2.54	2.49	2.69	2.52	2.60	2.52	1.02	down	7.24E-01	9.12E-01	-	-
1398082_at	---	---	---	---	BF404767	2.44	2.43	2.51	2.44	2.46	2.41	1.02	down	4.53E-01	8.95E-01	-	-
1378752_at	---	---	---	Rn.200092	BF413430	2.35	2.34	2.45	2.34	2.39	2.33	1.02	down	5.55E-01	8.95E-01	-	-
1383943_at	Dnah7	dynein, axonemal, heavy polypeptide 7	252893	Rn.202150	AA817863	2.46	2.45	2.46	2.45	2.52	2.48	1.02	up	3.43E-01	8.95E-01	-	-
1381804_at	Bcl8b	B-cell CLL/lymphoma 8, member B (zinc finger protein)	360551	Rn.137148	BI283313	2.46	2.46	2.49	2.56	2.46	2.46	1.02	up	5.11E-01	8.95E-01	-	-
1384276_at	LOC363458	similar to procollagen, type IV, alpha 6	363458	Rn.182586	BI283340	2.50	2.48	2.58	2.49	2.53	2.47	1.02	down	5.26E-01	8.95E-01	-	-
1398287_at	Plau	plasminogen activator, urokinase	25619	Rn.6064	NM_013085	10.10	11.04	11.17	10.58	10.69	10.96	1.02	down	9.49E-01	9.85E-01	-	-
1395674_at	---	---	---	Rn.161314	BF408259	2.41	2.42	2.46	2.41	2.41	2.40	1.02	down	1.79E-01	8.95E-01	-	-
1371259_at	Ngf	nerve growth factor (beta polypeptide)	310738	Rn.22168	BM388972	2.46	2.46	2.77	2.84	2.47	2.45	1.02	up	8.90E-01	9.66E-01	-	-
1378361_at	Chd7	chromodomain helicase DNA binding protein 7	312974	Rn.37783	BF523068	3.53	2.94	2.41	2.94	2.95	2.91	1.02	down	9.44E-01	9.84E-01	-	-
1368816_at	Mpz	myelin protein zero	24564	Rn.8997	BG669096	2.37	2.36	2.44	2.37	2.37	2.36	1.02	down	3.86E-01	8.95E-01	-	-
1395924_at	---	---	---	---	AI575421	2.43	2.43	2.46	2.43	2.54	2.42	1.02	up	5.81E-01	8.95E-01	-	-
1391175_at	---	---	---	Rn.207592	BF400716	2.38	2.41	2.38	2.36	2.38	2.35	1.02	down	1.19E-01	8.95E-01	-	-
1392442_at	---	---	---	Rn.160501	BE109868	2.45	2.44	2.53	2.44	2.46	2.45	1.02	down	4.52E-01	8.95E-01	-	-
1373795_at	---	---	---	Rn.207771	BE106860	2.37	2.30	2.31	2.30	2.31	2.29	1.02	down	3.19E-01	8.95E-01	-	-
1382557_at	---	---	---	Rn.129495	AA946491	2.54	2.53	2.57	2.52	2.55	2.51	1.02	down	2.10E-01	8.95E-01	-	-
1390078_at	---	---	---	Rn.168223	BF407131	2.41	2.35	2.38	2.36	2.36	2.34	1.02	down	2.25E-01	8.95E-01	-	-
1369549_at	Klrk1	killer cell lectin-like receptor subfamily K, member 1	24934	Rn.14544	NM_130512	2.46	2.51	2.50	2.47	2.48	2.45	1.02	down	2.40E-01	8.95E-01	-	-
1388105_at	Cdc123	cell division cycle 123 homolog (S. cerevisiae)	116656	Rn.11096	BE113021	6.29	6.80	6.25	6.06	6.17	7.04	1.02	down	9.49E-01	9.85E-01	-	-
1370769_a_at	Icos	inducible T-cell co-stimulator	64545	Rn.168816	AB023133	2.37	2.39	2.36	2.35	2.36	2.34	1.02	down	5.17E-02	8.95E-01	-	-
1383284_at	---	---	---	Rn.147831	BG372598	2.40	2.47	2.40	2.40	2.40	2.39	1.02	down	3.36E-01	8.95E-01	-	-
1382474_at	Col13a1	collagen, type XIII, alpha 1	499431	Rn.17566	AA819747	2.52	2.65	2.71	3.09	2.76	2.70	1.02	up	9.05E-01	9.71E-01	-	-
1385558_at	---	---	---	Rn.47927	AW532330	2.37	2.36	2.45	2.35	2.38	2.36	1.02	down	4.67E-01	8.95E-01	-	-
1393555_at	// LOC363224 ///	heat shock protein 90kDa alpha (cytosolic), class B member 1 /// similar to he	66 /// 363224 /// 36	Rn.98667	BG153357	2.63	2.64	2.67	2.64	2.63	2.60	1.02	down	2.54E-01	8.95E-01	-	-
1381673_at	---	---	---	Rn.208285	BF413443	2.25	2.25	2.26	2.33	2.26	2.24	1.02	up	4.42E-01	8.95E-01	-	-
1390690_at	---	---	---	Rn.166552	BF564881	2.59	2.60	2.61	2.62	2.51	2.59	1.02	down	5.24E-01	8.95E-01	-	-
1368637_at	Card9	caspase recruitment domain family, member 9	64171	Rn.64486	NM_022303	2.35	2.34	2.40	2.35	2.32	2.32	1.02	down	2.79E-01	8.95E-01	-	-
1373359_at	---	---	---	Rn.73218	BI298204	2.32	2.37	2.32	2.31	2.32	2.31	1.02	down	2.65E-01	8.95E-01	-	-
1368864_at	Lrrn3	leucine rich repeat neuronal 3	81514	Rn.39124	NM_030856	2.53	2.49	2.50	2.48	2.50	2.47	1.02	down	1.69E-01	8.95E-01	-	-
1382147_at	Tmem132c	transmembrane protein 132C	363915	Rn.23050	AI229479	2.43	2.39	2.44	2.40	2.41	2.38	1.02	down	2.31E-01	8.95E-01	-	-
1375418_at	Trrap	transformation/transcription domain-associated protein	288471	Rn.92036	BI275823	3.41	4.02	3.66	3.65	3.73	3.64	1.02	down	9.01E-01	9.69E-01	-	-
1386450_at	Odf4	outer dense fiber of sperm tails 4	303236	Rn.13716	AI639253	2.52	2.51	2.56	2.52	2.52	2.48	1.02	down	2.57E-01	8.95E-01	-	-
1396728_at	---	---	---	Rn.204527	AI556127	2.49	2.48	2.52	2.49	2.49	2.44	1.02	down	2.99E-01	8.95E-01	-	-
1395103_at	---	---	---	Rn.172918	BF397372	2.44	2.44	2.48	2.43	2.45	2.41	1.02	down	2.57E-01	8.95E-01	-	-
1396276_at	---	---	---	Rn.59568	BG662898	2.46	2.45	2.49	2.47	2.57	2.44	1.02	up	5.79E-01	8.95E-01	-	-
1391870_at	---	---	---	Rn.63320	BF418037	2.43	2.40	2.41	2.41	2.44	2.42	1.02	down	2.12E-01	8.95E-01	-	-
1370343_at	Xab2	XPA binding protein 2	245976	Rn.24921	AF277899	5.97	6.44	5.07	5.91	5.39	6.11	1.02	down	9.60E-01	9.89E-01	-	-
1395523_at	Rbmx	RNA binding motif protein, X-linked	302855	Rn.40449	AW523475	2.48	2.47	2.49	2.43	2.48	2.47	1.02	down	2.28E-01	8.95E-01	-	-
1368942_at	Hes5	hairy and enhancer of split 5 (Drosophila)	79225	Rn.22422	NM_024383	2.33	2.32	2.39	2.32	2.33	2.31	1.02	down	3.68E-01	8.95E-01	-	-
1393176_at	---	---	---	Rn.146930	BF387254	2.73	2.80	2.73	2.72	2.71	2.76	1.02	down	4.48E-01	8.95E-01	-	-
1399080_at	LOC688495	hypothetical protein LOC688495	688495	Rn.40562	BI292036	6.71	7.54	7.23	7.22	6.91	7.43	1.02	up	9.37E-01	9.82E-01	-	-
1396083_at	---	---	---	Rn.13949	BM390018	2.41	2.39	2.41	2.50	2.41	2.37	1.02	up	5.61E-01	8.95E-01	-	-
1376365_at	Twf1	twinfilin, actin-binding protein, homolog 1 (Drosophila)	315265	Rn.162971	BF419802	2.64	2.59	2.61	2.60	2.60	2.57	1.02	down	2.49E-01	8.95E-01	-	-
1369954_at	Idh1	isocitrate dehydrogenase 1 (NADP+), soluble	24479	Rn.3561	NM_031510	11.16	10.73	10.99	10.94	10.90	11.11	1.02	up	8.74E-01	9.61E-01	-	-
1367568_a_at	Mgp	matrix Gla protein	25333	Rn.2379	NM_012862	8.57	7.83	7.19	8.48	8.13	7.05	1.02	up	9.69E-01	9.91E-01	-	-
1381379_at	---	---	---	Rn.206158	BE096536	2.42	2.40	2.44	2.40	2.41	2.38	1.02	down	1.88E-01	8.95E-01	-	-
1382090_at	---	---	---	Rn.204244	AI070376	2.53	2.52	2.61	2.53	2.58	2.48	1.02	down	5.93E-01	8.95E-01	-	-
1393339_at	---	---	---	Rn.204763	AW535172	2.39	2.38	2.46	2.38	2.39	2.38	1.02	down	3.85E-01	8.95E-01	-	-
1381880_at	---	---	---	Rn.160177	AW530117	2.33	2.32	2.37	2.33	2.33	2.29	1.02	down	3.01E-01	8.95E-01	-	-
1396905_at	---	---	---	Rn.205172	AI501578	2.45	2.37	2.38	2.36	2.40	2.36	1.02	down	4.56E-01	8.95E-01	-	-
1378637_at	Nfx1	nuclear transcription factor, X-box binding 1	313166	Rn.55459	BG374464	9.62	9.31	9.07	9.27	8.97	9.70	1.02	down	9.32E-01	9.81E-01	-	-
1367762_at	Sst	somatostatin	24797	Rn.34418	NM_012659	2.45	2.44	2.47	2.40	2.46	2.43	1.02	down	3.30E-01	8.95E-01	-	-
1396433_at	---	---	---	---	BF413338	2.41	2.40	2.47	2.41	2.42	2.39	1.02	down	3.40E-01	8.95E-01	-	-
1379116_at	---	---	---	Rn.207817	BM386353	2.56	2.54	2.59	2.55	2.60	2.47	1.02	down	5.87E-01	8.95E-01	-	-
1370901_at	RGD1306215	similar to hypothetical protein MGC36831	296565	Rn.96042	AI407120	6.05	5.92	5.49	5.83	5.85	5.85	1.02	up	8.94E-01	9.67E-01	-	-
1390427_at	---	---	---	Rn.165769	BF397491	2.74	2.78	2.68	2.42	2.93	2.77	1.02	down	8.84E-01	9.64E-01	-	-
1367712_at	Timp1	TIMP metallopeptidase inhibitor 1	116510	Rn.25754	NM_053819	2.37	2.36	2.38	2.45	2.37	2.36	1.02	up	4.58E-01	8.95E-01	-	-
1392021_at	---	---	---	---	BF388754	2.49	2.46	2.50	2.56	2.52	2.43	1.02	up	5.70E-01	8.95E-01	-	-
1380150_at	---	---	---	Rn.168175	AI008553	2.61	2.55	2.67	2.57	2.67	2.52	1.02	down	6.84E-01	9.03E-01	-	-
1387013_at	Tmem27	transmembrane protein 27	57395	Rn.32298	NM_020976	11.51	11.51	11.55	11.54	11.50	11.47	1.02	down	4.05E-01	8.95E-01	-	-
1394578_at	---	---	---	Rn.212188	BI299761	2.55	2.53	2.62	2.54	2.60	2.49	1.02	down	6.06E-01	8.95E-01	-	-
1394534_at	---	---	---	Rn.201929	AW532329	2.47	2.42	2.44	2.42	2.43	2.41	1.02	down	2.31E-01	8.95E-01	-	-
1391884_at	F12	coagulation factor XII (Hageman factor)	306761	Rn.53943	BF416651	2.53	2.52	2.59	2.50	2.53	2.54	1.02	down	3.84E-01	8.95E-01	-	-
1391532_at	Rap2ip	Rap2 interacting protein	303569	Rn.102473	AI535169	2.54	2.47	2.64	2.50	2.55	2.52	1.02	down	6.73E-01	9.01E-01	-	-
1397026_at	---	---	---	Rn.210105	BF393981	2.44	2.43	2.50	2.43	2.45	2.42	1.02	down	3.94E-01	8.95E-01	-	-
1396023_at	---	---	---	Rn.45459	AW522736	2.64	2.56	2.83	2.62	2.81	2.53	1.02	down	8.43E-01	9.51E-01	-	-
1395639_at	---	---	---	Rn.216731	AW254678	2.74	2.70	2.73	2.71	2.71	2.68	1.02	down	1.91E-01	8.95E-01	-	-
1394801_at	---	---	---	Rn.199355	AI555464	3.06	3.06	3.07	3.03	3.07	3.16	1.02	up	5.63E-01	8.95E-01	-	-
1394336_at	Spag16	sperm associated antigen 16	501158	Rn.220565	BF564356	2.67	2.65	2.76	2.65	2.74	2.63	1.02	down	6.53E-01	8.97E-01	-	-
1391520_at	---	---	---	Rn.146175	BE109256	2.53	2.50	2.58	2.51	2.56	2.47	1.02	down	5.13E-01	8.95E-01	-	-
1379446_at	---	---	---	Rn.150261	BF282187	2.43	2.43	2.45	2.43	2.44	2.38	1.02	down	2.76E-01	8.95E-01	-	-
1396867_at	---	---	---	Rn.31601	BF283047	2.44	2.39	2.41	2.39	2.40	2.38	1.02	down	1.74E-01	8.95E-01	-	-
1375212_at	Ankrd52	ankyrin repeat domain 52	362811	Rn.8972	AA964250	2.39	2.38	2.39	2.46	2.40	2.37	1.02	up	4.25E-01	8.95E-01	-	-
1398458_at	RGD1307284	similar to protein kinase, lysine deficient 1; kinase deficient protein	306811	Rn.204068	BE104506	2.31	2.30	2.32	2.31	2.40	2.30	1.02	up	4.88E-01	8.95E-01	-	-
1391968_at	---	---	---	---	BM389535	2.95	3.76	3.54	3.64	2.71	3.96	1.02	up	9.60E-01	9.89E-01	-	-
1390011_at	---	---	---	Rn.212106	BI296601	2.56	2.54	2.64	2.56	2.57	2.55	1.02	down	4.69E-01	8.95E-01	-	-
1387240_at	Rdh7	retinol dehydrogenase 7	360420	Rn.31786	NM_133543	2.49	2.46	2.54	2.46	2.52	2.42	1.02	down	5.46E-01	8.95E-01	-	-
1377404_at	Stc1	stanniocalcin 1	81801	Rn.10647	BM386683	2.40	2.34	2.35	2.34	2.35	2.33	1.02	down	3.01E-01	8.95E-01	-	-
1394617_at	Abhd15	abhydrolase domain containing 15	303343	Rn.31213	BF284367	2.38	2.37	2.38	2.37	2.47	2.36	1.02	up	5.27E-01	8.95E-01	-	-
1395291_at	---	---	---	Rn.210287	BF396777	2.62	2.62	2.63	2.60	2.64	2.55	1.02	down	4.24E-01	8.95E-01	-	-
1387313_at	Myoc	myocilin	81523	Rn.30051	NM_030865	2.42	2.35	2.36	2.35	2.37	2.34	1.02	down	3.53E-01	8.95E-01	-	-
1369620_at	Hint1	histidine triad nucleotide binding protein 1	690660	Rn.138667	NM_022192	2.56	2.52	2.61	2.55	2.57	2.50	1.02	down	5.03E-01	8.95E-01	-	-
1380274_at	RGD1560795 /// S	similar to Sepiapterin reductase (SPR) /// sepiapterin reductase (7,8-dihydrob	29270 /// 297402	Rn.6658	AI103974	3.91	3.81	3.73	4.54	3.18	3.66	1.02	down	9.56E-01	9.87E-01	-	-
1395070_at	---	---	---	Rn.204550	AI136959	2.38	2.32	2.36	2.33	2.34	2.32	1.02	down	2.57E-01	8.95E-01	-	-
1376921_at	---	---	---	Rn.42737	BG381722	2.69	2.67	2.69	2.67	2.75	2.70	1.02	up	3.91E-01	8.95E-01	-	-
1378438_at	---	---	---	---	BF405026	2.36	2.33	2.34	2.40	2.38	2.33	1.02	up	3.94E-01	8.95E-01	-	-
1384745_at	Piwil2	piwi-like 2 (Drosophila)	306011	Rn.144968	BE111824	2.48	2.48	2.51	2.49	2.56	2.48	1.02	up	4.27E-01	8.95E-01	-	-
1381006_at	Hgfac	hepatocyte growth factor activator	58947	Rn.144587	BE119649	2.38	2.37	2.38	2.38	2.47	2.36	1.02	up	5.04E-01	8.95E-01	-	-
1392390_at	---	---	---	Rn.206242	AW524258	2.68	2.64	2.76	2.66	2.75	2.61	1.02	down	6.86E-01	9.04E-01	-	-
1396455_at	Upk1a	uroplakin 1A	365227	Rn.140554	BI302778	2.44	2.41	2.45	2.42	2.43	2.38	1.02	down	2.79E-01	8.95E-01	-	-
1385446_at	---	---	---	---	AA866240	2.47	2.44	2.48	2.44	2.46	2.42	1.02	down	2.63E-01	8.95E-01	-	-
1382919_at	Slc39a14	solute carrier family 39 (zinc transporter), member 14	306009	Rn.7037	BI294340	2.44	2.42	2.45	2.44	2.52	2.43	1.02	up	4.70E-01	8.95E-01	-	-
1395041_at	Mttp	microsomal triglyceride transfer protein	310900	Rn.81556	BM385230	2.51	2.49	2.53	2.48	2.52	2.47	1.02	down	2.88E-01	8.95E-01	-	-
1397829_at	---	---	---	Rn.41566	AA943636	2.45	2.44	2.53	2.44	2.48	2.43	1.02	down	5.10E-01	8.95E-01	-	-
1388152_at	Map2	microtubule-associated protein 2	25595	Rn.10484	BG374290	2.50	2.47	2.53	2.46	2.52	2.45	1.02	down	4.56E-01	8.95E-01	-	-
1396288_s_at	---	---	---	Rn.136371	BI273954	2.52	2.50	2.56	2.50	2.54	2.46	1.02	down	4.59E-01	8.95E-01	-	-
1392970_at	Tmem108	transmembrane protein 108	300967	Rn.44026	BI285605	2.50	2.42	2.41	2.49	2.44	2.48	1.02	up	5.11E-01	8.95E-01	-	-
1393943_at	Matn3	Matrilin 3	313954	Rn.41528	AI716693	2.56	2.52	2.62	2.53	2.60	2.49	1.02	down	6.31E-01	8.95E-01	-	-
1371635_at	Gpr175	G protein-coupled receptor 175	85494	Rn.3566	AI559069	3.69	4.15	5.82	3.94	5.51	4.15	1.02	down	9.78E-01	9.93E-01	-	-
1389410_s_at	---	---	---	---	AI412389	2.43	2.42	2.43	2.43	2.51	2.43	1.02	up	4.48E-01	8.95E-01	-	-
1370479_x_at	Obp3	alpha-2u globulin PGCL4	259247	Rn.86413	J00738	2.39	2.38	2.46	2.38	2.41	2.36	1.02	down	4.79E-01	8.95E-01	-	-
1367503_at	Bcap31	B-cell receptor-associated protein 31	293852	Rn.96419	AI409930	8.76	8.78	8.93	8.69	8.70	9.02	1.02	down	8.56E-01	9.55E-01	-	-
1371172_at	Atp2b3	ATPase, Ca++ transporting, plasma membrane 3	29599	Rn.11053	M96626	2.47	2.45	2.48	2.45	2.46	2.43	1.02	down	1.68E-01	8.95E-01	-	-
1392224_at	Rasa3	RAS p21 protein activator 3	29372	Rn.23055	AI237779	2.57	2.52	2.69	2.59	2.60	2.51	1.02	down	7.07E-01	9.08E-01	-	-
1395889_at	---	---	---	---	AW921250	2.91	2.90	2.93	2.91	3.04	2.85	1.02	up	6.97E-01	9.07E-01	-	-
1381223_at	Anxa9	annexin A9	689830	Rn.73434	BG372869	2.38	2.32	2.34	2.32	2.33	2.31	1.02	down	2.93E-01	8.95E-01	-	-
1392202_at	---	---	---	Rn.153805	BE120418	2.47	2.45	2.50	2.54	2.49	2.48	1.02	up	3.80E-01	8.95E-01	-	-
1379776_at	---	---	---	Rn.168897	BI395339	2.48	2.47	2.54	2.47	2.51	2.45	1.02	down	4.27E-01	8.95E-01	-	-
1392065_at	Kif18a	kinesin family member 18A	362186	Rn.35496	BE116803	2.38	2.38	2.44	2.38	2.39	2.36	1.02	down	3.35E-01	8.95E-01	-	-
1389117_at	Osgep	O-sialoglycoprotein endopeptidase	290028	Rn.220217	AW532161	5.82	6.31	5.40	5.95	5.37	6.28	1.02	up	9.53E-01	9.86E-01	-	-
1378760_at	LOC680874	hypothetical protein LOC680874	680874	Rn.160496	BF417605	2.66	2.56	2.61	2.59	2.60	2.56	1.02	down	4.96E-01	8.95E-01	-	-
1393579_at	Chrdl1	kohjirin	363455	Rn.211154	BF406384	2.52	2.50	2.58	2.50	2.54	2.49	1.02	down	4.68E-01	8.95E-01	-	-
1377324_at	RGD1564599	RGD1564599	293925	Rn.62289	BF412777	2.43	2.43	2.46	2.43	2.44	2.38	1.02	down	2.88E-01	8.95E-01	-	-
1376884_a_at	Rpl3l	ribosomal protein L3-like	287122	Rn.105722	BE111370	2.47	2.46	2.51	2.46	2.48	2.43	1.02	down	2.73E-01	8.95E-01	-	-
1382110_at	Cnpy3	canopy 3 homolog (zebrafish)	685174	Rn.43984	AA899630	7.09	6.65	5.69	6.37	6.34	6.79	1.02	up	9.60E-01	9.89E-01	-	-
1395782_at	Yeats4	YEATS domain containing 4	299810	Rn.103329	AW921463	2.83	2.86	2.90	2.89	2.89	2.88	1.02	up	2.90E-01	8.95E-01	-	-
1392310_at	---	---	---	Rn.211716	AI535319	2.50	2.48	2.50	2.50	2.56	2.50	1.02	up	3.39E-01	8.95E-01	-	-
1381772_at	RGD1309079	Similar to Ab2-095	315891	Rn.15757	BF415397	2.53	2.52	2.59	2.52	2.53	2.51	1.02	down	3.34E-01	8.95E-01	-	-
1384332_at	---	---	---	Rn.24418	AI501967	2.54	2.50	2.59	2.52	2.57	2.47	1.02	down	5.61E-01	8.95E-01	-	-
1384758_at	Rbak	RB-associated KRAB zinc finger	288489	Rn.137256	BE107825	2.51	2.44	2.46	2.45	2.46	2.44	1.02	down	3.38E-01	8.95E-01	-	-
1395051_at	---	---	---	Rn.148089	AI136856	2.37	2.36	2.37	2.45	2.37	2.35	1.02	up	4.92E-01	8.95E-01	-	-
1383277_at	Ppp1r7	protein phosphatase 1, regulatory (inhibitor) subunit 7	301618	Rn.19437	H32309	2.81	3.52	3.07	3.04	2.90	3.53	1.02	up	9.38E-01	9.82E-01	-	-
1396557_at	---	---	---	---	BE119958	2.51	2.43	2.43	2.44	2.44	2.42	1.02	down	4.05E-01	8.95E-01	-	-
1390005_at	Asxl2	additional sex combs like 2 (Drosophila)	313922	Rn.153991	BF404290	2.34	2.33	2.35	2.33	2.38	2.38	1.02	up	2.01E-01	8.95E-01	-	-
1393344_at	---	---	---	Rn.164720	AW528051	2.39	2.37	2.46	2.38	2.41	2.35	1.02	down	4.87E-01	8.95E-01	-	-
1370306_at	Pex14	peroxisomal biogenesis factor 14	64460	Rn.7844	AB017544	3.34	2.33	2.34	2.33	3.49	2.26	1.02	up	9.66E-01	9.90E-01	-	-
1396072_at	Appbp2	amyloid beta precursor protein (cytoplasmic tail) binding protein 2	303396	Rn.104856	BG662585	2.47	2.46	2.47	2.47	2.55	2.45	1.02	up	5.04E-01	8.95E-01	-	-
1381465_at	LOC685756	hypothetical protein LOC685756	685756	Rn.28477	BE099710	2.25	2.24	2.31	2.24	2.25	2.24	1.02	down	3.54E-01	8.95E-01	-	-
1383967_at	---	---	---	Rn.20516	BI275739	2.40	2.45	2.40	2.39	2.40	2.39	1.02	down	2.17E-01	8.95E-01	-	-
1381359_at	---	---	---	Rn.23635	AI102874	2.61	2.57	2.64	2.57	2.62	2.55	1.02	down	4.72E-01	8.95E-01	-	-
1380397_at	---	---	---	Rn.43120	AI707044	2.56	2.55	2.58	2.56	2.57	2.49	1.02	down	4.24E-01	8.95E-01	-	-
1391678_at	Pax1	paired box 1	311505	Rn.40296	BI294574	2.53	2.57	2.57	2.51	2.67	2.51	1.02	up	6.61E-01	8.98E-01	-	-
1391901_at	---	---	---	Rn.18217	AA956085	2.43	2.42	2.44	2.43	2.51	2.42	1.02	up	4.55E-01	8.95E-01	-	-
1391358_at	---	---	---	Rn.209725	BF392781	2.45	2.47	2.45	2.45	2.40	2.40	1.02	down	2.61E-01	8.95E-01	-	-
1380752_at	---	---	---	Rn.211307	BF410207	2.47	2.47	2.55	2.48	2.50	2.45	1.02	down	4.67E-01	8.95E-01	-	-
1382676_at	Wdr20a	WD repeat domain 20a	314453	Rn.17925	AI013980	2.36	2.35	2.42	2.35	2.36	2.35	1.02	down	3.49E-01	8.95E-01	-	-
1396871_at	Kcnv2	Potassium channel, subfamily V, member 2	294065	Rn.168638	AI764002	2.43	2.42	2.47	2.42	2.43	2.40	1.02	down	2.49E-01	8.95E-01	-	-
1371942_at	Gstt3	glutathione S-transferase, theta 3	499422	Rn.92581	BM390376	12.14

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1371405_at	RGD1565095	similar to hypothetical protein MGC52110	503252	Rn.3412	BE109143	9.01	9.47	9.39	8.88	9.33	9.60	1.02	down	9.32E-01	9.81E-01	-	-
1391493_at	---	---	---	---	AI071685	2.41	2.43	2.44	2.43	2.44	2.48	1.02	up	2.58E-01	8.95E-01	-	-
1392381_at	---	---	---	---	BM382852	2.37	2.36	2.44	2.37	2.38	2.36	1.02	down	4.05E-01	8.95E-01	-	-
1387271_at	Phyh	phytanoyl-CoA 2-hydroxylase	114209	Rn.7279	NM_053674	8.68	8.69	8.71	8.72	8.56	8.73	1.02	down	7.02E-01	9.07E-01	-	-
1396010_at	---	---	---	Rn.171384	BF411744	2.67	2.58	2.64	2.63	2.64	2.55	1.02	down	5.85E-01	8.95E-01	-	-
1393010_at	---	---	---	Rn.88974	AI008808	2.42	2.40	2.48	2.41	2.43	2.39	1.02	down	4.33E-01	8.95E-01	-	-
1378847_x_at	H2afx	H2A histone family, member X	500987	Rn.2850	BI284313	2.45	2.45	2.47	2.46	2.52	2.46	1.02	up	3.10E-01	8.95E-01	-	-
1397653_at	---	---	---	Rn.38286	AI578063	2.39	2.38	2.45	2.38	2.39	2.38	1.02	down	3.79E-01	8.95E-01	-	-
1385669_at	Madl1l	MAD1 mitotic arrest deficient-like 1 (yeast)	680006	Rn.95132	BF551518	2.44	2.42	2.42	2.41	2.41	2.38	1.02	down	1.39E-01	8.95E-01	-	-
1394249_x_at	Tmem131	transmembrane protein 131	316335	Rn.63731	BG153340	2.54	2.51	2.61	2.52	2.58	2.49	1.02	down	5.87E-01	8.95E-01	-	-
1392888_at	Gpc4	glypican 4	317322	Rn.19945	AI071251	8.93	8.72	8.80	8.83	8.83	8.86	1.02	up	7.35E-01	9.15E-01	-	-
1378915_x_at	LOC308990	hypothetical protein LOC308990	308990	Rn.98391	AI059468	2.71	2.67	2.79	2.69	2.73	2.68	1.02	down	5.68E-01	8.95E-01	-	-
1380462_at	RGD1562146	RGD1562146	500612	Rn.154972	BF283078	2.58	2.62	2.52	2.57	2.58	2.64	1.02	up	5.61E-01	8.95E-01	-	-
1381830_x_at	Stk11	Serine/threonine kinase 11	114821	Rn.12052	AI113337	2.49	2.48	2.49	2.43	2.56	2.53	1.02	up	6.05E-01	8.95E-01	-	-
1377465_at	---	---	---	Rn.12465	AI407752	2.48	2.75	2.49	2.83	2.51	2.46	1.02	up	8.82E-01	9.64E-01	-	-
1375414_at	Taf9	TAF9 RNA polymerase II, TATA box binding protein (TBP)-associated factor	373541	Rn.8139	AA944572	4.96	5.27	5.83	5.12	5.31	5.69	1.02	up	9.44E-01	9.84E-01	-	-
1388057_a_at	Dlgap1	discs, large (Drosophila) homolog-associated protein 1	65040	Rn.90059	AB003594	2.52	2.54	2.57	2.51	2.54	2.51	1.02	down	2.69E-01	8.95E-01	-	-
1380328_at	---	---	---	Rn.147446	AW533453	2.70	2.73	2.71	2.69	2.70	2.68	1.02	down	1.38E-01	8.95E-01	-	-
1397999_at	---	---	---	Rn.209154	BI386502	2.38	2.39	2.39	2.48	2.39	2.35	1.02	up	5.91E-01	8.95E-01	-	-
1373172_at	---	---	---	Rn.32516	AI044483	2.41	2.40	2.48	2.40	2.41	2.40	1.02	down	4.20E-01	8.95E-01	-	-
1393538_at	---	---	---	Rn.134320	AI044886	2.32	2.32	2.38	2.32	2.33	2.31	1.02	down	3.47E-01	8.95E-01	-	-
1367990_at	Crybb3	crystallin, beta B3	64349	Rn.19693	NM_031690	2.39	2.31	2.33	2.32	2.32	2.32	1.02	down	3.75E-01	8.95E-01	-	-
1380025_at	Dgcr8	DiGeorge syndrome critical region gene 8	287954	Rn.17134	AW530337	2.35	2.34	2.43	2.35	2.36	2.35	1.02	down	4.92E-01	8.95E-01	-	-
1392266_at	Rnf190	ring finger protein 190	303596	Rn.160625	BI280114	2.55	2.55	2.56	2.54	2.67	2.52	1.02	up	6.47E-01	8.95E-01	-	-
1397502_at	---	---	---	Rn.205161	AI501394	2.71	2.71	2.75	2.73	2.82	2.70	1.02	up	5.73E-01	8.95E-01	-	-
1389911_at	Metrnl	meteorin, glial cell differentiation regulator-like	316842	Rn.64557	BM389126	2.47	3.17	2.42	2.41	2.42	3.28	1.02	up	9.54E-01	9.87E-01	-	-
1377886_at	---	---	---	Rn.80076	BI274321	2.47	2.40	2.43	2.40	2.43	2.40	1.02	down	3.75E-01	8.95E-01	-	-
1387976_at	Slc9a3r2	solute carrier family 9 (sodium/hydrogen exchanger), member 3 regulator 2	116501	Rn.39351	AF294257	2.47	2.44	2.45	2.44	2.45	2.40	1.02	down	2.39E-01	8.95E-01	-	-
1394338_x_at	Ptk2	PTK2 protein tyrosine kinase 2	25614	Rn.2809	BF290004	2.73	2.55	2.86	2.69	2.81	2.71	1.02	up	8.27E-01	9.45E-01	-	-
1397193_at	---	---	---	---	BM385669	2.37	2.29	2.30	2.30	2.31	2.29	1.02	down	4.36E-01	8.95E-01	-	-
1371312_at	Chchd2	coiled-coil-helix-coiled-coil-helix domain containing 2	316643	Rn.108412	AA799736	10.76	10.83	10.64	10.50	10.81	10.87	1.02	down	8.64E-01	9.58E-01	-	-
1393927_at	Wnt2	wingless-type MMTV integration site family member 2	114487	Rn.203764	AA997477	2.36	2.36	2.36	2.36	2.41	2.34	1.02	down	6.00E-01	8.95E-01	-	-
1385362_at	---	---	---	---	BF388014	2.60	2.55	2.70	2.59	2.68	2.51	1.02	down	7.40E-01	9.16E-01	-	-
1397632_at	Slitrk1	SLIT and NTRK-like family, member 1	306147	Rn.31034	AW523107	2.31	2.30	2.31	2.30	2.31	2.38	1.02	up	4.02E-01	8.95E-01	-	-
1394564_at	---	---	---	Rn.129685	BE106791	2.43	2.42	2.45	2.50	2.48	2.40	1.02	up	4.95E-01	8.95E-01	-	-
1397522_at	Sbf1	SET binding factor 1	300147	Rn.7632	BF554377	2.71	2.72	2.80	2.83	2.63	2.85	1.02	up	7.77E-01	9.27E-01	-	-
1380239_at	---	---	---	Rn.207709	BE106083	2.43	2.42	2.51	2.42	2.44	2.42	1.02	down	4.48E-01	8.95E-01	-	-
1375079_at	---	---	---	Rn.149392	BE115776	2.49	2.48	2.53	2.48	2.51	2.44	1.02	down	4.04E-01	8.95E-01	-	-
1385313_at	Pogk	pogo transposable element with KRAB domain	304941	Rn.18738	BF386923	2.43	2.42	2.49	2.43	2.43	2.41	1.02	down	3.36E-01	8.95E-01	-	-
1394986_at	Fam120b	Family with sequence similarity 120B	308218	Rn.2666	BE108719	2.32	2.32	2.33	2.32	2.37	2.34	1.02	up	2.22E-01	8.95E-01	-	-
1387736_at	Chrm1	cholinergic receptor, muscarinic 1	25229	Rn.119306	NM_080773	2.41	2.40	2.41	2.40	2.41	2.35	1.02	down	3.02E-01	8.95E-01	-	-
1381127_at	---	---	---	Rn.199521	AI712728	2.34	2.33	2.35	2.42	2.34	2.32	1.02	up	5.09E-01	8.95E-01	-	-
1396427_at	---	---	---	Rn.173464	BF416565	2.47	2.44	2.51	2.45	2.47	2.42	1.02	down	3.97E-01	8.95E-01	-	-
1393301_at	---	---	---	Rn.199419	AI555172	2.27	2.27	2.27	2.27	2.35	2.26	1.02	up	4.46E-01	8.95E-01	-	-
1396972_at	---	---	---	Rn.173061	BF399801	2.32	2.31	2.37	2.30	2.33	2.29	1.02	down	3.76E-01	8.95E-01	-	-
1375234_at	Ncoa5	nuclear receptor coactivator 5	296372	Rn.8482	AI009170	2.42	2.41	2.44	2.42	2.43	2.36	1.02	down	3.98E-01	8.95E-01	-	-
1374359_at	Ccne2	cyclin E2	362485	Rn.98992	BM383329	2.61	2.84	3.38	2.81	3.26	2.84	1.02	up	9.37E-01	9.82E-01	-	-
1379594_at	---	---	---	Rn.93081	AW524408	2.37	2.36	2.37	2.42	2.36	2.38	1.02	up	3.11E-01	8.95E-01	-	-
1370930_at	---	---	---	---	BF417285	8.82	8.79	8.54	8.41	8.74	8.92	1.02	down	9.02E-01	9.70E-01	-	-
1398337_at	LOC290341	Similar to RIKEN cDNA 9430077D24 gene	290341	Rn.3259	AI169116	3.92	5.10	5.59	4.73	4.79	5.02	1.02	down	9.66E-01	9.90E-01	-	-
1397125_at	---	---	---	Rn.56868	BF388547	2.50	2.49	2.55	2.50	2.51	2.47	1.02	down	3.48E-01	8.95E-01	-	-
1372159_at	---	---	---	Rn.6206	BI285456	2.62	2.61	2.67	2.61	2.62	2.61	1.02	down	2.96E-01	8.95E-01	-	-
1372760_at	---	---	---	Rn.119131	AI176579	11.23	10.63	10.62	11.18	10.94	10.42	1.02	up	9.43E-01	9.84E-01	-	-
1386439_at	Tomm34	Translocase of outer mitochondrial membrane 34	311621	Rn.16749	H31323	3.04	3.98	4.34	3.34	3.94	4.14	1.02	up	9.63E-01	9.89E-01	-	-
1368350_at	Ptpn21	protein tyrosine phosphatase, receptor-type, Z polypeptide 1	256113	Rn.10088	NM_013080	2.41	2.40	2.42	2.41	2.42	2.47	1.02	up	3.18E-01	8.95E-01	-	-
1367565_a_at	Fth1	ferritin, heavy polypeptide 1	25319	Rn.54447	NM_012848	13.61	13.62	13.61	13.58	13.55	13.78	1.02	up	7.64E-01	9.23E-01	-	-
1391549_at	Dcun1d4	DCN1, defective in cullin neddylation 1, domain containing 4 (S. cerevisiae)	360928	Rn.20231	BF288456	6.73	6.39	6.51	6.50	6.47	6.73	1.02	up	8.67E-01	9.58E-01	-	-
1368524_at	Kcnc1	potassium voltage gated channel, Shaw-related subfamily, member 1	25327	Rn.33095	NM_012856	2.57	2.49	2.56	2.52	2.54	2.49	1.02	down	4.63E-01	8.95E-01	-	-
1381936_at	Camk2g	calcium/calmodulin-dependent protein kinase II gamma	171140	Rn.10961	BF390092	2.46	2.41	2.44	2.42	2.42	2.41	1.02	down	2.33E-01	8.95E-01	-	-
1382209_at	Ccdc28b	coiled coil domain containing 28B	682445	Rn.216577	BI280344	2.55	2.53	2.62	2.54	2.56	2.54	1.02	down	4.69E-01	8.95E-01	-	-
1387468_at	Sstr5	somatostatin receptor 5	25354	Rn.91342	NM_012882	2.36	2.35	2.38	2.45	2.36	2.34	1.02	up	5.33E-01	8.95E-01	-	-
1372158_at	Macrod1	MACRO domain containing 1	246233	Rn.98178	BI295768	7.49	7.72	7.29	7.48	7.47	7.50	1.02	down	8.65E-01	9.58E-01	-	-
1376023_at	Rarg	retinoic acid receptor, gamma	685072	Rn.198797	BM386555	2.30	2.30	2.36	2.30	2.31	2.29	1.02	down	3.44E-01	8.95E-01	-	-
1393879_at	---	---	---	Rn.152575	BF391763	2.65	2.67	2.65	2.65	2.68	2.58	1.02	down	5.15E-01	8.95E-01	-	-
1397153_at	---	---	---	Rn.208664	BE115262	2.38	2.45	2.40	2.40	2.39	2.37	1.02	down	4.06E-01	8.95E-01	-	-
1376711_at	Cldn11	claudin 11	84588	Rn.8282	BG673439	2.41	2.41	2.43	2.42	2.50	2.41	1.02	up	4.64E-01	8.95E-01	-	-
1379719_at	---	---	---	Rn.169131	AI408386	6.40	6.57	5.84	6.29	6.31	6.29	1.02	up	9.22E-01	9.77E-01	-	-
1395593_at	---	---	---	Rn.155254	BI275754	2.37	2.36	2.38	2.36	2.46	2.35	1.02	up	5.48E-01	8.95E-01	-	-
1375716_at	Ifngr2	interferon gamma receptor 2	360697	Rn.23305	AI602715	2.53	2.48	2.50	2.48	2.50	2.46	1.02	down	2.58E-01	8.95E-01	-	-
1377087_at	---	---	---	Rn.203616	AA963029	2.43	2.42	2.43	2.42	2.53	2.40	1.02	up	6.10E-01	8.95E-01	-	-
1385388_at	---	---	---	---	AI045847	2.56	2.53	2.61	2.54	2.61	2.48	1.02	down	6.33E-01	8.95E-01	-	-
1371453_at	Farsb	phenylalanyl-tRNA synthetase, beta subunit	301544	Rn.17054	BE113146	5.84	5.40	5.83	5.48	5.62	6.03	1.02	up	9.22E-01	9.77E-01	-	-
1386203_at	---	---	---	Rn.218970	AA851194	2.34	2.33	2.34	2.45	2.33	2.31	1.02	up	6.37E-01	8.95E-01	-	-
1396121_at	---	---	---	Rn.206454	AW527234	2.49	2.47	2.54	2.47	2.51	2.45	1.02	down	4.19E-01	8.95E-01	-	-
1392179_at	---	---	---	Rn.147045	BI297081	2.43	2.42	2.48	2.43	2.44	2.40	1.02	down	3.28E-01	8.95E-01	-	-
1379956_at	---	---	---	---	AI013395	2.31	2.29	2.32	2.30	2.40	2.29	1.02	up	5.68E-01	8.95E-01	-	-
1377863_at	Kdm5b	lysine (K)-specific demethylase 5B	304809	Rn.22866	BI303977	3.29	3.11	3.34	2.63	3.62	3.43	1.02	down	9.46E-01	9.84E-01	-	-
1382739_at	Gpr19	G protein-coupled receptor 19	312787	Rn.96370	AI045718	2.36	2.35	2.37	2.35	2.46	2.34	1.02	up	5.77E-01	8.95E-01	-	-
1381086_at	---	---	---	Rn.26789	AW523816	2.65	2.61	2.76	2.63	2.75	2.56	1.02	down	7.67E-01	9.24E-01	-	-
1377451_at	RGD1305704	Similar to c-Mpl binding protein	307452	Rn.116140	AI599250	9.33	9.66	9.86	9.17	9.76	9.85	1.02	down	9.36E-01	9.82E-01	-	-
1371179_a_at	Fgfr2	fibroblast growth factor receptor 2	25022	Rn.12732	AJ312745	2.57	2.55	2.63	2.56	2.61	2.52	1.02	down	5.43E-01	8.95E-01	-	-
1395874_at	---	---	---	Rn.30592	AW621461	2.36	2.35	2.44	2.35	2.39	2.34	1.02	down	5.30E-01	8.95E-01	-	-
1369313_at	Fhl2	four and a half LIM domains 2	63839	Rn.3849	NM_031677	2.56	2.53	2.51	2.50	2.51	2.65	1.02	up	6.80E-01	9.03E-01	-	-
1395497_at	LOC684771	similar to cell division cycle associated 5	684771	Rn.219526	BF418066	2.52	2.49	2.54	2.50	2.53	2.46	1.02	down	3.95E-01	8.95E-01	-	-
1374978_at	Cbx2	chromobox homolog 2 (Pc class homolog, Drosophila)	303730	Rn.13839	AI102524	2.36	2.36	2.38	2.36	2.37	2.44	1.02	up	4.30E-01	8.95E-01	-	-
1391904_at	---	---	---	Rn.208849	BE120522	2.36	2.34	2.37	2.36	2.44	2.34	1.02	up	5.22E-01	8.95E-01	-	-
1383803_at	---	---	---	---	BF283176	2.50	2.52	2.50	2.48	2.50	2.47	1.02	down	1.13E-01	8.95E-01	-	-
1382726_at	Nkd1	naked cuticle homolog 1 (Drosophila)	364952	Rn.8826	BF386091	2.44	2.43	2.48	2.43	2.44	2.42	1.02	down	2.79E-01	8.95E-01	-	-
1374356_at	LOC302999	similar to tripartite motif protein 32	302999	Rn.163131	BI298463	2.46	2.45	2.49	2.46	2.47	2.40	1.02	down	4.00E-01	8.95E-01	-	-
1389266_at	---	---	---	Rn.176544	BI296566	2.38	2.44	2.39	2.38	2.38	2.37	1.02	down	2.79E-01	8.95E-01	-	-
1390538_at	---	---	---	Rn.148039	BF414192	3.04	2.97	3.07	2.94	3.16	3.05	1.02	up	7.64E-01	9.23E-01	-	-
1393695_at	---	---	---	Rn.205166	AI501474	2.56	2.81	2.58	2.59	2.86	2.57	1.02	up	8.64E-01	9.58E-01	-	-
1372079_at	---	---	---	Rn.164556	AI410099	7.82	7.86	7.83	7.20	8.24	8.00	1.02	down	9.47E-01	9.85E-01	-	-
1387584_at	Shh	sonic hedgehog	29499	Rn.10432	NM_017221	2.39	2.38	2.44	2.38	2.40	2.37	1.02	down	3.16E-01	8.95E-01	-	-
1395670_at	---	---	---	Rn.173380	BF406267	2.37	2.36	2.45	2.37	2.38	2.36	1.02	down	4.65E-01	8.95E-01	-	-
1394006_at	Psme1	Proteasome (prosome, macropain) activator subunit 1	29630	Rn.2742	AA899618	2.32	2.31	2.32	2.32	2.32	2.38	1.02	up	3.40E-01	8.95E-01	-	-
1392628_at	---	---	---	Rn.149326	AI012134	2.59	2.56	2.70	2.57	2.68	2.53	1.02	down	7.40E-01	9.16E-01	-	-
1390488_a_at	Stk38	serine/threonine kinase 38	361813	Rn.13142	AI176077	3.02	4.17	3.25	4.14	3.01	3.35	1.02	up	9.65E-01	9.90E-01	-	-
1378486_at	---	---	---	Rn.210885	BF409825	2.26	2.26	2.28	2.26	2.27	2.33	1.02	up	3.75E-01	8.95E-01	-	-
1369555_at	Ccr4	chemokine (C-C motif) receptor 4	171054	Rn.81076	NM_133532	2.36	2.41	2.37	2.36	2.37	2.35	1.02	down	2.47E-01	8.95E-01	-	-
1396675_at	---	---	---	Rn.209988	BF401461	2.42	2.42	2.43	2.50	2.43	2.41	1.02	up	4.27E-01	8.95E-01	-	-
1391634_at	RGD1562078	similar to RIKEN cDNA 2310057N15	501766	---	BF552826	2.27	2.20	2.21	2.21	2.21	2.20	1.02	down	3.64E-01	8.95E-01	-	-
1383635_at	Ddx59	DEAD (Asp-Glu-Ala-Asp) box polypeptide 59	289402	Rn.34313	BM385099	4.01	4.67	4.86	4.48	3.97	5.17	1.02	up	9.81E-01	9.89E-01	-	-
1367895_at	Hnrnpk	heterogeneous nuclear ribonucleoprotein K	117282	Rn.11854	NM_057141	9.42	9.86	9.18	9.35	9.41	9.64	1.02	down	9.23E-01	9.77E-01	-	-
1376210_at	Foxo3	forkhead box O3	294515	Rn.24593	AI231684	2.36	2.32	2.33	2.33	2.37	2.38	1.02	up	2.41E-01	8.95E-01	-	-
1395283_at	---	---	---	Rn.153838	BF411821	2.69	2.66	2.75	2.67	2.72	2.65	1.02	down	5.30E-01	8.95E-01	-	-
1375455_at	Guca1a	guanylate cyclase activator 1a (retina)	301233	Rn.39165	AI716086	2.47	2.43	2.44	2.43	2.46	2.39	1.02	down	3.79E-01	8.95E-01	-	-
1374814_at	---	---	---	---	AI101530	2.29	2.28	2.29	2.36	2.29	2.28	1.02	up	4.37E-01	8.95E-01	-	-
1386269_x_at	Sorl1	sortilin-related receptor, LDLR class A repeats-containing	300652	Rn.92871	AI177589	2.56	2.52	2.56	2.55	2.61	2.54	1.02	up	4.29E-01	8.95E-01	-	-
1369352_at	Hipk3	homeodomain interacting protein kinase 3	83617	Rn.8099	NM_031787	3.80	4.86	4.66	4.64	4.01	4.61	1.02	down	9.56E-01	9.87E-01	-	-
1374841_at	RGD1560065	similar to RIKEN cDNA 2410004B18	499724	Rn.15356	AI237644	4.57	3.90	3.84	3.94	4.04	4.26	1.02	down	9.34E-01	9.81E-01	-	-
1370232_at	Ivd	isovaleryl coenzyme A dehydrogenase	24513	Rn.147	AI102838	8.67	9.12	8.73	8.74	9.11	8.73	1.02	up	9.10E-01	9.73E-01	-	-
1388972_at	Rtn4r	reticulon 4 receptor	113912	Rn.45686	BF386649	2.51	2.50	2.55	2.49	2.51	2.48	1.02	down	2.87E-01	8.95E-01	-	-
1391019_at	Slitrk1	SLIT and NTRK-like family, member 1	306147	Rn.31034	BF285698	2.64	2.55	2.64	2.58	2.61	2.59	1.02	down	5.14E-01	8.95E-01	-	-
1369435_at	Ttpa	tocopherol (alpha) transfer protein	25571	Rn.64565	NM_013048	2.54	2.50	2.58	2.51	2.57	2.47	1.02	down	5.79E-01	8.95E-01	-	-
1370649_at	krb2 /// RGD13084	bradykinin receptor B2 /// similar to RIKEN cDNA 4933439P14 gene	25245 /// 362778	Rn.3701	M59967	2.57	2.57	2.62	2.56	2.57	2.56	1.02	down	2.86E-01	8.95E-01	-	-
1370408_at	Nid67	putative small membrane protein NID67	286919	Rn.8865	AF313411	2.33	2.32	2.33	2.39	2.34	2.32	1.02	up	3.14E-01	8.95E-01	-	-
1394720_at	Tal1	T-cell acute lymphocytic leukemia 1	313507	Rn.9434	AI577495	2.44	2.43	2.45	2.43	2.54	2.41	1.02	up	6.11E-01	8.95E-01	-	-
1393504_at	---	---	---	---	AI072549	2.69	2.60	2.78	2.68	2.91	2.54	1.02	up	8.63E-01	9.58E-01	-	-
1373518_at	---	---	---	Rn.3006	AA866231	7.33	8.06	7.30	7.27	7.24	8.10	1.02	down	9.55E-01	9.87E-01	-	-
1381215_at	Numbl	numb homolog (Drosophila)-like	292732	Rn.15133	AA900967	2.29	2.26	2.27	2.26	2.37	2.26	1.02	up	5.89E-01	8.95E-01	-	-
1395104_at	---	---	---	Rn.16756	BF390608	2.48	2.42	2.44	2.42	2.44	2.41	1.02	down	3.18E-01	8.95E-01	-	-
1370699_a_at	Egfr /// Pepd	epidermal growth factor receptor /// peptidase D	24329 /// 292808	Rn.37227	AF187818	11.82	11.83	11.66	11.68	11.78	11.79	1.02	down	7.50E-01	9.19E-01	-	-
1396405_at	---	---	---	Rn.98620	BE097557	2.45	2.40	2.41	2.40	2.41	2.38	1.02	down	2.35E-01	8.95E-01	-	-
1370722_at	Cngb1	cyclic nucleotide gated channel beta 1	83686	Rn.10733	AJ224680	2.32	2.31	2.32	2.40	2.32	2.30	1.02	up	4.83E-01	8.95E-01	-	-
1369710_a_at	Snap91	synaptosomal-associated protein 91	65178	Rn.11022	NM_031728	2.46	2.40	2.42	2.40	2.42	2.39	1.02	down	3.48E-01	8.95E-01	-	-
1396503_at	---	---	---	Rn.209170	BF405056	2.48	2.47	2.52	2.47	2.49	2.44	1.02	down	3.51E-01	8.95E-01	-	-
1395091_at	---	---	---	Rn.207229	BE095757	2.43	2.46	2.43	2.43	2.54	2.43	1.02	up	6.00E-01	8.95E-01	-	-
1384241_at	Crygn	crystallin, gamma N	296730	Rn.23610	BE096332	2.41	2.35	2.37	2.36	2.36	2.34	1.02	down	3.03E-01	8.95E-01	-	-
1393301_at	---	---	---	Rn.30125	AW618896	3.72	4.03	4.51	4.13	4.36	3.83	1.02	up	9.40E-01	9.83E-01	-	-
1372140_at	Ccdc28a	coiled-coil domain containing 28A	361454	Rn.11855	BI295141	2.38	2.37	2.38	2.29	2.38	2.51	1.02	up	7.42E-01	9.17E-01	-	-
1369497_at	LOC24906	RoBo-1	24906	Rn.48721	NM_031537	2.37	2.34	2.39	2.35	2.35	2.33	1.02	down	2.08E-01	8.95E-01	-	-
1396718_at	---	---	---	---	AW522657	2.36	2.35	2.42	2.36	2.37	2.34	1.02	down	3.60E-01	8.95E-01	-	-
1393682_at	Gpr34	G protein-coupled receptor 34	554353	Rn.163444	BF410504	2.49	2.47	2.56	2.48	2.52	2.45	1.02	down	5.79E-01	8.95E-01	-	-
1377549_at	Cpne5	copine V	309650	Rn.21919	BF410265	2.56	2.56	2.64	2.54	2.61	2.54	1.02	down	5.61E-01	8.95E-01	-	-
1385135_at	---	---	---	---	BE118923	2.92	2.74	2.94	2.83	2.94	2.77	1.02	down	7.99E-01	9.35E-01	-	-
1389049_at	Kctd4	potassium channel tetramerisation domain containing 4	691835	Rn.169515	AI228222	2.51	2.56	2.52	2.49	2.55	2.48	1.02	down	4.63E-01	8.95E-01	-	-
1390870_at	Rnf207	ring finger protein 207	691246	Rn.155693	BF408540	2.64	2.62	2.65	2.62	2.73	2.62	1.02	up	5.73E-01	8.95E-01	-	-
1380267_at	Tekt3	tektin 3	287392	Rn.11745	AI029135	2.58	2.51	2.55	2.70	2.55	2.46	1.02	up	7.72E-01	9.26E-01	-	-
1372703_at	LOC689226	similar to ubiquitin-conjugating enzyme E2R 2	689226	Rn.203082	BG380680	10.05	9.37	9.50	9.70	9.63	9.51	1.02	down	9.23E-01	9.77E-01	-	-
1395183_at	---	---	---	Rn.73529	BM391096	2.41	2.37	2.42	2.40	2.47	2.39	1.02	up	5.01E-01	8.95E-01	-	-
1381357_at	Ptpn22	protein tyrosine phosphatase, non-receptor type 22 (lymphoid)	295338	Rn.22891	AI176755	2.63	2.62	2.67	2.63	2.64	2.59	1.02	down	3.79E-01	8.95E-01	-	-
1395322_at	Slbp	Stem-loop binding protein	681062	Rn.198386	BE116752	2.68	2.67	2.75	2.66	2.70	2.66	1.02	down	5.01E-01	8.95E-01	-	-
1385478_at	Rbm10	RNA binding motif protein 10	64510	Rn.8822	BF410579	2.43	2.41	2.44	2.42

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicats)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1370526_at	Itgae	integrin, alpha E, epithelial-associated	83577	Rn.128291	AF020045	2.67	3.85	3.44	3.62	3.50	2.90	1.02	up	9.60E-01	9.89E-01	-	-
1395016_at	Andpro	androgen regulated 20 kDa protein	25030	Rn.9977	BM388042	2.42	2.41	2.46	2.41	2.43	2.39	1.02	down	3.29E-01	8.95E-01	-	-
1373061_at	Snx17	sorting nexin 17	298836	Rn.162846	BE329329	8.13	7.37	7.77	8.05	7.93	7.34	1.02	up	9.47E-01	9.85E-01	-	-
1378684_at	Rem1	RAS (RAD and GEM)-like GTP-binding 1	366232	Rn.88325	BG375958	2.46	2.47	2.48	2.47	2.52	2.48	1.02	up	2.56E-01	8.95E-01	-	-
1369876_at	Gnb3	guanine nucleotide binding protein (G protein), beta polypeptide 3	60449	Rn.27065	NM_021858	2.42	2.42	2.46	2.42	2.42	2.39	1.02	down	2.82E-01	8.95E-01	-	-
1395506_at	---	---	---	Rn.167827	AW530922	2.44	2.39	2.40	2.39	2.39	2.37	1.02	down	3.17E-01	8.95E-01	-	-
1384043_at	---	---	---	Rn.173529	BG667918	2.36	2.34	2.41	2.35	2.35	2.33	1.02	down	3.83E-01	8.95E-01	-	-
1383602_at	Pum1	pumilio homolog 1 (Drosophila)	362609	Rn.44196	BE112428	8.03	7.69	7.54	7.81	7.49	7.90	1.02	down	9.14E-01	9.74E-01	-	-
1372904_at	Mobkl2a	MOB1, Mps One Binder kinase activator-like 2A (yeast)	362833	Rn.9147	BI285628	2.35	2.36	2.36	2.35	2.36	2.43	1.02	up	4.43E-01	8.95E-01	-	-
1375329_at	---	---	---	Rn.204242	BF520837	2.57	2.53	2.63	2.56	2.60	2.50	1.02	down	6.28E-01	8.95E-01	-	-
1394709_at	---	---	---	Rn.205882	AI406967	2.38	2.32	2.33	2.32	2.33	2.31	1.02	down	3.34E-01	8.95E-01	-	-
1397514_at	---	---	---	Rn.56010	BF283101	2.47	2.47	2.50	2.47	2.47	2.43	1.02	down	2.70E-01	8.95E-01	-	-
1394007_at	Prm1	protamine 1	24685	Rn.27657	AI144723	2.76	2.54	2.68	2.59	2.73	2.59	1.02	down	7.94E-01	9.34E-01	-	-
1397093_at	---	---	---	Rn.210499	BF398550	2.36	2.36	2.43	2.36	2.37	2.35	1.02	down	4.16E-01	8.95E-01	-	-
1368539_at	Scn9a	sodium channel, voltage-gated, type IX, alpha	78956	Rn.88082	NM_133289	2.51	2.47	2.55	2.48	2.52	2.45	1.02	down	5.08E-01	8.95E-01	-	-
1395550_at	RGD1565629	similar to collagen and calcium binding EGF domains 1	307358	Rn.91552	BE098003	2.44	2.45	2.56	2.45	2.46	2.47	1.02	down	6.11E-01	8.95E-01	-	-
1380463_at	Aak1	AP2 associated kinase 1	500244	Rn.203307	AI102811	2.55	2.52	2.55	2.54	2.55	2.46	1.02	down	4.91E-01	8.95E-01	-	-
1371247_at	Tnnt3	troponin T type 3 (skeletal, fast)	24838	Rn.15488	BF521859	2.46	2.43	2.52	2.45	2.45	2.43	1.02	down	4.73E-01	8.95E-01	-	-
1391496_at	Polr3f	polymerase (RNA) III (DNA directed) polypeptide F, 39 kDa	311487	Rn.22329	AA819635	2.89	2.87	3.16	2.90	3.15	2.80	1.02	down	8.83E-01	9.64E-01	-	-
1385858_at	---	---	---	---	AI071537	2.58	2.51	2.59	2.53	2.55	2.53	1.02	down	4.30E-01	8.95E-01	-	-
1398272_at	B4galnt1	beta-1,4-N-acetyl-galactosaminyl transferase 1	64828	Rn.10119	NM_022860	2.36	2.35	2.34	2.40	2.37	2.34	1.02	up	2.36E-01	8.95E-01	-	-
1381523_at	---	---	---	Rn.205932	BE112754	2.41	2.40	2.46	2.40	2.42	2.39	1.02	down	3.52E-01	8.95E-01	-	-
1393196_at	Klhl23	kelch-like 23 (Drosophila)	311114	Rn.125724	BE104114	2.34	2.33	2.35	2.34	2.43	2.33	1.02	up	5.49E-01	8.95E-01	-	-
1382588_at	LOC679578	similar to Protein C18orf1	679578	Rn.206948	AW532202	2.76	3.52	3.52	2.76	3.81	3.30	1.02	up	9.59E-01	9.89E-01	-	-
1384784_at	Clca2 /// Clca4l	chloride channel calcium activated 2 /// chloride channel calcium activated 4-l	362052 /// 499721	Rn.93762	AI111432	2.46	2.43	2.50	2.44	2.47	2.41	1.02	down	4.12E-01	8.95E-01	-	-
1384901_at	---	---	---	Rn.205365	BF523017	3.57	3.54	3.63	3.58	3.61	3.61	1.02	up	4.86E-01	8.95E-01	-	-
1379024_at	---	---	---	Rn.147769	BF392308	2.56	2.55	2.65	2.53	2.65	2.50	1.02	down	7.20E-01	9.11E-01	-	-
1396683_at	---	---	---	Rn.207411	BE099973	2.42	2.39	2.43	2.48	2.42	2.41	1.02	up	4.12E-01	8.95E-01	-	-
1378206_a_at	Meig1	meiosis expressed gene 1	679834	Rn.46511	BF565261	2.59	2.57	2.65	2.57	2.61	2.56	1.02	down	5.05E-01	8.95E-01	-	-
1377329_at	---	---	---	Rn.203438	BE113460	2.44	2.43	2.46	2.44	2.44	2.38	1.02	down	3.41E-01	8.95E-01	-	-
1385355_at	---	---	---	Rn.209860	BF391308	2.70	2.79	2.70	2.91	2.69	2.65	1.02	up	8.16E-01	9.41E-01	-	-
1368250_at	Tekt1	tektin 1	85270	Rn.46442	NM_053508	2.53	2.45	2.47	2.46	2.47	2.45	1.02	down	4.24E-01	8.95E-01	-	-
1393005_at	Sft2d2	SFT2 domain containing 2	360868	Rn.8424	AW916965	8.16	8.06	7.44	7.50	7.98	8.13	1.02	down	9.45E-01	9.84E-01	-	-
1384598_at	---	---	---	Rn.163090	AA894105	2.55	2.56	2.55	2.63	2.54	2.54	1.02	up	4.80E-01	8.95E-01	-	-
1373756_at	Cend1	cell cycle exit and neuronal differentiation 1	361675	Rn.64460	BI298757	2.46	2.46	2.54	2.46	2.46	2.47	1.02	down	4.47E-01	8.95E-01	-	-
1391947_at	---	---	---	Rn.177235	BM386499	2.48	2.46	2.52	2.47	2.50	2.44	1.02	down	4.08E-01	8.95E-01	-	-
1390751_at	---	---	---	---	BF415798	2.41	2.40	2.47	2.39	2.43	2.40	1.02	down	4.17E-01	8.95E-01	-	-
1395607_at	---	---	---	---	BF402418	2.47	2.45	2.50	2.46	2.47	2.43	1.02	down	3.07E-01	8.95E-01	-	-
1380458_at	---	---	---	Rn.3993	AA849609	2.45	2.43	2.45	2.44	2.52	2.43	1.02	up	5.09E-01	8.95E-01	-	-
1384300_at	---	---	---	Rn.119594	AW921534	2.47	2.46	2.49	2.45	2.48	2.43	1.02	down	2.88E-01	8.95E-01	-	-
1383608_at	Arrdc2	arrestin domain containing 2	306344	Rn.22853	AI145231	2.48	3.80	3.12	3.40	2.80	3.27	1.02	up	9.62E-01	9.89E-01	-	-
1370321_at	Aifm1	apoptosis-inducing factor, mitochondrion-associated 1	83533	Rn.203165	AF262320	8.97	9.08	9.00	8.88	8.95	9.15	1.02	down	8.20E-01	9.42E-01	-	-
1380382_at	---	---	---	Rn.64787	AW520863	2.36	2.35	2.36	2.35	2.45	2.33	1.02	up	5.75E-01	8.95E-01	-	-
1375229_at	Klc1	Kinesin light chain 1	171041	Rn.106230	AA818427	3.89	3.89	4.04	4.11	3.76	3.89	1.02	down	8.57E-01	9.55E-01	-	-
1391835_at	---	---	---	---	AW531843	2.44	2.43	2.46	2.44	2.44	2.40	1.02	down	2.37E-01	8.95E-01	-	-
1379914_at	Klf11	Kruppel-like factor 11	313994	Rn.18589	AI716050	3.41	2.64	2.58	2.66	2.60	3.43	1.02	up	9.57E-01	9.88E-01	-	-
1377039_at	---	---	---	Rn.19277	BF401480	2.36	2.31	2.33	2.31	2.32	2.30	1.02	down	2.75E-01	8.95E-01	-	-
1394686_at	Ercc4	excision repair cross-complementing rodent repair deficiency, complementatic	304719	Rn.195555	AI013171	2.44	2.42	2.45	2.42	2.43	2.40	1.02	down	2.14E-01	8.95E-01	-	-
1384399_at	Ankrd50	ankyrin repeat domain 50	294988	Rn.7482	AW526620	2.40	2.37	2.41	2.37	2.38	2.37	1.02	down	1.36E-01	8.95E-01	-	-
1380133_at	Osr2	odd-skipped related 2 (Drosophila)	315039	Rn.13228	BI289743	2.43	2.41	2.45	2.42	2.42	2.38	1.02	down	2.23E-01	8.95E-01	-	-
1394702_at	---	---	---	Rn.88737	AI137904	2.21	2.20	2.21	2.20	2.28	2.19	1.01	up	5.07E-01	8.95E-01	-	-
1392402_at	---	---	---	---	BF417576	2.55	2.51	2.59	2.52	2.57	2.49	1.01	down	5.25E-01	8.95E-01	-	-
1396054_at	---	---	---	Rn.210626	BF399535	6.26	5.58	5.54	5.84	5.73	5.88	1.01	up	9.32E-01	9.81E-01	-	-
1371143_at	Serpina7	serine (or cysteine) peptidase inhibitor, clade A (alpha-1 antiproteinase, antitry	81806	Rn.9948	M63991	2.51	2.47	2.56	2.49	2.53	2.46	1.01	down	5.56E-01	8.95E-01	-	-
1370881_at	Tst	thiosulfate sulfurtransferase, mitochondrial	25274	Rn.6360	AI411117	9.01	8.40	8.34	8.63	8.56	8.62	1.01	up	9.26E-01	9.79E-01	-	-
1375950_a_at	---	---	---	Rn.12955	BI294235	2.52	3.21	3.01	3.21	2.58	3.01	1.01	up	9.42E-01	9.83E-01	-	-
1387374_at	Tcf12	transcription factor 12	25720	Rn.9916	NM_013176	7.28	6.66	7.30	7.60	6.65	7.06	1.01	up	9.53E-01	9.86E-01	-	-
1389192_at	Atp5si	ATP5S-like	361520	Rn.31959	AA800521	6.47	6.46	6.77	6.79	6.51	6.46	1.01	up	8.90E-01	9.68E-01	-	-
1394660_at	Ephb2	Eph receptor B2	313633	Rn.27233	AI136749	2.34	2.33	2.40	2.33	2.35	2.32	1.01	down	3.85E-01	8.95E-01	-	-
1392400_at	Glmn	glomulin, FKBP associated protein	289437	Rn.44333	AI764065	2.53	2.53	2.56	2.51	2.56	2.48	1.01	down	4.52E-01	8.95E-01	-	-
1391989_at	---	---	---	---	AI179410	2.43	2.37	2.38	2.37	2.39	2.36	1.01	down	3.60E-01	8.95E-01	-	-
1397513_at	RGD1305844	hypothetical LOC294883	294883	Rn.24012	BE097409	2.66	2.60	2.72	2.64	2.72	2.54	1.01	down	7.48E-01	9.18E-01	-	-
1377824_a_at	Igf2bp3	insulin-like growth factor 2 mRNA binding protein 3	312320	Rn.100446	AI230709	2.64	2.57	2.79	2.59	2.70	2.63	1.01	down	7.79E-01	9.28E-01	-	-
1375794_at	---	---	---	Rn.63100	BF403635	2.37	2.33	2.43	2.34	2.39	2.34	1.01	down	5.69E-01	8.95E-01	-	-
1398074_at	---	---	---	Rn.208072	BE109876	2.43	2.42	2.48	2.42	2.43	2.41	1.01	down	3.93E-01	8.95E-01	-	-
1394845_at	Aqr	aquarius homolog (mouse)	366163	Rn.37299	BF542818	2.60	2.55	2.68	2.57	2.65	2.54	1.01	down	6.99E-01	9.07E-01	-	-
1391063_at	Klf23	kinesin family member 23	315740	Rn.63734	BE113443	2.40	2.39	2.42	2.38	2.40	2.37	1.01	down	1.81E-01	8.95E-01	-	-
1373223_at	---	---	---	Rn.22383	AI101361	2.33	2.33	2.38	2.33	2.33	2.32	1.01	down	3.29E-01	8.95E-01	-	-
1395685_at	---	---	---	Rn.15647	BF392586	2.42	2.40	2.44	2.42	2.43	2.35	1.01	down	4.70E-01	8.95E-01	-	-
1368045_at	Slc31a1	solute carrier family 31 (copper transporters), member 1	171135	Rn.2789	NM_133600	10.59	10.40	10.43	10.60	10.26	10.63	1.01	up	8.82E-01	9.64E-01	-	-
1388285_at	---	---	---	---	X14264	2.47	2.45	2.52	2.46	2.48	2.44	1.01	down	4.65E-01	8.95E-01	-	-
1374491_at	Cmtm8	CKLF-like MARVEL transmembrane domain containing 8	301045	Rn.10184	AI408279	2.45	2.44	2.48	2.44	2.46	2.41	1.01	down	3.79E-01	8.95E-01	-	-
1390022_at	Arpc5	actin related protein 2/3 complex, subunit 5	360854	Rn.1639	AA946538	7.65	7.99	8.07	7.73	7.90	8.01	1.01	down	8.95E-01	9.67E-01	-	-
1379979_at	---	---	---	Rn.199306	AI548961	2.38	2.37	2.39	2.37	2.47	2.36	1.01	up	5.90E-01	8.95E-01	-	-
1381860_at	---	---	---	Rn.173878	BF420440	2.48	2.45	2.51	2.46	2.47	2.43	1.01	down	3.33E-01	8.95E-01	-	-
1381566_at	---	---	---	Rn.216623	BE097780	2.33	2.32	2.39	2.33	2.32	2.31	1.01	down	4.12E-01	8.95E-01	-	-
1391447_at	---	---	---	Rn.166172	BI299229	2.32	2.32	2.33	2.39	2.33	2.31	1.01	up	4.30E-01	8.95E-01	-	-
1379227_at	---	---	---	Rn.160805	BF392832	2.58	2.55	2.69	2.57	2.66	2.52	1.01	down	7.36E-01	9.15E-01	-	-
1372035_at	Ift52	intraflagellar transport 52 homolog (Chlamydomonas)	362265	Rn.36626	BG381014	5.85	6.19	5.22	5.71	5.72	5.91	1.01	up	9.45E-01	9.84E-01	-	-
1380384_at	---	---	---	Rn.147651	BF398176	2.44	2.43	2.49	2.44	2.45	2.42	1.01	down	3.62E-01	8.95E-01	-	-
1367852_s_at	Gp1bb /// Sept5	glycoprotein Ib (platelet), beta polypeptide /// septin 5	116727 /// 116728	Rn.96497	BM387903	2.44	2.40	2.46	2.41	2.43	2.40	1.01	down	3.28E-01	8.95E-01	-	-
1395034_at	---	---	---	---	AI408816	2.34	2.29	2.30	2.29	2.29	2.28	1.01	down	2.87E-01	8.95E-01	-	-
1387042_at	Cacnb3	calcium channel, voltage-dependent, beta 3 subunit	25297	Rn.2808	NM_012828	2.45	2.44	2.46	2.43	2.45	2.41	1.01	down	1.62E-01	8.95E-01	-	-
1392369_at	---	---	---	Rn.209277	BF388926	2.41	2.36	2.40	2.37	2.38	2.36	1.01	down	2.12E-01	8.95E-01	-	-
1393873_s_at	---	---	---	---	AI639528	2.65	2.63	2.67	2.64	2.76	2.62	1.01	up	6.60E-01	8.98E-01	-	-
1380652_at	---	---	---	Rn.202023	BF396394	2.47	2.45	2.53	2.46	2.49	2.44	1.01	down	5.14E-01	8.95E-01	-	-
1398691_at	---	---	---	Rn.205910	AI408578	2.56	2.54	2.59	2.65	2.56	2.55	1.01	up	5.54E-01	8.95E-01	-	-
1381797_at	---	---	---	Rn.205682	AW530275	2.52	2.46	2.49	2.47	2.48	2.45	1.01	down	3.73E-01	8.95E-01	-	-
1374100_at	---	---	---	Rn.8384	AI102771	5.22	4.87	4.47	4.69	4.76	5.18	1.01	up	9.40E-01	9.83E-01	-	-
1370971_at	Myh1	myosin, heavy polypeptide 1, skeletal muscle, adult	287408	---	BI277545	2.49	2.48	2.52	2.48	2.50	2.44	1.01	down	3.78E-01	8.95E-01	-	-
1370030_at	Gclm	glutamate cysteine ligase, modifier subunit	29739	Rn.2460	NM_017305	11.75	11.96	12.26	11.89	12.08	12.06	1.01	up	9.01E-01	9.70E-01	-	-
1376322_at	---	---	---	Rn.207625	BF405165	2.44	2.38	2.39	2.38	2.39	2.37	1.01	down	3.23E-01	8.95E-01	-	-
1374327_at	Bbs4	Bardet-Biedl syndrome 4 homolog (human)	300754	Rn.25002	AW531530	4.98	5.57	5.17	5.32	5.17	5.16	1.01	down	9.12E-01	9.74E-01	-	-
1397933_at	---	---	---	Rn.148276	BF390265	2.45	2.44	2.51	2.40	2.48	2.45	1.01	down	5.49E-01	8.95E-01	-	-
1373192_at	Wdr60	WD repeat domain 60	314523	Rn.41144	BE102484	2.94	2.94	2.94	3.01	2.94	2.94	1.01	up	3.90E-01	8.95E-01	-	-
1386995_at	---	---	---	Rn.47315	BF565756	2.48	2.46	2.53	2.47	2.50	2.44	1.01	down	4.92E-01	8.95E-01	-	-
1375092_at	---	---	---	---	AW252664	2.46	2.44	2.51	2.45	2.47	2.43	1.01	down	3.73E-01	8.95E-01	-	-
1386435_at	Tcfap4	transcription factor AP4	360482	Rn.145139	AI101186	2.72	3.15	3.00	2.70	3.37	2.85	1.01	up	9.33E-01	9.81E-01	-	-
1395791_at	RGD1306404	similar to mKIAA1402 protein	296733	Rn.37536	BF287167	2.69	2.85	2.77	2.81	2.76	2.80	1.01	up	6.86E-01	9.04E-01	-	-
1385451_at	---	---	---	---	BF420260	2.54	2.62	2.55	2.54	2.56	2.54	1.01	down	4.43E-01	8.95E-01	-	-
1382855_at	RGD1305899	similar to Protein C20orf158	311715	---	BI295963	2.34	2.28	2.29	2.28	2.29	2.27	1.01	down	3.15E-01	8.95E-01	-	-
1382414_at	---	---	---	Rn.203992	AI043787	2.51	2.49	2.52	2.47	2.50	2.49	1.01	down	1.50E-01	8.95E-01	-	-
1379656_at	---	---	---	Rn.8962	AA855863	2.45	2.45	2.50	2.46	2.44	2.45	1.01	down	2.71E-01	8.95E-01	-	-
1380477_at	---	---	---	Rn.167687	BE112382	2.28	2.28	2.34	2.28	2.28	2.27	1.01	down	3.60E-01	8.95E-01	-	-
1369927_at	Mdh2	malate dehydrogenase 2, NAD (mitochondrial)	81829	Rn.1011	NM_031151	9.46	10.11	10.00	9.57	9.89	10.08	1.01	down	9.36E-01	9.82E-01	-	-
1389917_at	RGD1564778	similar to RIKEN cDNA 4121402D02	303514	Rn.22437	BF284375	2.29	2.30	2.32	2.34	2.31	2.33	1.01	up	1.61E-01	8.95E-01	-	-
1390234_at	Sf3b1	splicing factor 3b, subunit 1	84486	Rn.198843	BE115465	9.34	8.80	8.92	9.00	9.01	9.12	1.01	up	9.07E-01	9.71E-01	-	-
1391961_a_at	---	---	---	Rn.171199	BI283648	2.53	2.52	2.59	2.53	2.56	2.49	1.01	down	5.14E-01	8.95E-01	-	-
1375500_at	---	---	---	---	AI600078	2.62	2.59	2.60	2.59	2.60	2.55	1.01	down	3.43E-01	8.95E-01	-	-
1389878_at	---	---	---	Rn.212201	BI296752	2.44	2.38	2.39	2.38	2.39	2.37	1.01	down	3.37E-01	8.95E-01	-	-
1389772_at	---	---	---	Rn.48930	AI575785	2.28	2.33	2.29	2.28	2.29	2.28	1.01	down	2.47E-01	8.95E-01	-	-
1390469_at	Nrm	nurim (nuclear envelope membrane protein)	361791	Rn.38521	BM391488	2.30	2.29	2.30	2.30	2.37	2.28	1.01	up	4.92E-01	8.95E-01	-	-
1380633_at	---	---	---	Rn.209128	BG381596	2.33	2.32	2.34	2.32	2.41	2.32	1.01	up	5.40E-01	8.95E-01	-	-
1370537_at	Xrcc6	X-ray repair complementing defective repair in Chinese hamster cells 6	25019	Rn.161996	AB066102	3.88	4.14	4.08	4.05	4.07	4.03	1.01	up	8.04E-01	9.37E-01	-	-
1385400_at	Atp6v1b1	ATPase, H transporting, lysosomal V1 subunit B1	312488	Rn.103610	BI288461	2.40	2.39	2.45	2.40	2.40	2.38	1.01	down	3.16E-01	8.95E-01	-	-
1375409_at	---	---	---	Rn.208831	BE120389	2.52	2.49	2.55	2.53	2.59	2.50	1.01	up	5.43E-01	8.95E-01	-	-
1387292_s_at	Capn8	calpain 8	170808	Rn.80837	NM_133309	2.37	2.32	2.33	2.32	2.31	2.31	1.01	down	2.77E-01	8.95E-01	-	-
1382138_at	Nrarp	Notch-regulated ankyrin repeat protein	499745	Rn.22790	BG380221	2.40	2.38	2.41	2.48	2.40	2.38	1.01	up	5.36E-01	8.95E-01	-	-
1396143_at	---	---	---	Rn.60419	BI293013	2.55	2.54	2.58	2.53	2.56	2.51	1.01	down	3.58E-01	8.95E-01	-	-
1368306_at	Grin2c	glutamate receptor, ionotropic, N-methyl D-aspartate 2C	24411	Rn.9709	U08259	2.44	2.42	2.44	2.42	2.44	2.50	1.01	up	4.15E-01	8.95E-01	-	-
1380900_at	---	---	---	Rn.204445	BE120504	2.43	2.34	2.36	2.37	2.35	2.33	1.01	down	5.12E-01	8.95E-01	-	-
1378875_a_at	RGD1303066	similar to RIKEN cDNA 2610110G12	361789	Rn.136935	AW522817	2.80	3.20	2.99	3.54	2.45	3.06	1.01	up	9.53E-01	9.86E-01	-	-
1385954_at	rCG_58138	hypothetical protein LOC100125362	100125362	Rn.18127	AI029023	2.51	2.46	2.58	2.48	2.54	2.46	1.01	down	6.39E-01	8.95E-01	-	-
1381506_at	---	---	---	Rn.146835	BF417935	2.57	2.53	2.58	2.54	2.57	2.51	1.01	down	4.25E-01	8.95E-01	-	-
1368443_at	Necab2	N-terminal EF-hand calcium binding protein 2	170928	Rn.62703	NM_133415	2.47	2.49	2.50	2.46	2.48	2.46	1.01	down	1.01E-01	8.95E-01	-	-
1396410_at	---	---	---	Rn.208414	BE116258	2.45	2.42	2.47	2.45	2.52	2.44	1.01	up	4.99E-01	8.95E-01	-	-
1382490_at	---	---	---	Rn.203853	BF284288	2.20	2.63	3.12	3.39	2.33	2.29	1.01	up	9.65E-01	9.90E-01	-	-
1372542_at	---	---	---	Rn.203756	BE113281	6.60	6.28	5.52	6.23	5.92	6.32	1.01	up	9.54E-01	9.86E-01	-	-
1370414_at	Rab38	RAB38, member RAS oncogene family	252916	Rn.9824	M94043	2.37	2.30	2.31	2.31	2.30	2.31	1.01	down	3.82E-01	8.95E-01	-	-
1378193_at	Ms4a7	membrane-spanning 4-domains, subfamily A, member 7	293744	Rn.44037	AI408286	2.34	2.43	2.35	2.39	2.34	2.32	1.01	down	5.72E-01	8.95E-01	-	-
1386769_at	---	---	---	Rn.145684	BF552679	2.50	2.46	2.52	2.47	2.51	2.44	1.01	down	5.02E-01	8.95E-01	-	-
1369368_at	Trpc5	transient receptor potential cation channel, subfamily C, member 5	140933	Rn.212751	NM_080898	2.41	2.43	2.42	2.39	2.41	2.38	1.01	down	8.36E-02	8.95E-01	-	-
1382121_at	Stim1	stromal interaction molecule 1	361618	Rn.106771	BI292282	2.30	2.34	2.31	2.30	2.30	2.29	1.01	down	1.53E-01	8.95E-01	-	-
1370629_at	Art2b	ADP-ribosyltransferase 2b	293152	Rn.107075	M85193	2.52	2.50	2.56	2.50	2.54	2.46	1.01	down	5.19E-01	8.95E-01	-	-
1385433_at	Mtss1	metastasis suppressor 1	362918	Rn.38488	AI576354	6.86	5.39	5.98	5.98	5.89	6.30	1.01	down	9.64E-01	9.90E-01	-	-
1385123_at	Ik /// Wdr55	IK cytokine /// WD repeat domain 55	291659 /// 307494	Rn.162302	BM386845	2.35	2.33	2.38	2.33	2.34	2.32	1.01	down	1.98E-01	8.95E-01	-	-
1374831_at	Ath1	ATH1, acid trehalase-like 1 (yeast)	309103	Rn.23728	AI172579	5.16	4.49	4.45	4.45	4.55	4.55	1.01	up	9.51E-01	9.88E-01	-	-
1381839_at	---	---	---	---	AA957129	2.87	2.86	3.06	3.15	2.80	2.76	1.01	down	8.88E-01	9.65E-01	-	-
1370865_at	Idh3g	isocitrate dehydrogenase 3 (NAD), gamma	25179	Rn.2837	BI277627	10.33	10.16	10.60	10.25	10.38	10.39	1.01	down	8.84E-01	9.64E-01	-	-
1368889_at	Vti1a	vesicle transport through interaction with t-SNAREs homolog 1A (yeast)	65277	Rn.154408	NM_023101	4.29	4.44	4.11	4.23	4.25	4.41	1.01	up	8.61E-01	9.57E-01	-	-
1380727_at	---	---	---	Rn.206262	AW524544	2.36	2.35	2.41	2.36	2.37	2.34	1.01	down	3.47E-01	8.95E-01	-	-
1377753_at	---	---	---	Rn.104110	BI295763	2.32	2.31	2.32	2.38	2.32	2.30	1.01	up	4.42E-01	8.95E-01	-	-
1384171_x_at	Vav2	vav 2 guanine nucleotide exchange factor	296603	Rn.98555	AA800477	2.55	2.58	2.61	2.58	2.59	2.63	1.01	up	3.84E-01	8.95E-01	-	-
1392031_at	---	---	---	Rn.78130	BI280974	2.55	2.51	2.66	2.54	2.62	2.49	1.01	down	7.41E-01	9.17E-01	-	-
1394764_at	Lmtk2	lemur tyrosine kinase 2	304286	Rn.26715	AW531730	2.88	2.97

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1385655_at	Riok1	RIO kinase 1 (yeast)	291061	Rn.132553	AA925880	2.48	2.46	2.54	2.47	2.51	2.44	1.01	down	5.39E-01	8.95E-01	-	-
1391017_at	Farp1	FERM, RhoGEF (Arhgef) and pleckstrin domain protein 1 (chondrocyte-derive	306183	Rn.92109	AI058490	2.46	2.45	2.49	2.45	2.57	2.44	1.01	up	6.68E-01	9.00E-01	-	-
1379820_at	Ptchd2	patched domain containing 2	313705	Rn.103010	AW529839	2.45	2.42	2.45	2.42	2.43	2.41	1.01	down	1.61E-01	8.95E-01	-	-
1387639_at	Hpcal4	hippocalcin-like 4	50872	Rn.34529	NM_017357	2.50	2.48	2.52	2.49	2.64	2.44	1.01	up	7.49E-01	9.19E-01	-	-
1380484_at	Pi16	peptidase inhibitor 16	294312	Rn.9448	AI044661	2.37	2.34	2.41	2.36	2.36	2.34	1.01	down	3.59E-01	8.95E-01	-	-
1389555_at	Tcf19	transcription factor 19	406195	Rn.216465	BM387190	3.78	4.63	4.00	5.37	3.01	4.10	1.01	up	9.79E-01	9.94E-01	-	-
1390615_at	Kpna1	Karyopherin (importin) alpha 1	288064	Rn.6272	BI281629	2.36	2.36	2.37	2.44	2.36	2.35	1.01	up	5.10E-01	8.95E-01	-	-
1381197_at	---	---	---	---	BF409085	2.53	2.51	2.57	2.52	2.52	2.52	1.01	down	3.38E-01	8.95E-01	-	-
1382772_at	---	---	---	---	BF289261	2.71	2.63	2.70	2.68	2.69	2.62	1.01	down	5.71E-01	8.95E-01	-	-
1381950_at	---	---	---	Rn.166007	AI044440	2.47	2.45	2.50	2.45	2.48	2.42	1.01	down	3.98E-01	8.95E-01	-	-
1393167_at	---	---	---	Rn.166086	AI231826	2.51	2.45	2.53	2.52	2.53	2.50	1.01	up	4.55E-01	8.95E-01	-	-
1384072_at	---	---	---	Rn.153731	BI288828	2.52	2.50	2.56	2.51	2.54	2.47	1.01	down	5.22E-01	8.95E-01	-	-
1391065_at	---	---	---	Rn.169569	BG373309	2.84	2.35	2.63	2.67	2.63	2.59	1.01	up	8.92E-01	9.67E-01	-	-
1389914_at	RGD1563533	similar to novel protein	313713	Rn.91524	AI535202	2.39	2.38	2.40	2.39	2.48	2.38	1.01	up	5.76E-01	8.95E-01	-	-
1380202_at	Znf821	zinc finger protein 821	307834	Rn.18256	AI070003	2.66	2.66	2.84	2.66	2.67	2.77	1.01	down	7.87E-01	9.31E-01	-	-
1397396_at	RGD1308297	Similar to CG10084-PA	306137	Rn.28431	BE109259	2.47	2.45	2.47	2.52	2.47	2.46	1.01	up	3.63E-01	8.95E-01	-	-
1368320_at	Ncam1	neural cell adhesion molecule 1	24586	Rn.11283	NM_031521	2.95	2.58	2.75	2.82	2.70	2.70	1.01	down	8.65E-01	9.58E-01	-	-
1392076_at	---	---	---	Rn.58146	BF393849	2.53	2.52	2.62	2.52	2.57	2.51	1.01	down	6.16E-01	8.95E-01	-	-
1382459_at	RGD1307201	similar to chromosome 13 open reading frame 3	361047	Rn.218204	BF287235	2.44	2.41	2.43	2.41	2.42	2.39	1.01	down	2.59E-01	8.95E-01	-	-
1390175_at	Ccdc85b	coiled-coil domain containing 85B	309161	---	AI072997	2.46	2.41	2.43	2.41	2.41	2.41	1.01	down	2.25E-01	8.95E-01	-	-
1381365_at	---	---	---	Rn.169729	AW535275	2.44	2.43	2.48	2.44	2.57	2.40	1.01	up	7.23E-01	9.12E-01	-	-
1388876_at	---	---	---	Rn.164113	AI231802	2.38	2.37	2.42	2.37	2.38	2.36	1.01	down	3.03E-01	8.95E-01	-	-
1397377_at	---	---	---	Rn.165274	AA955664	3.83	3.90	5.26	4.06	5.55	3.43	1.01	up	9.80E-01	9.94E-01	-	-
1395508_at	Cct5	chaperonin containing Tcp1, subunit 5 (epsilon)	294864	Rn.92645	BG665309	7.11	7.79	7.64	7.24	7.57	7.66	1.01	down	9.37E-01	9.82E-01	-	-
1393338_at	Scx	scleraxis	680712	Rn.198233	AW528719	2.36	2.36	2.42	2.36	2.37	2.36	1.01	down	3.96E-01	8.95E-01	-	-
1379935_at	Ccl7	chemokine (C-C motif) ligand 7	287561	Rn.26815	BF419899	2.40	2.35	2.36	2.35	2.36	2.34	1.01	down	3.05E-01	8.95E-01	-	-
1387597_at	Dmrt1	doublesex and mab-3 related transcription factor 1	114498	Rn.74260	NM_053706	2.47	2.42	2.43	2.43	2.43	2.42	1.01	down	2.76E-01	8.95E-01	-	-
1391954_at	---	---	---	Rn.206558	BF400813	2.56	2.49	2.51	2.50	2.52	2.48	1.01	down	4.36E-01	8.95E-01	-	-
1381733_at	---	---	---	Rn.210526	BF404543	2.37	2.38	2.38	2.34	2.41	2.31	1.01	down	5.32E-01	8.95E-01	-	-
1397138_at	---	---	---	Rn.135933	BF396994	2.40	2.39	2.44	2.39	2.39	2.38	1.01	down	2.75E-01	8.95E-01	-	-
1372162_at	Acsa1	acyl-CoA synthetase short-chain family member 1	296259	Rn.98236	AI176565	7.51	6.08	7.19	6.92	7.11	6.68	1.01	down	9.66E-01	9.90E-01	-	-
1380696_at	---	---	---	Rn.199679	AW530527	2.46	2.43	2.45	2.52	2.44	2.44	1.01	up	5.20E-01	8.95E-01	-	-
1397283_at	---	---	---	Rn.167263	AI176618	2.40	2.39	2.44	2.39	2.40	2.38	1.01	down	2.71E-01	8.95E-01	-	-
1372378_at	Dis3l2	DIS3 mitotic control homolog (S. cerevisiae)-like 2	367307	Rn.2940	BE117729	4.69	4.49	3.71	3.52	5.30	4.01	1.01	down	9.75E-01	9.92E-01	-	-
1367888_at	Pcdh21	protocadherin 21	93662	Rn.19780	NM_053572	2.37	2.31	2.33	2.32	2.32	2.31	1.01	down	3.07E-01	8.95E-01	-	-
1393157_at	---	---	---	Rn.216467	BF389860	2.33	2.33	2.33	2.32	2.40	2.33	1.01	up	5.01E-01	8.95E-01	-	-
1397571_at	Casc3	Cancer susceptibility candidate 3	259170	Rn.162194	BF554256	3.12	3.60	3.13	3.57	3.03	3.19	1.01	down	9.33E-01	9.81E-01	-	-
1375904_at	---	---	---	Rn.16505	AI011285	7.46	7.49	7.45	7.38	7.46	7.63	1.01	up	7.96E-01	9.34E-01	-	-
1392560_at	Pip5k1a	phosphatidylinositol-4-phosphate 5-kinase, type 1, alpha	365865	Rn.1836	BG153281	3.56	3.55	4.50	3.99	4.16	3.52	1.01	up	9.58E-01	9.89E-01	-	-
1398222_at	Rnf24	ring finger protein 24	362218	Rn.59409	BF399554	2.45	2.53	2.43	2.45	2.46	2.44	1.01	down	5.43E-01	8.95E-01	-	-
1396500_at	---	---	---	Rn.219452	BE120381	2.50	2.50	2.53	2.49	2.52	2.46	1.01	down	3.70E-01	8.95E-01	-	-
1393788_at	Catl10	cystatin 10 (chondrocytes)	366219	Rn.148733	BI283606	2.42	2.40	2.46	2.41	2.42	2.39	1.01	down	3.95E-01	8.95E-01	-	-
1384176_at	---	---	---	---	BF419876	2.42	2.40	2.43	2.38	2.42	2.40	1.01	down	1.72E-01	8.95E-01	-	-
1368980_at	Plce1	phospholipase C, epsilon 1	114633	Rn.64650	NM_053758	2.39	2.38	2.47	2.38	2.42	2.37	1.01	down	5.74E-01	8.95E-01	-	-
1377965_at	Rasip1	Ras interacting protein 1	292912	Rn.23451	BE114146	2.27	2.27	2.28	2.27	2.35	2.26	1.01	up	5.42E-01	8.95E-01	-	-
1381444_at	---	---	---	---	BF386605	2.55	2.54	2.59	2.55	2.58	2.49	1.01	down	5.43E-01	8.95E-01	-	-
1384324_at	Rbm14	RNA binding motif protein 14	170900	Rn.8556	AW522810	2.53	2.54	2.57	2.54	2.53	2.51	1.01	down	2.39E-01	8.95E-01	-	-
1396763_at	---	---	---	Rn.208892	BF412654	2.44	2.37	2.38	2.39	2.38	2.36	1.01	down	4.17E-01	8.95E-01	-	-
1398640_at	---	---	---	Rn.166069	AI044871	2.34	2.34	2.40	2.34	2.35	2.33	1.01	down	3.94E-01	8.95E-01	-	-
1368278_at	Lgals2	lectin, galactoside-binding, soluble 2	171134	Rn.2982	NM_133599	2.29	2.28	2.35	2.29	2.29	2.28	1.01	down	3.94E-01	8.95E-01	-	-
1394894_at	---	---	---	Rn.207043	AW534121	2.40	2.39	2.42	2.39	2.47	2.41	1.01	up	4.30E-01	8.95E-01	-	-
1388552_at	Smpd1	sphingomyelin phosphodiesterase 1, acid lysosomal	308909	Rn.18277	BI283738	4.48	5.17	5.03	4.47	4.93	5.22	1.01	down	9.50E-01	9.85E-01	-	-
1379029_at	RGD1560191	similar to Zinc finger protein 62 homolog (Zfp-62) (ZT3)	497894	---	BI284478	4.18	4.41	5.45	5.08	3.49	5.42	1.01	down	9.79E-01	9.93E-01	-	-
1396785_at	---	---	---	Rn.161134	BF419700	2.67	2.66	2.76	2.67	2.72	2.65	1.01	down	6.17E-01	8.95E-01	-	-
1384281_at	---	---	---	Rn.13852	BI285209	7.18	6.17	6.28	6.62	6.16	6.91	1.01	up	9.80E-01	9.89E-01	-	-
1388123_at	Psbpc2	prostatic steroid-binding protein C2	293731	Rn.10394	BI279003	2.52	2.49	2.58	2.52	2.54	2.47	1.01	down	5.73E-01	8.95E-01	-	-
1398591_at	Ccrl2	chemokine (C-C motif) receptor-like 2	316019	Rn.67232	AI707080	2.30	2.29	2.36	2.29	2.30	2.29	1.01	down	3.94E-01	8.95E-01	-	-
1396336_at	---	---	---	Rn.156697	AI112744	2.32	2.31	2.37	2.32	2.33	2.31	1.01	down	3.63E-01	8.95E-01	-	-
1390425_at	---	---	---	Rn.156007	BF398716	2.39	2.37	2.39	2.38	2.44	2.39	1.01	up	3.45E-01	8.95E-01	-	-
1393595_at	Utp6	UTP6, small subunit (SSU) processome component, homolog (yeast)	360574	Rn.145141	BI289182	4.75	5.22	4.21	4.48	4.75	5.02	1.01	up	9.54E-01	9.86E-01	-	-
1395904_at	---	---	---	Rn.60146	BF388148	2.47	2.44	2.52	2.46	2.48	2.44	1.01	down	4.58E-01	8.95E-01	-	-
1398862_at	Npc2	Niemann-Pick disease, type C2	286898	Rn.3491	BI287980	8.17	7.71	7.75	7.77	7.88	8.03	1.01	up	9.08E-01	9.72E-01	-	-
1396749_at	Cabp1	calcium binding protein 1	171051	Rn.23560	BF390144	2.43	2.41	2.44	2.43	2.45	2.47	1.01	up	1.99E-01	8.95E-01	-	-
1379913_at	---	---	---	---	BE100916	2.36	2.35	2.36	2.36	2.36	2.42	1.01	up	3.83E-01	8.95E-01	-	-
1384259_at	Racgap1	Rac GTPase-activating protein 1	315298	Rn.101301	BF559151	2.49	2.48	2.50	2.48	2.58	2.47	1.01	up	5.86E-01	8.95E-01	-	-
1396954_at	---	---	---	Rn.156355	BM386206	2.51	3.18	2.72	2.44	2.83	3.08	1.01	down	9.44E-01	9.84E-01	-	-
1369159_at	Ar	androgen receptor	24208	Rn.9813	NM_012502	5.37	5.70	5.75	5.74	5.40	5.74	1.01	up	9.08E-01	9.72E-01	-	-
1387038_at	Ccs	copper chaperone for superoxide dismutase	84485	Rn.12311	NM_053425	7.09	7.51	7.51	7.08	6.73	8.24	1.01	down	9.68E-01	9.91E-01	-	-
1397906_at	---	---	---	Rn.126653	AW251988	2.62	2.62	2.69	2.62	2.64	2.72	1.01	up	6.25E-01	8.95E-01	-	-
1390086_at	---	---	---	Rn.203989	BF404536	2.34	2.33	2.40	2.33	2.34	2.32	1.01	down	4.03E-01	8.95E-01	-	-
1381862_at	---	---	---	Rn.160392	AW524296	2.50	2.44	2.50	2.47	2.48	2.43	1.01	down	4.62E-01	8.95E-01	-	-
1370858_at	Psbpc1	prostatic steroid binding protein C1	309203	Rn.10393	BI285057	2.47	2.45	2.49	2.46	2.58	2.43	1.01	up	6.93E-01	9.05E-01	-	-
1379848_at	Dfnb59	deafness, autosomal recessive 59 (human)	679552	Rn.56059	AF401801	4.44	4.84	6.11	5.10	5.90	4.33	1.01	down	9.77E-01	9.93E-01	-	-
1393926_at	Stap1	signal transducing adaptor family member 1	305269	Rn.205047	AW920039	2.46	2.44	2.49	2.44	2.46	2.42	1.01	down	3.46E-01	8.95E-01	-	-
1369819_at	Bsn	bassoon	29138	Rn.29999	NM_019146	2.44	2.38	2.40	2.39	2.39	2.39	1.01	down	3.03E-01	8.95E-01	-	-
1376907_at	---	---	---	Rn.203128	AW521452	2.49	2.48	2.52	2.49	2.50	2.45	1.01	down	3.41E-01	8.95E-01	-	-
1383029_at	---	---	---	Rn.164825	AA946413	2.48	2.45	2.51	2.53	2.49	2.47	1.01	up	4.73E-01	8.95E-01	-	-
1392752_at	Sfrs12ip1	SFRS12-interacting protein 1	361888	Rn.15726	AI101540	2.74	2.53	2.34	2.53	2.62	2.52	1.01	up	8.74E-01	9.61E-01	-	-
1387550_a_at	Slc14a2	solute carrier family 14 (urea transporter), member 2	54302	Rn.10157	NM_019347	2.73	2.72	2.74	2.70	2.84	2.71	1.01	up	6.85E-01	9.03E-01	-	-
1383411_at	---	---	---	---	BM389444	2.37	2.34	2.40	2.35	2.40	2.41	1.01	up	4.70E-01	8.95E-01	-	-
1370977_at	Dpf1	D4, zinc and double PHD fingers family 1	50545	Rn.42906	X66022	2.54	2.50	2.55	2.54	2.57	2.54	1.01	up	3.65E-01	8.95E-01	-	-
1381345_at	---	---	---	---	BF403393	2.58	2.56	2.60	2.59	2.61	2.49	1.01	down	6.45E-01	8.95E-01	-	-
1376332_at	---	---	---	Rn.210214	BF396082	2.33	2.32	2.34	2.32	2.39	2.33	1.01	up	4.13E-01	8.95E-01	-	-
1382546_at	84778 /// Phf11 ///	hypothetical protein LOC84778 /// PHD finger protein 11 /// PHD finger prote	51 /// 364393 /// 68	Rn.213394	AW920026	2.38	2.40	2.40	2.37	2.39	2.36	1.01	down	7.17E-02	8.95E-01	-	-
1393878_at	---	---	---	Rn.211597	BF416495	2.50	2.49	2.52	2.51	2.51	2.43	1.01	down	5.37E-01	8.95E-01	-	-
1383585_s_at	---	---	---	Rn.203366	AI043753	2.53	2.51	2.55	2.49	2.57	2.47	1.01	down	5.90E-01	8.95E-01	-	-
1391376_at	---	---	---	---	BF405737	2.29	2.27	2.32	2.27	2.29	2.26	1.01	down	2.96E-01	8.95E-01	-	-
1387813_at	Erbb2	v-erb-b2 erythroblastic leukemia viral oncogene homolog 2, neuro/glioblaston	24337	Rn.93966	NM_017003	3.47	2.44	2.40	2.58	2.99	2.68	1.01	down	9.59E-01	9.89E-01	-	-
1386592_at	---	---	---	---	AI639154	2.48	2.48	2.48	2.46	2.47	2.44	1.01	down	1.21E-01	8.95E-01	-	-
1376080_at	Rcor1	REST corepressor 1	314458	Rn.32217	BF409812	2.41	2.44	2.47	2.43	2.42	2.41	1.01	down	2.98E-01	8.95E-01	-	-
1382599_at	---	---	---	Rn.201887	BE103520	2.51	2.49	2.55	2.49	2.54	2.48	1.01	down	4.83E-01	8.95E-01	-	-
1369796_at	Gjd2	gap junction protein, delta 2	50564	Rn.9904	NM_019281	2.47	2.45	2.47	2.54	2.47	2.45	1.01	up	5.25E-01	8.95E-01	-	-
1396811_at	---	---	---	---	AI111472	2.44	2.43	2.47	2.43	2.44	2.41	1.01	down	2.60E-01	8.95E-01	-	-
1390280_at	---	---	---	Rn.206467	BF396115	2.38	2.42	2.38	2.38	2.38	2.36	1.01	down	2.04E-01	8.95E-01	-	-
1368611_at	Grp	gastrin releasing peptide	171101	Rn.10930	NM_133570	2.40	2.34	2.37	2.35	2.36	2.34	1.01	down	2.90E-01	8.95E-01	-	-
1395290_at	---	---	---	Rn.61424	BF393591	2.54	2.53	2.57	2.54	2.58	2.46	1.01	down	5.96E-01	8.95E-01	-	-
1376555_at	RGD1308958	Similar to chromosome 9 open reading frame 5	298020	Rn.39293	BE113184	2.30	2.29	2.30	2.30	2.30	2.35	1.01	up	3.03E-01	8.95E-01	-	-
1390747_at	---	---	---	Rn.147201	BF412714	2.61	2.59	2.63	2.59	2.62	2.55	1.01	down	4.45E-01	8.95E-01	-	-
1372980_at	Tspan33	tetraspanin 33	500065	Rn.1696	AA819250	7.43	7.33	6.98	7.39	7.59	6.81	1.01	up	9.44E-01	9.84E-01	-	-
1397038_at	---	---	---	---	BF394024	2.43	2.42	2.48	2.42	2.44	2.41	1.01	down	3.52E-01	8.95E-01	-	-
1369589_x_at	Amelx	amelogenin X chromosome	29160	Rn.11368	NM_019154	2.46	2.43	2.48	2.44	2.46	2.42	1.01	down	3.47E-01	8.95E-01	-	-
1369607_at	Fgf6	fibroblast growth factor 6	170700	Rn.81222	NM_131908	2.55	2.54	2.56	2.62	2.56	2.54	1.01	up	4.80E-01	8.95E-01	-	-
1369904_at	Gabrb1	gamma-aminobutyric acid (GABA) A receptor, beta 1	25450	Rn.207157	NM_012956	2.38	2.38	2.44	2.38	2.39	2.37	1.01	down	4.02E-01	8.95E-01	-	-
1395954_at	---	---	---	---	BF288399	2.62	3.13	2.64	3.13	2.63	2.56	1.01	down	9.39E-01	9.83E-01	-	-
1379319_at	RGD1564719	similar to RIKEN cDNA C230052I12	502320	Rn.159895	AI045149	2.41	2.40	2.41	2.41	2.47	2.41	1.01	up	3.80E-01	8.95E-01	-	-
1384143_at	Cgn	cingulin	310655	Rn.117014	BE114778	2.41	2.56	2.40	2.49	2.42	2.40	1.01	down	7.50E-01	9.19E-01	-	-
1378454_at	---	---	---	Rn.173163	BF405939	2.37	2.37	2.41	2.36	2.38	2.35	1.01	down	2.22E-01	8.95E-01	-	-
1397259_at	Fam126b	family with sequence similarity 126, member B	316415	Rn.149172	BF291133	2.53	2.50	2.58	2.51	2.56	2.47	1.01	down	6.12E-01	8.95E-01	-	-
1372716_at	---	---	---	---	BF284207	2.99	3.44	3.58	3.16	3.43	3.48	1.01	up	9.27E-01	9.79E-01	-	-
1377923_at	Stard8	StAR-related lipid transfer (START) domain containing 8	312113	Rn.14795	AA892818	5.15	4.02	5.53	4.77	4.09	3.78	1.01	down	9.73E-01	9.92E-01	-	-
1386143_at	RGD1309501	hypothetical LOC305552	305552	Rn.6266	AA799997	2.50	2.46	2.57	2.59	2.52	2.48	1.01	up	6.71E-01	9.01E-01	-	-
1396769_at	---	---	---	---	AW527250	2.38	2.41	2.40	2.38	2.39	2.36	1.01	down	1.36E-01	8.95E-01	-	-
1383033_at	---	---	---	---	AI059738	2.51	2.49	2.54	2.49	2.50	2.49	1.01	down	2.42E-01	8.95E-01	-	-
1397431_at	---	---	---	Rn.61741	BE102945	2.41	2.39	2.46	2.39	2.41	2.39	1.01	down	3.97E-01	8.95E-01	-	-
1383113_at	---	---	---	Rn.172117	AW523077	2.40	2.45	2.40	2.40	2.40	2.39	1.01	down	3.05E-01	8.95E-01	-	-
1388620_at	Tada3l	transcriptional adaptor 3 (NGG1 homolog, yeast)-like	362414	Rn.1326	AA818192	2.40	2.76	2.39	2.41	2.39	2.82	1.01	up	9.19E-01	9.76E-01	-	-
1387365_at	Nr1h3	nuclear receptor subfamily 1, group H, member 3	58852	Rn.11209	NM_031627	8.82	8.79	8.53	8.98	7.86	9.24	1.01	down	9.65E-01	9.90E-01	-	-
1393728_at	---	---	---	Rn.11836	AA964541	2.51	2.45	2.48	2.45	2.47	2.46	1.01	down	3.40E-01	8.95E-01	-	-
1374383_at	---	---	---	Rn.156608	BE121006	2.44	2.41	2.48	2.42	2.44	2.42	1.01	down	4.02E-01	8.95E-01	-	-
1385839_x_at	Tm2d1	TM2 domain containing 1	362545	Rn.198278	BF287928	8.18	8.51	9.01	8.47	8.69	8.47	1.01	down	9.40E-01	9.83E-01	-	-
1381318_at	Chia	chitinase, acidic	113901	Rn.43692	AI639227	2.42	2.40	2.44	2.40	2.42	2.39	1.01	down	2.69E-01	8.95E-01	-	-
1389748_at	---	---	---	Rn.169350	BE118122	2.69	2.51	2.47	2.58	2.52	2.51	1.01	down	7.89E-01	9.32E-01	-	-
1373322_at	---	---	---	Rn.146584	BF564703	2.45	2.45	2.47	2.45	2.46	2.41	1.01	down	2.63E-01	8.95E-01	-	-
1391277_at	S100a5	S100 calcium binding protein A5	295211	Rn.11640	BF548433	2.47	2.44	2.48	2.44	2.45	2.43	1.01	down	2.53E-01	8.95E-01	-	-
1384146_at	---	---	---	Rn.210466	AI236895	6.22	6.37	5.63	6.87	6.19	5.10	1.01	down	9.73E-01	9.92E-01	-	-
1381699_at	---	---	---	Rn.206850	BF389280	2.43	2.43	2.46	2.42	2.43	2.40	1.01	down	2.16E-01	8.95E-01	-	-
1374315_at	---	---	---	---	AI228079	3.11	2.95	2.68	2.90	2.91	2.87	1.01	down	8.82E-01	9.64E-01	-	-
1371647_at	Tm9sf3	transmembrane 9 superfamily member 3	309475	Rn.17150	AA963367	10.70	10.62	10.77	10.74	10.68	10.73	1.01	up	6.89E-01	9.05E-01	-	-
1397000_at	LOC680133	Similar to TBC1 domain family, member 8	680133	Rn.205305	AF419803	2.38	2.37	2.39	2.37	2.46	2.36	1.01	up	5.85E-01	8.95E-01	-	-
1378944_at	---	---	---	---	BE119619	2.45	2.45	2.46	2.41	2.45	2.44	1.01	down	2.41E-01	8.95E-01	-	-
1385138_at	---	---	---	Rn.156251	BF401469	4.96	5.04	5.94	5.40	5.00	5.61	1.01	up	9.59E-01	9.89E-01	-	-
1385298_at	RGD1564851	similar to putative anion transporter	366909	Rn.73969	AI555358	2.44	2.43	2.49	2.44	2.44	2.43	1.01	down	3.75E-01	8.95E-01	-	-
1384389_at	---	---	---	Rn.26706	AI112040	2.49	2.47	2.53	2.48	2.49	2.47	1.01	down	3.12E-01	8.95E-01	-	-
1375822_at	---	---	---	Rn.209883	BF413399	2.42	2.42	2.49	2.42	2.43	2.42	1.01	down	4.75E-01	8.95E-01	-	-
1373845_at	LOC688235	similar to Nucleolar protein 11	688235	---	AA944773	5.95	6.59	5.74	5.91	5.91	6.52	1.01	up	9.54E-01	9.86E-01	-	-
1395112_at	---	---	---	Rn.168138	AI555810	2.37	2.35	2.39	2.35	2.36	2.34	1.01	down	2.58E-01	8.95E-01	-	-
1395999_at	---	---	---	Rn.63656	BF419807	2.54	2.50	2.59	2.53	2.53	2.50	1.01	down	5.21E-01	8.95E-01	-	-
1380593_at	---	---	---	Rn.203808	AI008189	2.40	2.38	2.41	2.40	2.45	2.39	1.01	down	4.00E-01	8.95E-01	-	-
1369035_a_at	Kcnj6	potassium inwardly-rectifying channel, subfamily J, member 6	25743	Rn.10185	NM_013192	2.43	2.42	2.44	2.41	2.43	2.39	1.01	down	2.41E-01	8.95E-01	-	-
1391873_at	---	---	---	Rn.37683	AI176950	2.35	2.38	2.36	2.34	2.36	2.33	1.01	down	1.46E-01	8.95E-01	-	-
1390003_at	Jmjd3	jumonji domain containing 3	363630	Rn.205533	BE118720	2.29	2.28	2.29	2.33	2.32	2.28	1.01	up	2.29E-01	8.95E-01	-	-
1394134_at	Dock8	dedicator of cytokinesis 8	499337	Rn.164225	AA893933	2.26	2.26	2.27	2.33	2.26	2.25	1.01	up	4.47E-01	8.95E-01	-	-
1369848_at	Kcns2	potassium voltage-gated channel, delayed-rectifier, subfamily S, member 2	66022	Rn.64498	NM_023966	2.36	2.35	2.41	2.35	2.36	2.34	1.01	down	3.76E-01	8.95E-01	-	-
1396071_at	---	---	---	Rn.205225	AI502944	2.57	2.51	2.64	2.55	2.64	2.48	1.01	down	7.57E-01	9.21E-01	-	-
1374425_at	Tle1	transducin-like enhancer of split 1 (E(sp1) homolog, Drosophila)	362533	Rn.6875	BG380534	2.38	2.38	2.40	2.45	2.39	2.38	1.01	up	4.64E-01	8.95E-01	-	-
1370710_at	Asmt	acetylserotonin O-methyltransferase	246281	Rn.10768	L78306	2.51	2.47	2.54	2.49	2.53	2.45	1.01	down	5.23E-01

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1383857_at	---	---	---	---	BF411408	2.42	2.41	2.43	2.41	2.43	2.36	1.01	down	4.29E-01	8.95E-01	-	-
1393471_at	---	---	---	Rn.203836	AI175908	2.37	2.33	2.34	2.33	2.33	2.31	1.01	down	2.88E-01	8.95E-01	-	-
1397871_at	---	---	---	Rn.27629	AI446643	2.55	2.54	2.64	2.54	2.62	2.51	1.01	down	6.90E-01	9.05E-01	-	-
1390957_at	---	---	---	Rn.26760	AI112360	4.99	4.52	4.35	4.70	4.06	5.04	1.01	down	9.57E-01	9.88E-01	-	-
1394144_at	Tubb6	tubulin, beta 6	307351	Rn.98430	BG153275	2.57	2.54	2.61	2.55	2.57	2.54	1.01	down	4.28E-01	8.95E-01	-	-
1369147_at	Ahr	aryl hydrocarbon receptor	25690	Rn.91370	NM_013149	2.98	2.95	2.96	2.96	3.04	2.95	1.01	up	5.36E-01	8.95E-01	-	-
1397102_at	---	---	---	Rn.203093	AI502196	2.40	2.39	2.40	2.46	2.40	2.38	1.01	up	4.68E-01	8.95E-01	-	-
1377832_at	Plk4	polo-like kinase 4 (Drosophila)	310344	Rn.14848	BE109322	2.43	2.38	2.41	2.39	2.40	2.37	1.01	down	3.28E-01	8.95E-01	-	-
1395527_at	LOC314655	similar to a disintegrin-like and metalloprotease (reprolysin type) with thrombo	314655	Rn.135600	AW534755	2.45	2.41	2.44	2.42	2.43	2.39	1.01	down	2.93E-01	8.95E-01	-	-
1377003_at	---	---	---	---	AW528437	2.38	2.36	2.38	2.34	2.37	2.35	1.01	down	1.28E-01	8.95E-01	-	-
1391060_at	---	---	---	Rn.35547	BG371670	2.37	2.36	2.38	2.43	2.37	2.36	1.01	up	4.58E-01	8.95E-01	-	-
1390761_at	---	---	---	Rn.209783	BF403233	2.56	2.49	2.53	2.51	2.51	2.50	1.01	down	3.98E-01	8.95E-01	-	-
1381983_at	Dennd1a	DENN/MADD domain containing 1A	311913	Rn.92793	AI454019	2.99	2.98	2.99	2.98	3.09	2.95	1.01	up	6.62E-01	8.98E-01	-	-
1396612_at	Ank2	ankyrin 2, neuronal	362036	Rn.133131	BF413286	2.41	2.39	2.49	2.40	2.44	2.39	1.01	down	6.16E-01	8.95E-01	-	-
1370966_at	Hcn2	hyperpolarization activated cyclic nucleotide-gated potassium channel 2	114244	Rn.162907	AW532988	2.26	2.20	2.21	2.21	2.21	2.20	1.01	down	3.23E-01	8.95E-01	-	-
1396711_at	Obsl1	obscurin-like 1	363259	Rn.776	BF391506	2.32	2.31	2.32	2.31	2.32	2.26	1.01	down	3.13E-01	8.95E-01	-	-
1392252_at	---	---	---	Rn.148042	AA819893	2.32	2.31	2.37	2.31	2.32	2.30	1.01	down	3.72E-01	8.95E-01	-	-
1377831_at	---	---	---	Rn.16867	BF285316	2.58	2.60	2.62	2.57	2.59	2.58	1.01	down	2.31E-01	8.95E-01	-	-
1396734_at	---	---	---	---	BF394498	2.42	2.41	2.44	2.51	2.42	2.40	1.01	up	5.95E-01	8.95E-01	-	-
1373710_at	---	---	---	Rn.176436	BI296600	2.53	2.51	2.54	2.52	2.54	2.47	1.01	down	4.35E-01	8.95E-01	-	-
1394074_at	Zfp276	zinc finger protein (C2H2 type) 276	307924	Rn.140797	AI059004	2.31	2.30	2.34	2.30	2.31	2.29	1.01	down	2.66E-01	8.95E-01	-	-
1369339_at	Dcc	deleted in colorectal carcinoma	25311	Rn.10666	NM_012841	2.43	2.40	2.42	2.40	2.41	2.38	1.01	down	2.36E-01	8.95E-01	-	-
1370949_at	46 /// LOC681252	similar to Myristoylated alanine-rich C-kinase substrate (MARCKS) (ACAMP-43 ///	294446 /// 68	Rn.9560	BE111706	7.35	8.44	6.98	7.34	8.34	7.02	1.01	down	9.75E-01	9.93E-01	-	-
1393573_at	Pde8b	phosphodiesterase 8B, cGMP-specific, rod, beta	289878	Rn.19724	AI575628	2.46	2.45	2.49	2.46	2.58	2.43	1.01	up	6.97E-01	9.07E-01	-	-
1380774_at	---	---	---	Rn.171490	AI227918	3.30	3.38	3.07	3.52	3.17	3.11	1.01	up	9.09E-01	9.72E-01	-	-
1373802_at	Chm	Choroideremia (Rab escort protein 1)	24942	Rn.10191	BF392902	2.35	2.44	2.35	2.50	2.35	2.34	1.01	up	7.65E-01	9.23E-01	-	-
1378815_at	RGD1306924	similar to Gamma-tubulin complex component 4 (GCP-4)	362203	---	BG373276	2.44	2.45	2.47	2.43	2.46	2.41	1.01	down	3.16E-01	8.95E-01	-	-
1393297_at	Pou2af1	POU class 2 associating factor 1	690528	Rn.15298	BG377979	2.33	2.32	2.35	2.41	2.34	2.32	1.01	up	5.10E-01	8.95E-01	-	-
1370404_at	Cst12	cystatin 12	266776	Rn.58124	AF440736	2.36	2.35	2.36	2.35	2.43	2.35	1.01	up	5.07E-01	8.95E-01	-	-
1387429_at	Adrbk1	adrenergic, beta, receptor kinase 1	25238	Rn.13010	NM_012776	5.08	4.91	4.94	4.91	4.95	5.00	1.01	down	7.60E-01	9.22E-01	-	-
1377152_at	Rfx1	regulatory factor X, 1 (influences HLA class II expression)	288906	Rn.154447	AI111991	5.51	5.69	5.52	5.72	5.52	5.41	1.01	down	8.66E-01	9.58E-01	-	-
1371432_at	Vat1	vesicle amine transport protein 1 homolog (T californica)	287721	Rn.9118	BI284849	6.87	6.90	5.60	6.02	6.45	6.84	1.01	down	9.70E-01	9.91E-01	-	-
1397127_at	---	---	---	Rn.207526	BE102322	2.41	2.40	2.45	2.40	2.42	2.38	1.01	down	3.65E-01	8.95E-01	-	-
1380144_at	Mob4r1a	MOB1, Mps One Binder kinase activator-like 1A (yeast)	360920	Rn.7775	BE103512	4.82	4.74	4.39	4.54	4.12	5.23	1.01	down	9.58E-01	9.89E-01	-	-
1397824_at	RGD1562407	similar to WAC	307029	---	BG665671	4.19	4.95	4.52	4.82	4.37	4.43	1.01	down	9.45E-01	9.84E-01	-	-
1384492_at	---	---	---	---	AA998153	2.41	2.32	2.41	2.41	2.38	2.40	1.01	up	5.65E-01	8.95E-01	-	-
1397295_at	---	---	---	---	BF291108	2.44	2.44	2.45	2.51	2.44	2.44	1.01	up	4.57E-01	8.95E-01	-	-
1377910_at	Nol5	nucleolar protein 5	60373	Rn.43930	BF407333	2.60	2.57	2.65	2.55	2.63	2.57	1.01	down	6.06E-01	8.95E-01	-	-
1397460_at	---	---	---	Rn.208698	BE119491	2.52	2.49	2.56	2.50	2.54	2.46	1.01	down	5.57E-01	8.95E-01	-	-
1377368_at	---	---	---	Rn.206746	AW529710	2.48	2.48	2.53	2.48	2.50	2.45	1.01	down	4.00E-01	8.95E-01	-	-
1377954_at	---	---	---	Rn.15097	AA800691	2.48	2.46	2.52	2.47	2.49	2.44	1.01	down	4.04E-01	8.95E-01	-	-
1388166_at	OC314509 /// LO	immunoglobulin heavy chain 6 /// similar to single chain Fv antibody fragment	57 /// 314509 /// 67	Rn.201760	AI411693	2.38	2.33	2.34	2.33	2.34	2.33	1.01	down	2.71E-01	8.95E-01	-	-
1367899_at	F2r	coagulation factor II (thrombin) receptor	25439	Rn.2609	NM_012950	5.15	3.81	4.79	5.50	4.29	4.02	1.01	up	9.76E-01	9.93E-01	-	-
1378695_at	---	---	---	Rn.13760	AI007942	2.57	2.54	2.57	2.55	2.56	2.51	1.01	down	3.65E-01	8.95E-01	-	-
1393263_at	---	---	---	Rn.203498	AW522530	2.39	2.37	2.43	2.38	2.39	2.36	1.01	down	3.93E-01	8.95E-01	-	-
1371979_at	Srebf2	sterol regulatory element binding transcription factor 2	300095	Rn.41063	AI170663	3.59	3.61	3.14	3.21	3.08	4.12	1.01	up	9.60E-01	9.89E-01	-	-
1398249_at	Slc25a20	solute carrier family 25 (carnitine/acylcarnitine translocase), member 20	117035	Rn.3289	NM_053965	6.67	6.78	6.95	6.64	6.95	6.76	1.01	down	8.80E-01	9.63E-01	-	-
1376286_at	---	---	---	Rn.210145	BF403823	2.31	2.33	2.31	2.30	2.30	2.29	1.01	down	7.31E-02	8.95E-01	-	-
1373227_at	Slc35a2	solute carrier family 35, member A2	100158233	Rn.2866	BE098851	2.54	2.49	2.52	2.51	2.51	2.47	1.01	down	4.19E-01	8.95E-01	-	-
1380548_at	Ift57	intraflagellar transport 57 homolog (Chlamydomonas)	303968	Rn.63846	BF420494	8.98	9.19	9.81	8.89	9.59	9.56	1.01	up	9.57E-01	9.88E-01	-	-
1375394_at	Otx2	orthodenticle homolog 2 (Drosophila)	305858	Rn.35222	BG373112	2.31	2.31	2.37	2.31	2.32	2.30	1.01	down	3.54E-01	8.95E-01	-	-
1374926_at	Dmwd /// Rsh1	dystrophia myotonica, WD repeat containing /// radial spokehead-like 1	292684 /// 680252	Rn.138418	AI102985	2.75	2.76	3.20	2.77	3.11	2.77	1.01	down	9.23E-01	9.77E-01	-	-
1398138_at	---	---	---	Rn.41364	AI177693	2.41	2.40	2.46	2.41	2.43	2.39	1.01	down	4.16E-01	8.95E-01	-	-
1396703_at	Ccdc158	coiled-coil domain containing 158	289502	Rn.51864	BF412919	2.48	2.45	2.51	2.48	2.49	2.53	1.01	up	4.57E-01	8.95E-01	-	-
1392734_at	Nrcam	neuronal cell adhesion molecule	497815	Rn.10691	AI146667	2.51	2.48	2.55	2.49	2.53	2.46	1.01	down	5.43E-01	8.95E-01	-	-
1390568_at	---	---	---	Rn.6713	BF551027	2.48	2.44	2.50	2.46	2.46	2.43	1.01	down	3.85E-01	8.95E-01	-	-
1397775_at	---	---	---	Rn.59518	BF402577	2.37	2.36	2.42	2.36	2.37	2.35	1.01	down	3.93E-01	8.95E-01	-	-
1376121_at	---	---	---	Rn.205145	BE107051	2.61	2.57	2.67	2.65	2.63	2.62	1.01	up	5.67E-01	8.95E-01	-	-
1385577_at	---	---	---	---	AW531898	5.61	6.17	5.25	5.74	5.55	5.68	1.01	down	9.47E-01	9.85E-01	-	-
1396750_at	---	---	---	Rn.100561	AW528700	2.50	2.50	2.52	2.49	2.51	2.46	1.01	down	2.86E-01	8.95E-01	-	-
1377372_at	---	---	---	Rn.41487	AW254527	2.60	2.64	2.60	2.60	2.60	2.59	1.01	down	2.35E-01	8.95E-01	-	-
1377163_at	Inhbb	Inhibin beta-B	25196	Rn.35074	BM385741	2.38	2.37	2.38	2.37	2.39	2.42	1.01	up	2.57E-01	8.95E-01	-	-
1381240_at	---	---	---	Rn.199451	BF418971	2.48	2.48	2.52	2.59	2.49	2.46	1.01	up	6.61E-01	8.98E-01	-	-
1371654_at	RGD1305350	similar to RIKEN cDNA 2510039O18	313699	Rn.99087	BF417252	5.31	6.36	5.35	6.08	5.29	5.72	1.01	up	9.65E-01	9.90E-01	-	-
1369174_at	Smad1	SMAD family member 1	25671	Rn.10635	NM_013130	2.44	2.42	2.47	2.43	2.44	2.41	1.01	down	3.11E-01	8.95E-01	-	-
1383908_at	Nsun6	NOL1/NOP2/Sun domain family, member 6	307148	Rn.11617	BF416685	2.52	2.50	2.53	2.56	2.55	2.49	1.01	up	4.29E-01	8.95E-01	-	-
1391349_at	Sars	seryl-tRNA synthetase	266975	Rn.73067	BG375114	2.36	2.35	2.37	2.43	2.37	2.34	1.01	up	5.25E-01	8.95E-01	-	-
1382054_at	---	---	---	Rn.24009	BF285731	2.39	2.38	2.45	2.39	2.40	2.38	1.01	down	4.09E-01	8.95E-01	-	-
1393056_at	---	---	---	---	AI767722	2.54	2.50	2.56	2.52	2.54	2.48	1.01	down	5.14E-01	8.95E-01	-	-
1394483_at	Adamts5	ADAM metallopeptidase with thrombospondin type 1 motif, 5	304135	Rn.107051	AW535310	2.51	2.49	2.52	2.50	2.51	2.46	1.01	down	3.25E-01	8.95E-01	-	-
1369789_at	Glra3	glycine receptor, alpha 3	114516	Rn.10038	M55250	2.44	2.36	2.45	2.46	2.47	2.39	1.01	up	6.34E-01	8.95E-01	-	-
1392913_at	Znf710	zinc finger protein 710	293044	Rn.124431	AA964151	2.37	2.39	2.41	2.44	2.39	2.39	1.01	up	4.06E-01	8.95E-01	-	-
1392017_at	---	---	---	---	BF397766	2.47	2.41	2.46	2.42	2.44	2.41	1.01	down	3.72E-01	8.95E-01	-	-
1380520_at	---	---	---	Rn.134219	BI295810	2.54	2.50	2.56	2.52	2.54	2.48	1.01	down	4.80E-01	8.95E-01	-	-
1386018_at	---	---	---	---	AI176253	2.68	2.65	2.71	2.67	2.80	2.62	1.01	up	7.45E-01	9.17E-01	-	-
1383297_at	Wdr5	WD repeat domain 5	362093	Rn.106818	BI275422	2.58	2.58	2.59	2.65	2.59	2.57	1.01	up	4.36E-01	8.95E-01	-	-
1377945_at	Ddx18	DEAD (Asp-Glu-Ala-Asp) box polypeptide 18	308490	Rn.26598	AI111512	5.81	6.06	6.63	5.95	6.26	6.35	1.01	up	9.46E-01	9.85E-01	-	-
1394840_at	---	---	---	Rn.123716	AI511432	2.50	2.49	2.51	2.49	2.50	2.45	1.01	down	3.07E-01	8.95E-01	-	-
1386923_at	Ube2b	ubiquitin-conjugating enzyme E2B, RAD6 homology (S. cerevisiae)	81816	Rn.20766	NM_031138	6.64	6.85	6.41	6.82	6.51	6.51	1.01	down	9.11E-01	9.73E-01	-	-
1392214_at	---	---	---	Rn.136438	AW532375	2.43	2.41	2.45	2.42	2.44	2.49	1.01	up	4.63E-01	8.95E-01	-	-
1396687_at	---	---	---	---	BF412949	2.40	2.40	2.41	2.39	2.41	2.35	1.01	down	3.14E-01	8.95E-01	-	-
1388288_at	Slco2b1	solute carrier organic anion transporter family, member 2b1	140860	Rn.44538	X61106	2.65	2.65	2.67	2.65	2.66	2.62	1.01	down	1.92E-01	8.95E-01	-	-
1378580_at	---	---	---	Rn.134946	AI007848	2.51	2.50	2.54	2.50	2.52	2.48	1.01	down	3.21E-01	8.95E-01	-	-
1370603_a_at	Ptprc	protein tyrosine phosphatase, receptor type, C	24699	Rn.90166	M10072	2.42	2.37	2.39	2.38	2.39	2.36	1.01	down	3.30E-01	8.95E-01	-	-
1397045_at	---	---	---	Rn.211585	BF416297	2.36	2.40	2.38	2.36	2.37	2.35	1.01	down	1.88E-01	8.95E-01	-	-
1387310_at	Atp2c2	ATPase, Ca++ transporting, type 2C, member 2	171496	Rn.163411	NM_134462	2.70	2.69	2.75	2.70	2.69	2.61	1.01	down	3.70E-01	8.95E-01	-	-
1369110_x_at	RT1-Aw2	RT1 class Ib, locus Aw2	24737	Rn.40130	NM_012645	2.75	2.61	2.63	2.63	2.67	2.63	1.01	down	6.99E-01	9.07E-01	-	-
1389653_at	Pcdhb9	protocadherin beta 9	680047	Rn.169512	AW526087	2.45	2.44	2.51	2.44	2.48	2.42	1.01	down	5.48E-01	8.95E-01	-	-
1391156_at	Podn1	podocan-like 1	289907	Rn.103275	BI3040040	2.46	2.43	2.44	2.42	2.45	2.41	1.01	down	2.55E-01	8.95E-01	-	-
1379180_at	---	---	---	Rn.207356	BF394667	2.47	2.47	2.46	2.48	2.52	2.46	1.01	up	3.27E-01	8.95E-01	-	-
1388056_at	Oas1b	2-5 oligoadenylate synthetase 1B	246268	Rn.14530	AF068268	2.48	2.46	2.53	2.47	2.51	2.44	1.01	down	5.39E-01	8.95E-01	-	-
1375195_at	---	---	---	Rn.199969	BG376894	2.54	2.51	2.58	2.53	2.57	2.47	1.01	down	6.16E-01	8.95E-01	-	-
1387985_a_at	Otp3	alpha-2u globulin PGCL4	259247	Rn.86413	AB039825	2.59	2.57	2.67	2.58	2.64	2.55	1.01	down	6.43E-01	8.95E-01	-	-
1374104_at	Cldn5	claudin 5	65131	Rn.17420	BI281680	2.40	2.35	2.36	2.35	2.36	2.34	1.01	down	3.48E-01	8.95E-01	-	-
1388077_a_at	P2rx3	purinergic receptor P2X, ligand-gated ion channel, 3	81739	Rn.10388	AF084975	2.40	2.50	2.40	2.44	2.40	2.39	1.01	down	6.18E-01	8.95E-01	-	-
1388168_a_at	Fgfr2	fibroblast growth factor receptor 2	25222	Rn.12732	L19107	2.32	2.31	2.33	2.38	2.33	2.31	1.01	up	4.14E-01	8.95E-01	-	-
1376193_at	---	---	---	Rn.16652	AA819658	2.74	2.71	2.91	2.89	2.91	2.62	1.01	up	8.72E-01	9.61E-01	-	-
1381750_at	---	---	---	---	AW251098	2.64	2.61	2.42	2.58	2.61	2.53	1.01	up	8.06E-01	9.38E-01	-	-
1379014_at	Arf2	ADP-ribosylation factor 2	79119	Rn.62175	BF412835	2.44	2.43	2.49	2.44	2.45	2.42	1.01	down	4.21E-01	8.95E-01	-	-
1385599_at	RSA-14-44	RSA-14-44 protein	297173	Rn.47032	BF409564	2.40	2.36	2.41	2.37	2.39	2.34	1.01	down	3.96E-01	8.95E-01	-	-
1393976_at	Stbp	Stem-loop binding protein	288962	Rn.198386	BE110459	2.65	2.60	2.75	2.62	2.76	2.56	1.01	down	8.08E-01	9.38E-01	-	-
1398155_at	---	---	---	Rn.210118	BF394133	2.44	2.41	2.47	2.42	2.45	2.39	1.01	down	4.53E-01	8.95E-01	-	-
1389885_at	Limd2	LIM domain containing 2	360646	Rn.112761	BI294855	2.56	2.31	2.34	2.36	2.34	2.46	1.01	down	4.36E-01	9.48E-01	-	-
1398702_at	---	---	---	Rn.208539	BE117785	2.51	2.51	2.56	2.51	2.54	2.48	1.01	down	4.72E-01	8.95E-01	-	-
1377460_at	---	---	---	Rn.77696	BM383995	2.38	2.37	2.43	2.37	2.38	2.37	1.01	down	3.51E-01	8.95E-01	-	-
1381672_at	Ldlrap1	low density lipoprotein receptor adaptor protein 1	500564	Rn.62309	BE097787	4.53	3.97	3.22	3.67	4.28	3.71	1.01	down	9.67E-01	9.90E-01	-	-
1377452_at	---	---	---	---	AW251280	2.38	2.40	2.39	2.36	2.38	2.36	1.01	down	1.19E-01	8.95E-01	-	-
1393197_at	Abhd8	abhydrolase domain containing 8	306338	Rn.22147	BG376055	2.37	2.36	2.37	2.36	2.37	2.42	1.01	up	3.72E-01	8.95E-01	-	-
1372633_at	Spg20	spastic paraplegia 20, spartin (Troyer syndrome) homolog (human)	295053	Rn.7964	AI178531	2.98	2.95	2.98	2.95	3.00	3.02	1.01	up	4.80E-01	8.95E-01	-	-
1382136_at	Slc2a9	solute carrier family 2 (facilitated glucose transporter), member 9	501925	Rn.92551	AA858900	5.08	3.89	4.36	4.43	4.44	4.52	1.01	up	9.59E-01	9.89E-01	-	-
1394610_at	Grb10	growth factor receptor bound protein 10	498416	Rn.63942	BF408313	4.52	3.82	6.36	5.07	4.87	4.81	1.01	up	9.81E-01	9.94E-01	-	-
1397799_at	Ccdc40	coiled-coil domain containing 40	287867	Rn.58111	BF393651	2.54	2.53	2.59	2.52	2.56	2.52	1.01	down	4.89E-01	8.95E-01	-	-
1369239_at	Gabrr2	gamma-aminobutyric acid (GABA) receptor, rho 2	29695	Rn.48659	NM_017292	2.40	2.45	2.41	2.40	2.41	2.40	1.01	down	2.94E-01	8.95E-01	-	-
1397115_at	---	---	---	Rn.211128	BF409361	2.53	2.53	2.58	2.52	2.54	2.52	1.01	down	3.18E-01	8.95E-01	-	-
1384689_at	Pln	phospholamban	64672	Rn.9740	AI554976	2.51	2.48	2.54	2.49	2.50	2.48	1.01	down	3.66E-01	8.95E-01	-	-
1390368_at	Zfhx2	zinc finger homeobox 2	305888	Rn.161359	AI716535	2.51	2.49	2.54	2.50	2.52	2.47	1.01	down	4.02E-01	8.95E-01	-	-
1380887_at	---	---	---	Rn.146777	BF389417	2.34	2.34	2.35	2.32	2.33	2.31	1.01	down	7.63E-02	8.95E-01	-	-
1398013_at	---	---	---	Rn.26740	AI112236	2.54	2.53	2.58	2.53	2.56	2.51	1.01	down	4.76E-01	8.95E-01	-	-
1396206_at	RGD1562846	similar to Docking protein 5 (Downstream of tyrosine kinase 5) (Protein dok-5	502694	Rn.74088	BG665525	2.42	2.39	2.42	2.40	2.40	2.37	1.01	down	2.19E-01	8.95E-01	-	-
1386446_at	Cdh1	cadherin 1	83502	Rn.1303	BG057557	2.46	2.44	2.49	2.44	2.48	2.42	1.01	down	4.39E-01	8.95E-01	-	-
1394135_at	---	---	---	Rn.169196	AI639109	2.57	2.53	2.65	2.55	2.74	2.52	1.01	up	8.22E-01	9.43E-01	-	-
1376329_at	---	---	---	Rn.47467	BI295813	2.37	2.41	2.38	2.36	2.38	2.36	1.01	down	1.87E-01	8.95E-01	-	-
1395977_at	---	---	---	---	AW530722	2.48	2.49	2.49	2.47	2.49	2.44	1.01	down	3.14E-01	8.95E-01	-	-
1396979_at	MGC114440	similar to RIKEN cDNA 4930555I21	500566	Rn.211002	BF404542	2.37	2.36	2.42	2.36	2.38	2.35	1.01	down	3.79E-01	8.95E-01	-	-
1370650_s_at	krb2 /// RGD13084	bradykinin receptor B2 /// similar to RIKEN cDNA 4933433P14 gene	25245 /// 362778	Rn.3701	BF408558	2.45	2.43	2.44	2.43	2.44	2.39	1.01	down	3.06E-01	8.95E-01	-	-
1375263_at	---	---	---	Rn.212029	BI296498	2.59	2.56	2.68	2.59	2.66	2.53	1.01	down	7.32E-01	9.14E-01	-	-
1376557_at	---	---	---	Rn.154107	BF393295	2.47	2.44	2.49	2.45	2.47	2.42	1.01	down	3.96E-01	8.95E-01	-	-
1367605_at	Pfn1	profilin 1	64303	Rn.1152	NM_022511	10.14	9.87	9.96	10.29	9.88	9.85	1.01	up	9.13E-01	9.74E-01	-	-
1387771_at	Cggbp1	CGG triplet repeat binding protein 1	288353	Rn.101743	BG668182	6.09	5.30	6.24	5.56	6.33	5.69	1.01	down	9.62E-01	9.89E-01	-	-
1378201_at	---	---	---	Rn.203872	BF392915	2.30	2.34	2.30	2.30	2.30	2.29	1.01	down	2.51E-01	8.95E-01	-	-
1374167_at	rCG_51406	neuritin 1-like	100189544	Rn.220423	AW532828	2.47	2.46	2.47	2.46	2.47	2.41	1.01	down	4.26E-01	8.95E-01	-	-
1376548_at	Ppp1r12c	Protein phosphatase 1, regulatory (inhibitor) subunit 12C	499076	Rn.41379	BE099685	2.28	2.27	2.28	2.26	2.34	2.27	1.01	up	4.98E-01	8.95E-01	-	-
1372500_at	Tmod3	tropomodulin 3	300838	Rn.146101	BG378269	6.60	6.59	6.62	6.59	6.60	6.68	1.01	up	5.50E-01	8.95E-01	-	-
1369349_a_at	Pde1a	phosphodiesterase 1A	140928	Rn.212754	NM_080893	2.51	2.50	2.56	2.50	2.51	2.50	1.01	down	3.84E-01	8.95E-01	-	-
1392206_at	Slc35f4	solute carrier family 35, member F4	305865	Rn.102592	AI111510	2.40	2.39	2.44	2.40	2.41	2.37	1.01	down	3.82E-01	8.95E-01	-	-
1375489_at	RGD1565057	similar to hypothetical protein FLJ32871	309300	Rn.219529	BF405610	2.47	2.45	2.48	2.45	2.44	2.45	1.01	down	7.81E-02	8.95E-01	-	-
1381309_at	---	---	---	Rn.34540	AI453886	2.46	2.45	2.47	2.45	2.46	2.41	1.01	down	2.99E-01	8.95E-01	-	-
1375103_at	---	---	---	---	BF409504	2.32	2.31	2.33	2.31	2.40	2.30	1.01	up	5.70E-01	8.95E-01	-	-
1374106_at	---	---	---	---	AI412389	2.50	2.47	2.54	2.48	2.53	2.45	1.01	down	5.70E-01	8.95E-01	-	-
1389671_at	Trpc2	transient receptor potential cation channel, subfamily C, member 2	64573	Rn.48766	AW252088	2.31	2.36	2.32	2.31	2.32	2.31	1.01	down	3.21E-01	8.95E-01	-	-
1380739_at	---	---	---	Rn.148169	BE111708	2.35	2.34	2.40	2.34	2.35	2.33	1.01	down	3.84E-01	8.95E-01	-	-
1397184_at	42077 /// RGD130	hypothetical LOC292199 /// similar to intracellular protein transport like (XM_	292199 /// 308053	Rn.38655	AI574688	2.37	2.36	2.42	2.36	2.37	2.35	1.01	down	3.62E-01	8.95E-01	-	-
1387349_at	Shox2	short stature homeobox 2	25546	Rn.11258	NM_013028	2.47	2.45	2.47	2.45	2.46	2.41

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)				REG	MTC
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval		
1397738_at	---	---	---	Rn.207787	BF416112	2.59	2.55	2.62	2.54	2.65	2.50	1.01	down	7.26E-01	9.13E-01	-	-
1368227_at	Slc28a2	solute carrier family 28 (sodium-coupled nucleoside transporter), member 2	60423	Rn.10140	NM_031664	2.63	2.58	2.65	2.66	2.64	2.61	1.01	up	5.07E-01	8.95E-01	-	-
1398063_x_at	Stfa3	stefin A3	288075	Rn.78016	BI282513	2.38	2.36	2.40	2.37	2.47	2.36	1.01	up	6.32E-01	8.95E-01	-	-
1382799_at	---	---	---	Rn.202638	AA998800	2.49	2.47	2.53	2.48	2.51	2.45	1.01	down	5.18E-01	8.95E-01	-	-
1395395_at	---	---	---	Rn.25550	BF291053	4.87	4.86	5.26	4.91	5.07	5.05	1.01	up	9.02E-01	9.70E-01	-	-
1375041_at	RGD1563982	similar to F-box only protein 27	499114	Rn.105566	AI599362	2.28	2.28	2.34	2.28	2.29	2.27	1.01	down	4.10E-01	8.95E-01	-	-
1392234_at	---	---	---	Rn.119954	BF394183	2.50	2.47	2.54	2.48	2.52	2.45	1.01	down	5.67E-01	8.95E-01	-	-
1381200_at	---	---	---	---	BE106653	2.55	2.53	2.57	2.55	2.56	2.49	1.01	down	4.80E-01	8.95E-01	-	-
1387300_at	Cmkl1	crooked neck pre-mRNA splicing factor-like 1 (Drosophila)	116481	Rn.162694	NM_053797	5.47	6.32	6.50	5.99	5.55	6.80	1.01	up	9.71E-01	9.92E-01	-	-
1378549_at	---	---	---	Rn.210232	BF396244	2.40	2.43	2.42	2.40	2.41	2.39	1.01	down	1.38E-01	8.95E-01	-	-
1390732_at	---	---	---	Rn.207001	BI294940	2.61	2.55	2.61	2.69	2.61	2.52	1.01	up	7.37E-01	9.15E-01	-	-
1380291_at	RGD1564972	RGD1564972	499666	---	BM384766	2.30	2.30	2.35	2.30	2.31	2.29	1.01	down	3.29E-01	8.95E-01	-	-
1390321_at	RGD1304693	similar to CG14803-PA	313108	Rn.23932	BI302848	2.32	2.31	2.39	2.32	2.32	2.32	1.01	down	4.99E-01	8.95E-01	-	-
1398391_at	Gnl1	guanine nucleotide binding protein-like 1	309593	Rn.35325	BG379297	4.66	4.37	4.22	4.48	4.45	4.37	1.01	up	8.96E-01	9.67E-01	-	-
1391200_at	Spry3	sprouty homolog 3 (Drosophila)	498159	Rn.141220	AW530290	2.39	2.39	2.42	2.39	2.39	2.36	1.01	down	2.69E-01	8.95E-01	-	-
1368343_at	Kcnh2	potassium voltage-gated channel, subfamily H (eag-related), member 2	117018	Rn.10970	NM_053949	2.39	2.42	2.39	2.38	2.39	2.37	1.01	down	2.45E-01	8.95E-01	-	-
1377775_at	---	---	---	Rn.31654	AI234627	2.52	2.49	2.55	2.50	2.54	2.47	1.01	down	5.46E-01	8.95E-01	-	-
1370704_at	Kcnj6	potassium inwardly-rectifying channel, subfamily J, member 6	25743	Rn.10185	AB073756	2.48	2.48	2.49	2.60	2.49	2.41	1.01	up	7.63E-01	9.22E-01	-	-
1388977_at	Cept1	choline/ethanolamine phosphotransferase 1	310773	Rn.2636	BM390401	6.05	6.25	6.76	6.28	6.28	6.44	1.01	down	9.37E-01	9.82E-01	-	-
1384661_at	RGD1565551	similar to RIKEN cDNA 4833418A01	499807	Rn.21777	AI072552	2.35	2.35	2.42	2.35	2.37	2.34	1.01	down	4.78E-01	8.95E-01	-	-
1380826_at	Myrip	myosin VIIA and Rab interacting protein	360034	Rn.161974	BF416438	2.46	2.45	2.49	2.44	2.46	2.42	1.01	down	3.23E-01	8.95E-01	-	-
1384393_at	---	---	---	Rn.171726	BE120370	2.45	2.43	2.49	2.44	2.46	2.42	1.01	down	4.13E-01	8.95E-01	-	-
1387295_at	Slc6a12	solute carrier family 6 (neurotransmitter transporter, betaine/GABA), member	50676	Rn.11352	NM_017335	2.33	2.31	2.38	2.33	2.33	2.31	1.01	down	3.92E-01	8.95E-01	-	-
1397868_at	---	---	---	Rn.216746	BF395461	2.43	2.38	2.40	2.38	2.39	2.38	1.01	down	2.26E-01	8.95E-01	-	-
1395591_at	---	---	---	Rn.159915	BF416502	2.37	2.38	2.37	2.36	2.37	2.34	1.01	down	5.45E-02	8.95E-01	-	-
1399047_at	Mrpl27	mitochondrial ribosomal protein L27	287635	Rn.18445	BF283001	6.85	7.95	7.35	7.06	7.33	7.71	1.01	down	9.63E-01	9.89E-01	-	-
1373116_at	Fau	Finkel-Biskis-Reilly murine sarcoma virus (FBR-MuSV) ubiquitously expresse	29752	Rn.5998	AI177382	11.69	11.50	11.48	11.54	11.49	11.69	1.01	up	8.47E-01	9.52E-01	-	-
1371226_at	Col2a1	collagen, type II, alpha 1	25412	Rn.10124	AF305418	2.40	2.39	2.41	2.39	2.41	2.35	1.01	down	3.81E-01	8.95E-01	-	-
1389965_at	Tgoln1	trans-golgi network protein	192152	Rn.11349	AA799818	9.15	9.07	9.55	9.36	9.05	9.42	1.01	up	9.26E-01	9.79E-01	-	-
1381784_at	Tbc1d9b	TBC1 domain family, member 9B	360520	Rn.137185	BE099215	2.58	2.57	2.61	2.58	2.58	2.66	1.01	up	5.65E-01	8.95E-01	-	-
1386003_at	LOC309220	similar to mortality factor 4 like 1 isoform b	309220	Rn.112847	BF286548	2.46	2.44	2.50	2.44	2.48	2.42	1.01	down	5.12E-01	8.95E-01	-	-
1394171_at	---	---	---	---	AI639310	2.50	2.50	2.55	2.49	2.54	2.46	1.01	down	5.63E-01	8.95E-01	-	-
1368130_at	Aldh3a1	aldehyde dehydrogenase 3 family, member A1	25375	Rn.105627	NM_031972	2.40	2.39	2.43	2.39	2.40	2.38	1.01	down	2.34E-01	8.95E-01	-	-
1368257_at	Psg19	pregnancy specific glycoprotein 19	24256	Rn.100787	NM_019126	2.52	2.50	2.55	2.49	2.55	2.47	1.01	down	5.31E-01	8.95E-01	-	-
1396269_at	---	---	---	---	BI297876	2.55	2.53	2.59	2.53	2.57	2.51	1.01	down	5.15E-01	8.95E-01	-	-
1389698_at	---	---	---	Rn.30605	AI010312	2.51	2.50	2.51	2.50	2.26	2.71	1.01	down	8.94E-01	9.67E-01	-	-
1391204_at	Smap2	small ArfGAP2	298500	Rn.203765	BF415830	2.47	2.43	2.48	2.43	2.47	2.42	1.01	down	4.14E-01	8.95E-01	-	-
1388149_at	Tap1	transporter 1, ATP-binding cassette, sub-family B (MDR/TAP)	24811	Rn.10763	X57523	2.53	2.53	2.54	2.53	2.54	2.47	1.01	down	4.14E-01	8.95E-01	-	-
1384805_at	Defb24	defensin beta 24	641632	Rn.147317	BF550925	2.41	2.39	2.45	2.39	2.41	2.39	1.01	down	4.27E-01	8.95E-01	-	-
1393680_at	Cetn1	centrin 1	84592	Rn.74781	BE103209	2.46	2.44	2.46	2.45	2.50	2.46	1.01	up	3.59E-01	8.95E-01	-	-
1369444_at	Cyp19a1	cytochrome P450, family 19, subfamily a, polypeptide 1	25147	Rn.21402	NM_017085	2.30	2.32	2.32	2.30	2.40	2.30	1.01	up	6.14E-01	8.95E-01	-	-
1367853_at	Slc12a2	solute carrier family 12 (sodium/potassium/chloride transporters), member 2	83629	Rn.11523	NM_031798	4.61	4.58	5.24	4.51	5.02	4.96	1.01	up	9.49E-01	9.85E-01	-	-
1388231_at	Mcpt3	mast cell peptidase 3	290244	Rn.205841	U67888	2.53	2.48	2.52	2.48	2.53	2.46	1.01	down	5.13E-01	8.95E-01	-	-
1397638_at	---	---	---	Rn.156214	BF412682	2.48	2.47	2.50	2.47	2.49	2.45	1.01	down	3.11E-01	8.95E-01	-	-
1380843_at	---	---	---	Rn.172619	BF414449	2.37	2.36	2.42	2.36	2.38	2.35	1.01	down	4.15E-01	8.95E-01	-	-
1379117_at	---	---	---	Rn.52558	BF415415	2.44	2.42	2.48	2.43	2.44	2.40	1.01	down	4.36E-01	8.95E-01	-	-
1382740_at	---	---	---	Rn.166468	AI071726	2.44	2.40	2.50	2.43	2.44	2.41	1.01	down	5.54E-01	8.95E-01	-	-
1378400_at	Fam122b	family with sequence similarity 122B	501647	Rn.15660	AI170395	2.43	2.43	2.43	2.43	2.49	2.43	1.01	up	4.70E-01	8.95E-01	-	-
1394180_at	---	---	---	---	AI639379	2.54	2.51	2.59	2.54	2.57	2.47	1.01	down	6.56E-01	8.98E-01	-	-
1395423_at	---	---	---	---	AW920217	3.60	4.36	4.04	3.64	3.61	4.79	1.01	up	9.69E-01	9.91E-01	-	-
1384272_at	---	---	---	Rn.204945	BG378837	2.61	2.56	2.64	2.60	2.67	2.59	1.01	up	6.13E-01	8.95E-01	-	-
1389323_at	Wdr61	WD repeat domain 61	363064	Rn.3698	BF282629	6.21	7.06	7.12	6.37	6.83	7.13	1.01	down	9.63E-01	9.89E-01	-	-
1376672_at	---	---	---	Rn.18056	AW533083	2.49	2.48	2.50	2.48	2.49	2.45	1.01	down	2.71E-01	8.95E-01	-	-
1385663_at	Usp13	ubiquitin specific protease 13 (isopeptidase T-3)	310306	Rn.16802	BF567505	2.42	2.41	2.47	2.41	2.43	2.40	1.01	down	3.50E-01	8.95E-01	-	-
1379794_at	Gzmb	granzyme B	171528	Rn.21395	AI026386	2.44	2.43	2.47	2.43	2.44	2.41	1.01	down	2.77E-01	8.95E-01	-	-
1377546_at	---	---	---	---	BF397279	2.55	2.51	2.61	2.54	2.58	2.50	1.01	down	6.25E-01	8.95E-01	-	-
1390270_at	---	---	---	Rn.210689	BF400616	2.40	2.38	2.48	2.39	2.44	2.38	1.01	down	6.34E-01	8.95E-01	-	-
1388786_at	---	---	---	Rn.7071	BF401452	3.61	2.61	2.48	2.51	3.65	2.59	1.01	up	9.73E-01	9.92E-01	-	-
1390452_at	Epb4.1l1	erythrocyte protein band 4.1-like 1	59317	Rn.20361	AI112258	2.26	2.25	2.31	2.25	2.26	2.25	1.01	down	3.81E-01	8.95E-01	-	-
1395153_at	Cldn15	claudin 15	304388	Rn.202600	AW534829	2.45	2.42	2.59	2.44	2.56	2.41	1.01	down	8.08E-01	9.38E-01	-	-
1384422_at	---	---	---	Rn.15907	AI045140	2.54	2.53	2.58	2.54	2.55	2.51	1.01	down	3.80E-01	8.95E-01	-	-
1384513_at	---	---	---	Rn.19915	AI071056	2.48	2.47	2.57	2.48	2.53	2.46	1.01	down	6.62E-01	8.98E-01	-	-
1370487_a_at	Kalrn	kalirin, RhoGEF kinase	84009	Rn.87882	U88156	2.66	2.60	2.60	2.60	2.61	2.60	1.01	down	4.50E-01	8.95E-01	-	-
1395798_at	---	---	---	---	BF388518	2.42	2.42	2.46	2.41	2.44	2.39	1.01	down	4.00E-01	8.95E-01	-	-
1383367_at	Samd14	sterile alpha motif domain containing 14	287637	Rn.156072	AI136153	2.42	2.41	2.43	2.40	2.42	2.39	1.01	down	1.93E-01	8.95E-01	-	-
1380100_at	---	---	---	Rn.23142	AW526268	2.50	2.49	2.51	2.50	2.52	2.54	1.01	up	2.31E-01	8.95E-01	-	-
1378658_at	Clca4	chloride channel accessory 4	362053	Rn.44141	BI292185	2.38	2.36	2.39	2.37	2.46	2.36	1.01	up	5.95E-01	8.95E-01	-	-
1396527_at	---	---	---	Rn.172429	BF399373	2.53	2.47	2.54	2.52	2.54	2.53	1.01	up	4.28E-01	8.95E-01	-	-
1379502_at	---	---	---	Rn.146288	AA818107	2.41	2.37	2.39	2.37	2.38	2.36	1.01	down	2.98E-01	8.95E-01	-	-
1374787_at	---	---	---	Rn.166927	BI282169	2.36	2.34	2.39	2.35	2.35	2.34	1.01	down	2.63E-01	8.95E-01	-	-
1371238_at	Grm1	glutamate receptor, metabotropic 1	24414	Rn.87787	Y18809	2.31	2.30	2.39	2.31	2.34	2.30	1.01	down	5.63E-01	8.95E-01	-	-
1388229_a_at	Mug1	murinoglobulin 1	497794	Rn.198689	M22359	2.56	2.55	2.58	2.56	2.58	2.50	1.01	down	5.26E-01	8.95E-01	-	-
1374300_at	Entpd4	ectonucleoside triphosphate diphosphohydrolase 4	361063	Rn.34634	AA997139	9.35	8.98	9.59	9.28	9.29	9.29	1.01	down	9.23E-01	9.78E-01	-	-
1377720_x_at	---	---	---	---	AA892765	10.26	9.83	10.58	10.05	10.28	10.28	1.01	down	9.41E-01	9.83E-01	-	-
1389376_at	---	---	---	Rn.169615	BE113330	2.40	2.36	2.37	2.36	2.37	2.35	1.01	down	2.92E-01	8.95E-01	-	-
1372266_at	Rev3l	REV3-like, catalytic subunit of DNA polymerase zeta (yeast)	309812	Rn.8189	BI281607	2.93	2.97	2.89	2.99	2.93	2.92	1.01	up	5.80E-01	8.95E-01	-	-
1396510_at	---	---	---	Rn.173045	BF403278	2.40	2.38	2.45	2.50	2.41	2.37	1.01	up	7.02E-01	9.07E-01	-	-
1380494_at	---	---	---	Rn.203843	BG379580	2.46	2.45	2.47	2.46	2.53	2.45	1.01	up	5.26E-01	8.95E-01	-	-
1371931_at	Gtf2i	general transcription factor II I	353256	Rn.27575	BI274753	7.95	8.58	8.45	8.36	8.28	8.39	1.01	up	9.30E-01	9.81E-01	-	-
1384726_at	---	---	---	Rn.151168	AI058852	2.56	2.52	2.62	2.54	2.59	2.52	1.01	down	6.50E-01	8.96E-01	-	-
1379598_at	---	---	---	Rn.19450	AI071649	2.87	2.35	2.34	2.86	2.34	2.32	1.01	down	9.45E-01	9.84E-01	-	-
1374658_at	Iqsec2	IQ motif and Sec7 domain 2	317433	Rn.204879	AI176974	3.24	2.86	2.78	2.94	3.01	2.98	1.01	up	9.06E-01	9.71E-01	-	-
1379125_at	---	---	---	---	BF397335	2.42	2.40	2.42	2.39	2.41	2.38	1.01	down	2.06E-01	8.95E-01	-	-
1384826_a_at	---	---	---	---	AA849871	2.53	2.50	2.58	2.51	2.56	2.48	1.01	down	6.07E-01	8.95E-01	-	-
1382399_at	Ccdc55	coiled-coil domain containing 55	303346	Rn.145937	AW530026	6.09	6.07	6.14	6.03	6.14	6.08	1.01	down	6.43E-01	8.95E-01	-	-
1390530_at	---	---	---	Rn.227717	AI169239	9.32	8.84	9.45	9.02	9.43	9.20	1.01	up	9.38E-01	9.82E-01	-	-
1386597_s_at	Spdya	speedy homolog A (Xenopus laevis)	192209	Rn.19576	BF563673	2.38	2.38	2.44	2.38	2.40	2.37	1.01	down	4.54E-01	8.95E-01	-	-
1379040_at	---	---	---	Rn.204264	AI136672	2.34	2.29	2.31	2.30	2.30	2.29	1.01	down	3.16E-01	8.95E-01	-	-
1390059_at	Usp25	ubiquitin specific peptidase 25	304150	Rn.23509	AW523267	2.39	2.35	2.36	2.35	2.36	2.34	1.01	down	2.38E-01	8.95E-01	-	-
1385694_at	---	---	---	Rn.212692	BI297119	2.84	2.83	2.85	2.81	2.91	2.74	1.01	down	7.23E-01	9.12E-01	-	-
1397705_at	Nlgn2	neuroligin 2	117096	Rn.55111	BF542792	2.49	2.46	2.52	2.47	2.50	2.45	1.01	down	4.46E-01	8.95E-01	-	-
1373317_at	Calm4	calmodulin 4	364774	Rn.199023	BI278721	2.41	2.40	2.42	2.40	2.42	2.47	1.01	up	4.32E-01	8.95E-01	-	-
1372848_at	RGD1310269	hypothetical LOC314472	314472	Rn.22400	BI296915	2.30	2.26	2.27	2.26	2.27	2.26	1.01	down	2.35E-01	8.95E-01	-	-
1394804_at	---	---	---	---	AI599871	2.43	2.40	2.44	2.41	2.42	2.39	1.01	down	2.86E-01	8.95E-01	-	-
1394258_at	---	---	---	---	BF564756	2.45	2.41	2.45	2.42	2.44	2.40	1.01	down	3.70E-01	8.95E-01	-	-
1381657_at	---	---	---	Rn.151154	BF403903	2.55	2.53	2.57	2.53	2.56	2.49	1.01	down	4.71E-01	8.95E-01	-	-
1390292_at	Tmem8	transmembrane protein 8 (five membrane-spanning domains)	303004	Rn.21890	AW527467	8.18	8.96	9.16	9.04	8.58	8.62	1.01	down	9.60E-01	9.89E-01	-	-
1392288_at	---	---	---	Rn.146480	BE120230	2.42	2.39	2.47	2.42	2.43	2.39	1.01	down	5.14E-01	8.95E-01	-	-
1386721_at	Znf503	zinc finger protein 503	305687	Rn.37928	BF560938	6.14	4.58	5.83	5.66	5.78	5.05	1.01	down	9.74E-01	9.92E-01	-	-
1395896_at	---	---	---	---	AI233009	2.68	2.65	2.68	2.67	2.71	2.58	1.01	down	6.58E-01	8.98E-01	-	-
1395314_at	---	---	---	Rn.208520	AA824452	2.62	2.57	2.63	2.59	2.62	2.56	1.01	down	5.36E-01	8.95E-01	-	-
1387315_at	Sftpd	surfactant protein D	25350	Rn.11348	NM_012878	2.42	2.40	2.42	2.41	2.42	2.46	1.01	up	3.24E-01	8.95E-01	-	-
1370252_at	Avpi1	arginine vasopressin-induced 1	171386	Rn.13633	BI282724	4.01	5.22	5.34	4.57	4.92	5.02	1.01	down	9.70E-01	9.91E-01	-	-
1398380_at	Vwa1	von Willebrand factor A domain containing 1	298683	Rn.162159	AF413643	3.62	2.39	2.39	2.82	2.99	2.63	1.01	up	9.68E-01	9.91E-01	-	-
1373714_at	---	---	---	Rn.60163	BF401566	2.38	2.37	2.43	2.38	2.38	2.36	1.01	down	4.14E-01	8.95E-01	-	-
1395547_at	---	---	---	Rn.203053	BG686143	3.00	3.00	3.00	2.99	3.01	3.05	1.01	up	3.53E-01	8.95E-01	-	-
1397609_at	Traf4af1	TRAF4 associated factor 1	311325	Rn.20235	BF287466	2.48	2.44	2.49	2.44	2.49	2.42	1.01	down	5.25E-01	8.95E-01	-	-
1376231_at	Gins1	GINS complex subunit 1 (Psf1 homolog)	499914	Rn.117311	BF389244	2.39	2.37	2.39	2.45	2.38	2.37	1.01	up	5.40E-01	8.95E-01	-	-
1379892_at	---	---	---	Rn.20586	AI385306	2.42	2.41	2.48	2.42	2.43	2.41	1.01	down	4.63E-01	8.95E-01	-	-
1374741_at	Esrra	estrogen related receptor, alpha	293701	Rn.130171	AI171726	4.20	3.63	5.22	4.07	4.77	4.16	1.01	down	9.74E-01	9.92E-01	-	-
1397434_at	---	---	---	Rn.173039	BF399188	2.43	2.41	2.48	2.42	2.44	2.40	1.01	down	4.97E-01	8.95E-01	-	-
1375796_at	Ifgp	interferon gamma induced GTPase	303163	Rn.220163	BI300770	2.39	2.36	2.39	2.36	2.38	2.35	1.01	down	2.39E-01	8.95E-01	-	-
1388202_at	RT1-Aw2	RT1 class Ib, locus Aw2	24737	Rn.145377	BI395698	2.52	2.51	2.53	2.50	2.52	2.48	1.01	down	2.48E-01	8.95E-01	-	-
1387119_at	Mvk	mevalonate kinase	81727	Rn.6995	AW433971	2.77	2.46	2.49	2.80	2.45	2.53	1.01	up	9.08E-01	9.72E-01	-	-
1385447_at	RGD1308385	similar to RIKEN cDNA 1700010M22	311491	Rn.94281	BE102219	2.55	2.52	2.63	2.54	2.58	2.52	1.01	down	6.37E-01	8.95E-01	-	-
1373752_at	---	---	---	Rn.209106	BF410306	2.48	2.47	2.51	2.48	2.50	2.44	1.01	down	4.52E-01	8.95E-01	-	-
1370786_at	LOC257643	cystatin SC	257643	Rn.8641	AF442205	2.36	2.35	2.41	2.36	2.37	2.34	1.01	down	3.78E-01	8.95E-01	-	-
1376207_at	RGD1560070	Similar to ataxin 2-binding protein 1 isoform 2	287847	Rn.143966	BE105381	2.29	2.28	2.33	2.28	2.29	2.27	1.01	down	3.06E-01	8.95E-01	-	-
1373356_at	Gdpd5	glycerophosphodiester phosphodiesterase domain containing 5	499211	Rn.11632	AA963795	2.42	2.42	2.47	2.44	2.40	2.41	1.01	down	3.98E-01	8.95E-01	-	-
1395806_at	389083 /// LOC68	similar to spermatogenesis associated glutamate (E)-rich protein 4d /// similar	689083	Rn.198083	AI547628	2.35	2.34	2.40	2.34	2.36	2.33	1.01	down	3.85E-01	8.95E-01	-	-
1388286_at	Fgb	fibrinogen beta chain	24366	Rn.11416	M35602	2.45	2.44	2.47	2.45	2.46	2.40	1.01	down	4.13E-01	8.95E-01	-	-
1367933_at	Amd1	adenosylmethionine decarboxylase 1	81640	Rn.56270	NM_031011	5.58	5.96	5.86	5.61	6.07	5.78	1.01	up	9.24E-01	9.78E-01	-	-
1385174_at	Tessp6	testis-specific serine protease-6	408245	Rn.129743	BE101765	2.37	2.37	2.44	2.38	2.38	2.37	1.01	down	5.08E-01	8.95E-01	-	-
1369190_at	Cd2	Cd2 molecule	497761	Rn.10328	NM_012830	2.46	2.41	2.55	2.45	2.46	2.45	1.01	down	6.84E-01	9.03E-01	-	-
1377129_at	Fbxo39	F-box protein 39	303287	Rn.198886	BF419558	2.49	2.43	2.49	2.45	2.48	2.43	1.01	down	5.00E-01	8.95E-01	-	-
1383268_at	Vstm2a	V-set and transmembrane domain containing 2A	689106	Rn.207014	BG867725	2.46	2.44	2.53	2.46	2.48	2.44	1.01	down	5.64E-01	8.95E-01	-	-
1369133_a_at	Kcnc3	potassium voltage gated channel, Shaw-related subfamily, member 3	117101	Rn.9885	NM_053997	2.39	2.37	2.43	2.37	2.40	2.36	1.01	down	4.66E-01	8.95E-01	-	-
1375820_at	---	---	---	Rn.7551	BF403869	2.43	2.41	2.45	2.41	2.43	2.39	1.01	down	3.54E-01	8.95E-01	-	-
1385470_at	---	---	---	Rn.166139	AI045606	4.71	6.07	7.11	6.03	5.97	5.95	1.01	up	9.81E-01	9.94E-01	-	-
1372891_at	Cox19	COX19 cytochrome c oxidase assembly homolog (S. cerevisiae)	304330	Rn.205089	BF406856	8.88	8.77	8.72	8.26	8.77	9.38	1.01	up	9.59E-01	9.86E-01	-	-
1384320_at	Bai3	brain-specific angiogenesis inhibitor 3	301309	Rn.204758	BE121330	2.41	2.39	2.45	2.40	2.41	2.38	1.01	down	4.07E-01	8.95E-01	-	-
1384161_at	Csnk1e	Casein kinase 1, epsilon	58822	Rn.203721	BF398627	2.60	2.61	2.66	2.59	2.62	2.60	1.01	down	4.43E-01	8.95E-01	-	-
1370731_at	Sgp158	proline-rich glycoprotein (sgp158)	245985	Rn.10110	L08134	2.47	2.44	2.51	2.45	2.48	2.43	1.01	down	5.20E-01	8.95E-01	-	-
1385572_at	---	---	---	Rn.27718	AI144884	2.37	2.36	2.40	2.36	2.37	2.35	1.01	down	2.56E-01	8.95E-01	-	-
1392602_at	Cdc14b	CDC14 cell division cycle 14 homolog B (S. cerevisiae)	361195	Rn.162177	BF290959	2.35	2.36	2.39	2.35	2.36	2.34	1.01	down	2.68E-01	8.95E-01	-	-
1384460_at	---	---	---	Rn.20220	AI072669	2.45	2.49	2.46	2.45	2.46	2.44	1.01	down	1.92E-01	8.95E-01	-	-
1392587_at	---	---	---	Rn.51225	BE115141	8.01	7.54	7.60	7.90	7.90	7.90	1.01	down	9.46E-01	9.84E-01	-	-
1375987_at	Cerk	ceramide kinase	300129	Rn.99537	AW525194	2.57	2.53	2.58	2.57	2.60	2.57	1.01	up	3.99E-01	8.95E-01	-	-
1379670_at	Sgol2	shugoshin-like 2 (S. pombe)	316425	Rn.55827	BF289778	2.46	2.45	2.47	2.45	2.46	2.41	1.01	down	3.52E-01	8.95E-01	-	-
1379549_at	---	---	---	Rn.44903	BI288184	2.38	2.37	2.41	2.37	2.38	2.35	1.01	down	3.37E-01	8.95E-01	-	-
1370273_at	LOC360395	hypothetical gene supported by M31032; NM_181440	360395	Rn.219982	M58654	2.49	2.46	2.52	2.47	2.50	2.45	1.01	down	5.04E-01	8.95E-01	-	-
1383362_at	---	---	---	Rn.30219	BI275850	2.41	2.40	2.41	2.40	2.42	2.45	1.01	up	2.70E-01	8.95E-01	-	-
1396440_at	---	---	---	Rn.216977	BF419659	2.65	2.56	2.78	2.66	2.66	2.62	1.01	down	7.97E-01	9.35E-01	-	-
1390658_at	Mast4	microtubule associated serine/threonine kinase family member 4	310040	Rn.43251	BF408763	2.48	2.44	2.50	2.45	2.48	2.43	1.01	down	4.88E-01	8.95E-01	-	-
1398047_at	---	---	---	R

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1390745_at	---	---	---	---	BF417914	2.52	2.51	2.58	2.51	2.53	2.51	1.01	down	4.79E-01	8.95E-01	-	-
1394679_at	---	---	---	Rn.50850	BE105933	2.42	2.40	2.42	2.41	2.49	2.39	1.01	up	5.99E-01	8.95E-01	-	-
1393570_at	---	---	---	Rn.136018	AI111566	2.56	2.51	2.61	2.55	2.61	2.48	1.01	down	7.35E-01	9.15E-01	-	-
1377264_at	Il17f	interleukin 17F	301291	Rn.34022	BI288683	2.46	2.43	2.46	2.44	2.45	2.41	1.01	down	2.84E-01	8.95E-01	-	-
1387054_at	Abcg1	ATP-binding cassette, sub-family G (WHITE), member 1	85264	Rn.8398	AI712719	2.35	2.34	2.55	2.35	2.52	2.34	1.01	down	8.55E-01	9.55E-01	-	-
1398880_at	Sub1	SUB1 homolog (S. cerevisiae)	192269	Rn.8706	BM388890	8.73	8.79	8.98	8.86	8.82	8.87	1.01	up	8.33E-01	9.47E-01	-	-
1377783_at	Angpt4	angiopoietin 4	296269	Rn.9586	BI294141	2.35	2.30	2.32	2.30	2.31	2.30	1.01	down	3.15E-01	8.95E-01	-	-
1393022_at	Ankrd13d	ankyrin repeat domain 13 family, member D	361699	Rn.15704	BG380737	2.41	2.39	2.43	2.39	2.41	2.37	1.01	down	3.36E-01	8.95E-01	-	-
1391729_at	---	---	---	Rn.47716	BF409212	2.50	2.48	2.53	2.49	2.51	2.44	1.01	down	5.25E-01	8.95E-01	-	-
1390766_at	Tuba8	tubulin, alpha 8	500377	Rn.27364	AI137249	2.40	2.39	2.44	2.39	2.41	2.38	1.01	down	4.12E-01	8.95E-01	-	-
1391193_at	---	---	---	Rn.218101	BI288564	3.17	3.32	2.54	3.10	2.24	3.65	1.01	down	9.72E-01	9.92E-01	-	-
1395097_at	---	---	---	Rn.207296	BE097124	2.35	2.34	2.40	2.34	2.36	2.33	1.01	down	4.00E-01	8.95E-01	-	-
1377055_at	RGD1310754	similar to G2	311264	---	BF394089	2.90	2.89	2.92	2.97	2.91	2.88	1.01	up	5.54E-01	8.95E-01	-	-
1381413_at	---	---	---	---	AI547999	2.42	2.39	2.40	2.39	2.40	2.37	1.01	down	2.62E-01	8.95E-01	-	-
1381678_at	LOC683788	similar to Fascin (Singed-like protein)	683788	Rn.199526	AW525560	2.39	2.38	2.39	2.39	2.47	2.36	1.01	up	6.39E-01	8.95E-01	-	-
1387589_at	Rims3	regulating synaptic membrane exocytosis 3	65025	Rn.209039	NM_022931	2.38	2.37	2.39	2.45	2.38	2.36	1.01	up	5.22E-01	8.95E-01	-	-
1380853_at	---	---	---	Rn.148782	BE101772	2.48	2.44	2.51	2.46	2.47	2.44	1.01	down	4.53E-01	8.95E-01	-	-
1387204_at	Negr1	neuronal growth regulator 1	59318	Rn.205838	NM_021682	2.27	2.31	2.27	2.27	2.27	2.26	1.01	down	2.70E-01	8.95E-01	-	-
1388741_at	LOC688915	similar to cardiomyopathy associated 5	688915	Rn.7810	AW533234	2.42	2.42	2.48	2.42	2.43	2.42	1.01	down	4.19E-01	8.95E-01	-	-
1370790_at	Ifng	interferon gamma	25712	Rn.10795	AF010466	2.39	2.37	2.38	2.36	2.37	2.35	1.01	down	1.65E-01	8.95E-01	-	-
1369480_at	Slc16a8	solute carrier family 16, member 8 (monocarboxylic acid transporter 3)	65200	Rn.14526	NM_031744	2.39	2.33	2.35	2.34	2.35	2.33	1.01	down	3.49E-01	8.95E-01	-	-
1396481_at	---	---	---	Rn.167172	AW918413	2.59	2.56	2.62	2.58	2.74	2.51	1.01	up	8.18E-01	9.42E-01	-	-
1397199_at	---	---	---	Rn.171863	BF408180	2.38	2.39	2.39	2.37	2.38	2.36	1.01	down	6.15E-02	8.95E-01	-	-
1378802_at	Pyroxd2	pyridine nucleotide-disulphide oxidoreductase domain 2	306381	Rn.102445	AI105386	9.94	10.15	9.85	9.95	9.80	10.14	1.01	down	9.01E-01	9.70E-01	-	-
1396354_at	---	---	---	Rn.50366	BM390363	2.53	2.50	2.59	2.52	2.57	2.47	1.01	down	6.65E-01	8.99E-01	-	-
1388358_at	Etfb	electron-transfer-flavoprotein, beta polypeptide	292845	Rn.60152	AW252650	12.85	12.88	12.83	12.83	12.75	13.04	1.01	up	8.54E-01	9.55E-01	-	-
1393415_at	Ednra	endothelin receptor type A	24326	Rn.10915	BF548851	2.33	2.32	2.33	2.33	2.33	2.38	1.01	up	3.59E-01	8.95E-01	-	-
1394756_at	---	---	---	Rn.203519	AA955494	2.42	2.40	2.47	2.42	2.43	2.39	1.01	down	5.03E-01	8.95E-01	-	-
1367629_at	Cox7a2	cytochrome c oxidase, subunit VIIa 2	29507	Rn.1745	NM_022503	11.86	11.34	11.55	11.57	11.59	11.54	1.01	down	9.14E-01	9.75E-01	-	-
1371016_at	LOC290071	similar to RIKEN cDNA A430107P09 gene	290071	Rn.9949	BM386010	2.37	2.32	2.34	2.32	2.34	2.32	1.01	down	2.95E-01	8.95E-01	-	-
1391704_at	C1qtnf4	C1q and tumor necrosis factor related protein 4	311184	Rn.24378	BE103189	2.37	2.36	2.40	2.36	2.37	2.35	1.01	down	3.00E-01	8.95E-01	-	-
1392040_at	Sass6	spindle assembly 6 homolog (C. elegans)	310807	Rn.51026	BE107904	2.29	2.28	2.34	2.29	2.30	2.28	1.01	down	3.90E-01	8.95E-01	-	-
1381189_at	Fzr1	fizzy/cell division cycle 20 related 1 (Drosophila)	314642	Rn.12924	BF402538	2.38	2.37	2.39	2.37	2.45	2.37	1.01	up	5.34E-01	8.95E-01	-	-
1391288_at	---	---	---	---	BF402388	2.36	2.29	2.33	2.31	2.32	2.30	1.01	down	4.44E-01	8.95E-01	-	-
1397067_at	---	---	---	Rn.59164	BF403822	2.43	2.40	2.45	2.41	2.42	2.39	1.01	down	3.18E-01	8.95E-01	-	-
1397721_at	LOC691770	similar to Ankyrin repeat domain-containing protein 28	691770	Rn.27640	AW531134	2.40	2.39	2.41	2.40	2.48	2.38	1.01	up	6.07E-01	8.95E-01	-	-
1370160_at	Xpnpep1	X-prolyl aminopeptidase (aminopeptidase P) 1, soluble	170751	Rn.25763	AI178742	10.97	10.66	10.00	11.02	10.40	10.25	1.01	up	9.65E-01	9.90E-01	-	-
1386389_at	---	---	---	---	AI639126	2.43	2.43	2.47	2.43	2.44	2.41	1.01	down	2.95E-01	8.95E-01	-	-
1384641_at	---	---	---	Rn.9588	AA957600	2.31	2.27	2.28	2.27	2.27	2.26	1.01	down	2.42E-01	8.95E-01	-	-
1372190_at	Aqp4	aquaporin 4	25293	Rn.90091	AI235942	2.47	2.45	2.50	2.45	2.47	2.43	1.01	down	3.96E-01	8.95E-01	-	-
1389516_at	---	---	---	Rn.212265	BI300082	2.29	2.28	2.29	2.34	2.29	2.28	1.01	up	4.10E-01	8.95E-01	-	-
1369964_at	Coro1a	coronin, actin binding protein 1A	155151	Rn.6990	NM_130411	2.45	2.39	2.45	2.46	2.45	2.44	1.01	up	4.85E-01	8.95E-01	-	-
1396536_at	Gylltl1b	Glycosyltransferase-like 1B	311202	Rn.205174	BF399987	2.27	2.27	2.28	2.28	2.28	2.31	1.01	up	1.57E-01	8.95E-01	-	-
1378704_at	---	---	---	---	AI406658	3.76	3.79	3.73	3.76	3.81	3.76	1.01	up	5.24E-01	8.95E-01	-	-
1391653_at	Gabrg2	gamma-aminobutyric acid (GABA) A receptor, gamma 2	29709	Rn.159942	BE120391	2.45	2.43	2.48	2.44	2.46	2.41	1.01	down	4.23E-01	8.95E-01	-	-
1391615_at	---	---	---	---	BF400897	2.45	2.43	2.48	2.44	2.45	2.41	1.01	down	3.63E-01	8.95E-01	-	-
1394051_at	P2ry10	purinergic receptor P2Y, G-protein coupled 10	317219	Rn.17487	AI009791	2.59	2.56	2.64	2.58	2.61	2.55	1.01	down	5.93E-01	8.95E-01	-	-
1384395_at	Ldhal6b	lactate dehydrogenase A-like 6B	369018	Rn.208286	BE114359	2.62	2.59	2.72	2.63	2.69	2.57	1.01	down	7.46E-01	9.18E-01	-	-
1374433_at	---	---	---	Rn.199187	BI301532	6.37	6.90	6.34	6.12	6.75	6.79	1.01	up	9.54E-01	9.87E-01	-	-
1378421_at	---	---	---	Rn.15594	BG671734	2.38	2.31	2.32	2.31	2.33	2.30	1.01	down	4.95E-01	8.95E-01	-	-
1394538_at	---	---	---	Rn.211037	BF404879	2.51	2.46	2.51	2.58	2.50	2.45	1.01	up	6.91E-01	9.05E-01	-	-
1375836_at	---	---	---	Rn.210566	BF399108	2.56	2.52	2.58	2.53	2.59	2.49	1.01	down	6.56E-01	8.98E-01	-	-
1384111_at	Stat4	signal transducer and activator of transcription 4	367264	Rn.137580	AA955354	2.43	2.42	2.45	2.42	2.43	2.40	1.01	down	2.13E-01	8.95E-01	-	-
1396760_at	---	---	---	Rn.210795	BF405512	2.42	2.41	2.46	2.41	2.42	2.40	1.01	down	3.65E-01	8.95E-01	-	-
1385689_at	---	---	---	Rn.152531	BI290860	4.47	5.00	5.52	4.61	5.47	4.87	1.01	down	9.67E-01	9.91E-01	-	-
1394126_at	---	---	---	Rn.136393	AA893693	2.51	2.48	2.55	2.50	2.53	2.46	1.01	down	5.95E-01	8.95E-01	-	-
1391985_at	Nrip3	nuclear receptor interacting protein 3	361625	Rn.48099	BI288541	2.44	2.41	2.47	2.42	2.45	2.39	1.01	down	5.19E-01	8.95E-01	-	-
1373286_at	Fblim1	filamin binding LIM protein 1	362650	Rn.2851	AA875261	2.44	2.41	2.46	2.47	2.45	2.43	1.01	up	4.39E-01	8.95E-01	-	-
1389787_at	Ptk7	PTK7 protein tyrosine kinase 7	301242	Rn.198822	AI549469	2.49	2.48	2.50	2.49	2.49	2.45	1.01	down	3.25E-01	8.95E-01	-	-
1377120_at	---	---	---	Rn.216607	AI385307	2.52	2.51	2.57	2.52	2.53	2.50	1.01	down	3.96E-01	8.95E-01	-	-
1368364_at	Smcp	sperm mitochondria-associated cysteine-rich protein	24899	Rn.10492	NM_031536	2.45	2.44	2.46	2.43	2.46	2.42	1.01	down	2.56E-01	8.95E-01	-	-
1387696_a_at	Glra2	glycine receptor, alpha 2	24397	Rn.10379	X61159	2.42	2.40	2.45	2.41	2.42	2.39	1.01	down	3.97E-01	8.95E-01	-	-
1368491_at	Dnase2b	deoxyribonuclease II beta	59296	Rn.41640	NM_021664	2.35	2.33	2.40	2.34	2.35	2.33	1.01	down	4.30E-01	8.95E-01	-	-
1379225_at	---	---	---	---	AI071617	2.37	2.37	2.38	2.37	2.44	2.37	1.01	up	4.95E-01	8.95E-01	-	-
1390107_at	Syt2	synaptotagmin-like 2	361604	Rn.7634	BG670294	2.37	2.37	2.37	2.37	2.37	2.42	1.01	up	3.74E-01	8.95E-01	-	-
1382800_at	---	---	---	Rn.154134	AI234840	3.49	3.21	3.32	3.27	3.21	3.60	1.01	up	9.12E-01	9.74E-01	-	-
1389360_at	Fxyd3	FXYD domain-containing ion transport regulator 3	116831	Rn.3896	AI009597	2.32	2.31	2.37	2.32	2.32	2.31	1.01	down	4.38E-01	8.95E-01	-	-
1380803_at	---	---	---	---	AI176603	2.51	2.50	2.60	2.52	2.57	2.48	1.01	down	7.02E-01	9.07E-01	-	-
1379144_at	Rab36	RAB36, member RAS oncogene family	690407	Rn.210110	BF393973	2.43	2.44	2.45	2.43	2.40	2.40	1.01	down	2.21E-01	8.95E-01	-	-
1395401_at	Dos	downstream of Stk11	314622	Rn.91597	BE106038	2.36	2.35	2.38	2.34	2.36	2.35	1.01	down	2.06E-01	8.95E-01	-	-
1379618_at	---	---	---	---	AI172526	2.54	2.50	2.54	2.52	2.53	2.58	1.01	up	5.10E-01	8.95E-01	-	-
1381351_at	---	---	---	Rn.33295	AI599264	2.53	2.50	2.56	2.50	2.55	2.48	1.01	down	5.52E-01	8.95E-01	-	-
1398078_at	---	---	---	Rn.56275	BF391102	2.51	2.48	2.51	2.50	2.51	2.54	1.01	up	3.35E-01	8.95E-01	-	-
1374631_at	Obfc2b	oligonucleotide/oligosaccharide-binding fold containing 2B	362813	Rn.23934	AW914202	4.91	5.98	5.68	5.58	5.38	5.67	1.01	up	9.61E-01	9.89E-01	-	-
1393837_at	---	---	---	Rn.56493	AI577369	2.38	2.36	2.41	2.37	2.38	2.35	1.01	down	3.39E-01	8.95E-01	-	-
1390688_at	Ddx50	DEAD (Asp-Glu-Ala-Asp) box polypeptide 50	361848	Rn.98470	AA799576	7.70	7.47	7.60	7.30	7.86	7.67	1.01	up	9.27E-01	9.79E-01	-	-
1387737_at	Mat2a	methionine adenosyltransferase II, alpha	171347	Rn.41420	NM_134351	10.32	11.36	10.42	10.46	10.66	11.03	1.01	up	9.65E-01	9.90E-01	-	-
1379802_at	Agfg2	ArfGAP with FG repeats 2	304375	Rn.17775	BF287746	2.53	2.46	2.49	2.48	2.49	2.46	1.01	down	4.50E-01	8.95E-01	-	-
1396471_at	---	---	---	---	AI548716	2.67	2.93	2.73	2.61	3.06	2.60	1.01	down	9.25E-01	9.78E-01	-	-
1390348_at	Folr2	folate receptor 2 (fetal)	293154	Rn.8801	BI274054	2.33	2.32	2.33	2.32	2.39	2.32	1.01	up	4.85E-01	8.95E-01	-	-
1377450_s_at	Pvrl4	poliovirus receptor-related 4	498281	Rn.20370	AI073141	2.36	2.39	2.37	2.35	2.36	2.35	1.01	down	1.69E-01	8.95E-01	-	-
1384433_at	---	---	---	Rn.148816	AI072153	2.58	2.55	2.58	2.55	2.56	2.55	1.01	down	1.40E-01	8.95E-01	-	-
1397973_x_at	42077 /// RGD130	hypothetical LOC292199 /// similar to intracellular protein transport like (XM_	292199 /// 308053	Rn.38655	AW533355	2.44	2.42	2.49	2.43	2.46	2.41	1.01	down	4.90E-01	8.95E-01	-	-
1368369_at	Pnoc	preprononociceptin	25516	Rn.87935	NM_013007	2.30	2.30	2.35	2.30	2.31	2.29	1.01	down	3.64E-01	8.95E-01	-	-
1380534_at	---	---	---	Rn.205738	BF546444	2.51	2.48	2.55	2.51	2.61	2.47	1.01	up	7.23E-01	9.12E-01	-	-
1384133_at	Klf1a	kinesin family member 1A	363288	---	BF522755	2.41	2.44	2.42	2.40	2.42	2.39	1.01	down	1.67E-01	8.95E-01	-	-
1378881_at	---	---	---	---	BE098303	2.28	2.32	2.29	2.28	2.29	2.27	1.01	down	2.29E-01	8.95E-01	-	-
1369220_at	Dnm1l	dynamin 1-like	114114	Rn.216851	NM_053655	6.27	5.95	6.47	5.86	6.34	6.55	1.01	up	9.49E-01	9.85E-01	-	-
1367554_at	/cgb2a1 /// Scgb2a	secretoglobin, family 2A, member 1 /// secretoglobin, family 2A, member 2	25010 /// 361725	Rn.103180	NM_080770	2.31	2.30	2.36	2.31	2.31	2.30	1.01	down	3.55E-01	8.95E-01	-	-
1380750_at	---	---	---	---	BF393402	2.59	2.56	2.62	2.57	2.60	2.55	1.01	down	5.15E-01	8.95E-01	-	-
1394759_at	---	---	---	---	BF289157	2.52	2.48	2.52	2.51	2.56	2.50	1.01	up	4.55E-01	8.95E-01	-	-
1395062_at	---	---	---	Rn.170781	BE101553	2.41	2.39	2.45	2.40	2.42	2.38	1.01	down	4.96E-01	8.95E-01	-	-
1392191_at	LOC691093	similar to gene trap ROSA b-geo 22	691093	Rn.22319	BE329338	2.47	2.44	2.52	2.45	2.50	2.43	1.01	down	5.95E-01	8.95E-01	-	-
1379124_at	---	---	---	Rn.164957	BE103417	2.85	2.86	3.37	2.81	2.95	3.37	1.01	up	9.46E-01	9.85E-01	-	-
1387890_at	Rps29	ribosomal protein S29	25348	Rn.34942	AI229633	12.84	12.72	12.97	12.75	12.81	12.92	1.01	down	8.53E-01	9.55E-01	-	-
1390681_at	RGD1564927	similar to TGFB-induced factor 2	499929	Rn.214898	AA964074	2.47	2.48	2.49	2.56	2.48	2.45	1.01	up	6.29E-01	8.95E-01	-	-
1383882_at	---	---	---	Rn.166260	AW917556	2.46	2.44	2.50	2.45	2.48	2.42	1.01	down	4.98E-01	8.95E-01	-	-
1368256_at	Serpini1	serine (or cysteine) peptidase inhibitor, clade I, member 1	116459	Rn.52632	AF193015	2.49	2.48	2.52	2.47	2.51	2.46	1.01	down	4.10E-01	8.95E-01	-	-
1397552_at	Bbs12	Bardet-Biedl syndrome 12 (human)	365770	Rn.57468	BM389255	3.21	2.69	2.70	2.73	3.05	2.87	1.01	up	9.35E-01	9.82E-01	-	-
1370564_at	Dbh	dopamine beta-hydroxylase (dopamine beta-monooxygenase)	25699	Rn.87106	L12407	2.48	2.47	2.50	2.45	2.49	2.46	1.01	down	2.68E-01	8.95E-01	-	-
1369031_at	Il18bp	interleukin 18 binding protein	84388	Rn.20083	NM_053374	2.29	2.29	2.30	2.29	2.30	2.35	1.01	up	3.98E-01	8.95E-01	-	-
1373348_at	LOC687424	similar to Protein deltex-1 (Deltex-1) (Deltex1) (mDTX1) (FXl-T1)	687424	---	AI500940	2.30	2.33	2.31	2.30	2.31	2.28	1.01	down	1.86E-01	8.95E-01	-	-
1379300_at	Chst2	carbohydrate sulfotransferase 2	367145	Rn.95986	AW520944	7.07	7.57	7.18	7.20	7.14	7.52	1.01	up	9.34E-01	9.81E-01	-	-
1379206_at	Tmem38a	transmembrane protein 38a	306327	Rn.162265	BF410357	2.36	2.36	2.40	2.36	2.36	2.35	1.01	down	2.44E-01	8.95E-01	-	-
1385485_x_at	RGD1561571	similar to Riken cDNA C230021P08	315297	Rn.198253	BE110831	2.38	2.35	2.36	2.35	2.35	2.33	1.01	down	2.62E-01	8.95E-01	-	-
1379096_at	---	---	---	Rn.204202	AI070835	2.60	2.58	2.63	2.59	2.61	2.57	1.01	down	3.95E-01	8.95E-01	-	-
1376506_at	LOC690358	Similar to PR domain containing 11	690358	Rn.44730	BE097618	2.38	2.38	2.42	2.38	2.38	2.37	1.01	down	3.16E-01	8.95E-01	-	-
1394867_at	---	---	---	---	AA944444	4.86	4.63	5.19	4.65	4.81	5.17	1.01	down	9.43E-01	9.84E-01	-	-
1376855_at	Nxn	Nucleoredoxin	360577	Rn.105982	BE104776	2.32	2.29	2.33	2.30	2.31	2.28	1.01	down	3.00E-01	8.95E-01	-	-
1393524_at	---	---	---	Rn.160847	AI764585	2.54	2.54	2.55	2.54	2.62	2.52	1.01	up	6.17E-01	8.95E-01	-	-
1395288_at	---	---	---	Rn.155516	AI233739	2.31	2.26	2.27	2.26	2.27	2.26	1.01	down	3.02E-01	8.95E-01	-	-
1381848_at	---	---	---	---	AI228486	2.37	2.36	2.38	2.40	2.41	2.35	1.01	up	4.38E-01	8.95E-01	-	-
1391081_at	---	---	---	Rn.46298	AW526722	2.46	2.42	2.48	2.44	2.46	2.41	1.01	down	4.29E-01	8.95E-01	-	-
1397994_at	---	---	---	---	BF392228	2.46	2.44	2.49	2.44	2.45	2.44	1.01	down	2.80E-01	8.95E-01	-	-
1377478_at	---	---	---	Rn.219127	AI511173	2.43	2.40	2.45	2.41	2.43	2.39	1.01	down	4.17E-01	8.95E-01	-	-
1376757_at	LOC687536	similar to Forkhead box protein F1 (Forkhead-related protein FKHL5) (Forkhe	687536	---	AW532942	2.25	2.28	2.28	2.27	2.32	2.27	1.01	up	4.24E-01	8.95E-01	-	-
1385389_x_at	---	---	---	---	AI045847	2.59	2.55	2.65	2.56	2.63	2.55	1.01	down	6.90E-01	9.05E-01	-	-
1378099_at	---	---	---	Rn.101460	AI412479	2.45	2.43	2.45	2.43	2.44	2.40	1.01	down	2.99E-01	8.95E-01	-	-
1397850_at	---	---	---	Rn.150411	BE110348	2.45	2.43	2.49	2.43	2.47	2.41	1.01	down	5.47E-01	8.95E-01	-	-
1370876_at	Map7d1	MAP7 domain containing 1	681287	Rn.39212	BI285436	4.20	4.23	3.32	3.97	4.14	3.59	1.01	down	9.83E-01	9.89E-01	-	-
1370248_at	Fxyd6	FXYD domain-containing ion transport regulator 6	63847	Rn.839	AA851939	3.32	2.52	2.74	3.28	2.75	2.61	1.01	up	9.59E-01	9.89E-01	-	-
1378329_at	---	---	---	Rn.47606	BF419525	2.42	2.39	2.42	2.40	2.40	2.39	1.01	down	1.84E-01	8.95E-01	-	-
1371756_at	---	---	---	Rn.217091	BI286411	2.30	2.28	2.34	2.29	2.30	2.28	1.01	down	3.83E-01	8.95E-01	-	-
1396794_at	LOC306346	similar to KIAA1683	306346	---	BE119143	2.46	2.42	2.46	2.43	2.45	2.41	1.01	down	3.80E-01	8.95E-01	-	-
1396919_at	Wnk1	WNK lysine deficient protein kinase 1	116477	Rn.27409	AI137384	2.50	2.47	2.55	2.49	2.53	2.45	1.01	down	6.10E-01	8.95E-01	-	-
1378507_at	---	---	---	Rn.88974	BE108914	2.36	2.31	2.33	2.32	2.32	2.31	1.01	down	3.14E-01	8.95E-01	-	-
1380668_at	Klc3	kinesin light chain 3	171549	Rn.161815	AF166267	2.38	2.33	2.35	2.34	2.35	2.33	1.01	down	3.24E-01	8.95E-01	-	-
1370685_at	Trpv1	transient receptor potential cation channel, subfamily V, member 1	83810	Rn.3073	AB015231	2.41	2.38	2.41	2.38	2.40	2.37	1.01	down	2.91E-01	8.95E-01	-	-
1381353_at	MGC114427	similar to melanoma antigen family A, 5	317297	Rn.54113	AI179244	2.53	2.50	2.61	2.53	2.57	2.49	1.01	down	6.79E-01	9.02E-01	-	-
1370518_a_at	Stxbp1	syntaxin binding protein 1	25558	Rn.80843	U06069	2.61	2.60	2.66	2.60	2.62	2.59	1.01	down	4.25E-01	8.95E-01	-	-
1390889_at	LOC691543	hypothetical protein LOC691543	691543	Rn.55420	AI102132	4.70	3.95	3.35	3.96	3.86	4.22	1.01	up	9.69E-01	9.91E-01	-	-
1392204_at	Zfp90	zinc finger protein 90	498945	Rn.38916	AI763897	2.45	2.39	2.48	2.42	2.45	2.40	1.01	down	6.04E-01	8.95E-01	-	-
1385549_at	LOC685964	hypothetical protein LOC685964	685964	Rn.62380	BF413544	2.46	2.43	2.51	2.45	2.49	2.41	1.01	down	6.47E-01	8.95E-01	-	-
1381062_at	---	---	---	Rn.164993	AI113313	2.42	2.38	2.41	2.39	2.40	2.37	1.01	down	2.92E-01	8.95E-01	-	-
1383512_at	Mllt10	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila);	361285	Rn.3620	AW918674	2.50	2.61	2.71	2.70	2.49	2.57	1.01	down	8.54E-01	9.55E-01	-	-
1373975_at	Inmt	indolethylamine N-methyltransferase	368066	Rn.19133	AI232716	8.50	9.08	8.57	8.99	8.40	8.72	1.01	down	9.49E-01	9.85E-01	-	-
1383123_at	---	---	---	Rn.164625	BF559503	8.20	8.72	8.53	8.64	8.29	8.57	1.01	up	9.32E-01	9.81E-01	-	-
1371860_at	Vta1	Vps20-associated 1 homolog (S. cerevisiae)	292640	Rn.1896	AA944016	5.90	6.70	5.78	6.10	6.00	6.24	1.01	up	9.57E-01	9.88E-01	-	-
1385096_at	---	---	---	Rn.151464	BG380261	2.49	2.47	2.61	2.48	2.68	2.46	1.01	up	8.46E-01	9.52E-01	-	-
1375393_at	---	---	---	Rn.206042	BG377970	3.02	3.69	3.02	3.83	2.70	3.15	1.01	down	9.68E-01	9.91E-01	-	-
1396293_at	---	---	---	---	BI294274	2.48	2.46	2.51	2.47	2.48	2.45	1.01	down	4.14E-01	8.95E-01	-	-
1370411_at	Trpc1	transient receptor potential cation channel, subfamily C, member 1	89821	Rn.88592	AF061266	2.36	2.38	2.37	2.35	2.35	2.35	1.01	down	1.88E-02	8.95E-01	-	-
1386868_at	Rps10	ribosomal protein S10	81773	Rn.3359	NM_031109	10.64	11.04	10.44	10.60	10.63	10.93	1.01	up	9.38E-01	9.83E-01	-	-
1379099_at	---	---	---	Rn.203811	BE109030	2.42	2.40	2.42	2.41	2.49	2.40	1.01	up	5.86E-01	8.95E-01	-	-
1377583_at

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1397149_at	---	---	---	Rn.58463	BF395834	2.37	2.36	2.38	2.45	2.37	2.34	1.01	up	6.26E-01	8.95E-01	-	-
1381168_at	Hipk4	homeodomain interacting protein kinase 4	308449	Rn.41008	BF389548	2.34	2.33	2.39	2.33	2.34	2.33	1.01	down	4.20E-01	8.95E-01	-	-
1381877_at	---	---	---	Rn.204486	AI113234	2.39	2.34	2.35	2.34	2.34	2.34	1.01	down	3.62E-01	8.95E-01	-	-
1370296_at	Podn /// Scp2	podocan /// sterol carrier protein 2	25541 /// 313483	Rn.31887	M62763	9.82	10.11	9.74	9.75	10.00	9.97	1.01	up	9.10E-01	9.73E-01	-	-
1369892_at	LOC682649 /// LO	histone cluster 1, H2ai /// similar to histone 2a /// similar to Histone H2A type	29 /// 680063 /// 68	Rn.196555	NM_021840	2.59	2.55	2.65	2.58	2.62	2.56	1.01	down	6.51E-01	8.97E-01	-	-
1394851_at	Nkx2-3	NK2 transcription factor related, locus 3 (Drosophila)	309389	Rn.91986	BF290088	2.51	2.50	2.52	2.50	2.52	2.46	1.01	down	4.23E-01	8.95E-01	-	-
1381370_at	---	---	---	Rn.205572	AW254502	2.46	2.46	2.50	2.46	2.49	2.42	1.01	down	5.43E-01	8.95E-01	-	-
1383520_at	---	---	---	Rn.53896	AA859127	4.04	4.64	4.15	3.99	4.14	4.65	1.01	down	9.54E-01	9.86E-01	-	-
1381821_at	Mdga2	MAM domain containing glycosylphosphatidylinositol anchor 2	314180	Rn.205097	AI454542	2.59	2.55	2.58	2.58	2.64	2.55	1.01	up	6.02E-01	8.95E-01	-	-
1369540_at	Necab1	N-terminal EF-hand calcium binding protein 1	64169	Rn.64485	NM_022302	2.39	2.42	2.39	2.38	2.39	2.38	1.01	down	1.90E-01	8.95E-01	-	-
1387482_at	Grid2	glutamate receptor, ionotropic, delta 2	79220	Rn.10046	NM_024379	2.39	2.37	2.41	2.37	2.39	2.36	1.01	down	3.54E-01	8.95E-01	-	-
1373424_at	Dgcr6	DiGeorge syndrome critical region gene 6	303794	Rn.22467	BF284776	9.14	9.21	8.84	8.97	9.06	9.12	1.01	down	8.97E-01	9.68E-01	-	-
1397908_at	---	---	---	Rn.148196	AW915255	2.62	2.38	2.40	2.38	2.39	2.67	1.01	up	8.98E-01	9.68E-01	-	-
1381948_at	---	---	---	Rn.43478	AI547876	2.31	2.30	2.31	2.30	2.38	2.29	1.01	up	6.06E-01	8.95E-01	-	-
1390759_at	---	---	---	Rn.146681	BF399309	2.37	2.35	2.38	2.37	2.37	2.31	1.01	down	4.99E-01	8.95E-01	-	-
1372138_at	Cux1	Cut-like homeobox 1	116639	Rn.10455	BM390477	5.44	5.50	5.21	5.38	5.13	5.59	1.01	down	9.21E-01	9.77E-01	-	-
1378308_at	---	---	---	---	AI231054	3.56	3.55	4.91	4.65	3.56	3.76	1.01	down	9.78E-01	9.93E-01	-	-
1389734_x_at	H2-T24	histocompatibility 2, T region locus 24	414784	---	BI282965	7.80	7.73	8.07	8.04	7.92	7.59	1.01	down	9.26E-01	9.79E-01	-	-
1398646_at	RGD1565493	similar to DKFZP434I092 protein	500853	Rn.43509	AI639247	2.45	2.42	2.45	2.43	2.44	2.41	1.01	down	2.98E-01	8.95E-01	-	-
1378111_at	---	---	---	Rn.38662	AI576002	2.37	2.36	2.39	2.43	2.38	2.36	1.01	up	4.75E-01	8.95E-01	-	-
1393856_x_at	RGD1306959	similar to C11orf17 protein	361624	Rn.106344	AA799992	2.71	2.69	2.73	2.69	2.72	2.67	1.01	down	3.94E-01	8.95E-01	-	-
1385962_x_at	Blk	B lymphoid tyrosine kinase	364403	Rn.20030	BF287903	2.54	2.52	2.53	2.52	2.54	2.47	1.01	down	4.56E-01	8.95E-01	-	-
1392364_at	---	---	---	Rn.199775	BE102708	2.44	2.42	2.48	2.43	2.45	2.41	1.01	down	4.23E-01	8.95E-01	-	-
1391189_a_at	RGD1559747	similar to Zinc finger and SCAN domain containing protein 2 (Zinc finger prote	312310	---	AA892659	2.37	2.36	2.38	2.36	2.37	2.42	1.01	up	4.08E-01	8.95E-01	-	-
1369741_at	Kcnj3	potassium inwardly-rectifying channel, subfamily J, member 3	50599	Rn.9809	NM_031610	2.42	2.41	2.42	2.40	2.49	2.41	1.01	up	5.86E-01	8.95E-01	-	-
1385522_at	Orc1l	origin recognition complex, subunit 1-like (yeast)	313479	Rn.92486	AI059490	2.47	2.44	2.56	2.46	2.53	2.43	1.01	down	7.32E-01	9.14E-01	-	-
1373364_at	Stk11	serine/threonine kinase 11	314621	Rn.12052	AI070345	2.28	2.23	2.24	2.23	2.24	2.23	1.01	down	3.21E-01	8.95E-01	-	-
1380969_at	---	---	---	Rn.207728	BE106363	2.59	2.71	2.58	2.79	2.57	2.56	1.01	up	8.57E-01	9.55E-01	-	-
1381023_at	---	---	---	Rn.206324	AW526145	2.42	2.41	2.43	2.41	2.42	2.38	1.01	down	2.72E-01	8.95E-01	-	-
1392083_at	Ext1	Exostoses (multiple) 1	299907	Rn.106323	BF415852	2.47	2.44	2.52	2.47	2.48	2.42	1.01	down	5.80E-01	8.95E-01	-	-
1379212_at	---	---	---	---	BE103175	2.44	2.42	2.46	2.43	2.43	2.41	1.01	down	2.45E-01	8.95E-01	-	-
1378735_at	---	---	---	Rn.172718	BG378988	3.79	3.76	3.80	3.85	3.79	3.75	1.01	up	6.21E-01	8.95E-01	-	-
1380586_at	---	---	---	---	AI711267	2.48	2.49	2.48	2.48	2.48	2.44	1.01	down	2.72E-01	8.95E-01	-	-
1380916_at	---	---	---	Rn.170999	BE106557	2.54	2.53	2.56	2.53	2.54	2.50	1.01	down	3.40E-01	8.95E-01	-	-
1392812_at	---	---	---	Rn.92761	AI058726	2.33	2.32	2.34	2.33	2.34	2.38	1.01	up	3.93E-01	8.95E-01	-	-
1372416_at	Nr2c1	nuclear receptor subfamily 2, group C, member 1	252924	Rn.79894	BI291300	2.46	2.45	2.50	2.45	2.49	2.43	1.01	down	5.28E-01	8.95E-01	-	-
1393072_at	Ube2q2	ubiquitin-conjugating enzyme E2Q (putative) 2	363065	---	H32128	6.73	6.90	7.51	6.84	7.11	7.24	1.01	up	9.53E-01	9.86E-01	-	-
1382262_at	---	---	---	Rn.43318	BE111891	2.50	2.50	2.56	2.50	2.52	2.50	1.01	down	4.69E-01	8.95E-01	-	-
1379374_at	Lppr4	plasticity related gene 1	295401	Rn.58355	AW526088	2.41	2.40	2.46	2.40	2.42	2.38	1.01	down	4.78E-01	8.95E-01	-	-
1375546_at	Fzr1	fizzy/cell division cycle 20 related 1 (Drosophila)	314642	Rn.12924	AI009616	3.74	4.02	3.84	3.76	3.65	4.25	1.01	up	9.38E-01	9.83E-01	-	-
1383959_at	Lztr1	leucine-zipper-like transcription regulator 1	360745	Rn.15759	BE096059	2.28	2.26	2.28	2.26	2.27	2.26	1.01	down	9.84E-02	8.95E-01	-	-
1384515_at	Hey2	Hairy/enhancer-of-split related with YRPW motif 2	155430	Rn.58672	BF388057	2.45	2.44	2.47	2.44	2.45	2.41	1.01	down	3.40E-01	8.95E-01	-	-
1374450_at	Ino80b	INO80 complex subunit B	500225	Rn.106816	BF406124	2.49	2.52	2.60	2.48	2.55	2.52	1.01	down	6.88E-01	9.04E-01	-	-
1396558_at	---	---	---	Rn.200034	BF392155	2.51	2.48	2.53	2.49	2.52	2.45	1.01	down	5.56E-01	8.95E-01	-	-
1372296_at	Sh3bgr	SH3 domain binding glutamic acid-rich protein	498066	Rn.4128	AA800892	2.29	2.27	2.29	2.29	2.29	2.32	1.01	up	2.78E-01	8.95E-01	-	-
1395358_at	Rhobtb3	Rho-related BTB domain containing 3	309922	Rn.74134	BF562492	2.42	2.45	2.42	2.41	2.42	2.41	1.01	down	1.89E-01	8.95E-01	-	-
1375865_at	Tjap1	tight junction associated protein 1	316233	Rn.18395	BF408844	4.25	4.13	4.61	4.49	4.21	4.24	1.01	down	9.27E-01	9.79E-01	-	-
1379709_at	Krtap14l	keratin associated protein 14 like	363739	---	AI599514	2.32	2.32	2.34	2.32	2.33	2.37	1.01	up	4.00E-01	8.95E-01	-	-
1382977_at	---	---	---	---	AI234983	2.51	2.45	2.52	2.47	2.48	2.47	1.01	down	5.02E-01	8.95E-01	-	-
1398125_at	Ank2	ankyrin 2, neuronal	362036	Rn.133131	BF563203	2.32	2.31	2.33	2.32	2.37	2.31	1.01	up	4.83E-01	8.95E-01	-	-
1386960_at	Slc37a4	solute carrier family 37 (glucose-6-phosphate transporter), member 4	29573	Rn.1592	NM_031589	8.73	8.78	9.29	8.85	8.92	8.98	1.01	down	9.31E-01	9.81E-01	-	-
1390063_at	Mfap3	microfibrillar-associated protein 3	287299	Rn.163119	BG380473	2.81	3.82	3.71	3.70	3.32	3.27	1.01	down	9.64E-01	9.90E-01	-	-
1370894_at	Cldn7	claudin 7	65132	Rn.32259	AJ011811	2.40	2.40	2.41	2.40	2.42	2.45	1.01	up	3.32E-01	8.95E-01	-	-
1396664_at	---	---	---	Rn.172324	BF409427	2.42	2.40	2.44	2.38	2.42	2.41	1.01	down	4.13E-01	8.95E-01	-	-
1372041_at	---	---	---	---	BI290059	2.65	2.67	2.62	2.28	2.65	3.06	1.01	up	9.46E-01	9.84E-01	-	-
1373890_at	Chchd5	coiled-coil-helix-coiled-coil-helix domain containing 5	296147	Rn.8658	AA924522	5.10	5.10	5.16	4.87	5.46	5.08	1.01	up	9.28E-01	9.80E-01	-	-
1397385_at	---	---	---	Rn.221927	BM387110	4.46	4.36	4.55	4.45	4.46	4.50	1.01	up	7.81E-01	9.29E-01	-	-
1375405_at	---	---	---	Rn.173160	BF406058	2.56	2.55	2.61	2.54	2.61	2.52	1.01	down	6.22E-01	8.95E-01	-	-
1379237_at	Tax1bp3	Tax1 (human T-cell leukemia virus type I) binding protein 3	360564	Rn.34842	AA997638	2.43	2.41	2.47	2.42	2.45	2.40	1.01	down	4.69E-01	8.95E-01	-	-
1395517_at	Limd1	LIM domains containing 1	316101	Rn.3966	AW916690	2.34	2.34	2.35	2.34	2.41	2.33	1.01	up	5.78E-01	8.95E-01	-	-
1396247_at	---	---	---	Rn.139100	AI453997	2.79	2.79	2.76	2.83	2.80	2.77	1.01	up	4.96E-01	8.95E-01	-	-
1380366_at	gh-6 /// LOC31450	immunoglobulin heavy chain 6 /// similar to single chain Fv antibody fragment	299357 /// 314509	Rn.201760	AA996557	2.44	2.39	2.41	2.39	2.43	2.37	1.01	down	5.06E-01	8.95E-01	-	-
1394839_at	---	---	---	---	AA850773	2.46	2.41	2.44	2.42	2.45	2.40	1.01	down	4.72E-01	8.95E-01	-	-
1395847_at	LOC100188933	hypothetical protein LOC100188933	100188933	Rn.47244	BF417335	3.58	3.61	3.60	3.59	3.65	3.59	1.01	up	4.98E-01	8.95E-01	-	-
1368981_at	Aqp4	aquaporin 4	25293	Rn.90091	NM_012825	2.36	2.37	2.38	2.35	2.37	2.34	1.01	down	1.62E-01	8.95E-01	-	-
1369503_at	Amy2	amylase 2, pancreatic	497039	Rn.67070	NM_031502	2.54	2.51	2.61	2.53	2.60	2.48	1.01	down	7.28E-01	9.13E-01	-	-
1384585_at	LOC690418	similar to Acidic proline-rich protein PRP25 precursor	690418	---	BI279337	2.41	2.37	2.38	2.38	2.47	2.37	1.01	up	6.42E-01	8.95E-01	-	-
1397011_at	---	---	---	Rn.153647	BE108912	2.32	2.32	2.33	2.38	2.32	2.32	1.01	up	4.41E-01	8.95E-01	-	-
1387145_at	Gjb1	gap junction protein, beta 1	29584	Rn.10444	NM_017251	2.64	2.73	2.37	2.49	2.50	2.70	1.01	down	9.04E-01	9.70E-01	-	-
1377136_at	---	---	---	Rn.205527	AW254190	2.39	2.38	2.44	2.38	2.42	2.37	1.01	down	5.50E-01	8.95E-01	-	-
1397776_at	---	---	---	---	BF409525	2.76	2.72	2.77	2.75	2.81	2.73	1.01	up	5.89E-01	8.95E-01	-	-
1392647_at	LOC687992	similar to Serum amyloid A-3 protein precursor	687992	---	BF282318	2.52	2.52	2.55	2.52	2.52	2.50	1.01	down	2.73E-01	8.95E-01	-	-
1379527_at	Epc1	enhancer of polycomb homolog 1 (Drosophila)	307042	Rn.219240	AI502952	2.47	2.74	2.47	2.45	2.47	2.70	1.01	down	8.98E-01	9.68E-01	-	-
1392066_at	RGD1559885	Similar to hypothetical gene supported by BC063892	500059	Rn.20360	BF391001	2.35	2.34	2.38	2.34	2.35	2.33	1.01	down	3.00E-01	8.95E-01	-	-
1374781_at	---	---	---	Rn.166588	AW533214	2.42	2.41	2.42	2.47	2.42	2.40	1.01	up	4.73E-01	8.95E-01	-	-
1389881_at	---	---	---	Rn.176848	BI296516	2.40	2.39	2.42	2.39	2.41	2.37	1.01	down	3.13E-01	8.95E-01	-	-
1394299_at	Bex1 /// Bex2	brain expressed gene 1 /// brain expressed X-linked 2	363498 /// 501625	Rn.9190	BG669326	2.45	2.47	2.56	2.48	2.48	2.46	1.01	down	6.44E-01	8.95E-01	-	-
1396975_at	---	---	---	---	BI281220	2.46	2.43	2.48	2.46	2.47	2.50	1.01	up	4.11E-01	8.95E-01	-	-
1378067_at	Aes	Amino-terminal enhancer of split	29466	Rn.11495	BF396871	2.43	2.41	2.44	2.42	2.43	2.39	1.01	down	3.29E-01	8.95E-01	-	-
1369855_at	Hrh1	histamine receptor H 1	24448	Rn.81032	NM_017018	2.40	2.39	2.41	2.40	2.40	2.35	1.01	down	4.01E-01	8.95E-01	-	-
1389485_at	Mdm1	Mdm1 nuclear protein homolog (mouse)	314859	Rn.162942	BE099784	2.71	2.70	2.71	2.71	2.71	2.76	1.01	up	3.79E-01	8.95E-01	-	-
1384967_at	---	---	---	---	BM386930	2.75	2.67	2.80	2.74	2.79	2.63	1.01	down	7.94E-01	9.34E-01	-	-
1371178_at	Il5	interleukin 5	24497	Rn.44227	AJ011299	2.39	2.38	2.40	2.38	2.39	2.35	1.01	down	3.21E-01	8.95E-01	-	-
1397408_at	---	---	---	---	AI407913	2.40	2.39	2.40	2.38	2.39	2.36	1.01	down	1.48E-01	8.95E-01	-	-
1395094_at	---	---	---	Rn.96074	BF549339	2.40	2.38	2.43	2.40	2.48	2.38	1.01	up	6.58E-01	8.98E-01	-	-
1394517_at	---	---	---	Rn.19506	AW522148	2.43	2.42	2.45	2.42	2.44	2.39	1.01	down	3.96E-01	8.95E-01	-	-
1375520_at	Copz1	coatomer protein complex, subunit zeta 1	315345	Rn.159796	AI007763	7.15	8.08	8.11	6.94	8.34	8.01	1.01	down	9.77E-01	9.93E-01	-	-
1368991_at	Smpd3	sphingomyelin phosphodiesterase 3, neutral	94338	Rn.54555	NM_053605	2.42	2.36	2.38	2.37	2.38	2.37	1.01	down	3.44E-01	8.95E-01	-	-
1392489_at	---	---	---	Rn.8458	BE108956	2.41	2.38	2.41	2.40	2.47	2.38	1.01	up	6.01E-01	8.95E-01	-	-
1379156_at	---	---	---	Rn.173103	BF400248	2.36	2.34	2.35	2.32	2.35	2.33	1.01	down	1.80E-01	8.95E-01	-	-
1378818_at	---	---	---	Rn.173625	BE095996	2.28	2.27	2.33	2.28	2.29	2.27	1.01	down	4.22E-01	8.95E-01	-	-
1396106_at	---	---	---	Rn.58641	BF565241	2.37	2.33	2.35	2.34	2.34	2.32	1.01	down	2.61E-01	8.95E-01	-	-
1380240_at	---	---	---	Rn.212078	AI102982	2.48	2.26	2.28	2.54	2.27	2.26	1.01	up	8.93E-01	9.67E-01	-	-
1381946_at	---	---	---	---	AI535089	2.34	2.37	2.34	2.33	2.34	2.33	1.01	down	1.97E-01	8.95E-01	-	-
1378013_at	RGD1564391	RGD1564391	361199	Rn.24746	BF283303	2.52	2.51	2.53	2.52	2.53	2.47	1.01	down	4.25E-01	8.95E-01	-	-
1383195_at	---	---	---	---	AW521311	2.56	2.53	2.63	2.54	2.59	2.54	1.01	down	6.38E-01	8.95E-01	-	-
1371746_at	---	---	---	Rn.13646	AW525288	2.40	2.38	2.41	2.39	2.47	2.38	1.01	up	6.23E-01	8.95E-01	-	-
1390013_at	---	---	---	---	BF410427	2.38	2.37	2.39	2.37	2.38	2.34	1.01	down	2.75E-01	8.95E-01	-	-
1385795_at	---	---	---	---	AA859828	2.48	2.46	2.49	2.45	2.48	2.45	1.01	down	3.22E-01	8.95E-01	-	-
1385799_at	Nxph1	neurexophilin 1	25501	Rn.10610	AW531533	2.52	2.50	2.56	2.49	2.58	2.46	1.01	down	7.07E-01	9.08E-01	-	-
1387283_at	Mx2	myxovirus (influenza virus) resistance 2	286918	Rn.10374	NM_134350	2.66	2.62	2.69	2.65	2.77	2.60	1.01	up	7.84E-01	9.30E-01	-	-
1388996_at	Hdhd2	haloacid dehalogenase-like hydrolase domain containing 2	361351	Rn.7319	AI406527	5.74	5.92	6.60	5.54	6.76	6.00	1.01	up	9.72E-01	9.92E-01	-	-
1391134_at	Tmco3	transmembrane and coiled-coil domains 3	306607	Rn.59630	BF404833	2.40	2.37	2.41	2.45	2.41	2.38	1.01	up	5.39E-01	8.95E-01	-	-
1397657_at	---	---	---	---	BF416736	2.51	2.49	2.55	2.49	2.53	2.48	1.01	down	5.23E-01	8.95E-01	-	-
1387164_at	Lect1	leukocyte cell derived chemotaxin 1	81512	Rn.9900	NM_030854	2.36	2.35	2.42	2.36	2.38	2.35	1.01	down	5.15E-01	8.95E-01	-	-
1368185_at	Gnaz	guanine nucleotide binding protein (G protein), alpha z polypeptide	25740	Rn.10943	J03773	2.37	2.36	2.40	2.36	2.36	2.35	1.01	down	2.56E-01	8.95E-01	-	-
1397646_at	---	---	---	Rn.29919	AW524814	2.41	2.39	2.43	2.41	2.42	2.35	1.01	down	5.51E-01	8.95E-01	-	-
1396142_at	Mrps9	mitochondrial ribosomal protein S9	301371	Rn.13913	BI274476	5.96	6.80	5.76	5.81	5.79	6.96	1.01	up	9.76E-01	9.93E-01	-	-
1378534_at	LOC308394	similar to brain carcinoembryonic antigen	308394	Rn.161808	AI178797	2.41	2.40	2.43	2.40	2.42	2.37	1.01	down	4.10E-01	8.95E-01	-	-
1395021_at	---	---	---	Rn.201913	AW533225	2.47	2.45	2.50	2.53	2.49	2.46	1.01	up	5.44E-01	8.95E-01	-	-
1376535_at	Mdga1	MAM domain containing glycosylphosphatidylinositol anchor 1	309659	Rn.133657	BE104330	2.24	2.29	2.24	2.24	2.25	2.24	1.01	down	3.88E-01	8.95E-01	-	-
1382648_at	Eprs	glutamyl-prolyl-tRNA synthetase	289352	Rn.21240	AI235566	2.33	2.35	2.36	2.33	2.34	2.32	1.01	down	1.68E-01	8.95E-01	-	-
1387459_at	Pkib	protein kinase (cAMP-dependent, catalytic) inhibitor beta	24678	Rn.9748	NM_012627	2.48	2.45	2.48	2.46	2.56	2.44	1.01	up	6.90E-01	9.05E-01	-	-
1371183_a_at	Dlg4	discs, large homolog 4 (Drosophila)	29495	Rn.9765	U77090	2.38	2.37	2.38	2.44	2.38	2.35	1.01	up	5.94E-01	8.95E-01	-	-
1393764_at	---	---	---	Rn.204065	AI045104	2.68	2.67	2.68	2.68	2.74	2.67	1.01	up	5.12E-01	8.95E-01	-	-
1368478_at	Drd1a	dopamine receptor D1A	24316	Rn.24039	M35077	2.38	2.40	2.39	2.38	2.38	2.36	1.01	down	1.46E-01	8.95E-01	-	-
1383504_at	Cpa6	carboxypeptidase A6	299811	Rn.16480	AW530904	6.97	6.76	7.48	6.75	7.01	7.50	1.01	up	9.61E-01	9.89E-01	-	-
1381662_at	---	---	---	Rn.156489	BF409847	2.45	2.44	2.47	2.44	2.45	2.41	1.01	down	3.70E-01	8.95E-01	-	-
1388000_at	Slc24a2	solute carrier family 24 (sodium/potassium/calcium exchanger), member 2	84550	Rn.208755	AF021923	2.45	2.43	2.52	2.43	2.50	2.42	1.01	down	6.93E-01	9.05E-01	-	-
1386135_at	---	---	---	---	BI850153	2.38	2.37	2.42	2.37	2.38	2.36	1.01	down	3.97E-01	8.95E-01	-	-
1389473_at	Rgr	retinal G protein coupled receptor	306307	Rn.26828	BG374248	2.46	2.42	2.47	2.44	2.45	2.41	1.01	down	4.03E-01	8.95E-01	-	-
1391739_at	Rundc1	RUN domain containing 1	303552	---	BF393038	2.37	2.37	2.42	2.37	2.38	2.37	1.01	down	4.16E-01	8.95E-01	-	-
1388262_at	Kcna6	potassium voltage gated channel, shaker related subfamily, member 6	64358	Rn.162791	AJ276137	2.74	2.65	2.77	2.73	2.80	2.69	1.01	up	7.62E-01	9.22E-01	-	-
1370459_at	Aard	alanine and arginine rich domain containing protein	246323	Rn.38451	AY007690	2.29	2.28	2.33	2.29	2.28	2.28	1.01	down	3.84E-01	8.95E-01	-	-
1392332_at	Myt1	myelin transcription factor 1	362291	Rn.102945	AI070390	2.46	2.45	2.49	2.45	2.48	2.42	1.01	down	4.60E-01	8.95E-01	-	-
1378316_at	---	---	---	Rn.203212	AI145009	2.50	2.48	2.53	2.49	2.52	2.45	1.01	down	5.66E-01	8.95E-01	-	-
1393589_at	Khl4	kelch-like 4 (Drosophila)	317196	Rn.121914	AW524979	2.51	2.48	2.55	2.49	2.53	2.46	1.01	down	6.05E-01	8.95E-01	-	-
1385203_at	---	---	---	Rn.141273	BE120707	2.41	2.43	2.42	2.40	2.43	2.39	1.01	down	2.38E-01	8.95E-01	-	-
1372569_at	Fhl3	four and a half LIM domains 3	313582	Rn.100732	AI171676	2.45	2.41	2.42	2.41	2.42	2.39	1.01	down	3.84E-01	8.95E-01	-	-
1393945_at	---	---	---	Rn.147572	AI454487	2.51	2.48	2.55	2.50	2.53	2.46	1.01	down	6.09E-01	8.95E-01	-	-
1398534_at	---	---	---	Rn.44199	BF396426	2.49	2.48	2.56	2.49	2.52	2.48	1.01	down	6.06E-01	8.95E-01	-	-
1397256_at	---	---	---	---	BF284577	2.23	2.27	2.24	2.23	2.24	2.23	1.01	down	2.57E-01	8.95E-01	-	-
1369273_a_at	Npr3	natriuretic peptide receptor C/guanylate cyclase C (atrionatriuretic peptide rec	25339	Rn.11297	X78595	2.52	2.51	2.54	2.50	2.52	2.51	1.01	down	2.81E-01	8.95E-01	-	-
1398036_at	---	---	---	Rn.210678	BF400233	2.47	2.44	2.51	2.45	2.49	2.42	1.01	down	5.81E-01	8.95E-01	-	-
1378272_at	---	---	---	Rn.147652	BF411569	2.53	2.52	2.55	2.52	2.54	2.50	1.01	down	2.51E-01	8.95E-01	-	-
1381152_at	Mettl11a	methyltransferase like 11A	362103	Rn.12306	BF387456	2.45	2.42	2.44	2.42	2.43	2.40	1.01	down	2.55E-01	8.95E-01	-	-
1396961_at	---	---	---	Rn.60547	BF404960	2.38	2.37	2.39	2.37	2.44	2.37	1.01	up	5.53E-01	8.95E-01	-	-
1378811_at	---	---	---	---	BF402978	2.98	2.63	3.15	2.98	2.99	2.75	1.01	down	9.30E-01	9.81E-01	-	-
1394399_at	---	---	---	Rn.29946	AW523958	2.56	2.54	2.62	2.55	2.61	2.52	1.01	down	6.88E-01	9.04E-01	-	-
1397177_at	---	---	---	Rn.150275	BF409052	2.48	2.43	2.46	2.44	2.45	2.43	1.01	down	3.99E-01	8.95E-01	-	-
1390376_at	---	---	---	Rn.57986	BF406135	2.37	2.36	2.41	2.36	2.38	2.35	1.01	down	4.52E-01	8.95E-01	-	-
1380072_at	MGC93975	similar to 2310044H10Rik protein	292878	Rn.1470	AI233871	2.84	2.95	2.81	2.83	2.84	2.87	1.01	down	7.38E-01	9.16E-01	-	-
1389725_at	Tm7sf2	transmembrane 7 superfamily member 2	293688	Rn.8313	BM390364	4.82	4.52	4.81	4.66	4.80	4.65	1.01	down	8.88E-01	9.65E-01	-	-
1379761_at	---	---	---	Rn.129784	BE104517	2.50	2.46	2.47	2.46	2.46	2.45	1.01	down	2.37E-01	8.95E-01	-	-

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1397118_at	---	---	---	Rn.211449	BF413386	2.46	2.46	2.48	2.46	2.47	2.42	1.01	down	3.62E-01	8.95E-01	-	-
1372118_at	Nsg2	neuron specific gene family member 2	497878	Rn.14657	BI281674	2.43	2.41	2.44	2.41	2.42	2.40	1.01	down	1.81E-01	8.95E-01	-	-
1398992_at	---	---	---	Rn.2497	AI410311	4.35	4.61	4.54	4.46	4.45	4.55	1.01	down	8.56E-01	9.55E-01	-	-
1381747_at	---	---	---	Rn.207239	BM385105	2.49	2.47	2.53	2.48	2.51	2.45	1.01	down	5.80E-01	8.95E-01	-	-
1370617_at	Grb2	growth factor receptor bound protein 2	81504	Rn.3360	D49847	2.40	2.38	2.40	2.41	2.44	2.37	1.01	up	4.74E-01	8.95E-01	-	-
1368873_at	Hoxa2	homeo box A2	24452	Rn.91077	NM_012581	2.28	2.27	2.28	2.28	2.33	2.27	1.01	up	4.47E-01	8.95E-01	-	-
1370886_a_at	Klc1	kinesin light chain 1	171041	Rn.106230	AI576981	7.23	7.39	7.20	7.19	7.49	7.19	1.01	up	8.98E-01	9.68E-01	-	-
1381844_at	---	---	---	Rn.57260	BM389974	2.28	2.27	2.28	2.27	2.28	2.32	1.01	up	3.61E-01	8.95E-01	-	-
1382553_at	Rfx3	Regulatory factor X, 3 (influences HLA class II expression)	361746	Rn.23347	AI137120	2.63	2.62	2.66	2.62	2.63	2.61	1.01	down	3.73E-01	8.95E-01	-	-
1381274_at	---	---	---	Rn.147560	BE118993	2.46	2.45	2.50	2.45	2.46	2.45	1.01	down	3.58E-01	8.95E-01	-	-
1391108_at	Znf593	zinc finger protein 593	298546	Rn.147537	BI289413	2.35	2.35	2.36	2.35	2.36	2.40	1.01	up	3.91E-01	8.95E-01	-	-
1394429_at	---	---	---	Rn.173626	BF413088	2.42	2.40	2.45	2.41	2.42	2.39	1.01	down	3.58E-01	8.95E-01	-	-
1384802_at	---	---	---	---	AI715326	2.59	2.57	2.61	2.56	2.60	2.57	1.01	down	3.75E-01	8.95E-01	-	-
1385688_at	---	---	---	---	BI287225	2.27	2.26	2.27	2.27	2.33	2.26	1.01	up	4.96E-01	8.95E-01	-	-
1377591_at	Tiam1	T-cell lymphoma invasion and metastasis 1	304109	Rn.204561	BE109656	2.45	2.42	2.52	2.44	2.50	2.41	1.01	down	7.08E-01	9.09E-01	-	-
1393668_at	Pex11g	peroxisomal biogenesis factor 11 gamma	288369	Rn.138848	BF408421	2.68	2.67	2.71	2.68	2.72	2.61	1.01	down	6.56E-01	8.98E-01	-	-
1392236_at	---	---	---	Rn.208902	AI145441	2.44	2.47	2.45	2.44	2.45	2.43	1.01	down	2.15E-01	8.95E-01	-	-
1377802_at	RGD1566399	similar to MYST histone acetyltransferase monocytic leukemia 4	305681	Rn.221977	BE098769	2.26	2.25	2.31	2.26	2.26	2.25	1.01	down	4.39E-01	8.95E-01	-	-
1394100_at	Ftar2	free fatty acid receptor 2	292794	Rn.17909	AI012591	2.47	2.45	2.49	2.46	2.46	2.45	1.01	down	2.38E-01	8.95E-01	-	-
1397095_at	---	---	---	Rn.207542	BF411970	2.40	2.39	2.42	2.39	2.40	2.37	1.01	down	2.97E-01	8.95E-01	-	-
1393642_at	Golsyn	Golgi-localized protein	500865	Rn.99794	AI137139	2.50	2.46	2.52	2.48	2.50	2.45	1.01	down	5.10E-01	8.95E-01	-	-
1395509_at	---	---	---	Rn.108008	BG666117	2.44	2.44	2.46	2.44	2.51	2.44	1.01	up	5.33E-01	8.95E-01	-	-
1377529_at	---	---	---	Rn.210049	BF404045	2.47	2.45	2.51	2.46	2.49	2.43	1.01	down	5.73E-01	8.95E-01	-	-
1380614_at	---	---	---	Rn.152072	BM385169	2.53	2.49	2.57	2.52	2.57	2.45	1.01	down	7.25E-01	9.13E-01	-	-
1394744_at	Eef1g	Eukaryotic translation elongation factor 1 gamma	293725	Rn.43300	AI556327	2.35	2.34	2.38	2.35	2.35	2.32	1.01	down	3.00E-01	8.95E-01	-	-
1373829_at	Fgfr2	fibroblast growth factor receptor 2	25022	Rn.12732	AI412658	2.37	2.37	2.38	2.42	2.37	2.37	1.01	up	3.62E-01	8.95E-01	-	-
1376951_at	Mad2l1	MAD2 (mitotic arrest deficient, homolog)-like 1 (yeast)	297176	Rn.19771	AI101906	2.41	2.41	2.43	2.47	2.42	2.41	1.01	up	4.39E-01	8.95E-01	-	-
1398475_at	Dars2	aspartyl-tRNA synthetase 2 (mitochondrial)	304919	Rn.137838	AI172076	2.43	2.41	2.44	2.42	2.42	2.40	1.01	down	2.94E-01	8.95E-01	-	-
1394075_at	Fanca	Fanconi anemia, complementation group A	361435	Rn.163415	AI059004	2.55	2.55	2.72	2.50	2.98	2.29	1.01	down	9.44E-01	9.84E-01	-	-
1374974_at	---	---	---	Rn.16408	BI299365	2.45	2.45	2.46	2.52	2.46	2.43	1.01	up	5.91E-01	8.95E-01	-	-
1370513_at	Tpm1	tropomyosin 1, alpha	24851	Rn.87540	M34135	2.58	2.55	2.65	2.57	2.61	2.54	1.01	down	6.84E-01	9.03E-01	-	-
1385080_s_at	Gsdma1	gasdermin A1	360619	Rn.82083	BM387797	2.39	2.37	2.43	2.38	2.39	2.37	1.01	down	3.96E-01	8.95E-01	-	-
1396829_at	---	---	---	Rn.45635	AW523421	2.46	2.46	2.47	2.46	2.52	2.46	1.01	up	4.82E-01	8.95E-01	-	-
1389803_at	RGD1560784	similar to RIKEN cDNA B630019K06	363449	---	AI408089	2.28	2.23	2.24	2.24	2.23	2.23	1.01	down	3.62E-01	8.95E-01	-	-
1396640_at	---	---	---	Rn.154167	BF403481	2.50	2.47	2.54	2.48	2.54	2.44	1.01	down	6.73E-01	9.01E-01	-	-
1385082_at	---	---	---	Rn.131291	BE120904	2.42	2.42	2.43	2.42	2.48	2.41	1.01	up	4.73E-01	8.95E-01	-	-
1391606_at	---	---	---	Rn.17471	BE116345	2.45	2.43	2.47	2.43	2.46	2.41	1.01	down	4.50E-01	8.95E-01	-	-
1375359_at	Gfra2	GDNF family receptor alpha 2	25136	Rn.90137	BE114004	4.65	3.92	4.05	4.54	4.08	3.96	1.01	down	8.59E-01	9.89E-01	-	-
1367616_at	Nppb	natriuretic peptide precursor B	25105	Rn.3835	NM_031545	2.61	2.51	2.49	2.51	2.52	2.54	1.01	down	7.17E-01	9.10E-01	-	-
1387634_a_at	Amelx	amelogenin X chromosome	29160	Rn.11368	NM_019154	2.60	2.58	2.69	2.60	2.72	2.51	1.01	down	8.28E-01	9.46E-01	-	-
1376795_at	Pik3ap1	phosphoinositide-3-kinase adaptor protein 1	294048	Rn.15411	AW916092	2.29	2.29	2.31	2.34	2.31	2.29	1.01	up	4.30E-01	8.95E-01	-	-
1375761_at	Bag3	Bcl2-associated athanogene 3	293524	Rn.46304	AW532391	2.44	2.41	2.45	2.41	2.44	2.40	1.01	down	3.89E-01	8.95E-01	-	-
1393782_at	---	---	---	Rn.210289	BF396790	2.48	2.43	2.48	2.45	2.47	2.42	1.01	down	5.27E-01	8.95E-01	-	-
1380006_at	---	---	---	---	AW921301	2.39	2.37	2.42	2.37	2.40	2.37	1.01	down	3.96E-01	8.95E-01	-	-
1377025_at	Kif3a	kinesin family member 3a	84392	Rn.47400	BF563503	5.28	4.31	5.19	4.86	4.51	5.35	1.01	down	9.70E-01	9.91E-01	-	-
1396560_at	---	---	---	---	BF399126	2.40	2.39	2.44	2.39	2.42	2.37	1.01	down	4.95E-01	8.95E-01	-	-
1384496_at	---	---	---	Rn.156749	BI274749	2.36	2.31	2.34	2.32	2.33	2.31	1.01	down	3.12E-01	8.95E-01	-	-
1378980_at	RGD1305685	similar to hypothetical protein FLJ13089	360811	Rn.202650	AI044779	2.45	2.44	2.46	2.50	2.47	2.43	1.01	up	5.17E-01	8.95E-01	-	-
1384007_at	Spg3a	spastic paraplegia 3A homolog (human)	362750	Rn.135117	BG668983	2.46	2.44	2.46	2.45	2.52	2.43	1.01	up	6.06E-01	8.95E-01	-	-
1394817_at	---	---	---	---	AI548775	2.66	2.63	2.71	2.64	2.81	2.60	1.01	up	8.25E-01	9.45E-01	-	-
1378374_at	RGD1560137	similar to expressed sequence AU021034	290372	Rn.19611	BE100748	2.55	2.50	2.51	2.50	2.52	2.50	1.01	down	4.04E-01	8.95E-01	-	-
1391809_at	---	---	---	Rn.203835	BE106814	2.46	2.45	2.48	2.46	2.47	2.42	1.01	down	4.28E-01	8.95E-01	-	-
1388281_at	RT1.M4	MHC class Ib antigen	309584	---	AF024712	2.44	2.43	2.46	2.43	2.45	2.48	1.01	up	4.32E-01	8.95E-01	-	-
1394541_at	---	---	---	Rn.149196	BM387754	2.54	2.53	2.55	2.50	2.54	2.53	1.01	down	2.79E-01	8.95E-01	-	-
1398703_at	---	---	---	Rn.33990	AI178307	2.59	2.53	2.61	2.57	2.57	2.55	1.01	down	5.61E-01	8.95E-01	-	-
1375242_at	LOC687797	similar to tumor suppressor candidate 5	687797	---	BI296440	2.31	2.28	2.33	2.31	2.31	2.26	1.01	down	5.23E-01	8.95E-01	-	-
1378807_at	---	---	---	Rn.209664	BF400251	2.40	2.37	2.39	2.38	2.38	2.35	1.01	down	2.14E-01	8.95E-01	-	-
1375992_at	RGD1564114	similar to FLJ46082 protein	499765	Rn.22858	BM389934	2.33	2.35	2.33	2.33	2.33	2.31	1.01	down	1.84E-01	8.95E-01	-	-
1389768_at	Gpr110	G protein-coupled receptor 110	301266	Rn.66272	BI296720	2.39	2.39	2.40	2.39	2.40	2.44	1.01	up	4.17E-01	8.95E-01	-	-
1395487_at	---	---	---	Rn.48058	BF400826	2.54	2.51	2.56	2.51	2.58	2.47	1.01	down	6.88E-01	9.04E-01	-	-
1384514_at	---	---	---	Rn.123788	BF398600	2.38	2.37	2.42	2.38	2.38	2.37	1.01	down	3.30E-01	8.95E-01	-	-
1398465_at	Lrrc23	leucine rich repeat containing 23	312707	Rn.46210	AW526224	2.42	2.40	2.46	2.41	2.44	2.39	1.01	down	5.47E-01	8.95E-01	-	-
1376821_at	Tmie	transmembrane inner ear	501061	Rn.172713	BE101619	2.43	2.42	2.45	2.42	2.44	2.40	1.01	down	3.11E-01	8.95E-01	-	-
1384972_at	Top3a	topoisomerase (DNA) III alpha	303194	---	BF399656	2.39	2.38	2.39	2.39	2.40	2.42	1.01	up	2.49E-01	8.95E-01	-	-
1390896_at	---	---	---	Rn.28213	AW524502	2.55	2.51	2.58	2.53	2.56	2.50	1.01	down	5.58E-01	8.95E-01	-	-
1375278_at	Trim2	tripartite motif-containing 2	361970	Rn.16973	BG670916	4.24	3.72	3.74	3.67	3.86	4.12	1.01	down	9.45E-01	9.84E-01	-	-
1369670_at	Cd200	Cd200 molecule	24560	Rn.7085	NM_031518	2.37	2.35	2.37	2.35	2.44	2.36	1.01	up	6.00E-01	8.95E-01	-	-
1377398_at	---	---	---	Rn.209814	BF391031	2.34	2.33	2.35	2.34	2.43	2.31	1.01	up	6.87E-01	9.04E-01	-	-
1396454_at	---	---	---	---	BF391035	2.39	2.38	2.43	2.37	2.41	2.37	1.01	down	4.81E-01	8.95E-01	-	-
1382205_at	---	---	---	Rn.41179	AW527509	2.46	2.44	2.49	2.45	2.48	2.42	1.01	down	4.87E-01	8.95E-01	-	-
1394726_at	---	---	---	---	AI412564	2.56	2.52	2.61	2.54	2.58	2.53	1.01	down	6.28E-01	8.95E-01	-	-
1391542_at	---	---	---	Rn.43268	BF391191	2.52	2.39	2.43	2.48	2.42	2.39	1.01	down	7.48E-01	9.18E-01	-	-
1373810_at	Pla2g12a	phospholipase A2, group XIIA	362039	Rn.137418	BF284175	8.36	7.74	7.60	7.97	7.76	8.02	1.01	up	9.53E-01	9.86E-01	-	-
1378706_at	LOC686944	similar to Zinc finger protein 45 (BRC1744)	686944	---	BE101875	2.42	2.42	2.45	2.42	2.43	2.49	1.01	up	5.65E-01	8.95E-01	-	-
1374198_at	Cd276	Cd276 molecule	315716	Rn.76129	BF398424	2.57	2.51	2.65	2.57	2.57	2.54	1.01	down	7.27E-01	9.13E-01	-	-
1378189_at	---	---	---	---	AA852047	2.37	2.36	2.37	2.36	2.43	2.35	1.01	up	5.28E-01	8.95E-01	-	-
1386185_at	---	---	---	---	H31802	2.49	2.45	2.51	2.46	2.50	2.44	1.01	down	5.66E-01	8.95E-01	-	-
1377179_at	Pqlc2	PQ loop repeat containing 2	362642	Rn.41973	BI283849	3.37	3.37	3.37	3.42	3.37	3.36	1.01	up	4.65E-01	8.95E-01	-	-
1376377_at	Diaph3	diaphanous homolog 3 (Drosophila)	299396	Rn.205858	BF398599	2.52	2.47	2.54	2.48	2.59	2.50	1.01	up	7.01E-01	9.07E-01	-	-
1381524_at	---	---	---	Rn.210313	BF397008	2.47	2.42	2.44	2.43	2.43	2.42	1.01	down	3.27E-01	8.95E-01	-	-
1368577_at	Gjb6	gap junction protein, beta 6	84403	Rn.18935	NM_053388	2.44	2.43	2.48	2.43	2.46	2.41	1.01	down	5.02E-01	8.95E-01	-	-
1397249_at	---	---	---	Rn.28328	BF282722	2.49	2.46	2.52	2.47	2.51	2.45	1.01	down	5.62E-01	8.95E-01	-	-
1368941_at	Ptger4	prostaglandin E receptor 4 (subtype EP4)	84023	Rn.16062	NM_032076	2.35	2.31	2.34	2.32	2.33	2.31	1.01	down	2.82E-01	8.95E-01	-	-
1384316_at	---	---	---	Rn.12451	BF399317	2.46	2.45	2.48	2.45	2.46	2.43	1.01	down	2.88E-01	8.95E-01	-	-
1397327_at	---	---	---	---	AW919585	2.35	2.29	2.31	2.30	2.31	2.30	1.01	down	4.78E-01	8.95E-01	-	-
1395918_at	---	---	---	Rn.29409	BI282754	2.42	2.38	2.39	2.38	2.40	2.37	1.01	down	3.49E-01	8.95E-01	-	-
1390911_at	---	---	---	---	AW916020	2.34	2.32	2.36	2.33	2.34	2.31	1.01	down	2.53E-01	8.95E-01	-	-
1396015_at	---	---	---	Rn.154197	BF410640	2.39	2.44	2.40	2.38	2.46	2.34	1.01	down	6.94E-01	9.05E-01	-	-
1373257_at	rCG_25854	cyclic AMP-regulated phosphoprotein	363153	Rn.7511	AI412989	2.42	2.40	2.49	2.44	2.44	2.39	1.01	down	6.89E-01	9.00E-01	-	-
1382250_at	---	---	---	Rn.53869	AW526660	2.43	2.39	2.39	2.38	2.40	2.39	1.01	down	3.04E-01	8.95E-01	-	-
1369056_at	Rpe65	retinal pigment epithelium 65	89826	Rn.76724	NM_053562	2.44	2.41	2.48	2.43	2.45	2.41	1.01	down	5.23E-01	8.95E-01	-	-
1398070_at	---	---	---	Rn.172609	BF404998	2.42	2.41	2.46	2.42	2.44	2.39	1.01	down	4.47E-01	8.95E-01	-	-
1397082_at	Pfkfb3	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3	117276	Rn.10791	BF414044	2.18	2.18	2.18	2.18	2.22	2.21	1.01	up	3.62E-01	8.95E-01	-	-
1379056_at	Dbndd1	dysbindin (dystrobrevin binding protein 1) domain containing 1	361437	Rn.163416	BG380506	2.55	2.54	2.57	2.58	2.56	2.48	1.01	down	6.38E-01	8.95E-01	-	-
1376360_at	Nhlh1	nescient helix loop helix 1	289230	Rn.203557	BF398530	2.26	2.25	2.29	2.25	2.26	2.25	1.01	down	2.65E-01	8.95E-01	-	-
1392972_at	Trio	triple functional domain (PTPRF interacting)	310192	Rn.221920	BF554226	2.46	2.44	2.45	2.44	2.51	2.44	1.01	up	5.33E-01	8.95E-01	-	-
1379946_at	---	---	---	Rn.211364	AW526208	2.48	2.47	2.51	2.48	2.50	2.44	1.01	down	5.26E-01	8.95E-01	-	-
1392840_at	---	---	---	Rn.21138	AI764605	2.52	2.51	2.54	2.50	2.54	2.49	1.01	down	4.10E-01	8.95E-01	-	-
1381273_at	---	---	---	Rn.169083	AW532624	2.43	2.40	2.44	2.40	2.43	2.39	1.01	down	4.25E-01	8.95E-01	-	-
1372325_at	Emilin1	elastin microfibril interfacer 1	298845	Rn.99346	BI302596	2.22	2.52	2.28	2.39	2.31	2.28	1.01	down	8.83E-01	9.64E-01	-	-
1385780_at	---	---	---	---	BF416348	2.49	2.46	2.56	2.48	2.52	2.47	1.01	down	6.36E-01	8.95E-01	-	-
1374389_at	Gucy1b3	guanylate cyclase 1, soluble, beta 3	25202	Rn.87228	BF399387	2.63	2.56	3.50	3.51	2.59	2.55	1.01	down	9.73E-01	9.92E-01	-	-
1368539_at	Mmp12	matrix metallopeptidase 12	117033	Rn.33193	NM_053963	2.35	2.32	2.34	2.33	2.33	2.31	1.01	down	2.04E-01	8.95E-01	-	-
1381896_at	---	---	---	Rn.135452	AI411637	2.48	2.47	2.51	2.48	2.50	2.42	1.01	down	5.97E-01	8.95E-01	-	-
1396391_at	---	---	---	Rn.162458	BF413637	2.42	2.41	2.44	2.41	2.42	2.40	1.01	down	1.68E-01	8.95E-01	-	-
1375135_at	Gcn1l1	GCN1 general control of amino-acid synthesis 1-like 1 (yeast)	690832	Rn.98494	BE111689	7.08	5.43	4.59	6.17	5.97	5.92	1.01	down	9.85E-01	9.98E-01	-	-
1375095_at	---	---	---	Rn.171400	BF394091	2.41	2.39	2.44	2.40	2.41	2.38	1.01	down	4.15E-01	8.95E-01	-	-
1373911_at	Postn	periostin, osteoblast specific factor	361945	Rn.30516	BM389026	2.50	2.43	2.46	2.44	2.46	2.44	1.01	down	4.95E-01	8.95E-01	-	-
1392780_at	Nxf7	nuclear RNA export factor 7	501621	Rn.24735	BF283270	2.51	2.48	2.50	2.49	2.52	2.44	1.01	down	5.52E-01	8.95E-01	-	-
1379384_at	Sp1	Sp1 transcription factor	24790	Rn.44609	BF288328	3.54	4.03	3.48	3.46	3.50	4.05	1.01	down	9.55E-01	9.87E-01	-	-
1385386_at	Vof16	ischemia related factor vof-16	259227	Rn.206986	BI302745	2.48	2.47	2.51	2.47	2.50	2.44	1.01	down	4.86E-01	8.95E-01	-	-
1380270_at	Mfi2	antigen p97 (melanoma associated) identified by monoclonal antibodies 133.2	288038	Rn.85934	BF417890	2.46	2.45	2.49	2.45	2.46	2.44	1.01	down	4.03E-01	8.95E-01	-	-
1396596_at	---	---	---	Rn.208805	BF402645	2.40	2.38	2.42	2.38	2.41	2.37	1.01	down	3.96E-01	8.95E-01	-	-
1377435_at	---	---	---	Rn.210728	BF401680	2.44	2.41	2.45	2.42	2.44	2.40	1.01	down	3.47E-01	8.95E-01	-	-
1390516_at	---	---	---	---	BF401649	2.53	2.55	2.58	2.59	2.57	2.55	1.01	up	4.43E-01	8.95E-01	-	-
1380492_at	Freq	frequenin homolog (Drosophila)	65153	Rn.62653	BF415213	2.60	2.59	2.65	2.60	2.60	2.60	1.01	down	4.64E-01	8.95E-01	-	-
1392418_at	Mapk8	Mitogen-activated protein kinase 8	116554	Rn.4090	BE105603	2.51	2.48	2.53	2.47	2.54	2.45	1.01	down	6.45E-01	8.95E-01	-	-
1382712_at	---	---	---	Rn.204017	AI044245	2.47	2.40	2.48	2.44	2.50	2.42	1.01	up	6.56E-01	8.98E-01	-	-
1379037_at	---	---	---	Rn.149549	AW533389	2.45	2.43	2.49	2.44	2.47	2.42	1.01	down	5.39E-01	8.95E-01	-	-
1395873_at	---	---	---	Rn.208438	BF410050	2.41	2.40	2.42	2.46	2.44	2.40	1.01	up	4.54E-01	8.95E-01	-	-
1373084_at	Wdr20a	WD repeat domain 20a	314453	Rn.17925	BI300912	2.67	2.54	2.68	2.51	2.57	2.85	1.01	up	8.99E-01	9.69E-01	-	-
1395660_at	---	---	---	---	BE114185	2.59	2.55	2.66	2.57	2.65	2.53	1.01	down	7.71E-01	9.25E-01	-	-
1388452_at	Spock2	sparc/osteonectin, cwcv and kazal-like domains proteoglycan 2	361840	Rn.15590	AI716904	2.39	2.36	2.40	2.37	2.39	2.35	1.01	down	3.80E-01	8.95E-01	-	-
1380255_at	---	---	---	Rn.25371	AI235931	4.42	4.06	3.92	5.06	3.20	4.19	1.01	up	9.79E-01	9.94E-01	-	-
1376493_at	Commd7	COMM domain containing 7	296285	Rn.92689	AI408996	6.41	6.78	7.21	6.64	6.68	7.03	1.01	down	9.56E-01	9.87E-01	-	-
1373092_at	---	---	---	Rn.8191	BE109587	4.77	4.67	5.05	4.78	4.97	4.69	1.01	down	9.17E-01	9.75E-01	-	-
1398404_at	Ctsq2	cathepsin Q-like 2	408201	Rn.128678	BI284886	2.45	2.43	2.48	2.44	2.46	2.41	1.01	down	4.89E-01	8.95E-01	-	-
1372164_at	RGD1305793	similar to hypothetical protein FLJ20154	309456	Rn.105679	AI600255	9.50	9.36	9.48	9.31	9.73	9.34	1.01	up	9.19E-01	9.76E-01	-	-
1372815_at	Magoh	mago-nashi homolog, proliferation-associated (Drosophila)	298385	Rn.8332	BG673028	6.66	6.99	6.88	6.71	6.66	7.12	1.01	down	9.34E-01	9.81E-01	-	-
1374360_at	Cdc20	Cell division cycle 20 homolog (S. cerevisiae)	64515	Rn.9262	BI298458	2.30	2.29	2.33	2.29	2.29	2.29	1.01	up	6.74E-01	9.01E-01	-	-
1380454_at	---	---	---	---	AW526025	2.54	2.51	2.58	2.62	2.56	2.50	1.01	up	7.16E-01	9.10E-01	-	-
1394857_at	Hadha	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/en	170670	Rn.34751	AI535136	2.48	2.48	2.46	2.46	2.45	2.51	1.01	down	1.03E-01	8.95E-01	-	-
1390238_at	Clca3	chloride channel calcium activated 3	308015	Rn.66961	BI291875	2.39	2.38	2.46	2.41	2.39	2.37	1.01	down	6.13E-01	8.95E-01	-	-
1391347_at	Rabl6b	RABBB, member RAS oncogene family	266888	Rn.10995	BF398743	2.53	2.48	2.53	2.52	2.55	2.52	1.01	up	5.11E-01	8.95E-01	-	-
1384473_at	---	---	---	Rn.120662	AA998651	2.48	2.46	2.50	2.47	2.48	2.44	1.01	down	4.72E-01	8.95E-01	-	-
1379972_at	Msl3l2	male-specific lethal 3-like 2 (Drosophila)	309790	Rn.166372	AI070438	2.41	2.42	2.43	2.46	2.43	2.42	1.01	up	2.68E-01	8.95E-01	-	-
1390083_at	---	---	---	Rn.210964	BI289990	2.39	2.36	2.38	2.37	2.37	2.35	1.01	down	2.42E-01	8.95E-01	-	-
1382394_at	---	---	---	Rn.23931	AA955985	2.39	2.40	2.40	2.38	2.39	2.37	1.01	down	7.12E-02	8.95E-01	-	-
1380340_at	---	---	---	Rn.63789	BF387865	2.45	2.41	2.44	2.42	2.44	2.40	1.01	down	3.70E-01	8.95E-01	-	-
1377931_at	Rnf207	ring finger protein 207	691246	Rn.156893	BE109649	2.34	2.33	2.38	2.34	2.34	2.33	1.01	down	3.92E-01	8.95E-01	-	-
1374374_a_at	Shroom1	shroom family member 1	287285	Rn.209227	BF393390	3.02	2.86	3.28	3.02	3.23	2.86	1.01	down	9.29E-01	9.80E-01	-	-
1394915_at	---	---	---	Rn.170524	BF291136	2.44	2.42	2.45	2.42	2.51	2.41	1.01	up	6.46E-01	8.95E-01	-	-
1382728_at	---	---	---	Rn.203440	AA924018	2.57	2.58	2.69	2.70	2.58	2.51	1.01	down	8.29E-01	9.46E-01	-	-
1398067_at	---	---	---	Rn.210099	BF393939	2.53	2.50	2.61	2.51	2.60	2.48	1.01	down	7.56E-01	9.20E-01	-	-
1397008_at	---	---	---	Rn.209822	BF404563	2.43	2.42	2.43	2.43	2.48	2.42	1.01	up	5.06E-01	8.95E-01	-	-
1393901_at	Runx1t1	runt-related transcription factor 1; translocated to, 1 (cyclin D-related)	362489	Rn.218117	BF408914	2.40	2.37	2.42	2.39	2.43	2.41	1.01	up	4.34E-01	8.95E-01	-	-
1379386_at	Gtse1	G-2 and S-

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1391219_at	---	---	---	Rn.20266	BF391545	2.43	2.38	2.41	2.39	2.41	2.38	1.01	down	3.97E-01	8.95E-01	-	-
1375035_at	---	---	---	Rn.16486	AI169627	5.41	5.04	4.62	4.73	4.75	5.63	1.01	up	9.69E-01	9.91E-01	-	-
1396930_x_at	---	---	---	---	AI549391	2.38	2.37	2.42	2.37	2.39	2.37	1.01	down	4.24E-01	8.95E-01	-	-
1378795_at	---	---	---	Rn.165156	AI549094	2.41	2.39	2.42	2.39	2.40	2.38	1.01	down	2.06E-01	8.95E-01	-	-
1391121_at	Pragmin	pragma of Rnd2	306506	Rn.51831	BF404955	2.38	2.37	2.41	2.38	2.38	2.36	1.01	down	2.91E-01	8.95E-01	-	-
1385520_at	---	---	---	Rn.169469	AW524783	2.51	2.43	2.54	2.48	2.58	2.46	1.01	up	7.71E-01	9.25E-01	-	-
1379693_at	Robo2	Roundabout, axon guidance receptor, homolog 2 (Drosophila)	84409	Rn.24350	AI409154	2.45	2.42	2.48	2.43	2.46	2.41	1.01	down	5.13E-01	8.95E-01	-	-
1375445_at	Ky	kyphoscoliosis peptidase	315962	Rn.24084	BG375795	2.33	2.33	2.37	2.33	2.34	2.32	1.01	down	3.63E-01	8.95E-01	-	-
1387464_at	Glra1	glycine receptor, alpha 1	25674	Rn.10109	NM_013133	2.47	2.45	2.51	2.47	2.58	2.43	1.01	up	7.64E-01	9.23E-01	-	-
1384782_at	Abpa	androgen binding protein, alpha	361551	Rn.137089	BI284006	2.53	2.49	2.57	2.50	2.57	2.47	1.01	down	6.98E-01	9.07E-01	-	-
1396672_at	---	---	---	---	BF393007	2.39	2.38	2.43	2.38	2.41	2.36	1.01	down	5.23E-01	8.95E-01	-	-
1380616_at	---	---	---	---	BI294748	2.39	2.38	2.40	2.38	2.40	2.43	1.01	up	4.17E-01	8.95E-01	-	-
1394646_at	---	---	---	Rn.32370	AA899105	2.41	2.40	2.43	2.40	2.42	2.38	1.01	down	3.45E-01	8.95E-01	-	-
1385651_at	---	---	---	---	AI575761	2.59	2.55	2.63	2.58	2.65	2.49	1.01	down	7.87E-01	9.31E-01	-	-
1374648_at	Gpr155	G protein-coupled receptor 155	311730	Rn.2051	BM390626	2.37	2.36	2.41	2.36	2.37	2.35	1.01	down	3.90E-01	8.95E-01	-	-
1393283_at	Ankrd34b	ankyrin repeat domain 34B	499506	Rn.203372	AA924915	2.40	2.39	2.44	2.39	2.41	2.39	1.01	down	4.23E-01	8.95E-01	-	-
1395706_at	Lingo1	leucine rich repeat and Ig domain containing 1	315691	Rn.20289	BF414924	2.44	2.43	2.49	2.44	2.45	2.42	1.01	down	4.80E-01	8.95E-01	-	-
1385744_at	Thsd7b	thrombospondin, type I, domain containing 7B	289007	Rn.209569	BF389238	2.48	2.46	2.52	2.47	2.50	2.44	1.01	down	5.76E-01	8.95E-01	-	-
1392004_at	---	---	---	Rn.211688	AI231080	2.40	2.38	2.44	2.39	2.42	2.36	1.01	down	5.71E-01	8.95E-01	-	-
1379430_at	---	---	---	---	BM390207	2.41	2.40	2.44	2.40	2.42	2.38	1.01	down	4.30E-01	8.95E-01	-	-
1393908_at	---	---	---	---	AA899594	2.64	2.63	2.66	2.63	2.64	2.61	1.01	down	3.05E-01	8.95E-01	-	-
1392019_at	Asap1	ArfGAP with SH3 domain, ankyrin repeat and PH domain 1	314961	Rn.63466	BG669281	2.45	2.45	2.48	2.45	2.46	2.42	1.01	down	4.41E-01	8.95E-01	-	-
1392005_at	---	---	---	Rn.99685	BF396526	2.34	2.34	2.35	2.40	2.35	2.33	1.01	up	5.06E-01	8.95E-01	-	-
1391153_at	---	---	---	Rn.19718	BE101678	2.65	2.60	2.62	2.61	2.62	2.60	1.01	down	3.67E-01	8.95E-01	-	-
1369004_at	Rab26	RAB26, member RAS oncogene family	171111	Rn.10975	NM_133580	2.37	2.36	2.42	2.36	2.37	2.37	1.01	down	4.46E-01	8.95E-01	-	-
1381187_at	---	---	---	Rn.202745	BE102551	2.33	2.32	2.37	2.33	2.34	2.31	1.01	down	3.83E-01	8.95E-01	-	-
1379576_at	---	---	---	Rn.164399	AA848479	2.38	2.37	2.42	2.38	2.39	2.36	1.01	down	4.54E-01	8.95E-01	-	-
1369605_at	Hes2	hairy and enhancer of split 2 (Drosophila)	29567	Rn.44655	NM_019236	2.52	2.47	2.49	2.48	2.50	2.47	1.01	down	4.06E-01	8.95E-01	-	-
1383648_x_at	Crb3	crumbs homolog 3 (Drosophila)	301112	Rn.14560	BI283883	5.76	6.12	5.83	6.83	5.10	5.82	1.01	up	9.78E-01	9.93E-01	-	-
1391559_at	Tlcd1	TLC domain containing 1	287472	Rn.106119	AW525904	3.76	3.62	3.64	3.97	3.50	3.60	1.01	up	9.25E-01	9.78E-01	-	-
1374621_at	Taf1c	TATA box binding protein (Tbp)-associated factor, RNA polymerase I, C	361420	Rn.146894	AA892987	3.84	3.56	3.36	3.16	3.45	3.21	1.01	up	9.76E-01	9.93E-01	-	-
1387596_at	F2rl1	coagulation factor II (thrombin) receptor-like 1	116677	Rn.10543	NM_053897	2.39	2.39	2.36	2.40	2.40	2.39	1.01	up	2.18E-01	8.95E-01	-	-
1371090_at	Scamp2	secretory carrier membrane protein 2	65168	Rn.3752	BM387006	5.67	5.66	5.66	5.66	5.71	5.66	1.01	up	4.24E-01	8.95E-01	-	-
1382422_at	Pcdh7	protocadherin 7	360942	Rn.150477	AA856340	2.47	2.44	2.48	2.45	2.46	2.43	1.01	down	3.70E-01	8.95E-01	-	-
1369687_at	Kcnab3	potassium voltage-gated channel, shaker-related subfamily, beta member 3	58981	Rn.11260	NM_031652	2.43	2.41	2.44	2.48	2.44	2.42	1.01	up	4.98E-01	8.95E-01	-	-
1398041_at	---	---	---	Rn.161169	BF419478	2.39	2.38	2.44	2.39	2.42	2.36	1.01	down	5.70E-01	8.95E-01	-	-
1386805_at	LOC304558	similar to TPR repeat-containing protein KIAA1043	304558	Rn.137233	BF554446	2.47	2.45	2.48	2.45	2.46	2.44	1.01	down	2.85E-01	8.95E-01	-	-
1396479_at	Zbtb7c	zinc finger and BTB domain containing 7C	679155	Rn.21793	BF420007	2.59	2.54	2.59	2.58	2.62	2.57	1.01	up	5.63E-01	8.95E-01	-	-
1387432_at	Rod1	ROD1 regulator of differentiation 1 (S. pombe)	83515	Rn.162818	NM_031346	2.43	2.46	2.46	2.43	2.44	2.43	1.01	down	2.86E-01	8.95E-01	-	-
1393141_at	---	---	---	Rn.203385	BF285419	2.42	2.40	2.43	2.42	2.45	2.42	1.01	up	2.53E-01	8.95E-01	-	-
1388940_at	Arhgap25	Rho GTPase activating protein 25	500246	Rn.22776	AW225115	2.35	2.34	2.39	2.34	2.36	2.34	1.01	down	4.32E-01	8.95E-01	-	-
1395540_at	Slc35e3	solute carrier family 35, member E3	362883	Rn.21084	AW144387	2.59	2.89	3.24	2.97	2.87	2.93	1.01	up	9.41E-01	9.83E-01	-	-
1397484_at	Acot6 /// Dnal1	acyl-CoA thioesterase 6 /// dynein, axonemal, light chain 1	299193 /// 685664	Rn.156856	BF394767	2.53	2.52	2.57	2.53	2.55	2.51	1.01	down	4.80E-01	8.95E-01	-	-
1378742_at	---	---	---	Rn.161004	BM388241	2.54	2.50	2.59	2.52	2.59	2.47	1.01	down	7.42E-01	9.17E-01	-	-
1375333_at	---	---	---	---	BE120158	2.39	2.38	2.44	2.39	2.40	2.38	1.01	down	4.52E-01	8.95E-01	-	-
1386699_at	Dnali1	dynein, axonemal, light intermediate chain 1	298524	Rn.146087	BF563867	2.46	2.45	2.49	2.45	2.46	2.44	1.01	down	3.58E-01	8.95E-01	-	-
1384109_at	---	---	---	Rn.173183	BF285329	2.53	2.51	2.53	2.51	2.54	2.47	1.01	down	5.08E-01	8.95E-01	-	-
1392141_at	---	---	---	Rn.16539	AA818806	2.41	2.39	2.42	2.39	2.40	2.38	1.01	down	2.65E-01	8.95E-01	-	-
1373931_at	RGD1304952	similar to RIKEN cDNA C530028O21 gene	312711	Rn.13411	C07069	2.44	2.46	2.44	2.51	2.44	2.43	1.01	up	6.08E-01	8.95E-01	-	-
1391747_at	Rbm12	RNA binding motif protein 12	652928	Rn.7119	BE109766	2.30	2.29	2.31	2.35	2.30	2.30	1.01	up	4.20E-01	8.95E-01	-	-
1396224_at	---	---	---	---	BF388985	2.41	2.40	2.44	2.40	2.41	2.40	1.01	down	3.49E-01	8.95E-01	-	-
1396800_at	---	---	---	---	BF410358	2.52	2.42	2.47	2.45	2.46	2.44	1.01	down	6.51E-01	8.97E-01	-	-
1387609_at	Car5a	carbonic anhydrase 5a, mitochondrial	54233	Rn.9988	NM_019293	2.47	2.46	2.51	2.47	2.48	2.46	1.01	down	3.81E-01	8.95E-01	-	-
1385579_at	P4ha3	Procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), al	361612	Rn.37765	BF560587	2.35	2.34	2.37	2.34	2.35	2.33	1.01	down	3.02E-01	8.95E-01	-	-
1374179_at	---	---	---	---	BF285334	8.44	8.72	8.49	8.40	8.37	8.92	1.01	up	9.44E-01	9.84E-01	-	-
1382696_at	---	---	---	Rn.173963	AI229090	2.50	2.47	2.53	2.49	2.52	2.45	1.01	down	5.81E-01	8.95E-01	-	-
1370303_at	Slc35a4	solute carrier family 35, member A4	257647	Rn.15468	AF406814	3.79	4.34	3.33	3.79	3.80	3.93	1.01	up	9.62E-01	9.89E-01	-	-
1384642_at	---	---	---	Rn.18820	AI044912	2.39	2.38	2.42	2.38	2.40	2.36	1.01	down	3.55E-01	8.95E-01	-	-
1398671_at	---	---	---	---	BG153337	2.52	2.50	2.57	2.63	2.53	2.47	1.01	up	7.90E-01	9.32E-01	-	-
1377277_at	---	---	---	Rn.25418	BE117885	2.37	2.35	2.39	2.35	2.36	2.34	1.01	down	3.05E-01	8.95E-01	-	-
1381689_at	---	---	---	Rn.28762	BF404369	2.44	2.41	2.45	2.42	2.44	2.40	1.01	down	4.61E-01	8.95E-01	-	-
1382871_at	---	---	---	Rn.203880	BE105552	2.46	2.42	2.46	2.43	2.45	2.42	1.01	down	4.30E-01	8.95E-01	-	-
1391186_at	---	---	---	Rn.20435	BF397942	2.40	2.40	2.41	2.40	2.39	2.38	1.01	down	6.24E-02	8.95E-01	-	-
1370161_at	Ccdc80	coiled-coil domain containing 80	64387	Rn.2193	AI235465	2.45	2.44	2.46	2.52	2.47	2.39	1.01	up	7.24E-01	9.12E-01	-	-
1395667_at	RGD1565983	similar to apurinic/apyrimidinic endonuclease 2	317628	Rn.52592	BF418964	2.25	2.27	2.25	2.24	2.25	2.24	1.01	down	1.10E-01	8.95E-01	-	-
1368318_at	Homer1	homer homolog 1 (Drosophila)	29546	Rn.37500	AB007888	7.06	6.78	6.82	6.72	6.99	6.89	1.01	down	9.05E-01	9.71E-01	-	-
1381726_at	---	---	---	Rn.147790	BF393430	2.44	2.42	2.45	2.42	2.44	2.40	1.01	down	3.78E-01	8.95E-01	-	-
1385861_x_at	---	---	---	---	AW522259	2.65	2.62	2.74	2.63	2.72	2.62	1.01	down	7.70E-01	9.25E-01	-	-
1397750_at	---	---	---	Rn.149231	AI145087	7.59	8.28	8.14	7.75	7.84	8.37	1.01	down	9.61E-01	9.89E-01	-	-
1384132_at	Cadm1	cell adhesion molecule 1	363058	Rn.19928	H31111	4.36	3.93	4.03	3.69	3.70	4.98	1.01	up	9.75E-01	9.92E-01	-	-
1381755_x_at	RGD1304563	similar to RIKEN cDNA 4831426I19	299356	Rn.199826	BI288309	2.47	2.48	2.51	2.47	2.51	2.43	1.01	down	5.77E-01	8.95E-01	-	-
1385866_at	---	---	---	Rn.92634	AA901198	2.44	2.42	2.48	2.43	2.45	2.41	1.01	down	4.81E-01	8.95E-01	-	-
1383552_at	---	---	---	Rn.21974	AI071698	2.48	2.48	2.52	2.48	2.48	2.47	1.01	down	3.60E-01	8.95E-01	-	-
1381636_at	---	---	---	Rn.206000	BF396481	2.51	2.49	2.52	2.49	2.50	2.48	1.01	down	2.39E-01	8.95E-01	-	-
1379379_at	---	---	---	Rn.166395	BF392753	2.42	2.39	2.41	2.39	2.41	2.38	1.01	down	3.09E-01	8.95E-01	-	-
1374908_at	---	---	---	Rn.47336	BE113272	2.35	2.34	2.38	2.34	2.35	2.33	1.01	down	3.91E-01	8.95E-01	-	-
1397537_at	501092 /// LOC68	similar to Discs large homolog 5 (Placenta and prostate DLG) (Discs large pro	501092 /// 685863	Rn.145712	BG665530	2.75	2.68	2.69	2.68	2.71	2.69	1.01	down	5.62E-01	8.95E-01	-	-
1383178_at	Fbxo28	F-box protein 28	305105	Rn.12792	AA848470	3.23	3.28	3.24	3.35	4.41	2.95	1.01	down	9.82E-01	9.94E-01	-	-
1385523_at	---	---	---	Rn.150092	BI283507	2.44	2.44	2.45	2.44	2.50	2.43	1.01	up	5.48E-01	8.95E-01	-	-
1383641_at	Ednra	endothelin receptor type A	24326	Rn.10915	BF414702	2.51	2.48	2.55	2.50	2.54	2.46	1.01	down	6.50E-01	8.96E-01	-	-
1381909_at	Hspa12b	Heat shock protein 12B	311427	Rn.154616	AI501247	2.32	2.30	2.33	2.30	2.31	2.29	1.01	down	2.28E-01	8.95E-01	-	-
1396906_at	---	---	---	Rn.206407	BE105377	2.43	2.42	2.44	2.42	2.43	2.39	1.01	down	3.03E-01	8.95E-01	-	-
1395626_at	---	---	---	Rn.63405	BF402072	2.45	2.44	2.47	2.44	2.44	2.43	1.01	down	2.61E-01	8.95E-01	-	-
1398558_at	---	---	---	Rn.167219	AI175246	2.56	2.52	2.61	2.55	2.61	2.49	1.01	down	7.56E-01	9.21E-01	-	-
1387713_a_at	Fcer1a	Fc fragment of IgE, high affinity I, receptor for; alpha polypeptide	25047	Rn.9677	M17153	2.43	2.42	2.46	2.42	2.44	2.40	1.01	down	4.31E-01	8.95E-01	-	-
1376595_at	Pex1	peroxisome biogenesis factor 1	500006	Rn.162727	BF282695	9.14	9.64	9.69	9.60	9.38	9.55	1.01	up	9.41E-01	9.83E-01	-	-
1393556_at	Zfyve28	zinc finger, FYVE domain containing 28	305454	Rn.91545	BE119549	2.46	2.42	2.45	2.43	2.46	2.40	1.01	down	5.06E-01	8.95E-01	-	-
1383217_at	RGD1564952	similar to zinc finger, RAN-binding domain containing 3	304761	Rn.37804	BE112670	2.44	2.44	2.45	2.41	2.44	2.43	1.01	down	2.26E-01	8.95E-01	-	-
1387124_at	Inha	inhibin alpha	24504	Rn.8831	NM_012890	2.38	2.40	2.38	2.38	2.38	2.36	1.01	down	1.67E-01	8.95E-01	-	-
1380313_at	Klre1	killer cell lectin-like receptor, family E, member 1	297645	Rn.16199	AA848998	2.44	2.43	2.48	2.43	2.47	2.41	1.01	down	5.60E-01	8.95E-01	-	-
1378744_at	---	---	---	---	AI412523	2.38	2.37	2.40	2.37	2.39	2.43	1.01	up	4.48E-01	8.95E-01	-	-
1384360_at	---	---	---	Rn.124193	BI282303	2.61	2.60	2.61	2.61	2.67	2.48	1.01	down	8.06E-01	9.38E-01	-	-
1384720_at	---	---	---	---	AI232723	2.40	2.36	2.37	2.37	2.37	2.36	1.01	down	3.14E-01	8.95E-01	-	-
1385483_at	RGD1562464	similar to hypothetical protein A030011M19	289236	Rn.163232	BF400949	2.41	2.39	2.44	2.40	2.41	2.39	1.01	down	3.82E-01	8.95E-01	-	-
1395451_at	---	---	---	Rn.62441	AI413728	2.40	2.38	2.40	2.44	2.40	2.39	1.01	up	3.82E-01	8.95E-01	-	-
1375618_at	Tceg1l	transcription elongation regulator 1-like	361669	Rn.45649	BF393791	2.54	2.47	2.55	2.50	2.54	2.48	1.01	down	6.61E-01	8.98E-01	-	-
1392401_s_at	Ngdn	Neuroguidin, EIF4E binding protein	305887	Rn.98692	AI535411	2.34	2.30	2.32	2.30	2.31	2.30	1.01	down	2.72E-01	8.95E-01	-	-
1393469_at	---	---	---	---	BE102340	2.52	2.49	2.56	2.51	2.55	2.46	1.01	down	6.72E-01	9.01E-01	-	-
1377110_at	Arl5c	ADP-ribosylation factor-like 5C	497990	Rn.23998	BF420720	2.47	2.44	2.49	2.46	2.48	2.43	1.01	down	5.12E-01	8.95E-01	-	-
1395748_at	---	---	---	---	AW528866	2.51	2.50	2.51	2.51	2.56	2.50	1.01	up	4.54E-01	8.95E-01	-	-
1396862_at	---	---	---	---	AW530721	2.32	2.32	2.36	2.31	2.34	2.31	1.01	down	4.52E-01	8.95E-01	-	-
1392362_at	---	---	---	Rn.49674	BE097725	2.48	2.46	2.52	2.47	2.49	2.46	1.01	down	4.30E-01	8.95E-01	-	-
1381027_at	---	---	---	Rn.61119	BF393571	2.51	2.59	2.56	2.54	2.55	2.52	1.01	down	5.98E-01	8.95E-01	-	-
1386248_at	---	---	---	---	BG153352	2.36	2.35	2.37	2.36	2.41	2.35	1.01	up	4.94E-01	8.95E-01	-	-
1387131_at	Serpini1	serine (or cysteine) peptidase inhibitor, clade I, member 1	116459	Rn.52632	AF193015	2.51	2.50	2.54	2.51	2.52	2.47	1.01	down	4.67E-01	8.95E-01	-	-
1378864_at	Lrrc23	leucine rich repeat containing 23	312707	Rn.46210	BE103187	2.53	2.40	2.69	2.52	2.53	2.52	1.01	down	8.68E-01	9.59E-01	-	-
1395521_at	---	---	---	Rn.210315	BI299174	2.56	2.51	2.62	2.54	2.60	2.51	1.01	down	7.44E-01	9.17E-01	-	-
1398060_at	Rhbdl3	rhomboid, veinlet-like 3 (Drosophila)	287556	Rn.20693	BF386379	2.42	2.41	2.42	2.41	2.41	2.38	1.01	down	2.76E-01	8.95E-01	-	-
1383003_at	Lect2	leukocyte cell-derived chemotaxin 2	361205	Rn.23016	AA924735	2.40	2.36	2.38	2.36	2.38	2.36	1.01	down	2.86E-01	8.95E-01	-	-
1389226_at	Stag1	stromal antigen 1	315958	Rn.11715	BI295219	2.96	3.64	3.74	3.38	3.03	3.90	1.01	down	9.69E-01	9.91E-01	-	-
1398684_s_at	RGD1311823	similar to RIKEN cDNA 1700016G05	362346	Rn.28920	BF288608	2.47	2.46	2.49	2.46	2.49	2.43	1.01	down	4.96E-01	8.95E-01	-	-
1369686_at	Dclk1	doublecortin-like kinase 1	83825	Rn.80575	U78857	2.38	2.38	2.39	2.37	2.38	2.36	1.01	down	1.16E-01	8.95E-01	-	-
1384062_at	---	---	---	Rn.204352	AI072443	2.52	2.53	2.52	2.38	3.20	2.53	1.01	up	9.69E-01	9.91E-01	-	-
1370304_at	Timm17a	translocase of inner mitochondrial membrane 17 homolog A (yeast)	54311	Rn.22514	AB006450	7.56	7.73	7.28	7.64	7.14	7.74	1.01	down	9.52E-01	9.86E-01	-	-
1372273_at	Gypc	glycophorin C (Gerbich blood group)	364837	Rn.7693	AA944212	2.36	2.37	2.37	2.35	2.37	2.34	1.01	down	1.61E-01	8.95E-01	-	-
1376846_at	---	---	---	Rn.14533	AI013385	2.62	2.59	2.66	2.60	2.64	2.58	1.01	down	6.29E-01	8.95E-01	-	-
1396723_at	---	---	---	---	BF396078	2.36	2.39	2.38	2.36	2.37	2.35	1.01	down	1.62E-01	8.95E-01	-	-
1381986_at	LOC685707	similar to neuron navigator 1	685707	Rn.154566	BE112452	2.40	2.39	2.40	2.39	2.46	2.37	1.01	up	6.35E-01	8.95E-01	-	-
1392760_at	Hps1	Hermansky-Pudlak syndrome 1 homolog (human)	114638	Rn.17691	AW920326	2.81	2.65	2.85	3.03	2.73	2.60	1.01	up	9.22E-01	9.77E-01	-	-
1388714_at	Ell	elongation factor RNA polymerase II	306347	Rn.7876	AI008458	6.70	7.10	8.05	7.14	7.41	7.34	1.01	up	9.73E-01	9.92E-01	-	-
1390359_at	---	---	---	---	AI231635	2.38	2.38	2.41	2.38	2.39	2.36	1.01	down	3.74E-01	8.95E-01	-	-
1385089_at	Grhl1	grainyhead-like 1 (Drosophila)	313993	Rn.212889	BM386731	2.61	2.57	2.61	2.58	2.60	2.56	1.01	down	4.47E-01	8.95E-01	-	-
1381928_at	---	---	---	---	AI235537	2.51	2.45	2.61	2.47	2.62	2.44	1.01	down	8.50E-01	9.53E-01	-	-
1393198_at	366300 /// RGD13	hypothetical LOC366300 /// similar to RIKEN cDNA 5330414D10	312924 /// 366300	Rn.203101	AW920806	4.35	4.56	4.40	4.35	4.47	4.45	1.01	down	8.46E-01	9.52E-01	-	-
1391154_at	---	---	---	Rn.160261	BF394263	2.44	2.42	2.43	2.41	2.52	2.41	1.01	up	7.15E-01	9.10E-01	-	-
1377030_at	---	---	---	Rn.199946	BF390550	2.49	2.45	2.53	2.47	2.51	2.44	1.01	down	6.72E-01	9.01E-01	-	-
1385938_at	Mettl6	methyltransferase like 6	290564	Rn.29892	BI289749	2.45	2.49	2.47	2.56	2.46	2.44	1.01	up	7.18E-01	9.11E-01	-	-
1385255_at	Golga4 /// Itga9	golgi autoantigen, golgin subfamily a, 4 /// integrin alpha 9	501069 /// 685004	Rn.198229	BE111066	2.38	2.38	2.39	2.36	2.38	2.36	1.01	down	1.68E-01	8.95E-01	-	-
1391209_at	---	---	---	Rn.204386	AI556505	2.56	2.54	2.62	2.54	2.62	2.51	1.01	down	7.46E-01	9.18E-01	-	-
1391914_at	Wnt6	Wingless-type MMTV integration site family, member 6	316526	Rn.22149	BG371658	2.46	2.44	2.51	2.45	2.47	2.44	1.01	down	5.46E-01	8.95E-01	-	-
1373333_at	MGC109340	similar to Microsomal signal peptidase 23 kDa subunit (SPase 22 kDa subunit	317409	Rn.162344	AI102732	2.42	2.40	2.44	2.41	2.44	2.37	1.01	down	5.57E-01	8.95E-01	-	-
1369306_at	Klrd1	killer cell lectin-like receptor, subfamily D, member 1	25110	Rn.6025	NM_012745	2.38	2.37	2.38	2.36	2.37	2.35	1.01	down	1.03E-01	8.95E-01	-	-
1396738_at	---	---	---	Rn.172661	BF392185	2.48	2.48	2.52	2.48	2.48	2.47	1.01	down	3.42E-01	8.95E-01	-	-
1382292_at	---	---	---	---	BF285343	2.57	2.54	2.59	2.55	2.57	2.53	1.01	down	4.87E-01	8.95E-01	-	-
1382796_at	---	---	---	Rn.18166	AI029182	2.50	2.49	2.54	2.50	2.51	2.48	1.01	down	4.52E-01	8.95E-01	-	-
1381159_at	---	---	---	Rn.205794	AI548586	2.48	2.45	2.49	2.46	2.47	2.45	1.01	down	3.75E-01	8.95E-01	-	-
1392315_at	---	---	---	Rn.218118	BE107351	2.45	2.42	2.45	2.43	2.45	2.41	1.01	down	4.01E-01	8.95E-01	-	-
1383407_at	Sash3	SAM and SH3 domain containing 3	317578	Rn.15328	BM390872	2.42	2.40	2.43	2.39	2.42	2.39	1.01	down	3.23E-01	8.95E-01	-	-
1370059_at	Nefl	neurofilament, light polypeptide	83613	Rn.18568	BF394545	2.43	2.42	2.44	2.41	2.44	2.39	1.01	down	3.53E-01	8.95E-01	-	-
1378364_at	Znf668	zinc finger protein 668	309002	Rn.218034	AW144070	2.46	2.45	2.48	2.44	2.47	2.51	1.01	up	5.55E-01	8.95E-01	-	-
1393620_at	Sesn3	sestrin 3	315427	Rn.136987	AI113325	2.46	2.54	2.47	2.46	2.47	2.51	1.01	down	6.40E-01	8.95E-01	-	-
1393362_at	---	---	---	Rn.21080	AI554982	2.42	2.41	2.46	2.42	2.43	2.40	1.01	down	4.28E-01	8.95E-01	-	-
1396514_at	---	---	---	Rn.60627	BF404942	2.49	2.47	2.51	2.47	2.51	2.44	1.01	down	5.78E-01	8.95E-01	-	-
1381472_at	---	---	---	Rn.161952	BE110276	2.44	2.45	2.47	2.44	2.46	2.42	1.01	down	3.56E-01	8.95E-01	-	-
1374451_at	Hand2	Heart and neural crest derivatives expressed 2	64637	Rn.41057	AI577156	2.22	2.22	2.27	2.22	2.23	2.22	1.01	down

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1393575_at	---	---	---	Rn.148076	AW526013	2.48	2.47	2.52	2.48	2.51	2.44	1.01	down	6.02E-01	8.95E-01	-	-
1394584_at	---	---	---	---	AI232859	2.32	2.31	2.34	2.31	2.32	2.30	1.01	down	2.76E-01	8.95E-01	-	-
1383424_at	Cmpk2	cytidine monophosphate (UMP-CMP) kinase 2, mitochondrial	314004	Rn.100440	BI276216	2.41	2.39	2.44	2.40	2.41	2.39	1.01	down	3.91E-01	8.95E-01	-	-
1377178_at	---	---	---	Rn.131357	AA998606	2.68	2.63	2.67	2.71	2.67	2.64	1.01	up	5.82E-01	8.95E-01	-	-
1380096_at	---	---	---	---	AW520939	2.54	2.53	2.55	2.56	2.59	2.51	1.01	up	5.79E-01	8.95E-01	-	-
1385332_at	Dus4l	dihydrouridine synthase 4-like (S. cerevisiae)	366593	Rn.41975	BF409229	2.67	2.63	2.66	2.64	2.76	2.60	1.01	up	7.84E-01	9.30E-01	-	-
1394327_at	RGD1564804	similar to chromosome 1 open reading frame 50	313551	Rn.7322	BF543040	2.45	2.44	2.46	2.44	2.45	2.42	1.01	down	2.69E-01	8.95E-01	-	-
1380146_at	Smyd1	SET and MYND domain containing 1	297333	Rn.203854	AI010736	2.31	2.32	2.32	2.30	2.31	2.29	1.01	down	1.90E-01	8.95E-01	-	-
1368854_at	Vsnl1	visinin-like 1	24877	Rn.105934	AI227991	2.39	2.36	2.39	2.36	2.38	2.35	1.01	down	3.92E-01	8.95E-01	-	-
1387355_at	Acan	aggrecan	58968	Rn.54503	BM384639	2.30	2.30	2.31	2.30	2.31	2.26	1.01	down	3.79E-01	8.95E-01	-	-
1390565_at	RGD1559856	similar to potassium channel tetramerisation domain containing 16	291618	Rn.209823	BF391086	2.29	2.28	2.30	2.29	2.35	2.28	1.01	up	5.53E-01	8.95E-01	-	-
1376538_at	Btbd17	BTB (POZ) domain containing 17	303660	Rn.101489	AI228567	2.44	2.43	2.47	2.44	2.44	2.42	1.01	down	3.25E-01	8.95E-01	-	-
1368741_at	C9	complement component 9	117512	Rn.10252	NM_057146	2.33	2.32	2.37	2.32	2.33	2.32	1.01	down	4.22E-01	8.95E-01	-	-
1398083_at	---	---	---	Rn.216864	BF412562	2.41	2.39	2.44	2.41	2.40	2.39	1.01	down	3.95E-01	8.95E-01	-	-
1382688_at	Slc25a37	solute carrier family 25, member 37	306000	Rn.102664	AI229706	5.73	6.65	6.13	6.49	5.66	6.42	1.01	up	9.71E-01	9.92E-01	-	-
1390564_at	---	---	---	Rn.204966	BF406037	2.37	2.35	2.39	2.36	2.38	2.33	1.01	down	4.63E-01	8.95E-01	-	-
1390275_at	/// LOC689212 ///	similar to Cystatin S precursor (LM protein) /// similar to Cystatin S precursor (I4 /// 688251 /// 68	---	Rn.144315	BI285110	2.37	2.36	2.41	2.36	2.38	2.35	1.01	down	4.28E-01	8.95E-01	-	-
1385184_at	---	---	---	Rn.204709	AI145766	4.48	3.79	3.60	3.74	4.23	3.86	1.01	down	9.65E-01	9.90E-01	-	-
1397939_at	---	---	---	---	BF416814	2.49	2.48	2.54	2.46	2.58	2.42	1.01	down	7.98E-01	9.35E-01	-	-
1381514_at	---	---	---	Rn.133049	AI111456	2.42	2.40	2.45	2.41	2.42	2.39	1.01	down	4.35E-01	8.95E-01	-	-
1382768_at	LOC680835	similar to cullin 7	680835	Rn.91915	BF289486	2.49	2.48	2.51	2.48	2.51	2.44	1.01	down	5.20E-01	8.95E-01	-	-
1368653_a_at	Park7	Parkinson disease (autosomal recessive, early onset) 7	117287	Rn.30105	BI281756	10.54	10.83	10.30	10.36	10.71	10.64	1.01	up	9.42E-01	9.84E-01	-	-
1385784_at	Clca4l	chloride channel calcium activated 4-like	499721	Rn.26573	BF523821	2.39	2.38	2.43	2.38	2.40	2.37	1.01	down	4.46E-01	8.95E-01	-	-
1379200_at	RGD1563278	similar to Ubiquitin ligase protein DZIP3 (DAZ-interacting protein 3 homolog)	303963	Rn.162050	BE109271	2.56	2.62	2.54	2.55	2.56	2.56	1.01	down	5.75E-01	8.95E-01	-	-
1396690_at	---	---	---	Rn.146554	BF401284	2.46	2.45	2.49	2.46	2.48	2.42	1.01	down	5.46E-01	8.95E-01	-	-
1381464_at	Tbx3	T-box 3	353305	Rn.162144	AA957545	2.44	2.42	2.47	2.43	2.47	2.40	1.01	down	6.13E-01	8.95E-01	-	-
1379537_at	Rftn2	raftlin family member 2	363231	Rn.28137	AW525143	2.43	2.39	2.39	2.39	2.40	2.38	1.01	down	3.38E-01	8.95E-01	-	-
1390211_at	Slc27a3	Solute carrier family 27 (fatty acid transporter), member 3	295219	Rn.22977	AA943570	2.36	2.39	2.37	2.36	2.36	2.35	1.01	down	2.04E-01	8.95E-01	-	-
1385402_at	Galnt2	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltran	292090	Rn.144772	AI011863	2.44	2.43	2.45	2.44	2.44	2.40	1.01	down	3.27E-01	8.95E-01	-	-
1396243_at	---	---	---	Rn.168780	AI548947	2.48	2.47	2.56	2.47	2.54	2.46	1.01	down	7.34E-01	9.15E-01	-	-
1398539_at	---	---	---	Rn.146626	BF404302	2.31	2.33	2.31	2.30	2.31	2.29	1.01	down	1.79E-01	8.95E-01	-	-
1383971_at	---	---	---	Rn.17786	AA818159	2.54	2.50	2.59	2.51	2.55	2.54	1.01	down	6.31E-01	8.95E-01	-	-
1385347_at	---	---	---	Rn.123415	BE103484	2.59	2.56	2.64	2.64	2.62	2.59	1.01	up	6.45E-01	8.95E-01	-	-
1386493_at	---	---	---	---	AA893985	2.39	2.38	2.43	2.38	2.40	2.37	1.01	down	4.56E-01	8.95E-01	-	-
1381363_at	---	---	---	Rn.217998	BF388580	2.40	2.37	2.40	2.38	2.39	2.36	1.01	down	2.44E-01	8.95E-01	-	-
1384347_at	Shc2	SHC (Src homology 2 domain containing) transforming protein 2	314612	Rn.120041	BF386587	2.41	2.40	2.44	2.40	2.42	2.39	1.01	down	3.67E-01	8.95E-01	-	-
1389186_at	---	---	---	---	AA944175	2.37	2.33	2.35	2.34	2.34	2.32	1.01	down	2.93E-01	8.95E-01	-	-
1380036_at	---	---	---	Rn.199310	BE101298	2.39	2.35	2.38	2.36	2.37	2.35	1.01	down	3.95E-01	8.95E-01	-	-
1398090_at	LOC687873	similar to kallikrein 5 preproprotein	687873	---	BI282561	2.54	2.50	2.58	2.52	2.57	2.49	1.01	down	6.87E-01	9.04E-01	-	-
1388051_at	Slc26a3	solute carrier family 26, member 3	114629	Rn.81026	AF337809	2.49	2.47	2.49	2.48	2.48	2.46	1.01	down	2.43E-01	8.95E-01	-	-
1391092_at	---	---	---	Rn.94903	AW522900	2.48	2.46	2.50	2.47	2.49	2.43	1.01	down	5.24E-01	8.95E-01	-	-
1369749_a_at	Semg1	semenogelin I	25013	Rn.34331	NM_012710	2.49	2.46	2.50	2.47	2.48	2.46	1.01	down	4.08E-01	8.95E-01	-	-
1381474_at	Mbnl3	muscleblind-like 3 (Drosophila)	302492	Rn.105030	AI010322	2.43	2.41	2.46	2.42	2.44	2.40	1.01	down	4.93E-01	8.95E-01	-	-
1391715_at	---	---	---	Rn.116561	BF288175	2.37	2.37	2.38	2.36	2.43	2.37	1.01	up	5.11E-01	8.95E-01	-	-
1377340_at	Tfpi2	tissue factor pathway inhibitor 2	286926	Rn.15772	AI179507	2.45	2.42	2.49	2.44	2.46	2.41	1.01	down	5.80E-01	8.95E-01	-	-
1378884_at	---	---	---	Rn.146567	BF409365	2.39	2.36	2.39	2.36	2.38	2.35	1.01	down	3.30E-01	8.95E-01	-	-
1386239_at	Dmrta1	DMRT-like family A1	313352	Rn.43064	AI639210	2.52	2.51	2.53	2.51	2.54	2.46	1.01	down	5.87E-01	8.95E-01	-	-
1381409_at	---	---	---	Rn.124335	AA863978	2.32	2.32	2.35	2.32	2.33	2.31	1.01	down	2.80E-01	8.95E-01	-	-
1386831_at	LOC691396	similar to Zinc finger protein 551 (Zinc finger protein KOX23)	691396	Rn.38959	BF561330	2.81	2.82	2.80	2.79	2.83	2.77	1.01	down	4.69E-01	8.95E-01	-	-
1369449_at	Plin	perilipin	25629	Rn.9737	NM_013094	2.33	2.32	2.37	2.32	2.34	2.31	1.01	down	4.28E-01	8.95E-01	-	-
1371293_at	LOC688228	similar to Myosin light polypeptide 4 (Myosin light chain 1, atrial isoform)	688228	Rn.216832	AI103218	2.58	2.53	2.55	2.53	2.55	2.54	1.01	down	4.26E-01	8.95E-01	-	-
1392182_at	---	---	---	Rn.204651	BG380589	2.47	2.45	2.50	2.46	2.47	2.45	1.01	down	4.20E-01	8.95E-01	-	-
1392009_at	---	---	---	Rn.169417	AW523649	2.43	2.43	2.44	2.41	2.44	2.41	1.01	down	1.98E-01	8.95E-01	-	-
1381824_at	Alg1	Androgen-induced 1	292486	Rn.14443	AI602689	2.89	2.88	2.91	2.88	2.89	2.87	1.01	down	3.04E-01	8.95E-01	-	-
1393733_at	Pap2d	phosphatidic acid phosphatase type 2	310812	Rn.151385	BF402788	2.46	2.42	2.51	2.45	2.49	2.41	1.01	down	6.82E-01	9.03E-01	-	-
1386286_at	---	---	---	---	AI639322	2.45	2.44	2.47	2.44	2.46	2.41	1.01	down	4.24E-01	8.95E-01	-	-
1396480_at	---	---	---	Rn.206736	BG372249	2.53	2.53	2.56	2.53	2.54	2.52	1.01	down	3.33E-01	8.95E-01	-	-
1377574_at	---	---	---	Rn.147907	BF392065	2.45	2.43	2.50	2.44	2.48	2.42	1.01	down	6.12E-01	8.95E-01	-	-
1388632_at	Rab6b	RAB6B, member RAS oncogene family	363123	Rn.13756	BG665929	2.34	2.33	2.34	2.39	2.34	2.32	1.01	up	5.62E-01	8.95E-01	-	-
1394587_at	---	---	---	Rn.168383	AI576038	2.40	2.38	2.44	2.39	2.40	2.39	1.01	down	4.78E-01	8.95E-01	-	-
1377778_at	Vof16	ischemia related factor vof-16	259227	Rn.206986	BE107282	2.36	2.35	2.38	2.35	2.36	2.34	1.01	down	2.70E-01	8.95E-01	-	-
1389330_at	RGD1310127	similar to cDNA sequence BC017158	361854	Rn.138258	AA894060	4.54	4.70	4.54	4.78	4.48	4.56	1.01	up	9.01E-01	9.69E-01	-	-
1371095_at	Kif6	kinesin family member 6	171291	Rn.207571	AY035403	2.30	2.33	2.30	2.30	2.30	2.28	1.01	down	2.50E-01	8.95E-01	-	-
1396696_at	Gria4	glutamate receptor, ionotropic, AMPA4	29629	Rn.10938	BF390683	2.41	2.40	2.45	2.40	2.44	2.38	1.01	down	5.82E-01	8.95E-01	-	-
1380823_at	---	---	---	Rn.148728	AW535469	2.47	2.46	2.49	2.46	2.47	2.43	1.01	down	4.12E-01	8.95E-01	-	-
1396767_at	---	---	---	Rn.210759	BF401424	2.27	2.29	2.27	2.26	2.27	2.26	1.01	down	1.89E-01	8.95E-01	-	-
1373659_at	LOC689926	hypothetical protein LOC689926	689926	Rn.198906	AI639350	2.27	2.26	2.27	2.26	2.27	2.23	1.01	down	3.61E-01	8.95E-01	-	-
1373486_at	Shisa4	shisa homolog 4 (Xenopus laevis)	360848	Rn.40771	BG375421	2.39	2.38	2.40	2.38	2.39	2.37	1.01	down	1.75E-01	8.95E-01	-	-
1387293_at	Zp2	zona pellucida glycoprotein 2 (sperm receptor)	81828	Rn.10857	NM_031150	2.42	2.41	2.43	2.41	2.42	2.38	1.01	down	3.33E-01	8.95E-01	-	-
1398586_at	---	---	---	Rn.25292	BF289133	2.45	2.44	2.48	2.44	2.47	2.41	1.01	down	4.91E-01	8.95E-01	-	-
1395083_at	---	---	---	Rn.32739	AA926313	2.44	2.44	2.46	2.44	2.45	2.41	1.01	down	3.94E-01	8.95E-01	-	-
1379433_at	---	---	---	Rn.160333	BF400033	2.46	2.46	2.47	2.46	2.47	2.42	1.01	down	3.72E-01	8.95E-01	-	-
1371107_a_at	Tp73l	tumor protein p73-like	246334	Rn.42907	AJ277449	2.41	2.39	2.44	2.40	2.42	2.38	1.01	down	4.24E-01	8.95E-01	-	-
1374021_at	Wipi1	WD repeat domain, phosphoinositide interacting 1	303630	Rn.203725	BI299233	2.48	2.47	2.48	2.47	2.47	2.44	1.01	down	2.95E-01	8.95E-01	-	-
1395675_at	Sec61a1	Sec61 alpha 1 subunit (S. cerevisiae)	80843	Rn.47029	BF412173	2.37	2.33	2.35	2.34	2.34	2.33	1.01	down	2.91E-01	8.95E-01	-	-
1393774_at	Tcf20	transcription factor 20	366964	Rn.220442	BF406434	2.40	2.42	2.43	2.40	2.42	2.39	1.01	down	3.07E-01	8.95E-01	-	-
1374140_at	---	---	---	Rn.205662	AI716756	2.48	2.46	2.49	2.47	2.48	2.45	1.01	down	3.59E-01	8.95E-01	-	-
1369509_a_at	A1bg	alpha-1-B glycoprotein	140656	Rn.53990	AJ302031	2.37	2.36	2.41	2.36	2.37	2.36	1.01	down	4.31E-01	8.95E-01	-	-
1390720_at	---	---	---	Rn.129728	AI145419	2.40	2.39	2.42	2.39	2.40	2.37	1.01	down	3.33E-01	8.95E-01	-	-
1373130_at	Myom2	Myomesin 2	306616	Rn.33916	AI407239	2.30	2.27	2.29	2.27	2.28	2.26	1.01	down	2.54E-01	8.95E-01	-	-
1396355_at	---	---	---	Rn.207699	BF411289	2.32	2.29	2.31	2.30	2.29	2.29	1.01	down	2.55E-01	8.95E-01	-	-
1377231_at	---	---	---	Rn.61995	BF412078	2.47	2.47	2.47	2.46	2.45	2.45	1.01	down	3.05E-02	8.95E-01	-	-
1383057_at	Asf1a	ASF1 anti-silencing function 1 homolog A (S. cerevisiae)	294408	Rn.163427	BF558602	3.59	3.45	3.48	3.43	3.64	3.50	1.01	up	8.59E-01	9.56E-01	-	-
1387098_at	Polr1a	polymerase (RNA) I polypeptide A	83581	Rn.24877	NM_031772	3.60	3.60	3.60	3.59	3.59	3.58	1.01	down	3.42E-02	8.95E-01	-	-
1397919_at	Ccdc37	coiled-coil domain containing 37	297444	Rn.138053	BE121191	2.45	2.44	2.48	2.44	2.45	2.42	1.01	down	4.11E-01	8.95E-01	-	-
1381512_at	---	---	---	Rn.209231	BF386977	2.60	2.58	2.63	2.59	2.62	2.56	1.01	down	5.68E-01	8.95E-01	-	-
1372878_at	Zfr	zinc finger RNA binding protein	365703	Rn.11634	BG668247	8.54	8.06	8.10	8.29	8.20	8.16	1.01	down	9.33E-01	9.81E-01	-	-
1369474_a_at	P2rx2	purinergic receptor P2X, ligand-gated ion channel, 2	114115	Rn.88799	AF020757	2.48	2.46	2.53	2.46	2.52	2.44	1.01	down	6.70E-01	9.00E-01	-	-
1390774_at	---	---	---	Rn.210090	BF394099	2.52	2.50	2.52	2.50	2.52	2.48	1.01	down	3.30E-01	8.95E-01	-	-
1378664_at	Tsnaxip1	translin-associated factor X interacting protein 1	498944	Rn.210041	BF416541	2.32	2.35	2.33	2.32	2.32	2.32	1.01	down	1.68E-01	8.95E-01	-	-
1385060_at	RGD1562342	similar to RIKEN cDNA 1110012D08	500762	Rn.152999	BF401036	2.27	2.26	2.27	2.27	2.27	2.31	1.01	up	3.24E-01	8.95E-01	-	-
1375792_at	Znf532	zinc finger protein 532	307362	Rn.55564	AW252149	2.66	2.99	2.53	2.64	2.94	2.64	1.01	up	9.37E-01	9.82E-01	-	-
1379486_at	Sh3gl2	Sh3-domain GRB2-like endophilin B2	311848	Rn.26881	BG381092	2.55	2.42	2.42	2.42	2.51	2.42	1.01	down	7.92E-01	9.33E-01	-	-
1371204_at	Slc14a2	Solute carrier family 14 (urea transporter), member 2	54302	Rn.10157	AF230638	2.31	2.31	2.35	2.31	2.32	2.30	1.01	down	4.11E-01	8.95E-01	-	-
1380123_at	Tmem79	transmembrane protein 79	310626	Rn.13463	BG374569	3.20	2.54	2.56	2.61	2.56	3.08	1.01	down	9.61E-01	9.89E-01	-	-
1382956_at	LOC361016	similar to RIKEN cDNA 4933406L09	361016	Rn.203378	AA943750	2.41	2.40	2.43	2.43	2.44	2.41	1.01	up	1.73E-01	8.95E-01	-	-
1379787_at	Uck1	Uridine-cytidine kinase 1	311864	Rn.20148	BI290392	2.34	2.33	2.34	2.34	2.33	2.33	1.01	down	4.56E-01	8.95E-01	-	-
1375917_at	Irb4 /// LOC49907	leukocyte immunoglobulin-like receptor, subfamily B, member 4 /// similar to C292594 /// 499078	---	Rn.24628	BF282961	2.54	2.51	2.55	2.52	2.55	2.50	1.01	down	5.00E-01	8.95E-01	-	-
1379445_at	---	---	---	Rn.96236	BF283378	2.41	2.38	2.44	2.40	2.42	2.36	1.01	down	5.93E-01	8.95E-01	-	-
1384022_at	Agfg1	ArfGAP with FG repeats 1	363266	Rn.3794	BI288173	5.88	5.24	5.31	5.40	5.17	5.81	1.01	down	9.62E-01	9.89E-01	-	-
1395142_at	---	---	---	Rn.203970	BG371864	2.75	2.62	2.71	2.66	2.79	2.60	1.01	down	8.47E-01	9.52E-01	-	-
1389975_at	Elavl4	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 4 (Hu antigen D)	432358	Rn.134702	BE116949	2.29	2.28	2.33	2.28	2.29	2.28	1.01	down	4.10E-01	8.95E-01	-	-
1381863_at	---	---	---	Rn.166432	AI071253	2.50	2.50	2.52	2.52	2.58	2.46	1.01	up	7.16E-01	9.10E-01	-	-
1391004_at	Svil	Supervillin	361256	Rn.36337	AW535541	3.56	5.19	4.97	4.61	3.89	5.17	1.01	down	9.83E-01	9.95E-01	-	-
1370434_a_at	Mobp	myelin-associated oligodendrocyte basic protein	25037	Rn.91185	X89638	2.44	2.42	2.47	2.43	2.46	2.40	1.01	down	5.61E-01	8.95E-01	-	-
1380209_at	---	---	---	Rn.21104	AI176102	2.35	2.34	2.38	2.34	2.36	2.33	1.01	down	3.85E-01	8.95E-01	-	-
1394401_at	Elovl6	ELOVL family member 6, elongation of long chain fatty acids (yeast)	171402	Rn.46942	BF396857	2.93	2.91	2.93	3.10	2.81	2.90	1.01	up	8.79E-01	9.63E-01	-	-
1374955_at	---	---	---	Rn.63318	BF418034	2.39	2.38	2.40	2.39	2.45	2.36	1.01	up	6.10E-01	8.95E-01	-	-
1370818_at	Decr2	2,4-dienoyl CoA reductase 2, peroxisomal	64461	Rn.144598	AF044574	11.43	10.80	10.80	11.00	10.95	11.03	1.01	down	9.50E-01	9.85E-01	-	-
1370644_at	Vom2r18	vomeronasal 2 receptor, 18	286984	Rn.10809	AF016181	2.40	2.38	2.44	2.39	2.41	2.38	1.01	down	5.02E-01	8.95E-01	-	-
1389499_at	---	---	---	Rn.40836	AW254246	2.48	2.48	2.49	2.53	2.49	2.47	1.01	up	5.15E-01	8.95E-01	-	-
1397462_at	---	---	---	---	BF415997	2.47	2.44	2.49	2.46	2.48	2.42	1.01	down	5.36E-01	8.95E-01	-	-
1371128_at	Il4	interleukin 4	287287	Rn.108255	X16058	2.33	2.32	2.37	2.33	2.34	2.32	1.01	down	3.63E-01	8.95E-01	-	-
1384437_at	Smarca1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin,	317575	Rn.39117	AI576309	2.52	2.50	2.57	2.51	2.56	2.48	1.01	down	6.71E-01	9.00E-01	-	-
1390539_at	---	---	---	Rn.13736	BF285569	2.45	2.43	2.47	2.44	2.46	2.41	1.01	down	5.08E-01	8.95E-01	-	-
1396834_at	---	---	---	Rn.206686	AW529263	2.57	2.54	2.61	2.55	2.58	2.54	1.01	down	5.90E-01	8.95E-01	-	-
1381446_at	Fam75a4	family with sequence similarity 75, member A4	353306	Rn.96432	BF410122	2.42	2.40	2.43	2.40	2.42	2.38	1.01	down	4.22E-01	8.95E-01	-	-
1383772_at	---	---	---	Rn.165369	AA996760	5.55	6.25	6.54	5.82	6.31	6.18	1.01	down	9.68E-01	9.91E-01	-	-
1368605_at	Sh2b2	SH2B adaptor protein 2	114203	Rn.163202	NM_053669	2.39	2.39	2.42	2.39	2.40	2.37	1.01	down	3.49E-01	8.95E-01	-	-
1384951_at	Arfgap1	ADP-ribosylation factor GTPase activating protein 1	246310	Rn.11219	AW531209	2.43	2.36	2.44	2.43	2.44	2.41	1.01	up	6.26E-01	8.95E-01	-	-
1391342_at	---	---	---	Rn.18897	AI058512	2.42	2.38	2.39	2.39	2.39	2.38	1.01	down	2.58E-01	8.95E-01	-	-
1371228_at	Csf2	colony stimulating factor 2 (granulocyte-macrophage)	116630	Rn.44285	U00620	2.37	2.35	2.36	2.41	2.36	2.35	1.01	up	5.11E-01	8.95E-01	-	-
1395885_at	---	---	---	Rn.65838	AA957955	2.44	2.42	2.45	2.42	2.45	2.40	1.01	down	4.77E-01	8.95E-01	-	-
1386518_at	Zfp91	Zinc finger protein 91	246282	Rn.1772	BE112093	2.87	2.84	2.85	3.03	2.85	2.72	1.01	up	8.85E-01	9.64E-01	-	-
1374267_at	---	---	---	Rn.200204	BG378154	2.49	2.48	2.52	2.48	2.49	2.47	1.01	down	3.95E-01	8.95E-01	-	-
1373340_at	Dusp9	dual specificity phosphatase 9	293847	Rn.100548	AI179321	2.43	2.40	2.46	2.40	2.49	2.43	1.01	up	6.83E-01	9.03E-01	-	-
1384862_at	---	---	---	Rn.156710	AW521749	2.50	2.47	2.54	2.48	2.53	2.45	1.01	down	6.76E-01	9.02E-01	-	-
1393557_at	---	---	---	Rn.13163	AI176280	2.36	2.35	2.40	2.36	2.36	2.36	1.01	down	4.40E-01	8.95E-01	-	-
1378719_at	---	---	---	Rn.199687	BF411797	2.39	2.38	2.40	2.38	2.39	2.35	1.01	down	3.58E-01	8.95E-01	-	-
1396709_at	---	---	---	Rn.207985	BE108621	2.42	2.38	2.45	2.39	2.43	2.39	1.01	down	5.79E-01	8.95E-01	-	-
1381158_at	Spdya	speedy homolog A (Xenopus laevis)	192209	Rn.19576	AI101556	2.51	2.49	2.54	2.50	2.52	2.48	1.01	down	5.31E-01	8.95E-01	-	-
1390735_at	---	---	---	---	BG375163	2.42	2.41	2.43	2.41	2.42	2.39	1.01	down	3.43E-01	8.95E-01	-	-
1391313_at	---	---	---	---	AA818873	2.48	2.45	2.51	2.47	2.49	2.44	1.01	down	5.66E-01	8.95E-01	-	-
1397498_at	---	---	---	Rn.222067	AI547846	2.56	2.52	2.63	2.54	2.63	2.50	1.01	down	7.88E-01	9.31E-01	-	-
1380769_at	---	---	---	---	BF394344	2.37	2.36	2.39	2.37	2.37	2.34	1.01	down	3.01E-01	8.95E-01	-	-
1378425_at	LOC687300	hypothetical protein LOC687300	687300	---	AI710552	2.41	2.40	2.42	2.39	2.41	2.38	1.01	down	2.61E-01	8.95E-01	-	-
1377075_at	---	---	---	---	AW553613	2.36	2.34	2.38	2.34	2.35	2.34	1.01	down	3.61E-01	8.95E-01	-	-
1377640_at	---	---	---	Rn.164355	AA945708	2.49	2.47	2.51	2.54	2.51	2.45	1.01	up	6.47E-01	8.95E-01	-	-
1370820_at	Fbxo6	F-box protein 6	192351	Rn.57325	AF393484	6.36	6.60	6.17	6.21	6.35	6.61	1.01	up	9.39E-01	9.83E-01	-	-
1394697_at	RGD1311723	similar to KIAA1731 protein	363018	Rn.160168	BF391048	2.43	2.41	2.44	2.42	2.43	2.40	1.01	down	3.36E-01	8.95E-01	-	-
1396880_at	---	---	---	Rn.161723	AI548656	2.49	2.48	2.51	2.49	2.50	2.46	1.01	down	3.85E-01	8.95E-01	-	-
1369665_a_at	Il18	interleukin 18	29197	Rn.11118	AJ222813	2.42	2.38	2.40	2.39	2.39	2.37	1.01	down	3.65E-01	8.95E-01	-	-
1397699_at	Dak	dihydroxyacetone kinase 2 homolog (S. cerevisiae)	361730	Rn.55630	BF288726	2.32	2.31	2.34	2.31	2.32	2.30	1.01	down	2.35E-01	8.95E-01	-	-
1394757_at	Ogfod1	2-oxoglutarate and iron-dependent oxygenase domain containing 1	307657	Rn.19163	BF412566	3.39	3.

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1373668_at	Polr2i	polymerase (RNA) II (DNA directed) polypeptide I, 14.5kDa	292778	Rn.6227	BG373075	6.33	6.46	6.21	6.52	5.37	7.07	1.01	down	9.80E-01	9.94E-01	-	-
1376109_at	---	---	---	Rn.48053	BM387711	2.38	2.37	2.40	2.37	2.37	2.36	1.01	down	2.13E-01	8.95E-01	-	-
1396375_at	---	---	---	Rn.209355	BF417934	2.42	2.41	2.46	2.41	2.43	2.41	1.01	down	4.52E-01	8.95E-01	-	-
1394824_at	Itga11	integrin, alpha 11	315744	Rn.64478	BF398348	2.33	2.31	2.35	2.32	2.32	2.31	1.01	down	3.34E-01	8.95E-01	-	-
1398967_at	Med24	mediator complex subunit 24	619436	Rn.7360	AI410050	3.15	2.86	2.43	3.03	2.38	2.99	1.01	down	9.65E-01	9.90E-01	-	-
1385372_at	Gkn1	gastrokine 1	297418	Rn.43048	AI639014	2.45	2.42	2.45	2.44	2.48	2.44	1.01	up	4.83E-01	8.95E-01	-	-
1395022_at	---	---	---	Rn.148763	AA859303	2.49	2.48	2.49	2.48	2.49	2.45	1.01	down	3.40E-01	8.95E-01	-	-
1372225_at	---	---	---	Rn.8780	BE119802	8.10	7.51	6.95	8.37	6.52	7.72	1.01	up	9.84E-01	9.95E-01	-	-
1392208_at	---	---	---	Rn.151234	BF401148	2.42	2.40	2.48	2.42	2.45	2.40	1.01	down	6.59E-01	8.98E-01	-	-
1398890_at	MGC93975	similar to 2310044H10Rik protein	292878	Rn.1470	AI410096	3.83	3.83	3.84	3.83	3.84	3.88	1.01	up	4.02E-01	8.95E-01	-	-
1372516_at	Kif22	kinesin family member 22	293502	Rn.8601	AI317842	2.39	2.38	2.39	2.44	2.39	2.38	1.01	up	4.99E-01	8.95E-01	-	-
1382882_x_at	---	---	---	200086 /// Rn.201	AA963228	2.48	2.46	2.51	2.47	2.49	2.44	1.01	down	5.13E-01	8.95E-01	-	-
1370941_at	Pdgfra	platelet derived growth factor receptor, alpha polypeptide	25267	Rn.55127	AI232379	8.12	8.52	8.47	8.08	8.75	8.32	1.01	up	9.55E-01	9.87E-01	-	-
1381288_at	Il1f5	interleukin 1 family, member 5 (delta)	311783	Rn.63170	BI282543	2.46	2.44	2.47	2.45	2.42	2.42	1.01	down	3.62E-01	8.95E-01	-	-
1370676_at	RGD1564614	similar to complement factor H-related protein	498241	---	AF436847	2.35	2.34	2.39	2.34	2.36	2.33	1.01	down	4.41E-01	8.95E-01	-	-
1384253_at	LOC364558	similar to palladin; CGI-151 protein	364558	Rn.160897	AW251334	2.46	2.45	2.49	2.45	2.47	2.43	1.01	down	4.23E-01	8.95E-01	-	-
1389320_at	Fbxo25	F-box protein 25	364637	Rn.3663	BF419881	3.45	3.91	3.04	3.44	2.99	4.02	1.01	up	9.74E-01	9.92E-01	-	-
1374975_at	---	---	---	Rn.60896	BF402601	2.30	2.30	2.31	2.30	2.31	2.34	1.01	up	3.33E-01	8.95E-01	-	-
1398721_at	Fsd1	fibronectin type III and SPRY domain containing 1	301506	Rn.45600	BF399295	2.45	2.43	2.48	2.44	2.46	2.42	1.01	down	5.10E-01	8.95E-01	-	-
1369071_at	S1pr1	sphingosine-1-phosphate receptor 1	29733	Rn.109455	NM_017301	2.39	2.37	2.43	2.38	2.41	2.36	1.01	down	5.82E-01	8.95E-01	-	-
1371628_at	Ceacam11	carcinoembryonic antigen-related cell adhesion molecule 11	292668	Rn.205326	BI284359	2.48	2.45	2.50	2.47	2.49	2.43	1.01	down	5.68E-01	8.95E-01	-	-
1397108_at	---	---	---	Rn.171239	BE110342	2.50	2.48	2.51	2.48	2.58	2.47	1.01	up	7.30E-01	9.14E-01	-	-
1381412_at	---	---	---	Rn.203952	BE095850	2.43	2.41	2.45	2.41	2.43	2.39	1.01	down	4.77E-01	8.95E-01	-	-
1391772_at	---	---	---	---	BF414775	2.43	2.42	2.45	2.42	2.42	2.42	1.01	down	1.21E-01	8.95E-01	-	-
1386565_at	---	---	---	Rn.15385	BF556081	3.78	4.10	3.98	4.00	3.94	3.96	1.01	up	8.93E-01	9.67E-01	-	-
1370698_at	Ugt2b17	UDP glucuronosyltransferase 2 family, polypeptide B17	286954	Rn.9969	M13506	2.41	2.39	2.43	2.40	2.42	2.38	1.01	down	4.17E-01	8.95E-01	-	-
1380944_at	---	---	---	Rn.28781	AI146245	2.33	2.32	2.35	2.33	2.34	2.38	1.01	up	4.78E-01	8.95E-01	-	-
1395961_at	---	---	---	Rn.161881	BI298336	2.36	2.35	2.39	2.35	2.38	2.33	1.01	down	5.57E-01	8.95E-01	-	-
1377746_at	Rbm12	RNA binding motif protein 12	652928	Rn.7119	AI010418	2.41	2.41	2.42	2.40	2.41	2.39	1.01	down	1.40E-01	8.95E-01	-	-
1396342_at	---	---	---	Rn.147575	BF392211	2.48	2.46	2.51	2.47	2.50	2.44	1.01	down	6.11E-01	8.95E-01	-	-
1377883_at	---	---	---	Rn.29913	AI717530	2.51	2.52	2.52	2.50	2.52	2.49	1.01	down	2.94E-01	8.95E-01	-	-
1378701_at	---	---	---	Rn.172498	BF401392	2.40	2.40	2.43	2.40	2.41	2.38	1.01	down	4.01E-01	8.95E-01	-	-
1396970_at	---	---	---	Rn.172417	BF404956	2.34	2.34	2.35	2.38	2.35	2.35	1.01	up	2.69E-01	8.95E-01	-	-
1384883_at	---	---	---	Rn.146209	AA858571	2.46	2.44	2.49	2.45	2.48	2.42	1.01	down	5.60E-01	8.95E-01	-	-
1369028_at	Six3	SIX homeobox 3	78974	Rn.123641	NM_023990	3.51	3.49	3.53	3.49	3.53	3.46	1.01	down	5.98E-01	8.95E-01	-	-
1395093_at	---	---	---	---	AI145025	2.32	2.31	2.33	2.37	2.32	2.31	1.01	up	4.77E-01	8.95E-01	-	-
1372842_at	Psgb1	pregnancy-specific beta 1-glycoprotein	59313	Rn.42878	BI285898	2.46	2.45	2.49	2.45	2.46	2.44	1.01	down	3.51E-01	8.95E-01	-	-
1396340_at	---	---	---	Rn.207941	BF417789	2.48	2.41	2.50	2.46	2.53	2.45	1.01	up	7.18E-01	9.11E-01	-	-
1395849_at	---	---	---	---	BF401574	2.35	2.35	2.39	2.35	2.36	2.34	1.01	down	3.61E-01	8.95E-01	-	-
1385627_at	Bcl3	B-cell CLL/lymphoma 3	680611	Rn.198135	BF407019	2.44	2.45	2.47	2.45	2.46	2.41	1.01	down	4.45E-01	8.95E-01	-	-
1369475_x_at	P2rx2	purinergic receptor P2X, ligand-gated ion channel, 2	114115	Rn.88799	AF028804	2.36	2.36	2.39	2.35	2.37	2.34	1.01	down	3.21E-01	8.95E-01	-	-
1383135_at	---	---	---	Rn.203281	BG669126	2.36	2.35	2.41	2.36	2.38	2.34	1.01	down	5.38E-01	8.95E-01	-	-
1384290_at	Rbbp6	Retinoblastoma binding protein 6	308968	Rn.95305	BG373809	5.02	5.14	5.23	5.47	5.08	4.89	1.01	up	9.43E-01	9.84E-01	-	-
1382933_at	---	---	---	Rn.147263	BE102157	2.38	2.38	2.39	2.37	2.38	2.35	1.01	down	1.68E-01	8.95E-01	-	-
1391784_at	Repin1	replication initiator 1	445541	Rn.204397	AI784765	2.33	2.34	2.33	2.34	2.40	2.31	1.01	up	6.52E-01	8.97E-01	-	-
1385291_a_at	Sc65	synaptonemal complex protein SC65	59101	Rn.90100	BI303187	2.47	2.45	2.47	2.46	2.47	2.43	1.01	down	3.95E-01	8.95E-01	-	-
1395040_at	RGD1561777	similar to Na+ dependent glucose transporter 1	499463	Rn.204745	AI103846	2.36	2.35	2.38	2.35	2.35	2.35	1.01	down	3.06E-01	8.95E-01	-	-
1375398_at	Tmem163	Transmembrane protein 163	360839	Rn.25191	AW251322	2.69	2.65	2.66	2.65	2.66	2.64	1.01	down	3.07E-01	8.95E-01	-	-
1396946_at	---	---	---	Rn.212656	BI294771	2.75	2.71	2.72	2.71	2.72	2.79	1.01	up	6.31E-01	8.95E-01	-	-
1396764_at	---	---	---	Rn.210675	BF400138	2.34	2.32	2.36	2.33	2.34	2.32	1.01	down	3.39E-01	8.95E-01	-	-
1376973_at	Sdcbp2	syndecan binding protein (syntenin) 2	311532	Rn.15848	BM386809	2.36	2.34	2.39	2.35	2.35	2.35	1.01	down	4.21E-01	8.95E-01	-	-
1390038_at	Adcy5	Adenylate cyclase 5	64532	Rn.6278	BE109625	2.54	2.49	2.53	2.49	2.53	2.50	1.01	down	5.52E-01	8.95E-01	-	-
1374825_at	Sez6l2	seizure related 6 homolog (mouse)-like 2	309888	Rn.30285	BG380338	2.42	2.41	2.47	2.41	2.43	2.41	1.01	down	4.92E-01	8.95E-01	-	-
1384448_at	RGD1565844	similar to RIKEN cDNA 1700045I19	317486	Rn.11609	AA963712	2.38	2.37	2.40	2.37	2.39	2.36	1.01	down	2.78E-01	8.95E-01	-	-
1377497_at	Oasl	2'-5'-oligoadenylate synthetase-like	304545	Rn.7429	BF419319	2.43	2.39	2.40	2.39	2.40	2.38	1.01	down	3.45E-01	8.95E-01	-	-
1387311_at	Nox1	NADPH oxidase 1	114243	Rn.220465	NM_053683	2.56	2.40	2.40	2.39	2.42	2.51	1.01	down	8.40E-01	9.50E-01	-	-
1397941_at	LOC678741	similar to Zinc finger CCCH-type domain containing protein 6	678741	Rn.98823	AW533522	2.24	2.24	2.25	2.29	2.25	2.24	1.01	up	4.37E-01	8.95E-01	-	-
1381971_at	Sox18	SRY (sex determining region Y)-box 18	311723	Rn.22446	AW534157	2.34	2.36	2.34	2.34	2.32	2.32	1.01	down	2.63E-01	8.95E-01	-	-
1377548_at	---	---	---	Rn.219427	BF402404	2.46	2.45	2.49	2.45	2.48	2.42	1.01	down	5.50E-01	8.95E-01	-	-
1371994_at	Arhgap1	Rho GTPase activating protein 1	311193	Rn.64898	AI412316	4.37	4.39	4.46	4.51	4.21	4.53	1.01	up	9.04E-01	9.70E-01	-	-
1381961_at	Amn1	Antagonist of mitotic exit network 1 homolog (S. cerevisiae)	302032	Rn.104358	AI502554	2.68	2.67	2.70	2.77	2.69	2.55	1.01	down	8.44E-01	9.52E-01	-	-
1384763_at	RGD1306626	similar to RIKEN cDNA 4930500J03	362319	Rn.209992	BF392435	2.42	2.40	2.45	2.41	2.43	2.39	1.01	down	4.95E-01	8.95E-01	-	-
1380441_at	Tax1bp3	Tax1 (human T-cell leukemia virus type I) binding protein 3	360564	Rn.34842	AI009637	2.39	2.38	2.42	2.39	2.40	2.37	1.01	down	3.98E-01	8.95E-01	-	-
1391696_at	---	---	---	---	AI599889	2.36	2.35	2.35	2.34	2.34	2.33	1.01	down	1.43E-01	8.95E-01	-	-
1398121_at	---	---	---	Rn.44049	AI408889	2.37	2.35	2.38	2.35	2.36	2.34	1.01	down	2.87E-01	8.95E-01	-	-
1376527_at	---	---	---	Rn.200266	BI291223	2.41	2.39	2.41	2.40	2.40	2.38	1.01	down	2.24E-01	8.95E-01	-	-
1370231_at	Gtf3c1	general transcription factor III C 1	171063	Rn.11288	AI234022	3.38	3.36	3.38	3.16	3.42	3.59	1.01	up	9.20E-01	9.76E-01	-	-
1381745_at	---	---	---	---	BF413395	2.38	2.36	2.42	2.38	2.46	2.36	1.01	up	7.37E-01	9.15E-01	-	-
1397594_at	---	---	---	Rn.60729	BF405308	2.45	2.43	2.51	2.43	2.49	2.43	1.01	down	6.92E-01	9.05E-01	-	-
1396611_at	---	---	---	Rn.194910	BF404562	2.48	2.46	2.52	2.46	2.50	2.45	1.01	down	6.10E-01	8.95E-01	-	-
1392379_at	---	---	---	Rn.62088	BF413731	2.55	2.51	2.61	2.53	2.63	2.48	1.01	down	8.04E-01	9.37E-01	-	-
1381674_at	---	---	---	---	BF396526	2.51	2.53	2.53	2.52	2.53	2.48	1.01	down	4.94E-01	8.95E-01	-	-
1379817_at	Purg	purine-rich element binding protein G	361162	Rn.88554	AI227924	3.30	3.82	2.77	2.71	3.03	4.19	1.01	up	9.81E-01	9.94E-01	-	-
1391142_at	---	---	---	Rn.210695	BF400657	2.34	2.33	2.35	2.33	2.40	2.33	1.01	up	6.14E-01	8.95E-01	-	-
1395964_at	---	---	---	Rn.41069	BI301241	2.40	2.40	2.43	2.40	2.41	2.37	1.01	down	4.62E-01	8.95E-01	-	-
1369694_at	Slc1a2	solute carrier family 1 (glial high affinity glutamate transporter), member 2	29482	Rn.10240	AY069978	2.49	2.45	2.49	2.46	2.48	2.44	1.01	down	4.21E-01	8.95E-01	-	-
1374091_at	---	---	---	Rn.8987	AW526005	2.31	2.30	2.32	2.31	2.37	2.30	1.01	up	5.80E-01	8.95E-01	-	-
1382301_at	---	---	---	Rn.171733	BE120448	2.49	2.48	2.53	2.48	2.51	2.47	1.01	down	5.54E-01	8.95E-01	-	-
1386418_at	---	---	---	---	AI636330	2.45	2.44	2.48	2.45	2.47	2.42	1.01	down	4.96E-01	8.95E-01	-	-
1387600_at	Gabrp	gamma-aminobutyric acid (GABA-A) receptor, pi	81658	Rn.21401	NM_031029	2.44	2.41	2.47	2.43	2.45	2.40	1.01	down	5.94E-01	8.95E-01	-	-
1397597_at	---	---	---	Rn.203195	AW531942	2.41	2.40	2.41	2.41	2.46	2.40	1.01	up	5.36E-01	8.95E-01	-	-
1380877_at	---	---	---	Rn.149250	BF401719	2.42	2.39	2.43	2.41	2.41	2.38	1.01	down	3.72E-01	8.95E-01	-	-
1393553_at	---	---	---	Rn.41732	AI059872	2.45	2.44	2.49	2.45	2.46	2.44	1.01	down	4.52E-01	8.95E-01	-	-
1393709_at	---	---	---	Rn.147473	BF394784	2.40	2.38	2.40	2.38	2.39	2.37	1.01	down	2.84E-01	8.95E-01	-	-
1398352_at	Plas4	protein inhibitor of activated STAT, 4	362827	Rn.12810	AI412927	3.50	3.75	3.71	3.76	3.90	3.25	1.01	down	9.52E-01	9.86E-01	-	-
1381569_at	---	---	---	---	BE111190	2.45	2.45	2.46	2.49	2.46	2.44	1.01	up	4.37E-01	8.95E-01	-	-
1382954_at	---	---	---	Rn.131875	AI577630	2.38	2.38	2.39	2.37	2.38	2.36	1.01	down	1.87E-01	8.95E-01	-	-
1396464_at	---	---	---	---	AI501766	4.56	3.34	3.09	3.31	3.94	3.77	1.01	up	9.79E-01	9.94E-01	-	-
1386505_at	---	---	---	---	AI639214	2.40	2.39	2.44	2.39	2.42	2.39	1.01	down	5.06E-01	8.95E-01	-	-
1378731_at	// Prr14 /// RGD15	fibrosin /// proline rich 14 /// similar to CDNA sequence BC006909	67 /// 691898 /// 69	Rn.201735	BF404871	2.29	2.26	2.29	2.29	2.31	2.29	1.01	up	3.56E-01	8.95E-01	-	-
1381212_at	---	---	---	Rn.209339	BG378695	2.38	2.38	2.38	2.38	2.38	2.35	1.01	down	2.29E-01	8.95E-01	-	-
1395235_at	Nxnl1	nucleoredoxin-like 1	306342	Rn.48965	BE108041	2.33	2.32	2.36	2.32	2.33	2.31	1.01	down	3.09E-01	8.95E-01	-	-
1380828_at	Gabra1	gamma-aminobutyric acid (GABA) A receptor, alpha 1	29705	Rn.28463	AI145413	2.41	2.39	2.43	2.40	2.41	2.38	1.01	down	3.28E-01	8.95E-01	-	-
1394110_at	---	---	---	---	H35830	2.44	2.43	2.45	2.44	2.44	2.40	1.01	down	3.77E-01	8.95E-01	-	-
1390676_at	---	---	---	Rn.209429	BF415506	2.39	2.35	2.39	2.36	2.38	2.35	1.01	down	4.32E-01	8.95E-01	-	-
1393278_at	Creb3l4	CAMP responsive element binding protein 3-like 4	310616	Rn.19624	BM389370	2.42	2.44	2.42	2.48	2.41	2.41	1.01	up	5.96E-01	8.95E-01	-	-
1378085_at	Epn3	epsin 3	360605	Rn.26582	BM387330	2.40	2.40	2.44	2.40	2.41	2.40	1.01	down	4.28E-01	8.95E-01	-	-
1385956_at	---	---	---	Rn.119429	BF289086	6.77	4.71	6.16	5.26	6.92	5.50	1.01	up	9.87E-01	9.96E-01	-	-
1384674_at	---	---	---	Rn.23180	BF560339	2.48	2.45	2.49	2.46	2.49	2.44	1.01	down	4.89E-01	8.95E-01	-	-
1392871_at	---	---	---	Rn.17736	BM392092	2.21	2.20	2.21	2.21	2.25	2.20	1.01	up	4.26E-01	8.95E-01	-	-
1397338_at	---	---	---	Rn.187348	AI137999	2.57	2.54	2.67	2.56	2.73	2.54	1.01	up	8.66E-01	9.58E-01	-	-
1375976_a_at	Mus81	MUS81 endonuclease homolog (S. cerevisiae)	293678	Rn.137652	AA849388	3.06	3.51	2.79	3.84	2.73	2.73	1.01	down	9.76E-01	9.93E-01	-	-
1388272_at	Igh-1a	immunoglobulin heavy chain 1a (serum IgG2a)	293352	Rn.202986	AI411947	2.37	2.37	2.38	2.37	2.42	2.37	1.01	up	5.22E-01	8.95E-01	-	-
1378287_at	Rdx	radixin	315655	Rn.203261	BI297296	9.22	8.93	8.73	8.88	8.89	9.07	1.01	down	9.36E-01	9.82E-01	-	-
1382381_at	---	---	---	Rn.16713	AA818480	6.12	5.83	5.46	6.22	5.57	5.67	1.01	up	9.63E-01	9.90E-01	-	-
1386309_at	LOC304558	Similar to TPR repeat-containing protein KIAA1043	304558	Rn.137233	AI176361	2.46	2.44	2.51	2.45	2.48	2.43	1.01	down	5.99E-01	8.95E-01	-	-
1394883_at	---	---	---	Rn.156482	AI179616	2.38	2.37	2.38	2.37	2.38	2.34	1.01	down	3.33E-01	8.95E-01	-	-
1395031_at	---	---	---	Rn.210525	BF398717	2.56	2.55	2.56	2.56	2.56	2.52	1.01	down	3.87E-01	8.95E-01	-	-
1385511_at	Centd2	centaurin, delta 2	361617	Rn.41376	AI412079	3.73	3.47	3.26	3.48	3.49	3.54	1.01	up	9.26E-01	9.79E-01	-	-
1398484_at	RGD1308221	similar to TBC1 domain family, member 8 (with GRAM domain); vascular Rab	304645	Rn.19710	AI070306	2.29	2.32	2.29	2.29	2.28	2.28	1.01	down	2.10E-01	8.95E-01	-	-
1378709_at	---	---	---	Rn.212263	BI300330	2.35	2.34	2.39	2.35	2.36	2.33	1.01	down	4.44E-01	8.95E-01	-	-
1375582_at	Zfhx4	zinc finger homeobox 4	310250	Rn.133363	AW531902	2.38	2.37	2.43	2.37	2.41	2.36	1.01	down	6.18E-01	8.95E-01	-	-
1379324_at	---	---	---	Rn.21975	AW535283	2.36	2.36	2.37	2.42	2.37	2.35	1.01	up	5.51E-01	8.95E-01	-	-
1379198_at	---	---	---	Rn.199522	AI712874	2.56	2.60	2.60	2.64	2.66	2.50	1.01	up	8.00E-01	9.35E-01	-	-
1387330_at	Mepe	matrix extracellular phosphoglycoprotein	79110	Rn.160717	NM_024142	2.49	2.48	2.49	2.48	2.49	2.45	1.01	down	3.12E-01	8.95E-01	-	-
1383930_at	---	---	---	Rn.19519	AI058455	2.41	2.39	2.44	2.40	2.42	2.38	1.01	down	5.25E-01	8.95E-01	-	-
1396805_at	---	---	---	Rn.209100	BF391383	2.93	2.91	2.93	3.07	2.93	2.73	1.01	down	8.98E-01	9.68E-01	-	-
1395979_at	---	---	---	Rn.154053	BF403475	2.37	2.36	2.40	2.36	2.38	2.35	1.01	down	4.29E-01	8.95E-01	-	-
1387661_a_at	Opri1	opiate receptor-like 1	29256	Rn.9762	U05239	2.48	2.47	2.48	2.47	2.47	2.44	1.01	down	2.56E-01	8.95E-01	-	-
1388545_at	Smoc1	SPARC related modular calcium binding 1	314280	Rn.55639	BG373119	2.43	2.41	2.46	2.42	2.43	2.41	1.01	down	4.45E-01	8.95E-01	-	-
1386739_at	Etv4	ets variant 4	360635	Rn.195602	BF545627	2.35	2.34	2.37	2.34	2.35	2.33	1.01	down	2.27E-01	8.95E-01	-	-
1384872_at	---	---	---	---	AI556568	2.33	2.29	2.30	2.30	2.30	2.28	1.01	down	2.94E-01	8.95E-01	-	-
1369893_at	Hist1h2aa	histone cluster 1, H2aa	24828	Rn.18107	NM_021839	2.37	2.36	2.37	2.36	2.37	2.33	1.01	down	3.09E-01	8.95E-01	-	-
1379653_a_at	Sh2d1a	SH2 domain protein 1A	501502	Rn.12805	AI176327	2.49	2.47	2.53	2.48	2.51	2.45	1.01	down	6.31E-01	8.95E-01	-	-
1388793_at	Pigq	phosphatidylinositol glycan anchor biosynthesis, class Q	287159	Rn.12777	AI408261	3.92	4.82	5.30	4.21	4.20	5.59	1.01	down	9.84E-01	9.95E-01	-	-
1376721_at	Trio	triple functional domain (PTPRF interacting)	310192	Rn.221920	BF400666	2.38	2.40	2.39	2.39	2.38	2.35	1.01	down	2.77E-01	8.95E-01	-	-
1392383_at	---	---	---	Rn.210052	BF405619	2.64	2.58	2.77	2.73	2.66	2.56	1.01	down	8.68E-01	9.59E-01	-	-
1396714_at	---	---	---	Rn.210119	BF394289	2.63	2.54	2.70	2.61	2.67	2.56	1.01	down	8.23E-01	9.43E-01	-	-
1399022_at	Clk1	CDC-like kinase 1	301434	Rn.36770	AI177513	8.95	8.29	7.85	8.38	8.67	8.08	1.01	up	9.72E-01	9.92E-01	-	-
1393844_at	Mff1p	myeloid leukemia factor 1 interacting protein	306464	Rn.128609	AW525736	2.47	2.48	2.48	2.47	2.47	2.45	1.01	down	1.72E-01	8.95E-01	-	-
1385205_at	---	---	---	Rn.173484	BF409092	2.47	2.45	2.48	2.44	2.49	2.43	1.01	down	5.75E-01	8.95E-01	-	-
1390865_at	Tmem72	transmembrane protein 72	362424	Rn.194940	AA848412	2.44	2.43	2.45	2.42	2.46	2.40	1.01	down	5.02E-01	8.95E-01	-	-
1391343_at	---	---	---	Rn.101964	BF396067	2.26	2.26	2.26	2.26	2.31	2.25	1.01	up	4.96E-01	8.95E-01	-	-
1383299_at	---	---	---	Rn.19762	BI291730	5.10	5.91	4.16	4.24	5.11	5.86	1.01	up	9.85E-01	9.96E-01	-	-
1395491_at	---	---	---	Rn.51835	BF409377	2.52	2.48	2.55	2.50	2.54	2.47	1.01	down	6.77E-01	9.02E-01	-	-
1398097_at	---	---	---	---	AI412543	2.52	2.49	2.53	2.49	2.52	2.49	1.01	down	4.69E-01	8.95E-01	-	-
1391971_at	---	---	---	Rn.160358	BG669026	2.30	2.33	2.31	2.30	2.31	2.30	1.01	down	2.00E-01	8.95E-01	-	-
1371640_at	Znf706	zinc finger protein 706	500855	Rn.40403	BF289183	8.81	9.22	8.79	8.90	8.97	8.91	1.01	down	9.30E-01	9.81E-01	-	-
1395832_at	Zfp53	zinc finger protein 53	308236	Rn.198476	AW529599	2.37	2.41	2.37	2.46	2.37	2.36	1.01	up	7.14E-01	9.10E-01	-	-
1371559_at	Nadk	NAD kinase	100125370	Rn.28371	AI103384	7.66	8.44	8.68	8.76	7.65	8.34	1.01	down	9.78E-01	9.93E-01	-	-
1390950_at	---	---	---	Rn.204894	AI234865	2.47	2.44	2.50	2.45	2.48	2.43	1.01	down	5.76E-01	8.95E-01	-	-
1378924_at	Ints10	Integrator complex subunit 10	290679	Rn.2385	AI233807	2.39	2.38	2.40	2.38	2.39	2.36	1.01	down	2.71E-01	8.95E-01	-	-
1388299_at	Dnal1	dynein, axonemal, light chain 1	685664	Rn.156856	BF406304	2.40	2.38	2.41	2.38	2.40	2.37	1.01	down	3.01E-01	8.95E-01	-	-
1396495_at	---	---	---	Rn.76772	BI300244	2.43	2.42	2.45	2.43	2.44	2.40	1.01	down	4.11E-01	8.95E-01	-	-
1384065_at	---	---	---	Rn.23380	BG663648	2.64	2.61	2.67	2.62	2.66	2.59	1.01	down	6.50E-01	8.96E-01	-	-
1389936_at	LOC687035	similar to Tripartite motif protein 56	687035	---	BI291361	2.55	2.54	2.55	2.54	2.55	2.59	1.01	up	4.47E-01	8.95E-01	-	-
1377894_at	---	---	---	Rn.204903	BF404700	2.39	2.33	2.35	2.33

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1398278_at	Prl	prolactin	24683	Rn.9759	NM_012629	2.35	2.34	2.39	2.35	2.36	2.33	1.01	down	5.02E-01	8.95E-01	-	-
1392623_at	---	---	---	Rn.15656	AA926097	2.45	2.42	2.46	2.43	2.46	2.41	1.01	down	5.19E-01	8.95E-01	-	-
1391509_at	Tacstd2	tumor-associated calcium signal transducer 2	494343	Rn.24809	AA891826	2.35	2.35	2.36	2.35	2.40	2.35	1.01	up	4.93E-01	8.95E-01	-	-
1381701_at	Aak1	AP2 associated kinase 1	500244	Rn.203307	AW433655	2.50	2.48	2.55	2.49	2.60	2.48	1.01	up	7.84E-01	9.30E-01	-	-
1383337_at	---	---	---	Rn.203648	AA963875	2.43	2.40	2.42	2.48	2.41	2.40	1.01	up	6.22E-01	8.95E-01	-	-
1396341_at	Mrm1	Mitochondrial rRNA methyltransferase 1 homolog (S. cerevisiae)	363661	Rn.43486	BI276792	2.53	2.51	2.56	2.53	2.54	2.49	1.01	down	5.47E-01	8.95E-01	-	-
1376540_at	---	---	---	Rn.163053	BE105373	2.45	2.43	2.48	2.44	2.46	2.42	1.01	down	5.00E-01	8.95E-01	-	-
1386023_at	Lgi1	leucine-rich, glioma inactivated 1	252892	Rn.83615	AI229354	2.48	2.46	2.54	2.47	2.52	2.44	1.01	down	7.12E-01	9.10E-01	-	-
1388316_at	RGD1566320	RGD1566320	296207	Rn.4025	BG668062	6.76	7.23	7.02	7.19	6.74	7.13	1.01	up	9.50E-01	9.85E-01	-	-
1398698_at	---	---	---	Rn.66894	BG371721	2.48	2.56	2.48	2.48	2.48	2.61	1.01	up	8.11E-01	9.39E-01	-	-
1371208_at	Nupl1	nucleoporin like 1	245922	Rn.11099	AF000898	2.36	3.03	2.58	2.88	2.57	2.57	1.01	up	9.56E-01	9.87E-01	-	-
1385668_at	---	---	---	---	AI044864	2.42	2.41	2.44	2.48	2.44	2.39	1.01	up	6.54E-01	8.97E-01	-	-
1378220_at	LOC497860	similar to RIKEN cDNA 4930517K11	497860	Rn.26687	AI111983	2.45	2.42	2.48	2.44	2.47	2.41	1.01	down	6.14E-01	8.95E-01	-	-
1391354_at	---	---	---	Rn.209302	BF387447	2.39	2.40	2.40	2.39	2.39	2.36	1.01	down	2.46E-01	8.95E-01	-	-
1395252_at	---	---	---	Rn.148202	BE101587	2.56	2.53	2.64	2.54	2.69	2.54	1.01	up	8.32E-01	9.47E-01	-	-
1368034_at	Chgb	chromogranin B	24259	Rn.11090	NM_012526	2.46	2.46	2.50	2.46	2.48	2.44	1.01	down	5.17E-01	8.95E-01	-	-
1371272_at	/// LOC502908 ///	killer cell lectin-like receptor, subfamily A, member 5 /// Ly49s8 /// Ly49 stimulat	56 /// 494203 /// 50	Rn.37467	U56824	2.57	2.52	2.63	2.57	2.62	2.49	1.01	down	8.05E-01	9.37E-01	-	-
1386697_at	Nxph1	neurexophilin 1	25501	Rn.10610	BF567897	2.48	2.46	2.55	2.47	2.52	2.46	1.01	down	7.03E-01	9.07E-01	-	-
1368375_a_at	Il15	interleukin 15	25670	Rn.2490	AF015718	4.41	3.11	2.66	3.28	3.84	3.02	1.01	down	9.83E-01	9.95E-01	-	-
1377386_at	Atp2c1	ATPase, Ca++ transporting, type 2C, member 1	170699	Rn.5805	AI029639	2.45	2.43	2.47	2.44	2.47	2.42	1.01	down	5.35E-01	8.95E-01	-	-
1368857_at	Ugt8	UDP glycosyltransferase 8	50555	Rn.9744	L21698	2.48	2.45	2.51	2.46	2.51	2.43	1.01	down	5.46E-01	8.95E-01	-	-
1383109_at	Prcc	papillary renal cell carcinoma (translocation-associated)	310687	Rn.12346	BG669807	3.17	3.11	3.17	3.17	3.15	3.11	1.01	up	5.94E-01	8.95E-01	-	-
1377647_at	Scmh1	sex comb on midleg homolog 1 (Drosophila)	362581	Rn.7761	AA924088	2.26	2.25	2.26	2.25	2.26	2.29	1.01	up	3.50E-01	8.95E-01	-	-
1393838_at	---	---	---	Rn.203806	AA998494	2.49	2.47	2.53	2.48	2.51	2.46	1.01	down	6.30E-01	8.95E-01	-	-
1380417_at	Cmtm4	CKLF-like MARVEL transmembrane domain containing 4	498902	Rn.160026	AI412138	2.66	2.61	2.92	3.01	2.65	2.57	1.01	up	9.41E-01	9.83E-01	-	-
1372682_at	RGD1307218	similar to RIKEN cDNA 2810432L12	362518	Rn.161029	BI289460	2.70	2.67	2.68	2.67	2.68	2.66	1.01	down	3.30E-01	8.95E-01	-	-
1393258_at	---	---	---	---	AI112121	2.47	2.46	2.48	2.46	2.53	2.45	1.01	up	6.54E-01	8.97E-01	-	-
1391102_at	---	---	---	Rn.46371	BI275672	2.38	2.37	2.41	2.37	2.39	2.36	1.01	down	4.27E-01	8.95E-01	-	-
1391075_at	Rgs17	regulator of G-protein signaling 17	308118	Rn.166916	AI179271	2.45	2.43	2.47	2.43	2.46	2.41	1.01	down	5.29E-01	8.95E-01	-	-
1390809_at	---	---	---	Rn.15026	AI599392	2.41	2.39	2.41	2.46	2.41	2.38	1.01	up	5.82E-01	8.95E-01	-	-
1380849_at	---	---	---	Rn.208966	BI274299	2.41	2.35	2.37	2.36	2.37	2.36	1.01	down	4.67E-01	8.95E-01	-	-
1397410_at	---	---	---	Rn.206330	BI301687	2.96	2.67	2.84	2.88	2.86	2.69	1.01	down	9.06E-01	9.71E-01	-	-
1381385_at	RGD1565584	similar to tyrosine kinase-associated leucine zipper protein LAZIpII	293112	Rn.35776	AI579106	2.71	2.74	2.71	2.71	2.72	2.70	1.01	down	2.56E-01	8.95E-01	-	-
1385820_at	Ube2v1	ubiquitin-conjugating enzyme E2 variant 1	296390	Rn.220168	AW520508	2.47	2.43	2.49	2.46	2.55	2.42	1.01	up	7.67E-01	9.24E-01	-	-
1396297_at	---	---	---	Rn.160330	BG374359	2.30	2.29	2.33	2.30	2.30	2.28	1.01	down	4.45E-01	8.95E-01	-	-
1384902_at	---	---	---	Rn.204096	BF545275	2.45	2.44	2.46	2.44	2.45	2.41	1.01	down	3.92E-01	8.95E-01	-	-
1383903_at	St8sia5	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 5	364901	Rn.199050	AW529294	2.38	2.37	2.39	2.37	2.38	2.35	1.01	down	3.47E-01	8.95E-01	-	-
1385064_at	Lao1	L-amino acid oxidase 1	298483	Rn.158854	BM384729	2.44	2.43	2.47	2.43	2.46	2.42	1.01	down	3.77E-01	8.95E-01	-	-
1397890_at	RGD1564053	similar to hypothetical protein	500390	Rn.219789	BE108121	2.48	2.45	2.51	2.47	2.50	2.44	1.01	down	6.21E-01	8.95E-01	-	-
1372186_a_at	Top2a	topoisomerase (DNA) II alpha	360243	Rn.90996	BM385445	2.46	2.42	2.46	2.44	2.45	2.42	1.01	down	4.81E-01	8.95E-01	-	-
1375890_at	RGD1563892	similar to MGC15476 protein	499088	Rn.93232	BI286994	2.30	2.27	2.29	2.29	2.32	2.28	1.01	up	4.34E-01	8.95E-01	-	-
1368196_at	Clps	colipase, pancreatic	25680	Rn.6714	NM_013139	2.38	2.40	2.39	2.38	2.39	2.37	1.01	down	2.10E-01	8.95E-01	-	-
1395254_at	---	---	---	Rn.156522	BF388342	2.37	2.36	2.41	2.37	2.37	2.36	1.01	down	3.93E-01	8.95E-01	-	-
1390847_at	Tmem86a	transmembrane protein 86A	308602	Rn.23056	BF558827	2.14	2.13	2.14	2.14	2.14	2.18	1.01	up	3.78E-01	8.95E-01	-	-
1387339_at	Sepp1	selenoprotein P, plasma, 1	29360	Rn.1451	NM_019192	4.10	3.54	4.35	3.89	4.18	3.89	1.01	down	9.63E-01	9.89E-01	-	-
1391831_at	---	---	---	Rn.137550	BI276470	2.47	2.44	2.49	2.45	2.48	2.43	1.01	down	5.60E-01	8.95E-01	-	-
1380567_at	---	---	---	Rn.179110	AI410020	2.49	2.48	2.56	2.48	2.52	2.49	1.01	down	6.75E-01	9.01E-01	-	-
1387566_at	Pla2g4a	phospholipase A2, group IVA (cytosolic, calcium-dependent)	24653	Rn.10162	NM_133551	2.50	2.48	2.54	2.48	2.53	2.47	1.01	down	6.19E-01	8.95E-01	-	-
1382708_at	---	---	---	Rn.20838	AI045073	2.34	2.33	2.36	2.33	2.35	2.31	1.01	down	3.83E-01	8.95E-01	-	-
1369561_at	Cysltr1	cysteinyl leukotriene receptor 1	114099	Rn.74253	NM_053641	2.29	2.29	2.33	2.29	2.30	2.28	1.01	down	3.90E-01	8.95E-01	-	-
1392020_at	Cep164	centrosomal protein 164kDa	363055	Rn.106595	BF410474	2.49	2.48	2.51	2.48	2.49	2.47	1.01	down	2.82E-01	8.95E-01	-	-
1385034_at	Lhx9	LIM homeobox 9	289048	Rn.150335	AW527447	2.25	2.28	2.26	2.25	2.26	2.24	1.01	down	3.50E-01	8.95E-01	-	-
1395113_at	---	---	---	Rn.52612	BE116051	2.31	2.30	2.34	2.30	2.31	2.29	1.01	down	3.09E-01	8.95E-01	-	-
1391987_at	---	---	---	Rn.210617	BF399470	2.32	2.28	2.30	2.29	2.30	2.28	1.01	down	3.18E-01	8.95E-01	-	-
1386939_a_at	Cacna1a	calcium channel, voltage-dependent, P/Q type, alpha 1A subunit	25398	Rn.87769	AF051527	2.48	2.46	2.51	2.46	2.49	2.45	1.01	down	4.96E-01	8.95E-01	-	-
1394717_at	Tbc1d5	TBC1 domain family, member 5	501088	Rn.203950	BE106041	2.39	2.38	2.40	2.38	2.39	2.36	1.01	down	2.71E-01	8.95E-01	-	-
1393681_at	Tessp5	testis serine protease 5	408244	Rn.126315	BF390882	2.39	2.38	2.39	2.37	2.39	2.36	1.01	down	2.53E-01	8.95E-01	-	-
1374121_at	---	---	---	Rn.9	AI102735	2.44	2.44	2.46	2.44	2.46	2.41	1.01	down	4.43E-01	8.95E-01	-	-
1372230_at	Tmem147	transmembrane protein 147	292792	Rn.66215	AI105430	8.26	7.45	7.97	7.49	7.89	8.35	1.01	up	9.72E-01	9.92E-01	-	-
1387065_at	Plcd4	phospholipase C, delta 4	140693	Rn.37434	NM_080688	2.39	2.35	2.51	2.38	2.46	2.37	1.01	down	8.33E-01	9.47E-01	-	-
1386742_at	---	---	---	---	BF544387	2.44	2.42	2.48	2.43	2.46	2.41	1.01	down	5.81E-01	8.95E-01	-	-
1385376_at	---	---	---	---	AA997046	2.73	2.75	2.79	2.75	2.77	2.71	1.01	down	6.72E-01	9.01E-01	-	-
1393505_x_at	Fam63b	family with sequence similarity 63, member B	363089	Rn.15746	AI045965	4.02	4.11	5.20	4.74	4.85	3.78	1.01	up	9.81E-01	9.94E-01	-	-
1387389_at	Ramp3	receptor (G protein-coupled) activity modifying protein 3	56820	Rn.48672	NM_020100	2.36	2.36	2.37	2.36	2.36	2.33	1.01	down	3.25E-01	8.95E-01	-	-
1397791_at	---	---	---	Rn.160335	BF398985	2.42	2.40	2.43	2.41	2.42	2.39	1.01	down	3.85E-01	8.95E-01	-	-
1387761_at	Prp15	proline-rich protein 15	24687	Rn.9841	NM_012632	2.36	2.37	2.38	2.36	2.37	2.35	1.01	down	1.76E-01	8.95E-01	-	-
1395882_at	---	---	---	Rn.206437	AW527138	2.51	2.46	2.58	2.50	2.55	2.45	1.01	down	7.86E-01	9.31E-01	-	-
1368572_a_at	Grin1	glutamate receptor, ionotropic, N-methyl D-aspartate 1	24408	Rn.9840	NM_017010	2.33	2.32	2.38	2.33	2.42	2.32	1.01	up	7.45E-01	9.17E-01	-	-
1371260_at	/// Mcpt2 ///	mast cell protease 1-like 3 /// mast cell protease 1-like 4 /// mast cell protease	29266 /// 408209	Rn.9443	AA957923	2.36	2.38	2.37	2.35	2.37	2.34	1.01	down	2.27E-01	8.95E-01	-	-
1396234_at	Ebf3	early B-cell factor 3	361668	Rn.64435	AI136886	2.39	2.37	2.41	2.39	2.44	2.38	1.01	up	6.13E-01	8.95E-01	-	-
1374132_at	---	---	---	Rn.24195	BI294788	2.46	2.44	2.48	2.45	2.47	2.42	1.01	down	5.42E-01	8.95E-01	-	-
1382600_at	---	---	---	Rn.165169	AA956022	2.42	2.40	2.42	2.41	2.42	2.38	1.01	down	4.11E-01	8.95E-01	-	-
1393984_at	---	---	---	Rn.99062	BF521686	2.51	2.47	2.50	2.47	2.51	2.47	1.01	down	5.23E-01	8.95E-01	-	-
1390951_at	---	---	---	Rn.9566	BE107735	3.89	3.90	3.90	3.89	3.90	3.87	1.01	down	3.05E-01	8.95E-01	-	-
1375667_at	Ccdc102a	coiled-coil domain containing 102A	361363	Rn.41567	AI710579	2.26	2.25	2.29	2.25	2.26	2.25	1.01	down	3.89E-01	8.95E-01	-	-
1377256_at	---	---	---	Rn.146881	BG380135	2.39	2.36	2.38	2.36	2.38	2.35	1.01	down	3.72E-01	8.95E-01	-	-
1397990_at	---	---	---	Rn.51549	BE108616	2.35	2.34	2.39	2.35	2.36	2.34	1.01	down	4.39E-01	8.95E-01	-	-
1392558_at	Ppp2r5e	protein phosphatase 2, regulatory subunit B', epsilon isoform	299147	Rn.24394	AI101600	2.59	2.59	2.60	2.64	2.60	2.59	1.01	up	4.93E-01	8.95E-01	-	-
1381965_at	---	---	---	Rn.38431	AI136271	2.51	2.49	2.53	2.49	2.52	2.47	1.01	down	5.51E-01	8.95E-01	-	-
1384229_at	Gnal	guanine nucleotide binding protein, alpha stimulating, olfactory type	24611	---	AI576080	2.47	2.43	2.46	2.44	2.54	2.42	1.01	up	7.65E-01	9.23E-01	-	-
1398120_at	---	---	---	Rn.148463	AW531770	2.44	2.42	2.46	2.45	2.44	2.39	1.01	down	5.93E-01	8.95E-01	-	-
1397456_at	RGD1560620	similar to hypothetical protein	291940	Rn.29121	BI293930	2.36	2.35	2.37	2.40	2.37	2.35	1.01	up	4.44E-01	8.95E-01	-	-
1368593_at	Cd1d1	CD1d1 molecule	25109	Rn.11120	NM_017079	4.51	5.16	4.64	3.04	6.20	5.12	1.01	up	9.90E-01	9.97E-01	-	-
1398178_at	---	---	---	Rn.132174	BF404392	2.41	2.40	2.42	2.40	2.49	2.38	1.01	up	7.27E-01	9.13E-01	-	-
1387712_at	Hes3	hairy and enhancer of split 3 (Drosophila)	64628	Rn.48807	NM_022687	2.38	2.35	2.38	2.36	2.37	2.35	1.01	down	3.32E-01	8.95E-01	-	-
1387825_at	Ugt2b	UDP glycosyltransferase 2 family, polypeptide B	24862	Rn.2521	NM_031533	2.50	2.45	2.50	2.47	2.49	2.46	1.01	down	5.58E-01	8.95E-01	-	-
1378663_at	---	---	---	---	BF401737	2.46	2.44	2.49	2.45	2.48	2.43	1.01	down	5.05E-01	8.95E-01	-	-
1387936_at	Sult2a2	sulfotransferase family 2A, dehydroepiandrosterone (DHEA)-preferring, memt	361510	---	D14989	2.69	2.67	2.72	2.69	2.71	2.64	1.01	down	6.50E-01	8.96E-01	-	-
1395528_at	---	---	---	Rn.49063	BE100564	2.42	2.41	2.45	2.41	2.44	2.40	1.01	down	5.10E-01	8.95E-01	-	-
1369305_at	Rab3il1	RAB3A interacting protein (rabin3)-like 1	171452	Rn.162492	NM_134411	2.36	2.35	2.39	2.35	2.37	2.34	1.01	down	4.31E-01	8.95E-01	-	-
1383394_at	---	---	---	Rn.216613	BG372099	2.39	2.38	2.42	2.38	2.39	2.37	1.01	down	3.24E-01	8.95E-01	-	-
1395286_at	---	---	---	---	BF398465	2.61	2.59	2.63	2.60	2.66	2.54	1.01	down	7.58E-01	9.21E-01	-	-
1375758_at	---	---	---	Rn.210800	BF404935	2.47	2.46	2.50	2.46	2.50	2.43	1.01	down	6.20E-01	8.95E-01	-	-
1385584_at	---	---	---	Rn.146296	AI111406	2.41	2.39	2.44	2.40	2.43	2.38	1.01	down	5.50E-01	8.95E-01	-	-
1376528_at	Med16	mediator complex subunit 16	299607	Rn.144449	BI296471	2.47	2.46	2.48	2.46	2.53	2.46	1.01	up	6.39E-01	8.95E-01	-	-
1378861_at	---	---	---	Rn.46219	BE105498	2.44	2.42	2.46	2.43	2.45	2.41	1.01	down	5.16E-01	8.95E-01	-	-
1398243_at	Csrp3	cysteine and glycine-rich protein 3	117505	Rn.11345	NM_057144	2.33	2.32	2.34	2.37	2.34	2.33	1.01	up	4.25E-01	8.95E-01	-	-
1381781_at	---	---	---	Rn.209199	BF386770	2.38	2.36	2.41	2.36	2.39	2.35	1.01	down	5.20E-01	8.95E-01	-	-
1375082_at	---	---	---	---	BF410005	2.37	2.36	2.39	2.37	2.38	2.34	1.01	down	4.51E-01	8.95E-01	-	-
1371364_a_at	Andpro	androgen regulated 20 kDa protein	25030	Rn.9977	BI285417	2.42	2.41	2.44	2.41	2.43	2.39	1.01	down	4.12E-01	8.95E-01	-	-
1379887_at	RGD1304792	similar to chromosome 2 open reading frame 3; transcription factor 9 (binds G	312474	Rn.38790	BI290897	2.54	2.45	2.55	2.44	2.51	2.62	1.01	up	8.52E-01	9.54E-01	-	-
1388541_at	---	---	---	Rn.12649	BE116383	6.77	6.71	6.52	6.45	6.81	6.78	1.01	up	9.31E-01	9.81E-01	-	-
1378665_at	---	---	---	Rn.208937	BF415436	2.53	2.51	2.55	2.51	2.54	2.50	1.01	down	4.88E-01	8.95E-01	-	-
1384952_at	---	---	---	Rn.33254	AI028968	2.56	2.54	2.63	2.55	2.62	2.51	1.01	down	7.78E-01	9.28E-01	-	-
1387895_s_at	Cdc20	cell division cycle 20 homolog (S. cerevisiae)	64515	Rn.9282	U05341	2.40	2.39	2.41	2.39	2.39	2.38	1.01	down	1.98E-01	8.95E-01	-	-
1370980_at	Sftpb	surfactant protein B	192155	Rn.1952	X14778	2.37	2.34	2.36	2.35	2.35	2.34	1.01	down	2.43E-01	8.95E-01	-	-
1374985_at	---	---	---	Rn.207326	BF399485	2.44	2.42	2.44	2.43	2.44	2.40	1.01	down	3.11E-01	8.95E-01	-	-
1389822_at	Stard7	StAR-related lipid transfer (START) domain containing 7	296128	Rn.20506	AI176601	2.18	2.18	2.19	2.18	2.23	2.18	1.01	up	4.79E-01	8.95E-01	-	-
1384807_at	---	---	---	Rn.2209	AW530736	2.41	2.40	2.43	2.40	2.42	2.38	1.01	down	3.60E-01	8.95E-01	-	-
1398077_at	---	---	---	Rn.208916	BF416304	2.33	2.32	2.37	2.32	2.34	2.32	1.01	down	4.50E-01	8.95E-01	-	-
1372896_at	---	---	---	Rn.16961	BM390440	2.41	2.41	2.43	2.47	2.42	2.40	1.01	up	6.04E-01	8.95E-01	-	-
1395692_at	---	---	---	---	AW921106	2.38	2.37	2.40	2.37	2.39	2.35	1.01	down	4.45E-01	8.95E-01	-	-
1397720_at	---	---	---	---	BF286268	2.52	2.50	2.57	2.52	2.55	2.48	1.01	down	7.00E-01	9.07E-01	-	-
1382990_at	---	---	---	Rn.204274	AI236245	2.72	2.71	2.74	2.71	2.75	2.68	1.01	down	6.22E-01	8.95E-01	-	-
1372702_at	PRP-2	proline-rich protein	287750	Rn.198334	BI284972	2.46	2.43	2.49	2.44	2.47	2.42	1.01	down	5.96E-01	8.95E-01	-	-
1376911_at	---	---	---	Rn.45827	BM386385	2.40	2.41	2.40	2.39	2.47	2.38	1.01	up	6.84E-01	9.03E-01	-	-
1389776_at	---	---	---	Rn.23584	BE105589	4.99	4.75	4.52	4.51	5.00	4.77	1.01	up	9.51E-01	9.86E-01	-	-
1374616_at	Pdgfrl	platelet-derived growth factor receptor-like	290771	Rn.217523	BM384311	2.34	2.32	2.34	2.32	2.33	2.31	1.01	down	2.00E-01	8.95E-01	-	-
1376639_at	Rnf126	ring finger protein 126	314613	Rn.143411	AW252111	6.49	6.48	6.50	6.56	6.91	6.05	1.01	up	9.62E-01	9.89E-01	-	-
1396430_at	---	---	---	Rn.61588	BF410086	2.52	2.50	2.58	2.51	2.61	2.52	1.01	up	7.73E-01	9.28E-01	-	-
1373604_at	LOC680199	hypothetical protein LOC680199	680199	Rn.40201	BI288870	2.41	2.39	2.44	2.39	2.43	2.38	1.01	down	5.56E-01	8.95E-01	-	-
1396717_at	---	---	---	Rn.211460	BF413539	2.57	2.52	2.57	2.53	2.59	2.50	1.01	down	7.06E-01	9.08E-01	-	-
1381533_at	Rnd1	Rho family GTPase 1	362993	Rn.198250	AI144754	2.50	2.47	2.50	2.48	2.49	2.46	1.01	down	2.83E-01	8.95E-01	-	-
1391596_at	---	---	---	Rn.15765	AI040603	2.39	2.41	2.39	2.39	2.39	2.37	1.01	down	1.95E-01	8.95E-01	-	-
1397688_at	---	---	---	---	BG667330	2.49	2.47	2.49	2.48	2.54	2.47	1.01	up	5.86E-01	8.95E-01	-	-
1393071_at	Tulp1	tubby like protein 1	309900	Rn.254	BG372018	2.42	2.40	2.44	2.41	2.42	2.39	1.01	down	4.43E-01	8.95E-01	-	-
1381658_at	---	---	---	---	BF405906	2.34	2.30	2.33	2.30	2.33	2.29	1.01	down	5.22E-01	8.95E-01	-	-
1396327_at	Cyp2j10	cytochrome P450, family 2, subfamily j, polypeptide 10	313373	Rn.34638	BG374493	2.51	2.50	2.54	2.50	2.52	2.49	1.01	down	4.33E-01	8.95E-01	-	-
1397656_at	---	---	---	Rn.172690	BF399269	2.47	2.45	2.49	2.46	2.49	2.43	1.01	down	5.88E-01	8.95E-01	-	-
1368127_at	Neu2	sialidase 2 (cytosolic sialidase)	29204	Rn.9731	NM_017130	2.27	2.27	2.28	2.27	2.28	2.31	1.01	up	3.99E-01	8.95E-01	-	-
1393440_at	---	---	---	Rn.149046	AI071835	2.44	2.43	2.46	2.44	2.45	2.40	1.01	down	5.62E-01	8.95E-01	-	-
1392556_at	Shroom3	shroom family member 3	305230	Rn.15243	BF410961	2.39	2.38	2.41	2.38	2.40	2.37	1.01	down	4.05E-01	8.95E-01	-	-
1377715_at	---	---	---	Rn.19529	BI303075	2.35	2.32	2.34	2.32	2.33	2.31	1.01	down	2.64E-01	8.95E-01	-	-
1367749_at	Lum	lumican	81682	Rn.3087	NM_031050	2.40	2.38	2.41	2.38	2.40	2.37	1.01	down	4.21E-01	8.95E-01	-	-
1381210_at	---	---	---	Rn.43708	AI639521	2.55	2.53	2.60	2.55	2.57	2.52	1.01	down	6.36E-01	8.95E-01	-	-
1385693_at	---	---	---	---	BI295028	2.43	2.41	2.44	2.45	2.45	2.43	1.01	up	3.30E-01	8.95E-01	-	-
1373342_at	Igf3	IGF-like family member 3	361516	Rn.17980	AI013253	2.56	2.52	2.58	2.54	2.60	2.50	1.01	down	7.31E-01	9.14E-01	-	-
1368098_a_at	Snrpn	small nuclear ribonucleoprotein polypeptide N	81781	Rn.11169	M29294	2.37	2.58	2.79	2.37	2.60	2.73	1.01	down	9.42E-01	9.84E-01	-	-
1394297_at	Hoxd1	homeo box D1	288151	Rn.47291	BG670107	2.41	2.40	2.44	2.41	2.43	2.39	1.01	down	5.06E-01	8.95E-01	-	-
1376399_at	---	---	---	---	BI296449	2.40	2.38	2.40	2.39	2.39	2.36	1.01	down	3.62E-01	8.95E-01	-	-
1388373_at	Adipor1	adiponectin receptor 1	289036	Rn.104556	BI289063	8.18	8.42	8.62	8.33	8.19	8.66	1.01	down	9.50E-01	9.85E-01	-	-
1397695_at	---	---	---	Rn.209152	BF386452	2.46	2.44	2.49	2.45	2.48	2.42	1.01	down	5.93E-01	8.95E-01	-	-
1377057_at	---	---	---	Rn.210146	BF409786	2.43	2.42	2.43	2.42	2.49	2.40	1.01	up	6.49E-01	8.96E-01	-	-
1395609_at	---	---	---	---	BF543078	2.54	2.48	2.53	2.49	2.53	2.48	1.01	down	6.29E-01	8.95E-01	-	-
1375885_at	Mtmr1	myotubularin related protein 1	317296	Rn.18311	AA925482	2.43	2.42	2.44	2.42	2.37	2.53	1.01	up	8.04E-01	9.37E-01	-	-
1393751_at	Fabp12	Fatty acid binding protein 12	499570	Rn.23613	AA859029	2

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicats)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1395953_at	---	---	---	Rn.8838	AA955517	2.26	2.26	2.30	2.25	2.27	2.26	1.01	down	4.11E-01	8.95E-01	-	-
1390320_at	---	---	---	---	BF415486	2.36	2.35	2.38	2.35	2.37	2.34	1.01	down	3.77E-01	8.95E-01	-	-
1371477_at	---	---	---	Rn.18132	BG380735	5.66	6.48	5.41	5.59	5.86	6.07	1.01	down	9.74E-01	9.92E-01	-	-
1385125_at	Myocd	transcription factor myocardin	246297	Rn.163103	BF397140	2.43	2.42	2.45	2.42	2.44	2.41	1.01	down	4.46E-01	8.95E-01	-	-
1396585_at	---	---	---	---	BF392430	2.40	2.40	2.42	2.40	2.41	2.38	1.01	down	3.29E-01	8.95E-01	-	-
1375384_at	---	---	---	---	AI715114	2.87	2.82	2.86	2.84	2.84	2.82	1.01	down	4.75E-01	8.95E-01	-	-
1392844_at	---	---	---	Rn.171646	BE119432	2.43	2.42	2.45	2.42	2.44	2.40	1.01	down	4.12E-01	8.95E-01	-	-
1385425_at	Vwa3a	von Willebrand factor A domain containing 3A	293449	Rn.127486	BI293713	2.40	2.40	2.41	2.40	2.40	2.37	1.01	down	3.08E-01	8.95E-01	-	-
1372359_at	Dusp26	dual specificity phosphatase 26 (putative)	306527	Rn.22231	BI291423	2.42	2.41	2.44	2.41	2.43	2.40	1.01	down	4.13E-01	8.95E-01	-	-
1388286_a_at	Cdc34	cell division cycle 34 homolog (S. cerevisiae)	299502	Rn.2427	L38482	6.65	6.43	5.07	5.74	5.72	6.73	1.01	up	9.84E-01	9.95E-01	-	-
1378640_at	Uhrf1	ubiquitin-like with PHD and ring finger domains 1	316129	Rn.54318	BE098732	2.45	2.43	2.47	2.44	2.46	2.41	1.01	down	5.49E-01	8.95E-01	-	-
1394941_at	---	---	---	Rn.148118	AW533289	2.44	2.41	2.46	2.43	2.45	2.38	1.01	down	6.45E-01	8.95E-01	-	-
1384074_at	---	---	---	---	AW920694	2.47	2.46	2.47	2.45	2.49	2.42	1.01	down	6.09E-01	8.95E-01	-	-
1385717_at	Gdap1	ganglioside-induced differentiation-associated-protein 1	312890	Rn.45830	AW524331	2.45	2.44	2.49	2.44	2.48	2.42	1.01	down	6.41E-01	8.95E-01	-	-
1393392_at	---	---	---	Rn.146617	BE120352	2.43	2.41	2.46	2.42	2.45	2.39	1.01	down	6.07E-01	8.95E-01	-	-
1370791_at	RatNP-3b	defensin RatNP-3 precursor	498659	Rn.114810	U16683	2.45	2.44	2.48	2.45	2.45	2.43	1.01	down	3.85E-01	8.95E-01	-	-
1385161_x_at	---	---	---	---	C06786	2.51	2.51	2.51	2.55	2.51	2.50	1.01	up	4.55E-01	8.95E-01	-	-
1398479_at	Ryr3	ryanodine receptor 3	170546	Rn.20282	AI072862	2.43	2.42	2.44	2.42	2.43	2.39	1.01	down	3.96E-01	8.95E-01	-	-
1380505_at	---	---	---	Rn.44936	BF563556	2.42	2.38	2.44	2.41	2.47	2.39	1.01	up	7.09E-01	9.09E-01	-	-
1393819_x_at	Gas2l1	growth arrest-specific 2 like 1	360973	Rn.22189	BG371690	2.46	2.45	2.49	2.45	2.46	2.44	1.01	down	3.70E-01	8.95E-01	-	-
1394861_at	---	---	---	Rn.210087	BF393712	2.41	2.39	2.42	2.39	2.40	2.39	1.01	down	3.25E-01	8.95E-01	-	-
1388014_at	Obp1f	odorant binding protein 1 f	192267	Rn.9718	J03093	2.43	2.49	2.86	2.42	2.46	2.86	1.01	down	9.52E-01	9.86E-01	-	-
1375094_at	Cd200	Cd200 molecule	24560	Rn.7085	BF406208	2.41	2.38	2.49	2.40	2.47	2.39	1.01	down	7.79E-01	9.28E-01	-	-
1380625_at	---	---	---	Rn.208047	BE109276	2.47	2.47	2.48	2.46	2.47	2.52	1.01	up	5.62E-01	8.95E-01	-	-
1395975_at	---	---	---	---	AI235040	2.52	2.49	2.57	2.50	2.56	2.48	1.01	down	7.49E-01	9.19E-01	-	-
1390256_at	---	---	---	---	AW530389	2.38	2.38	2.40	2.37	2.39	2.43	1.01	up	5.65E-01	8.95E-01	-	-
1372952_at	LOC292069	similar to RIKEN cDNA 2310061F22	292069	Rn.20640	BI291286	2.33	2.37	2.39	2.37	2.38	2.37	1.01	up	5.22E-01	8.95E-01	-	-
1367785_at	Cnn1	calponin 1, basic, smooth muscle	65204	Rn.31788	NM_031747	2.41	2.41	2.44	2.41	2.42	2.39	1.01	down	4.13E-01	8.95E-01	-	-
1398223_at	---	---	---	---	BE107923	2.49	2.41	2.43	2.42	2.47	2.40	1.01	down	7.09E-01	9.09E-01	-	-
1372253_at	Cnot8	CCR4-NOT transcription complex, subunit 8	363603	Rn.203142	AI408162	2.49	2.53	2.49	2.42	2.50	2.63	1.01	up	8.48E-01	9.53E-01	-	-
1396693_at	---	---	---	Rn.59512	BF391854	2.40	2.40	2.43	2.39	2.42	2.38	1.01	down	4.42E-01	8.95E-01	-	-
1382747_at	Rttn	rotatin	291377	Rn.139347	AI410331	2.56	2.55	2.56	2.55	2.56	2.51	1.01	down	4.32E-01	8.95E-01	-	-
1389449_at	Fitm1	fat storage-inducing transmembrane protein 1	290223	Rn.22380	AI171994	2.31	2.30	2.34	2.30	2.32	2.30	1.01	down	4.24E-01	8.95E-01	-	-
1394735_at	Catsper2	cation channel, sperm associated 2	366174	Rn.198648	BF409552	2.43	2.42	2.45	2.42	2.44	2.40	1.01	down	4.51E-01	8.95E-01	-	-
1398302_at	Prl7a3	prolactin family 7, subfamily a, member 3	64361	Rn.1615	AI013501	2.40	2.39	2.41	2.40	2.47	2.38	1.01	up	6.80E-01	9.03E-01	-	-
1380173_at	---	---	---	Rn.169766	BE106938	2.45	2.43	2.52	2.44	2.51	2.42	1.01	down	7.60E-01	9.22E-01	-	-
1395281_at	---	---	---	Rn.207988	BE108512	2.41	2.39	2.44	2.39	2.42	2.38	1.01	down	5.73E-01	8.95E-01	-	-
1381105_at	---	---	---	Rn.204357	AW529713	2.50	2.47	2.55	2.48	2.54	2.46	1.01	down	7.32E-01	9.14E-01	-	-
1375067_at	---	---	---	Rn.167869	AI555354	5.17	4.36	4.70	4.97	4.41	4.89	1.01	up	9.69E-01	9.91E-01	-	-
1378956_at	---	---	---	Rn.169275	BF405977	2.41	2.40	2.43	2.40	2.41	2.38	1.01	down	3.83E-01	8.95E-01	-	-
1382525_at	Lypd6b	LY6/PLAUR domain containing 6B	362133	Rn.220607	BI293269	2.45	2.44	2.46	2.44	2.45	2.41	1.01	down	4.32E-01	8.95E-01	-	-
1393586_at	Nope	neighbor of Punc E11	363081	Rn.164673	AI101752	2.44	2.42	2.46	2.43	2.44	2.41	1.01	down	4.92E-01	8.95E-01	-	-
1378914_a_at	LOC308990	hypothetical protein LOC308990	308990	Rn.98391	AI059468	2.67	2.71	2.69	2.66	2.73	2.64	1.01	down	6.98E-01	9.07E-01	-	-
1394002_at	---	---	---	---	BM390752	2.44	2.41	2.45	2.42	2.46	2.39	1.01	down	6.48E-01	8.95E-01	-	-
1385317_s_at	Zfp112	zinc finger protein 112	308420	Rn.50186	BF392357	2.60	2.55	2.69	2.57	2.77	2.53	1.01	up	8.93E-01	9.67E-01	-	-
1398050_at	---	---	---	Rn.76761	BI300450	2.45	2.43	2.47	2.43	2.46	2.41	1.01	down	5.44E-01	8.95E-01	-	-
1373998_at	---	---	---	Rn.91446	BM389853	2.30	2.29	2.30	2.32	2.31	2.29	1.01	up	2.16E-01	8.95E-01	-	-
1394684_at	---	---	---	Rn.164657	AA908068	2.40	2.40	2.42	2.40	2.41	2.37	1.01	down	3.22E-01	8.95E-01	-	-
1369106_at	Tcea2	transcription elongation factor A (SII), 2	29575	Rn.78891	NM_057098	2.39	2.39	2.39	2.42	2.40	2.38	1.01	up	3.54E-01	8.95E-01	-	-
1391610_at	---	---	---	Rn.147327	AI555319	2.42	2.41	2.42	2.41	2.45	2.36	1.01	down	6.55E-01	8.97E-01	-	-
1377539_at	---	---	---	Rn.202818	BF404370	2.63	2.56	2.63	2.59	2.65	2.55	1.01	down	7.60E-01	9.22E-01	-	-
1378779_at	---	---	---	Rn.154787	BF386454	2.46	2.43	2.48	2.44	2.47	2.42	1.01	down	5.88E-01	8.95E-01	-	-
1394540_at	---	---	---	---	BF387197	2.37	2.36	2.37	2.36	2.37	2.34	1.01	down	2.31E-01	8.95E-01	-	-
1370510_a_at	Arntl	aryl hydrocarbon receptor nuclear translocator-like	29657	Rn.14532	AB012600	2.33	2.32	2.33	2.32	2.33	2.30	1.01	down	3.03E-01	8.95E-01	-	-
1395946_at	Rapsn	receptor-associated protein of the synapse	362161	Rn.171187	AW254429	2.42	2.41	2.45	2.41	2.42	2.40	1.01	down	4.31E-01	8.95E-01	-	-
1392930_at	Armc1	armadillo repeat containing 1	294948	Rn.17507	BI276980	6.08	5.99	6.34	5.75	6.23	6.45	1.01	up	9.60E-01	9.89E-01	-	-
1393313_at	---	---	---	Rn.204191	BE106204	2.26	2.25	2.29	2.25	2.26	2.25	1.01	down	4.48E-01	8.95E-01	-	-
1390438_at	---	---	---	Rn.216738	AW526136	2.64	2.64	2.65	2.64	2.69	2.63	1.01	up	5.80E-01	8.95E-01	-	-
1390834_at	Abcc10	ATP-binding cassette, sub-family C (CFTR/MRP), member 10	316231	Rn.39364	BM390369	2.38	2.38	2.43	2.38	2.42	2.36	1.01	down	6.57E-01	8.98E-01	-	-
1396731_at	RGD1310414	Similar to hypothetical protein FLJ23263	290811	Rn.12987	BE099580	2.51	2.47	2.52	2.47	2.53	2.47	1.01	down	6.51E-01	8.97E-01	-	-
1377804_at	Prtg	protogenin homolog (Gallus gallus)	315806	Rn.12313	AI030809	2.49	2.46	2.54	2.48	2.52	2.44	1.01	down	7.15E-01	9.10E-01	-	-
1380659_at	---	---	---	Rn.120334	BM386141	2.54	2.52	2.54	2.53	2.53	2.51	1.01	down	2.02E-01	8.95E-01	-	-
1380742_at	---	---	---	Rn.43780	AI406619	2.39	2.38	2.42	2.38	2.40	2.37	1.01	down	4.22E-01	8.95E-01	-	-
1372685_at	Cdkn3	cyclin-dependent kinase inhibitor 3	289993	Rn.107220	BE113362	2.39	2.46	2.41	2.38	2.40	2.45	1.01	down	7.18E-01	9.11E-01	-	-
1385283_at	Pex5	peroxisomal biogenesis factor 5	312703	Rn.14316	BE097537	2.49	2.49	2.50	2.49	2.53	2.48	1.01	up	4.31E-01	8.95E-01	-	-
1375750_at	---	---	---	Rn.145608	BE099067	2.50	2.50	2.52	2.50	2.51	2.48	1.01	down	2.75E-01	8.95E-01	-	-
1378845_at	Prkab2	Protein kinase, AMP-activated, beta 2 non-catalytic subunit	64562	Rn.207202	BF418781	2.36	2.35	2.39	2.40	2.38	2.36	1.01	up	4.85E-01	8.95E-01	-	-
1375584_at	---	---	---	Rn.204868	BG376873	2.50	2.48	2.49	2.48	2.49	2.46	1.01	down	2.47E-01	8.95E-01	-	-
1386370_at	---	---	---	Rn.125742	AI639519	2.51	2.48	2.54	2.50	2.53	2.46	1.01	down	6.89E-01	9.04E-01	-	-
1394463_at	---	---	---	Rn.141001	BE097727	2.44	2.91	2.46	2.92	2.46	2.39	1.01	down	9.60E-01	9.89E-01	-	-
1374240_at	---	---	---	Rn.208336	BF406127	2.40	2.39	2.41	2.39	2.40	2.36	1.01	down	4.00E-01	8.95E-01	-	-
1377360_at	Mark4	MAP/microtubule affinity-regulating kinase 4	680407	Rn.98278	AI599729	2.32	2.34	2.33	2.32	2.33	2.31	1.01	down	1.95E-01	8.95E-01	-	-
1382563_at	RGD1560818	similar to hypothetical protein FLJ38944	499112	Rn.52077	AI071510	2.49	2.48	2.50	2.47	2.49	2.47	1.01	down	2.93E-01	8.95E-01	-	-
1378218_at	Tcfcp2	transcription factor CP2	315309	Rn.202290	AW527419	3.17	2.79	2.57	2.80	2.78	2.98	1.01	up	9.51E-01	9.86E-01	-	-
1387518_at	Crisp2	cysteine-rich secretory protein 2	360445	Rn.32098	NM_031240	2.35	2.34	2.38	2.34	2.36	2.33	1.01	down	4.22E-01	8.95E-01	-	-
1395539_at	---	---	---	Rn.199396	AW523902	2.32	2.31	2.33	2.32	2.33	2.35	1.01	up	2.85E-01	8.95E-01	-	-
1398087_at	---	---	---	---	BE110617	2.40	2.39	2.43	2.40	2.41	2.38	1.01	down	4.64E-01	8.95E-01	-	-
1374971_at	---	---	---	Rn.16576	AA818954	2.40	2.64	2.40	2.70	2.40	2.39	1.01	up	9.30E-01	9.81E-01	-	-
1368798_at	Abo	ABO blood group (transferase A, alpha 1-3-N-acetylgalactosaminyltransferase	65270	Rn.112591	NM_023094	2.83	2.77	2.84	2.82	2.97	2.68	1.01	up	8.93E-01	9.67E-01	-	-
1374039_at	Car14	carbonic anhydrase 14	791259	Rn.201792	BI289989	2.47	2.43	2.47	2.44	2.45	2.44	1.01	down	4.61E-01	8.95E-01	-	-
1392045_at	Tmem22	transmembrane protein 22	315957	Rn.51858	BE110277	2.42	2.41	2.43	2.42	2.43	2.37	1.01	down	5.56E-01	8.95E-01	-	-
1386989_at	S1pr2	sphingosine-1-phosphate receptor 2	29415	Rn.2491	NM_017192	2.47	2.45	2.48	2.46	2.48	2.43	1.01	down	5.25E-01	8.95E-01	-	-
1380322_at	---	---	---	Rn.20182	AI502574	2.34	2.32	2.34	2.36	2.34	2.33	1.01	up	3.52E-01	8.95E-01	-	-
1378574_at	LOC100125377	hypothetical LOC100125377	100125377	Rn.136993	AA818104	2.51	2.48	2.52	2.49	2.51	2.48	1.01	down	4.73E-01	8.95E-01	-	-
1397801_at	---	---	---	---	BF563970	2.57	2.56	2.59	2.56	2.57	2.55	1.01	down	3.28E-01	8.95E-01	-	-
1384822_at	---	---	---	Rn.45231	AW521721	2.45	2.44	2.47	2.44	2.46	2.42	1.01	down	4.84E-01	8.95E-01	-	-
1390260_at	Cdc2l5	Cell division cycle 2-like 5 (cholinesterase-related cell division controller)	306998	Rn.23420	AI177766	2.39	2.38	2.42	2.39	2.39	2.38	1.01	down	3.78E-01	8.95E-01	-	-
1396316_at	---	---	---	Rn.147849	AW527987	2.44	2.42	2.46	2.43	2.45	2.40	1.01	down	5.07E-01	8.95E-01	-	-
1380088_at	---	---	---	Rn.28360	AW530021	2.32	2.32	2.34	2.32	2.32	2.30	1.01	down	2.84E-01	8.95E-01	-	-
1371694_at	Dpysl2	dihydropyrimidinase-like 2	25416	Rn.2889	AI317805	5.49	4.64	4.87	5.53	5.38	4.13	1.01	up	9.82E-01	9.95E-01	-	-
1398709_at	---	---	---	---	BI291207	2.41	2.40	2.43	2.41	2.42	2.38	1.01	down	4.77E-01	8.95E-01	-	-
1368415_at	Myh3	myosin, heavy chain 3, skeletal muscle, embryonic	24583	Rn.98847	NM_012604	2.39	2.39	2.42	2.39	2.40	2.38	1.01	down	3.95E-01	8.95E-01	-	-
1391745_at	---	---	---	Rn.203509	BI287873	2.55	2.50	2.52	2.51	2.52	2.51	1.01	down	4.42E-01	8.95E-01	-	-
1368338_at	Cd52	CD52 antigen	117054	Rn.34155	NM_053983	2.54	2.50	2.52	2.50	2.53	2.49	1.01	down	4.68E-01	8.95E-01	-	-
1384310_at	---	---	---	Rn.23945	BM383081	4.09	3.53	3.52	3.50	3.84	3.76	1.01	down	9.57E-01	9.88E-01	-	-
1380413_at	---	---	---	Rn.19411	BF564071	2.44	2.43	2.46	2.43	2.45	2.41	1.01	down	4.39E-01	8.95E-01	-	-
1396780_at	---	---	---	Rn.60404	BF403974	2.52	2.50	2.54	2.51	2.53	2.48	1.01	down	5.60E-01	8.95E-01	-	-
1375031_at	---	---	---	---	AI171653	2.42	2.40	2.43	2.40	2.42	2.39	1.01	down	4.04E-01	8.95E-01	-	-
1398219_at	LOC690918	hypothetical protein LOC690918	690918	Rn.53377	BE109914	2.46	2.43	2.51	2.45	2.46	2.45	1.01	down	6.10E-01	8.95E-01	-	-
1379481_at	---	---	---	Rn.146208	BG378577	2.41	2.40	2.43	2.40	2.41	2.39	1.01	down	3.31E-01	8.95E-01	-	-
1379857_at	---	---	---	Rn.172489	AA943994	2.36	2.35	2.37	2.35	2.36	2.33	1.01	down	3.41E-01	8.95E-01	-	-
1398356_at	Cpsf5	cleavage and polyadenylation specific factor 5	291877	Rn.199052	BF420718	7.80	7.45	6.24	7.72	5.84	7.89	1.01	down	9.89E-01	9.96E-01	-	-
1370024_at	Fabp7	fatty acid binding protein 7, brain	80841	Rn.10014	NM_030832	2.49	2.48	2.50	2.48	2.49	2.46	1.01	down	3.16E-01	8.95E-01	-	-
1390716_at	---	---	---	Rn.23254	BE098148	2.83	2.75	2.80	2.89	2.84	2.61	1.01	down	8.98E-01	9.68E-01	-	-
1381064_at	---	---	---	Rn.133430	AI137604	2.59	2.55	2.67	2.57	2.65	2.55	1.01	down	8.10E-01	9.39E-01	-	-
1373977_at	Klf5c	Kruppel-like factor 5 (intestinal)	311024	Rn.50843	BE108253	2.38	2.37	2.41	2.37	2.39	2.36	1.01	down	4.53E-01	8.95E-01	-	-
1391072_at	Fcer2	Fc fragment of IgE, low affinity II, receptor for (CD23)	171075	Rn.10328	AI410068	2.34	2.32	2.35	2.34	2.39	2.33	1.01	up	5.75E-01	8.95E-01	-	-
1387637_a_at	Fgf14	fibroblast growth factor 14	63851	Rn.44476	NM_022223	2.37	2.36	2.38	2.37	2.43	2.35	1.01	up	6.33E-01	8.95E-01	-	-
1394068_x_at	Klf2	Kruppel-like factor 2 (lung)	306330	Rn.92653	BF288243	2.42	2.38	2.42	2.40	2.41	2.37	1.01	down	5.28E-01	8.95E-01	-	-
1384590_at	---	---	---	Rn.22064	AA957900	2.43	2.41	2.47	2.42	2.46	2.41	1.01	down	6.16E-01	8.95E-01	-	-
1371262_at	a /// Igha /// LOC6	gamma-2a immunoglobulin heavy chain /// immunoglobulin heavy chain, alph	87 /// 367586 /// 67	Rn.219258	AJ391299	2.44	2.42	2.47	2.41	2.56	2.40	1.01	up	8.34E-01	9.48E-01	-	-
1394952_at	Hapln2	Hyaluronan and proteoglycan link protein 2	64057	Rn.76545	BF399794	2.34	2.32	2.36	2.33	2.34	2.32	1.01	down	4.10E-01	8.95E-01	-	-
1390567_at	Thap11	THAP domain containing 11	307806	Rn.2823	AI712547	2.26	2.25	2.28	2.26	2.25	2.25	1.01	down	2.98E-01	8.95E-01	-	-
1382785_at	Kif1a	kinesin family member 1A	363288	---	BE105549	2.44	2.44	2.47	2.44	2.45	2.42	1.01	down	4.35E-01	8.95E-01	-	-
1385197_at	---	---	---	Rn.136397	BF388053	2.37	2.33	2.36	2.35	2.35	2.32	1.01	down	4.80E-01	8.95E-01	-	-
1373082_at	---	---	---	Rn.164219	AA893743	2.86	2.60	2.68	2.78	2.76	2.63	1.01	up	9.01E-01	9.69E-01	-	-
1380543_at	---	---	---	Rn.159864	BF564294	4.58	3.23	3.19	4.53	3.05	3.45	1.01	up	9.86E-01	9.96E-01	-	-
1384444_at	---	---	---	---	BF415780	2.48	2.46	2.50	2.46	2.49	2.45	1.01	down	5.53E-01	8.95E-01	-	-
1391403_at	---	---	---	Rn.207267	BF399795	2.46	2.45	2.49	2.46	2.48	2.44	1.01	down	5.24E-01	8.95E-01	-	-
1389997_at	Cd3e	CD3 molecule, epsilon polypeptide	315609	Rn.96221	AA945909	2.48	2.45	2.52	2.46	2.58	2.45	1.01	up	8.03E-01	9.37E-01	-	-
1380950_at	---	---	---	Rn.201618	AW525135	2.36	2.35	2.39	2.35	2.38	2.33	1.01	down	5.63E-01	8.95E-01	-	-
1378899_at	Slc35d3	solute carrier family 35, member D3	308717	Rn.110407	BE108523	2.44	2.42	2.46	2.43	2.45	2.41	1.01	down	5.02E-01	8.95E-01	-	-
1374352_at	Actc1	actin, alpha, cardiac muscle 1	29275	---	AI711147	2.39	2.38	2.40	2.37	2.40	2.36	1.01	down	3.97E-01	8.95E-01	-	-
1398117_at	---	---	---	Rn.169751	AW533235	2.46	2.44	2.48	2.47	2.43	2.43	1.01	down	5.22E-01	8.95E-01	-	-
1395823_at	LOC691653	hypothetical protein LOC691653	691653	Rn.56087	BF284646	2.46	2.45	2.47	2.45	2.46	2.43	1.01	down	3.79E-01	8.95E-01	-	-
1384789_at	Tekt4	tektin 4	302991	Rn.27474	AA998672	2.45	2.44	2.46	2.52	2.45	2.43	1.01	up	7.01E-01	9.07E-01	-	-
1397832_at	Cdk5rap2	CDK5 regulatory subunit associated protein 2	286919	Rn.13247	BF564964	2.53	2.53	2.55	2.51	2.67	2.47	1.01	up	8.54E-01	9.55E-01	-	-
1371291_at	Creb1	cAMP responsive element binding protein 1	81646	Rn.90061	X69029	2.44	2.42	2.47	2.43	2.45	2.41	1.01	down	5.60E-01	8.95E-01	-	-
1397968_at	---	---	---	Rn.210644	BF399686	2.42	2.41	2.42	2.41	2.42	2.38	1.01	down	4.18E-01	8.95E-01	-	-
1394655_at	---	---	---	Rn.148063	AI601993	2.47	2.45	2.50	2.46	2.49	2.44	1.01	down	5.95E-01	8.95E-01	-	-
1388971_s_at	Krtdap	keratinocyte differentiation associated protein	65186	Rn.202626	BI282568	2.48	2.46	2.48	2.47	2.48	2.45	1.01	down	3.48E-01	8.95E-01	-	-
1397926_at	---	---	---	Rn.171251	BE110684	2.45	2.44	2.47	2.42	2.47	2.44	1.01	down	4.97E-01	8.95E-01	-	-
1381331_at	Cmtm2a	CKLF-like MARVEL transmembrane domain containing 2A	307616	Rn.163394	AI638953	2.40	2.39	2.43	2.39	2.40	2.39	1.01	down	3.77E-01	8.95E-01	-	-
1374892_at	Sat2	spermidine/spermine N1-acetyltransferase family member 2	365547	Rn.23795	AI410221	7.39	7.51	7.36	7.65	7.15	7.50	1.01	up	9.42E-01	9.84E-01	-	-
1370757_at	Cacng3	calcium channel, voltage-dependent, gamma subunit 3	140724	Rn.212756	AF361340	2.39	2.37	2.44	2.38	2.40	2.38	1.01	down	6.11E-01	8.95E-01	-	-
1393883_at	---	---	---	Rn.148191	AI556852	2.41	2.40	2.43	2.40	2.44	2.36	1.01	down	6.69E-01	9.00E-01	-	-
1396977_at	---	---	---	Rn.146281	BE110832	2.36	2.36	2.37	2.35	2.36	2.34	1.01	down	2.56E-01	8.95E-01	-	-
1382319_at	Gpr68	G protein-coupled receptor 68	314386	Rn.16653	BM389005	2.29	2.29	2.30	2.33	2.29	2.28	1.01	up	4.43E-01	8.95E-01	-	-
1391942_at	---	---	---	Rn.200013	BF402576	2.38	2.36	2.40	2.37	2.39	2.35	1.01	down	5.02E-01	8.95E-01	-	-
1392230_at	Plekha1	Pleckstrin homology domain containing, family A (phosphoinositide binding sp	361659	Rn.17662	BI287470	2.63	2.61	2.64	2.68	2.65	2.58	1.01	up	7.08E-01	9.09E-01	-	-
1397608_at	---	---	---	Rn.207801	BE107197	2.36	2.35	2.38	2.35	2.36	2.33	1.01	down	4.10E-01	8.95E-01	-	-
1396859_at	Zfp423	zinc finger protein 423	94188	Rn.9981	AW529230	2.35	2.32	2.34	2.32	2.33	2.32	1.01	down	2.78E-01	8.95E-01	-	-
1378601_at	---	---	---	Rn.147647	AI413056	2.43	2.40	2.44	2.41	2.43	2.40	1.01	down	4.96E-01	8.95E-01	-	-
1376254_at	---	---	---	---	AI549339	2.25	2.23	2.30	2.26	2.26	2.22	1.01	down	6.35E-01	8.95E-01	-	-
1384988_at	Fbxo5	F-box protein 5	292263	Rn.81585	BM385403	2.44	2.42	2.46	2.43	2.44	2.41	1.01	down	4.83E-01	8.95E-01	-	-
1389371_at	---	---	---	Rn.199177	AI104077	4.87	5.38	5.02	5.09	5.01	5.14	1.01	down	9.43E-01	9.84E-01	-	-
1395772_at	---	---	---	---	BF290181	2.62	2.58	2.71	2.60	2

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1376407_a_at	Lsm7	LSM7 homolog, U6 small nuclear RNA associated (S. cerevisiae)	362829	Rn.25010	BI289882	5.95	6.05	6.13	6.04	6.15	5.96	1.01	up	8.82E-01	9.64E-01	-	-
1392459_x_at	---	---	---	Rn.38431	AI136271	2.45	2.43	2.48	2.44	2.47	2.42	1.01	down	5.73E-01	8.95E-01	-	-
1375615_at	Ntrk1	Neurotrophic tyrosine kinase, receptor, type 1	59109	Rn.39098	AI575310	2.63	2.62	2.64	2.63	2.68	2.62	1.01	up	5.97E-01	8.95E-01	-	-
1377630_at	Tspan13	tetraspanin 13	366602	Rn.24284	AI408602	2.57	2.52	2.56	2.56	2.57	2.56	1.01	up	4.95E-01	8.95E-01	-	-
1385130_at	Fezf2	Fez family zinc finger 2	305719	Rn.69050	BE107866	2.42	2.37	2.39	2.37	2.39	2.38	1.01	down	4.75E-01	8.95E-01	-	-
1397857_at	---	---	---	Rn.169115	AI547502	2.47	2.44	2.49	2.45	2.54	2.43	1.01	up	7.63E-01	9.23E-01	-	-
1397746_at	---	---	---	Rn.212168	BG371972	2.40	2.40	2.42	2.40	2.46	2.39	1.01	up	6.47E-01	8.95E-01	-	-
1384882_at	---	---	---	Rn.24395	AI229056	2.59	2.53	2.54	2.52	2.53	2.64	1.01	up	7.92E-01	9.33E-01	-	-
1377083_at	---	---	---	Rn.9108	AA998190	2.43	2.42	2.43	2.43	2.43	2.39	1.01	down	4.26E-01	8.95E-01	-	-
1369671_at	Otc	ornithine carbamoyltransferase	25611	Rn.2393	K03940	2.50	2.57	2.42	2.40	2.42	2.71	1.01	up	9.17E-01	9.75E-01	-	-
1378984_at	---	---	---	Rn.40940	AW254072	2.42	2.40	2.43	2.40	2.42	2.39	1.01	down	3.79E-01	8.95E-01	-	-
1380704_a_at	---	---	---	Rn.153607	AI412161	2.54	2.52	2.62	2.55	2.58	2.51	1.01	down	7.52E-01	9.20E-01	-	-
1369529_at	Csf3	colony stimulating factor 3 (granulocyte)	25610	Rn.53973	NM_017104	2.41	2.39	2.43	2.40	2.42	2.38	1.01	down	4.81E-01	8.95E-01	-	-
1385186_at	---	---	---	Rn.114418	BE110083	2.43	2.41	2.44	2.42	2.42	2.41	1.01	down	3.07E-01	8.95E-01	-	-
1386381_at	---	---	---	---	AI639491	2.60	2.55	2.65	2.59	2.62	2.55	1.01	down	7.47E-01	9.18E-01	-	-
1388011_a_at	Tgfb2	transforming growth factor, beta 2	81809	Rn.24539	AF135598	2.38	2.36	2.38	2.40	2.38	2.38	1.01	up	3.54E-01	8.95E-01	-	-
1381227_at	---	---	---	Rn.146246	BF416819	2.52	2.50	2.58	2.51	2.56	2.49	1.01	down	7.31E-01	9.14E-01	-	-
1393858_at	LOC689656	hypothetical protein LOC689656	689656	Rn.212646	BI294306	2.51	2.48	2.54	2.50	2.52	2.47	1.01	down	6.38E-01	8.95E-01	-	-
1369392_at	Akap4	A kinase (PRKA) anchor protein 4	79254	Rn.10777	NM_024402	2.38	2.38	2.42	2.38	2.39	2.37	1.01	down	4.33E-01	8.95E-01	-	-
1375330_at	---	---	---	Rn.212274	BI291390	2.31	2.30	2.33	2.30	2.31	2.29	1.01	down	3.83E-01	8.95E-01	-	-
1380671_at	---	---	---	Rn.28727	BF405089	2.56	2.60	2.58	2.56	2.61	2.54	1.01	down	6.63E-01	8.99E-01	-	-
1369075_a_at	Gmeb2	glucocorticoid modulatory element binding protein 2	83635	Rn.40949	NM_031803	2.39	2.37	2.42	2.38	2.41	2.35	1.01	down	6.30E-01	8.95E-01	-	-
1380014_at	---	---	---	---	AW524490	2.42	2.40	2.44	2.41	2.42	2.39	1.01	down	4.27E-01	8.95E-01	-	-
1397030_at	---	---	---	---	AI406451	2.40	2.38	2.41	2.45	2.40	2.38	1.01	up	6.32E-01	8.95E-01	-	-
1387236_at	Dctn4	dynactin 4	84428	Rn.23941	NM_053404	5.46	5.88	5.72	5.76	5.91	5.43	1.01	up	9.53E-01	9.86E-01	-	-
1380168_at	Etv4	ets variant 4	360635	Rn.195602	BE102969	2.44	2.43	2.47	2.43	2.46	2.41	1.01	down	5.66E-01	8.95E-01	-	-
1395293_at	Sulf2	Sulfatase 2	311642	Rn.4228	BF388802	2.38	2.36	2.37	2.36	2.37	2.35	1.01	down	2.89E-01	8.95E-01	-	-
1388493_at	Ecop	EGFR-coamplified and overexpressed protein	362374	Rn.154707	AI600030	2.85	2.84	2.89	2.85	2.86	2.84	1.01	down	4.31E-01	8.95E-01	-	-
1392295_a_at	---	---	---	Rn.18590	AI030771	2.33	2.31	2.34	2.31	2.33	2.30	1.01	down	3.56E-01	8.95E-01	-	-
1381327_a_at	Cr2	complement receptor 2	289395	Rn.23490	AI556056	2.52	2.48	2.56	2.50	2.57	2.46	1.01	down	7.75E-01	9.27E-01	-	-
1384887_at	---	---	---	Rn.136780	AI070185	8.22	8.43	8.31	8.35	8.42	8.22	1.01	up	8.94E-01	9.67E-01	-	-
1397319_at	---	---	---	Rn.211751	BF542311	2.58	2.57	2.64	2.58	2.64	2.55	1.01	down	7.43E-01	9.17E-01	-	-
1398207_at	---	---	---	Rn.210250	BF396438	2.49	2.47	2.54	2.48	2.52	2.47	1.01	down	6.69E-01	9.00E-01	-	-
1374311_at	Rnf207	ring finger protein 207	691246	Rn.155693	BG373273	2.45	2.43	2.47	2.43	2.46	2.41	1.01	down	5.33E-01	8.95E-01	-	-
1391855_at	LOC690085	Similar to B-cell CLL/lymphoma 7A	690085	Rn.201710	AW534002	5.30	5.45	5.41	5.42	5.45	5.32	1.01	up	8.58E-01	9.56E-01	-	-
1397159_at	---	---	---	Rn.208918	BF394208	2.38	2.37	2.40	2.38	2.44	2.36	1.01	up	6.67E-01	8.99E-01	-	-
1383326_a_at	Pdcd4	programmed cell death 4	64031	Rn.206228	AI576297	7.55	7.55	7.41	7.38	7.86	7.31	1.01	up	9.51E-01	9.86E-01	-	-
1376748_at	Arx	aristaless related homeobox	317268	Rn.22484	AI406884	2.35	2.34	2.38	2.34	2.36	2.34	1.01	down	3.94E-01	8.95E-01	-	-
1369117_at	Calca	calcitonin/calcitonin-related polypeptide, alpha	24241	Rn.90085	NM_017338	2.38	2.37	2.40	2.37	2.38	2.37	1.01	down	3.53E-01	8.95E-01	-	-
1398156_at	---	---	---	Rn.147578	BF396516	2.36	2.35	2.37	2.35	2.43	2.34	1.01	up	6.92E-01	9.05E-01	-	-
1382821_at	Ptprfa3	Protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interactin	140591	Rn.10537	AA998957	2.44	2.44	2.47	2.43	2.46	2.43	1.01	down	3.68E-01	8.95E-01	-	-
1390377_at	---	---	---	Rn.169780	BF394108	2.44	2.43	2.45	2.42	2.45	2.41	1.01	down	4.21E-01	8.95E-01	-	-
1369195_at	Fabp2	fatty acid binding protein 2, intestinal	25598	Rn.91358	NM_013068	2.49	2.47	2.53	2.48	2.54	2.45	1.01	down	7.30E-01	9.14E-01	-	-
1369258_at	Fuf9	fucosyltransferase 9 (alpha (1,3) fucosyltransferase)	84597	Rn.212206	NM_053465	2.43	2.42	2.45	2.43	2.45	2.40	1.01	down	5.27E-01	8.95E-01	-	-
1368993_at	Odz2	odz, odd Oz/ten-m homolog 2 (Drosophila)	117242	Rn.205610	NM_020088	2.39	2.38	2.41	2.38	2.40	2.37	1.01	down	3.94E-01	8.95E-01	-	-
1383940_at	Nuf2	NUF2, NDC80 kinetochore complex component, homolog (S. cerevisiae)	304951	Rn.41428	BG375704	2.44	2.42	2.43	2.42	2.43	2.41	1.01	down	2.69E-01	8.95E-01	-	-
1387298_at	Pga5	pepsinogen 5, group I (pepsinogen A)	60372	Rn.43875	NM_021753	2.32	2.32	2.33	2.31	2.32	2.30	1.01	down	1.86E-01	8.95E-01	-	-
1391867_at	Txlnb	taxilin beta	308622	Rn.165855	BI290684	2.41	2.40	2.44	2.40	2.43	2.39	1.01	down	5.27E-01	8.95E-01	-	-
1397589_at	---	---	---	Rn.73063	BI296502	2.48	2.46	2.49	2.47	2.48	2.45	1.01	down	4.01E-01	8.95E-01	-	-
1396324_at	---	---	---	Rn.61226	BF390565	2.29	2.28	2.32	2.28	2.30	2.28	1.01	down	4.80E-01	8.95E-01	-	-
1376822_at	---	---	---	---	BI297481	2.48	2.45	2.48	2.47	2.48	2.49	1.01	up	3.64E-01	8.95E-01	-	-
1385539_at	---	---	---	Rn.199496	AI556222	2.30	2.30	2.31	2.34	2.32	2.29	1.01	up	4.47E-01	8.95E-01	-	-
1379743_at	Nubp2	Nucleotide binding protein 2	287125	Rn.203395	BF397271	2.32	2.30	2.32	2.31	2.31	2.30	1.01	down	2.17E-01	8.95E-01	-	-
1385456_at	---	---	---	Rn.8812	AA955079	2.42	2.41	2.43	2.41	2.42	2.38	1.01	down	4.84E-01	8.95E-01	-	-
1373449_at	Taf5l	TAF5-like RNA polymerase II, p300/CBP-associated factor (PCAF)-associated	307927	Rn.23853	BG375861	3.59	3.52	3.66	3.61	3.75	3.44	1.01	up	9.11E-01	9.73E-01	-	-
1386218_at	---	---	---	Rn.161398	AI639301	2.47	2.46	2.49	2.48	2.48	2.44	1.01	down	5.25E-01	8.95E-01	-	-
1394323_at	Cdk5r2	cyclin-dependent kinase 5, regulatory subunit 2 (p39)	501164	Rn.219411	BF523326	2.30	2.29	2.33	2.29	2.30	2.29	1.01	down	4.72E-01	8.95E-01	-	-
1395172_at	---	---	---	Rn.205721	BE096402	2.28	2.27	2.31	2.29	2.28	2.25	1.01	down	5.00E-01	8.95E-01	-	-
1388203_x_at	w2 /// RT1-CE10 ///	histocompatibility 2, T region locus 24 /// RT1 class Ia, locus A2 /// RT1 class	61787 /// 414779	Rn.120283	BI395698	2.38	2.38	2.42	2.38	2.39	2.37	1.01	down	4.48E-01	8.95E-01	-	-
1375310_at	Impact	Imprinted and ancient	497198	Rn.190651	AI409746	2.41	2.40	2.41	2.41	2.41	2.37	1.01	down	4.00E-01	8.95E-01	-	-
1387140_at	Taok2	TAO kinase 2	64666	Rn.9575	NM_022702	2.36	2.33	2.35	2.33	2.34	2.32	1.01	down	2.72E-01	8.95E-01	-	-
1397844_at	---	---	---	Rn.206885	BF400963	2.45	2.44	2.48	2.44	2.47	2.42	1.01	down	5.75E-01	8.95E-01	-	-
1368482_at	Bcl2a1d	B-cell leukemia/lymphoma 2 related protein A1d	170929	Rn.19770	NM_133416	2.52	2.51	2.54	2.51	2.53	2.50	1.01	down	4.71E-01	8.95E-01	-	-
1380420_at	---	---	---	Rn.205834	AI549585	2.46	2.45	2.46	2.46	2.46	2.42	1.01	down	3.70E-01	8.95E-01	-	-
1368193_at	Hip1	huntingtin interacting protein 1	192154	Rn.836	AI028905	2.41	2.40	2.41	2.40	2.46	2.40	1.01	up	6.17E-01	8.95E-01	-	-
1388291_at	---	---	---	---	L41558	2.43	2.42	2.45	2.43	2.44	2.40	1.01	down	5.22E-01	8.95E-01	-	-
1397022_at	---	---	---	Rn.211447	BF413347	2.37	2.34	2.36	2.35	2.36	2.33	1.01	down	3.28E-01	8.95E-01	-	-
1380401_at	---	---	---	Rn.169675	BF563413	2.48	2.47	2.50	2.47	2.48	2.46	1.01	down	3.72E-01	8.95E-01	-	-
1382023_at	---	---	---	Rn.8246	AI407113	2.39	2.43	2.40	2.38	2.41	2.41	1.01	down	5.06E-01	8.95E-01	-	-
1395711_at	---	---	---	Rn.205187	AW526713	2.53	2.48	2.50	2.50	2.62	2.43	1.01	up	8.53E-01	9.55E-01	-	-
1374988_at	---	---	---	---	BF390848	2.35	2.33	2.34	2.33	2.33	2.32	1.01	down	2.44E-01	8.95E-01	-	-
1389579_at	---	---	---	Rn.17918	BI294372	2.37	2.36	2.38	2.37	2.42	2.37	1.01	up	5.32E-01	8.95E-01	-	-
1381383_at	---	---	---	Rn.44674	AW434151	2.45	2.44	2.49	2.45	2.49	2.42	1.01	down	6.52E-01	8.97E-01	-	-
1376069_at	Psmd11	Proteasome (prosome, macropain) 26S subunit, non-ATPase, 11	303353	Rn.11861	BF414050	7.31	6.67	5.89	6.91	6.24	6.76	1.01	up	9.81E-01	9.94E-01	-	-
1389275_at	Sh3bp1	SH3-domain binding protein 1	300067	---	BM385271	2.28	2.33	2.29	2.28	2.30	2.28	1.01	down	4.98E-01	8.95E-01	-	-
1370152_at	Gp5	glycoprotein V (platelet)	25259	Rn.138111	NM_012795	2.36	2.35	2.38	2.35	2.36	2.34	1.01	down	3.83E-01	8.95E-01	-	-
1379605_at	---	---	---	Rn.147679	AW523671	2.40	2.38	2.43	2.39	2.41	2.38	1.01	down	5.35E-01	8.95E-01	-	-
1382080_at	RGD1563689	similar to KIAA0853 protein	498530	Rn.163283	AW523680	4.95	4.94	4.96	4.93	4.95	4.93	1.01	down	3.42E-01	8.95E-01	-	-
1398657_at	---	---	---	---	AI045896	2.40	2.40	2.42	2.40	2.41	2.38	1.01	down	3.86E-01	8.95E-01	-	-
1388572_at	LOC301128	similar to jumonji domain containing 2B	301128	Rn.6679	BM389961	3.44	2.93	3.03	3.44	2.96	2.97	1.01	down	9.61E-01	9.89E-01	-	-
1384676_at	---	---	---	---	AI232436	2.20	2.20	2.23	2.20	2.20	2.19	1.01	down	3.14E-01	8.95E-01	-	-
1396466_at	---	---	---	Rn.168052	BE097971	2.38	2.37	2.39	2.43	2.38	2.37	1.01	up	5.83E-01	8.95E-01	-	-
1380172_at	Klf5c	kinesin family member 5C	311024	Rn.50843	BE104278	2.41	2.40	2.42	2.41	2.42	2.38	1.01	down	4.04E-01	8.95E-01	-	-
1375977_at	Cetn2	centrin 2	84593	Rn.9472	AA958015	7.28	8.17	8.33	8.13	7.73	7.95	1.01	up	9.75E-01	9.92E-01	-	-
1390315_a_at	RGD1309414	similar to KIAA0913 protein	361004	Rn.24931	AA875438	2.40	2.41	2.40	2.39	2.41	2.45	1.01	up	5.45E-01	8.95E-01	-	-
1393841_at	RGD1310773	similar to hypothetical protein FLJ31810	313156	Rn.16998	AA859317	2.49	2.47	2.53	2.48	2.53	2.45	1.01	down	7.23E-01	9.12E-01	-	-
1382927_at	LOC308990	hypothetical protein LOC308990	308990	Rn.98391	BF282080	2.32	2.31	2.32	2.32	2.35	2.31	1.01	up	4.27E-01	8.95E-01	-	-
1385763_at	Cstl9l	cystatin 9-like	362231	Rn.60346	BF403691	2.42	2.37	2.39	2.37	2.40	2.37	1.01	down	5.73E-01	8.95E-01	-	-
1372640_at	Pi16	peptidase inhibitor 16	294312	Rn.9448	BI277758	2.39	2.37	2.40	2.37	2.39	2.37	1.01	down	3.95E-01	8.95E-01	-	-
1392173_at	Zcchc3	zinc finger, CCHC domain containing 3	690005	Rn.198655	BE115479	2.62	2.57	2.70	2.73	2.63	2.55	1.01	up	8.67E-01	9.58E-01	-	-
1390702_at	---	---	---	Rn.154138	BF388219	2.45	2.42	2.45	2.42	2.45	2.40	1.01	down	5.19E-01	8.95E-01	-	-
1380575_at	---	---	---	---	AI407274	2.38	2.36	2.38	2.37	2.41	2.37	1.01	up	4.41E-01	8.95E-01	-	-
1398305_at	Syt17	synaptotagmin XVII	192189	Rn.31973	U30831	2.44	2.42	2.44	2.43	2.49	2.41	1.01	up	6.35E-01	8.95E-01	-	-
1385657_at	Sptb	spectrin, beta, erythrocytic	314251	Rn.63940	BF549861	2.50	2.49	2.54	2.36	2.51	2.63	1.01	down	8.92E-01	9.66E-01	-	-
1378297_at	RGD1561517	similar to chromosome 20 open reading frame 144	499927	Rn.32947	AI144652	2.64	2.64	2.65	2.79	2.66	2.52	1.01	up	8.90E-01	9.66E-01	-	-
1390092_at	Tmem39b	transmembrane protein 39b	362608	Rn.5911	BG378899	3.84	3.48	3.57	3.77	3.52	3.56	1.01	down	9.35E-01	9.82E-01	-	-
1382430_at	Msl2l1	male-specific lethal 2-like 1 (Drosophila)	315959	Rn.9626	AI172357	6.86	7.32	8.32	7.11	7.19	8.17	1.01	down	9.84E-01	9.95E-01	-	-
1373805_at	Ctsr	cathepsin R	290975	Rn.106080	BI285778	2.42	2.40	2.47	2.42	2.43	2.40	1.01	down	6.07E-01	8.95E-01	-	-
1377538_at	---	---	---	---	BF393047	2.44	2.42	2.46	2.43	2.45	2.41	1.01	down	4.74E-01	8.95E-01	-	-
1377971_at	---	---	---	Rn.202616	BG378777	2.42	2.41	2.43	2.41	2.42	2.39	1.01	down	3.67E-01	8.95E-01	-	-
1385819_at	Msto1	misato homolog 1 (Drosophila)	295237	Rn.26620	BF287803	2.55	2.55	2.59	2.55	2.58	2.52	1.01	down	6.29E-01	8.95E-01	-	-
1398911_at	Mrpl2	mitochondrial ribosomal protein L2	301240	Rn.102111	AI171870	6.29	6.81	6.51	6.48	6.49	6.61	1.01	down	9.44E-01	9.84E-01	-	-
1379641_at	Rdx	Radixin	316855	Rn.203261	BE113016	2.43	2.41	2.44	2.42	2.43	2.40	1.01	down	4.16E-01	8.95E-01	-	-
1392811_at	Usp40	ubiquitin specific peptidase 40	316599	Rn.9343	BI289490	2.46	2.45	2.47	2.46	2.46	2.43	1.01	down	4.03E-01	8.95E-01	-	-
1383481_at	---	---	---	---	AI070144	2.45	2.43	2.48	2.44	2.47	2.42	1.01	down	5.81E-01	8.95E-01	-	-
1374850_at	---	---	---	Rn.154027	AI113301	2.37	2.37	2.38	2.37	2.38	2.34	1.01	down	3.34E-01	8.95E-01	-	-
1383053_x_at	Zfp91	zinc finger protein 91	246282	Rn.1772	BE112093	3.76	3.76	3.76	3.84	3.77	3.64	1.01	down	8.53E-01	9.54E-01	-	-
1385358_at	Zbtb24	zinc finger and BTB domain containing 24	365590	Rn.43308	BF403480	2.40	2.36	2.46	2.39	2.40	2.39	1.01	down	7.01E-01	9.07E-01	-	-
1395677_at	---	---	---	---	BF411677	2.51	2.44	2.54	2.50	2.51	2.51	1.01	up	6.94E-01	9.05E-01	-	-
1387018_at	Arg9p2	Arg/Abl-interacting protein ArgBP2	114901	Rn.24612	NM_053770	2.48	2.43	2.44	2.43	2.48	2.41	1.01	down	6.81E-01	9.03E-01	-	-
1392271_at	Rxrg	retinoid X receptor gamma	83574	Rn.40816	AW252290	2.30	2.29	2.31	2.34	2.30	2.29	1.01	up	5.21E-01	8.95E-01	-	-
1396737_at	RGD1307234	similar to RIKEN cDNA 4931400A14	316732	Rn.162279	BF403249	3.48	3.40	3.29	3.33	3.48	3.39	1.01	up	8.74E-01	9.61E-01	-	-
1384555_at	LOC363326	hypothetical LOC363326	363326	Rn.162357	BF416764	2.49	2.50	2.52	2.51	2.52	2.52	1.01	up	2.98E-01	8.95E-01	-	-
1377799_at	---	---	---	Rn.204853	BE114159	2.41	2.40	2.42	2.41	2.42	2.38	1.01	down	4.07E-01	8.95E-01	-	-
1390296_at	---	---	---	Rn.202801	BF410183	2.33	2.32	2.34	2.31	2.33	2.31	1.01	down	2.85E-01	8.95E-01	-	-
1394608_at	---	---	---	---	AI454756	2.45	2.42	2.45	2.43	2.44	2.42	1.01	down	3.72E-01	8.95E-01	-	-
1379463_at	Filip1	filamin A interacting protein 1	246776	Rn.44931	AW525176	2.40	2.40	2.41	2.39	2.40	2.38	1.01	down	2.54E-01	8.95E-01	-	-
1388725_at	Leprot	leptin receptor overlapping transcript	56766	---	AA892288	8.60	8.50	8.46	8.22	8.66	8.64	1.01	down	9.43E-01	9.84E-01	-	-
1380754_at	Zfyve20	zinc finger, FYVE domain containing 20	312562	Rn.172475	BI290505	2.53	2.50	2.52	2.51	2.51	2.50	1.01	down	2.63E-01	8.95E-01	-	-
1370089_at	Pam	peptidylglycine alpha-amidating monooxygenase	25508	Rn.1121	M82845	2.39	2.37	2.40	2.38	2.43	2.38	1.01	up	5.30E-01	8.95E-01	-	-
1398234_at	---	---	---	Rn.211467	AF413677	2.45	2.44	2.46	2.45	2.46	2.49	1.01	up	4.03E-01	8.95E-01	-	-
1386987_at	Il6ra	interleukin 6 receptor, alpha	24499	Rn.1716	NM_017020	2.49	2.48	2.50	2.53	2.50	2.48	1.01	up	5.21E-01	8.95E-01	-	-
1393721_at	RGD1308290	Similar to RIKEN cDNA 5730454B08	360845	Rn.73695	BF397181	2.42	2.39	2.40	2.39	2.40	2.39	1.01	down	2.78E-01	8.95E-01	-	-
1379490_at	---	---	---	Rn.204158	AI071599	2.61	2.55	2.69	2.61	2.61	2.59	1.01	down	7.93E-01	9.33E-01	-	-
1379896_at	Ddx42	DEAD (Asp-Glu-Ala-Asp) box polypeptide 42	303607	Rn.154550	BM390256	2.38	2.37	2.39	2.37	2.44	2.36	1.01	up	6.84E-01	9.03E-01	-	-
1397444_at	---	---	---	---	BE108044	2.45	2.43	2.46	2.43	2.46	2.42	1.01	down	5.21E-01	8.95E-01	-	-
1395305_at	---	---	---	Rn.32520	AW535218	2.39	2.37	2.43	2.38	2.48	2.38	1.01	up	7.76E-01	9.27E-01	-	-
1384928_at	Ankrd2	ankyrin repeat domain 2 (stretch responsive muscle)	309374	Rn.41952	AA849895	2.44	2.42	2.46	2.43	2.46	2.41	1.01	down	5.67E-01	8.95E-01	-	-
1381254_at	---	---	---	Rn.210793	BF403021	2.46	2.44	2.48	2.45	2.47	2.43	1.01	down	5.41E-01	8.95E-01	-	-
1381671_at	Sucla2	succinate-CoA ligase, ADP-forming, beta subunit	361071	Rn.62159	BF412750	2.42	2.42	2.45	2.41	2.43	2.41	1.01	down	4.05E-01	8.95E-01	-	-
1372207_at	Brd8	bromodomain containing 8	291691	Rn.98723	AI549477	7.34	6.75	6.47	6.42	7.05	7.06	1.01	down	9.74E-01	9.92E-01	-	-
1374216_at	---	---	---	Rn.24598	BI280277	2.41	2.39	2.40	2.38	2.39	2.38	1.01	down	1.53E-01	8.95E-01	-	-
1369315_at	Il12a	interleukin 12a	84405	Rn.207199	NM_053390	2.41	2.38	2.43	2.39	2.41	2.38	1.01	down	4.70E-01	8.95E-01	-	-
1375839_at	---	---	---	Rn.208198	BF393490	2.36	2.35	2.37	2.36	2.37	2.32	1.01	down	4.55E-01	8.95E-01	-	-
1377711_at	---	---	---	Rn.165309	BF284137	2.46	2.45	2.49	2.45	2.48	2.44	1.01	down	5.37E-01	8.95E-01	-	-
1377972_at	Mast4	microtubule associated serine/threonine kinase family member 4	310040	Rn.43251	BF402035	2.36	2.35	2.36	2.38	2.37	2.35	1.01	up	2.69E-01	8.95E-01	-	-
1396296_at	---	---	---	Rn.156349	BG374199	2.57	2.54	2.56	2.55	2.56	2.54	1.01	down	2.86E-01	8.95E-01	-	-
1397003_at	---	---	---	Rn.209900	BF399521	2.47	2.46	2.51	2.46	2.50	2.45	1.01	down	5.98E-01	8.95E-01	-	-
1368007_at	Dmbt1	deleted in malignant brain tumors 1	170568	Rn.10107	NM_022849	2.34	2.33	2.35	2.38	2.34	2.33	1.01	up	5.20E-01	8.95E-01	-	-
1384236_at	---	---	---	Rn.172334	BI281089	2.56	2.52	2.68	2.54	2.69	2.49	1.01	down	8.88E-01	9.65E-01	-	-
1370496_at	Cyp2d3	cytochrome P450, family 2, subfamily d, polypeptide 3	24303	Rn.32106	AB008424	2.37	2.36	2.41	2.37	2.38	2.37	1.01	down	5.10E-01	8.95E-01	-	-
1383983_at	---	---	---	Rn.15703	BF399458	2.50	2.48	2.60	2.49	2.65	2.48	1.01	up	8.66E-01	9.58E-01	-	-
1381417_at	Prox1	prospero homeobox 1	305066	Rn.26557	AI111346	2.43	2.42	2.44	2.42	2.43	2.40	1.01	down	3.41E-01	8.95E-01	-	-
1372872_at	---	---	---	Rn.136946	BI291271	2.81	3.40	2.81	2.81	2.82	3.43	1.01	up	9.70E-01	9.91E-01	-	-
1370202_at	Pla2g16	phospholipase A2, group XVI	24913	Rn.11377	BG378637	7.32	6.59	6.45	6.12	7.07	7.13	1.01	down	9.80E-01

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1392776_at	---	---	---	Rn.20984	AI058733	2.61	2.60	2.63	2.60	2.61	2.59	1.01	down	3.54E-01	8.95E-01	-	-
1381317_at	---	---	---	Rn.33665	BF400206	2.52	2.49	2.55	2.50	2.56	2.47	1.01	down	7.35E-01	9.15E-01	-	-
1385686_at	Stfa3	stefin A3	288075	Rn.78016	BI281097	2.52	2.50	2.60	2.50	2.58	2.50	1.01	down	7.92E-01	9.33E-01	-	-
1390629_at	---	---	---	Rn.210694	BF400629	2.43	2.42	2.43	2.42	2.43	2.40	1.01	down	2.84E-01	8.95E-01	-	-
1398306_at	Ampd1	adenosine monophosphate deaminase 1 (isoform M)	25028	Rn.9794	J02811	2.32	2.30	2.33	2.31	2.32	2.29	1.01	down	2.88E-01	8.95E-01	-	-
1393215_at	Iffo1	intermediate filament family orphan 1	362437	Rn.38932	AW523847	2.52	2.50	2.56	2.52	2.53	2.51	1.01	down	5.80E-01	8.95E-01	-	-
1383045_at	---	---	---	Rn.153471	AA943688	2.43	2.42	2.46	2.42	2.45	2.41	1.01	down	5.47E-01	8.95E-01	-	-
1382303_at	Phactr1	phosphatase and actin regulator 1	306844	Rn.22981	AA996943	2.42	2.39	2.43	2.40	2.42	2.38	1.01	down	4.52E-01	8.95E-01	-	-
1391150_at	---	---	---	Rn.134456	BM387773	2.51	2.48	2.54	2.50	2.53	2.46	1.01	down	7.11E-01	9.10E-01	-	-
1382041_at	Agpat3	1-acylglycerol-3-phosphate O-acyltransferase 3	294324	Rn.100251	BI290161	7.81	7.65	8.39	7.72	8.17	7.93	1.01	down	9.67E-01	9.90E-01	-	-
1376044_at	Leng9	leukocyte receptor cluster (LRC) member 9	292596	Rn.92802	BE099774	2.49	2.49	2.51	2.49	2.50	2.46	1.01	down	4.16E-01	8.95E-01	-	-
1370726_at	Vnr1	vomeronasal receptor 1	286893	Rn.144688	U36785	2.40	2.38	2.43	2.39	2.40	2.38	1.01	down	4.99E-01	8.95E-01	-	-
1367558_x_at	Andpro	androgen regulated 20 kDa protein	25030	Rn.9977	NM_012718	2.51	2.48	2.56	2.50	2.56	2.46	1.01	down	7.69E-01	9.24E-01	-	-
1390693_at	LOC689791	Hypothetical protein LOC689791	689791	Rn.134767	BF416413	2.51	2.49	2.53	2.50	2.53	2.47	1.01	down	6.36E-01	8.95E-01	-	-
1393219_at	C2	complement component 2	24231	Rn.98333	BF394142	2.39	2.39	2.44	2.38	2.42	2.38	1.01	down	6.28E-01	8.95E-01	-	-
1380228_at	RGD1306880	similar to hypothetical protein MGC47816	313553	---	BG672066	2.47	2.46	2.48	2.47	2.50	2.42	1.01	down	6.85E-01	9.03E-01	-	-
1390374_at	Fgfr1	fibroblast growth factor receptor-like 1	360903	Rn.44953	BM390970	6.06	6.14	6.32	6.12	6.13	6.30	1.01	up	9.12E-01	9.74E-01	-	-
1371282_at	Prm3	protamine 3	442921	Rn.126718	Z46939	2.49	2.49	2.49	2.49	2.49	2.46	1.01	down	3.30E-01	8.95E-01	-	-
1386827_at	LOC363458	similar to procollagen, type IV, alpha 6	363458	Rn.182586	BF546343	2.40	2.37	2.40	2.37	2.39	2.36	1.01	down	4.05E-01	8.95E-01	-	-
1377843_at	---	---	---	Rn.203357	BF548385	2.51	2.47	2.78	2.62	2.52	2.66	1.01	up	9.20E-01	9.76E-01	-	-
1390018_at	---	---	---	Rn.208936	BF400755	2.55	2.53	2.57	2.54	2.56	2.52	1.01	down	4.97E-01	8.95E-01	-	-
1381864_at	---	---	---	---	AI059122	2.47	2.45	2.51	2.47	2.49	2.43	1.01	down	6.54E-01	8.97E-01	-	-
1391797_at	Mef2b	myocyte enhancer factor 2B	498607	Rn.145490	AI013317	2.38	2.37	2.38	2.38	2.39	2.40	1.01	up	1.36E-01	8.95E-01	-	-
1385047_x_at	2685111 /// RGD15	similar to paired immunoglobin-like type 2 receptor beta /// similar to paired im	501815 /// 685048	Rn.217945	AI012782	2.44	2.42	2.46	2.55	2.44	2.36	1.01	up	8.50E-01	9.53E-01	-	-
1386378_at	Fam92a1	family with sequence similarity 92, member A1	297903	Rn.92601	AA850029	2.67	2.62	2.75	2.72	2.77	2.58	1.01	up	8.76E-01	9.61E-01	-	-
1385385_at	---	---	---	Rn.208451	BE116745	2.39	2.37	2.41	2.38	2.40	2.36	1.01	down	5.27E-01	8.95E-01	-	-
1380863_at	Fbxl19	f-box and leucine-rich repeat protein 19	308999	Rn.50190	BM390208	2.38	2.36	2.43	2.37	2.39	2.37	1.01	down	6.24E-01	8.95E-01	-	-
1369877_at	Cd8a	CD8a molecule	24930	Rn.10306	NM_031538	2.40	2.39	2.41	2.39	2.40	2.37	1.01	down	3.71E-01	8.95E-01	-	-
1368679_a_at	Lyn	v-yes-1 Yamaguchi sarcoma viral related oncogene homolog	81515	Rn.4338	NM_030857	2.38	2.39	2.39	2.39	2.38	2.36	1.01	down	2.87E-01	8.95E-01	-	-
1395792_at	---	---	---	Rn.205811	AI549034	2.37	2.35	2.37	2.36	2.37	2.33	1.01	down	4.59E-01	8.95E-01	-	-
1374020_at	Lrrc38	leucine rich repeat containing 38	313681	Rn.218649	BF281893	2.39	2.38	2.41	2.39	2.39	2.37	1.01	down	3.34E-01	8.95E-01	-	-
1389755_at	Cdca7l	cell division cycle associated 7 like	619566	Rn.201759	BM391858	2.36	2.35	2.39	2.36	2.36	2.35	1.01	down	4.67E-01	8.95E-01	-	-
1389219_at	LOC679692	Similar to lysophosphatidylglycerol acyltransferase 1	679692	Rn.101953	AI406322	7.31	8.16	7.48	7.49	7.09	8.35	1.01	down	9.81E-01	9.94E-01	-	-
1394862_at	---	---	---	---	AI502545	2.38	2.38	2.39	2.37	2.38	2.36	1.01	down	2.62E-01	8.95E-01	-	-
1375004_at	sg11 /// LOC68769	GSG1-like /// similar to germ cell associated 1	499263 /// 687697	Rn.18521	BF409055	2.46	2.39	2.42	2.45	2.41	2.39	1.01	down	6.95E-01	9.06E-01	-	-
1397069_at	---	---	---	Rn.138976	BE117298	2.49	2.47	2.54	2.49	2.50	2.48	1.01	down	6.10E-01	8.95E-01	-	-
1379628_at	---	---	---	Rn.21362	AI070862	2.38	2.36	2.44	2.38	2.36	2.42	1.01	down	7.20E-01	9.11E-01	-	-
1395334_at	Fam69b	family with sequence similarity 69, member B	362090	Rn.92162	BE112276	2.33	2.30	2.32	2.31	2.32	2.30	1.01	down	3.33E-01	8.95E-01	-	-
1382808_at	---	---	---	---	AW919353	2.43	2.41	2.45	2.42	2.44	2.40	1.01	down	5.48E-01	8.95E-01	-	-
1370090_at	Lcp2	lymphocyte cytosolic protein 2	155918	Rn.1057	NM_130421	2.49	2.43	2.44	2.43	2.46	2.43	1.01	down	6.19E-01	8.95E-01	-	-
1369598_at	Gdnf	glial cell derived neurotrophic factor	25453	Rn.53970	NM_019139	2.46	2.47	2.49	2.46	2.48	2.44	1.01	down	4.86E-01	8.95E-01	-	-
1394512_at	---	---	---	Rn.55853	BF289965	2.43	2.40	2.44	2.42	2.43	2.39	1.01	down	5.04E-01	8.95E-01	-	-
1382324_at	---	---	---	Rn.6710	AA851183	2.44	2.42	2.44	2.42	2.43	2.41	1.01	down	2.93E-01	8.95E-01	-	-
1395336_at	RGD1309930	Similar to 2810022L02Rik protein	316426	Rn.36675	BE098691	2.36	2.35	2.39	2.35	2.37	2.35	1.01	down	4.83E-01	8.95E-01	-	-
1368120_at	Nell1	NEL-like 1 (chicken)	81733	Rn.10695	NM_031069	2.38	2.37	2.41	2.37	2.39	2.37	1.01	down	4.66E-01	8.95E-01	-	-
1395736_at	Ripk5	receptor interacting protein kinase 5	304791	Rn.32539	BG666455	2.81	2.83	2.93	2.81	2.88	2.90	1.01	up	8.16E-01	9.41E-01	-	-
1397308_at	Thap3	THAP domain containing, apoptosis associated protein 3	362667	Rn.14849	BE119999	2.50	2.48	2.54	2.50	2.54	2.51	1.01	up	6.06E-01	8.95E-01	-	-
1378768_at	---	---	---	Rn.207291	BF388558	2.29	2.28	2.31	2.28	2.36	2.26	1.01	up	7.26E-01	9.13E-01	-	-
1369380_at	Kif2c	kinesin family member 2C	171529	Rn.152404	NM_134472	2.51	2.47	2.56	2.49	2.55	2.46	1.01	down	7.73E-01	9.26E-01	-	-
1396348_at	---	---	---	Rn.47169	BI287017	2.45	2.42	2.45	2.43	2.44	2.41	1.01	down	4.14E-01	8.95E-01	-	-
1396922_at	---	---	---	---	AI454930	2.56	2.55	2.59	2.56	2.57	2.54	1.01	down	4.33E-01	8.95E-01	-	-
1394635_at	---	---	---	---	AA963027	2.39	2.38	2.41	2.38	2.40	2.37	1.01	down	4.77E-01	8.95E-01	-	-
1370332_at	Unc13d	unc-13 homolog D (C. elegans)	192177	Rn.198919	AF159356	2.46	2.45	2.48	2.46	2.47	2.42	1.01	down	5.53E-01	8.95E-01	-	-
1382659_at	Pla2r1	phospholipase A2 receptor 1	295631	Rn.11694	BF289229	2.43	2.41	2.46	2.42	2.45	2.40	1.01	down	5.82E-01	8.95E-01	-	-
1369692_at	Tnr	tenascin R	25567	Rn.11028	NM_013045	2.44	2.42	2.44	2.42	2.43	2.40	1.01	down	3.89E-01	8.95E-01	-	-
1369746_a_at	Slco1b2	solute carrier organic anion transporter family, member 1b2	58978	Rn.48740	AF147740	2.37	2.35	2.39	2.36	2.37	2.35	1.01	down	4.42E-01	8.95E-01	-	-
1373827_at	Prlr7a4	prolactin family 7, subfamily a, member 4	306929	Rn.31448	AI179972	2.44	2.42	2.46	2.43	2.45	2.41	1.01	down	4.93E-01	8.95E-01	-	-
1375919_at	Ubqln2	ubiquilin 2	317396	Rn.23446	AW552982	2.48	2.47	2.49	2.47	2.49	2.45	1.01	down	4.16E-01	8.95E-01	-	-
1391265_at	LOC498236	LRRGT00186	498236	Rn.163219	BF400749	2.45	2.43	2.48	2.44	2.47	2.42	1.01	down	5.99E-01	8.95E-01	-	-
1396945_at	---	---	---	Rn.153704	BF406132	2.43	2.42	2.45	2.42	2.43	2.42	1.01	down	3.43E-01	8.95E-01	-	-
1390235_at	---	---	---	Rn.146514	BF410589	2.53	2.54	2.60	2.54	2.57	2.53	1.01	down	6.72E-01	9.01E-01	-	-
1387194_at	Adap1	ArfGAP with dual PH domains 1	171097	Rn.10539	U51013	2.39	2.40	2.41	2.38	2.39	2.38	1.01	down	1.41E-01	8.95E-01	-	-
1385667_x_at	---	---	---	Rn.6374	AI029796	2.67	2.59	2.59	2.67	2.62	2.59	1.01	up	7.74E-01	9.26E-01	-	-
1378650_at	Zfp61	zinc finger protein 61	499094	Rn.122263	BF396329	2.44	2.43	2.46	2.43	2.46	2.41	1.01	down	5.23E-01	8.95E-01	-	-
1373074_at	RGD1307279	similar to RIKEN cDNA 2700002I20	307210	Rn.16742	AI171367	7.35	7.15	7.78	7.36	7.22	7.66	1.01	down	9.83E-01	9.89E-01	-	-
1389939_at	---	---	---	Rn.147755	BI300781	2.36	2.34	2.37	2.35	2.36	2.33	1.01	down	4.03E-01	8.95E-01	-	-
1397028_at	---	---	---	Rn.209613	BF389733	2.47	2.46	2.48	2.47	2.47	2.43	1.01	down	4.80E-01	8.95E-01	-	-
1382890_at	---	---	---	Rn.148777	BF409134	2.40	2.38	2.41	2.39	2.40	2.37	1.01	down	3.84E-01	8.95E-01	-	-
1386795_at	Hepacam2	HEPACAM family member 2	296846	Rn.66067	BF291091	2.54	2.51	2.55	2.53	2.56	2.48	1.01	down	7.05E-01	9.08E-01	-	-
1398140_at	Ncor2	Nuclear receptor co-repressor 2	360801	Rn.113362	BF416372	2.83	2.77	2.90	2.83	3.03	2.60	1.01	down	9.36E-01	9.82E-01	-	-
1385140_at	Trim9	tripartite motif-containing 9	155812	Rn.209223	BF386925	2.43	2.41	2.45	2.42	2.44	2.40	1.01	down	5.39E-01	8.95E-01	-	-
1384506_at	Unc5c	unc-5 homolog C (C. elegans)	362049	Rn.47255	H33706	2.55	2.52	2.61	2.53	2.63	2.49	1.01	down	8.32E-01	9.47E-01	-	-
1385318_at	Ears2	glutamyl-tRNA synthetase 2 mitochondrial (putative)	361641	Rn.79288	AW528193	2.35	2.34	2.35	2.34	2.34	2.33	1.01	down	1.37E-01	8.95E-01	-	-
1377586_at	---	---	---	Rn.62020	BI288982	2.57	2.53	2.64	2.55	2.63	2.53	1.01	down	8.13E-01	9.40E-01	-	-
1385339_at	---	---	---	Rn.153485	BI304211	2.57	2.51	2.59	2.56	2.59	2.55	1.01	up	6.85E-01	9.03E-01	-	-
1395970_at	---	---	---	Rn.212009	BI297496	3.64	3.64	4.02	4.00	3.65	3.62	1.01	down	9.52E-01	9.86E-01	-	-
1378176_at	---	---	---	Rn.18215	AW531422	2.54	2.51	2.57	2.52	2.58	2.49	1.01	down	7.56E-01	9.21E-01	-	-
1384097_at	---	---	---	Rn.19690	AI146081	2.39	2.38	2.41	2.38	2.39	2.37	1.01	down	3.08E-01	8.95E-01	-	-
1391805_at	RGD1310364	Similar to KIAA1900 protein	313111	Rn.26637	BE096676	2.47	2.45	2.50	2.46	2.50	2.43	1.01	down	6.99E-01	9.07E-01	-	-
1381330_at	---	---	---	Rn.168679	AI763958	2.64	2.58	2.74	2.61	2.78	2.54	1.01	down	9.03E-01	9.70E-01	-	-
1370373_at	Rasd2	RASD family, member 2	171099	Rn.115571	BF404624	2.30	2.29	2.34	2.30	2.30	2.36	1.01	up	6.69E-01	9.00E-01	-	-
1376414_x_at	RGD1309414	similar to KIAA0913 protein	361004	Rn.24931	BE109634	3.28	3.28	4.01	3.48	3.50	3.62	1.01	up	9.66E-01	9.90E-01	-	-
1390758_at	---	---	---	Rn.209836	BF393473	2.51	2.48	2.55	2.48	2.57	2.46	1.01	down	7.88E-01	9.32E-01	-	-
1389024_at	Scfd2	sec1 family domain containing 2	498353	Rn.3326	BG380647	3.39	4.86	3.62	4.56	3.20	4.14	1.01	up	9.86E-01	9.96E-01	-	-
1384527_at	---	---	---	Rn.148086	AW535731	2.66	2.61	2.68	2.64	2.64	2.63	1.01	down	6.19E-01	8.95E-01	-	-
1394846_at	RGD1562625	similar to killer activatory receptor-like protein p91D	502291	Rn.216251	AI237640	2.48	2.45	2.51	2.46	2.51	2.43	1.01	down	7.22E-01	9.11E-01	-	-
1390325_at	Cd38	CD38 molecule	25668	Rn.11414	BI289418	2.48	2.48	2.49	2.48	2.52	2.48	1.01	up	4.49E-01	8.95E-01	-	-
1396426_at	Pak4	p21 protein (Cdc42/Rac)-activated kinase 4	292756	Rn.18543	BF404920	2.45	2.43	2.47	2.44	2.45	2.41	1.01	down	5.57E-01	8.95E-01	-	-
1395746_at	---	---	---	Rn.27932	BG666635	2.42	2.40	2.43	2.40	2.43	2.39	1.01	down	5.27E-01	8.95E-01	-	-
1388400_at	Cdc34	cell division cycle 34 homolog (S. cerevisiae)	299602	Rn.2427	BG375350	7.90	7.68	7.94	7.90	7.64	8.01	1.01	up	9.39E-01	9.83E-01	-	-
1395280_at	Col2a1	collagen, type II, alpha 1	25412	Rn.10124	AA899303	2.39	2.38	2.41	2.38	2.40	2.37	1.01	down	4.22E-01	8.95E-01	-	-
1387568_at	Lilrb3	leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domai	65146	Rn.207196	NM_031713	2.44	2.42	2.46	2.43	2.45	2.41	1.01	down	5.61E-01	8.95E-01	-	-
1385531_at	Psmb5	proteasome (prosome, macropain) subunit, beta type 5	29425	Rn.2	BI281524	2.41	2.39	2.45	2.40	2.43	2.38	1.01	down	6.53E-01	8.97E-01	-	-
1384798_at	---	---	---	Rn.216895	BE119818	2.50	2.47	2.53	2.48	2.61	2.44	1.01	up	8.53E-01	9.54E-01	-	-
1395333_at	Pmp2	peripheral myelin protein 2	688790	Rn.68131	AW533483	2.47	2.42	2.45	2.44	2.45	2.42	1.01	down	5.01E-01	8.95E-01	-	-
1368790_at	Serpina10	serine (or cysteine) peptidase inhibitor, clade A (alpha-1 antiproteinase, antitry	171154	Rn.10502	NM_133617	2.34	2.33	2.34	2.32	2.37	2.36	1.01	up	5.53E-01	8.95E-01	-	-
1367887_at	Lcat	lecithin cholesterol acyltransferase	24530	Rn.10481	NM_017024	2.42	2.41	2.45	2.41	2.43	2.40	1.01	down	4.42E-01	8.95E-01	-	-
1393710_at	Icam5	intercellular adhesion molecule 5, telencephalin	313785	Rn.59765	BE102418	2.29	2.28	2.30	2.29	2.33	2.29	1.01	up	4.64E-01	8.95E-01	-	-
1384274_at	LOC367746	similar to Spindlin-like protein 2 (SPIN-2)	367746	Rn.20107	BG377595	2.52	2.49	2.54	2.50	2.53	2.49	1.01	down	6.12E-01	8.95E-01	-	-
1395663_at	Mall	mal, T-cell differentiation protein-like	362211	Rn.48232	BM390756	2.59	3.76	3.28	3.27	2.80	3.53	1.01	down	9.79E-01	9.94E-01	-	-
1384852_at	Rab27a	RAB27A, member RAS oncogene family	50645	Rn.37360	AI043615	2.46	2.45	2.49	2.45	2.48	2.44	1.01	down	5.47E-01	8.95E-01	-	-
1397965_at	Porcn	porcupine homolog (Drosophila)	317368	Rn.63525	BF405066	2.46	2.44	2.45	2.44	2.45	2.50	1.01	up	5.84E-01	8.95E-01	-	-
1379895_at	---	---	---	Rn.156184	BF419411	2.53	2.50	2.54	2.52	2.57	2.45	1.01	down	7.72E-01	9.26E-01	-	-
1391316_at	---	---	---	Rn.166532	AI072558	2.48	2.46	2.52	2.47	2.56	2.46	1.01	up	7.79E-01	9.28E-01	-	-
1397060_at	---	---	---	Rn.169674	BF563411	2.44	2.42	2.46	2.43	2.45	2.41	1.01	down	5.64E-01	8.95E-01	-	-
1398154_at	---	---	---	---	BF406175	2.37	2.36	2.39	2.36	2.37	2.35	1.01	down	3.97E-01	8.95E-01	-	-
1372883_at	Cenpb	centromere protein B	362217	---	BE109061	2.67	2.61	2.75	2.68	2.73	2.58	1.01	down	8.59E-01	9.56E-01	-	-
1391390_at	Tns1	tensin 1	301509	Rn.3793	AA894192	10.29	9.80	9.69	10.10	9.84	9.88	1.01	up	9.59E-01	9.89E-01	-	-
1384165_at	---	---	---	Rn.141369	BG671473	2.40	2.38	2.41	2.38	2.41	2.37	1.01	down	5.41E-01	8.95E-01	-	-
1382693_a_at	---	---	---	Rn.30113	BF283375	2.82	2.86	2.96	2.87	2.81	2.93	1.01	down	8.47E-01	9.52E-01	-	-
1384611_at	LOC680889	Hypothetical protein LOC680889	680889	Rn.22365	AI171626	2.32	2.32	2.33	2.32	2.32	2.30	1.01	down	2.50E-01	8.95E-01	-	-
1387831_at	Xcl1	chemokine (C motif) ligand 1	171371	Rn.90962	NM_134361	2.43	2.41	2.46	2.41	2.45	2.40	1.01	down	6.19E-01	8.95E-01	-	-
1396113_at	Abhd14a	abhydrolase domain containing 14A	360982	Rn.41351	AI716909	5.31	5.93	6.20	5.60	5.53	6.27	1.01	down	9.77E-01	9.93E-01	-	-
1393592_at	Hs3st5	heparan sulfate (glucosamine) 3-O-sulfotransferase 5	294449	Rn.117403	AA998087	2.37	2.36	2.40	2.37	2.38	2.35	1.01	down	4.66E-01	8.95E-01	-	-
1375145_at	Rfwd2	Ring finger and WD repeat domain 2	360860	Rn.8617	AI548036	2.31	2.30	2.35	2.31	2.31	2.31	1.01	down	4.57E-01	8.95E-01	-	-
1379821_at	RGD1560166	similar to Probable G-protein coupled receptor 62 (hGPCR8)	501049	---	AW527863	2.34	2.31	2.33	2.32	2.32	2.31	1.01	down	3.06E-01	8.95E-01	-	-
1390823_at	Skp2	S-phase kinase-associated protein 2 (p45)	294790	Rn.154278	AA924839	2.43	2.42	2.45	2.42	2.44	2.41	1.01	down	3.81E-01	8.95E-01	-	-
1385146_at	---	---	---	Rn.157950	BF398614	2.27	2.27	2.28	2.31	2.28	2.27	1.01	up	4.50E-01	8.95E-01	-	-
1394747_at	Ankrd1	Ankyrin repeat domain 1 (cardiac muscle)	27064	Rn.3789	BE113012	2.35	2.35	2.36	2.34	2.36	2.33	1.01	down	2.84E-01	8.95E-01	-	-
1386433_at	---	---	---	---	AI639213	2.53	2.50	2.60	2.53	2.58	2.49	1.01	down	7.87E-01	9.31E-01	-	-
1398568_at	---	---	---	Rn.206858	AW531009	2.63	2.63	2.63	2.63	2.64	2.60	1.01	down	3.98E-01	8.95E-01	-	-
1370660_at	vom2r40 /// Vom2r4	vomeronasal 2 receptor, 40 /// vomeronasal 2 receptor, 41	286983 /// 293069	Rn.217629	AF016180	2.42	2.40	2.44	2.41	2.43	2.39	1.01	down	5.31E-01	8.95E-01	-	-
1393571_at	---	---	---	Rn.165009	AA963158	2.67	2.72	2.83	2.71	2.79	2.67	1.01	down	8.58E-01	9.56E-01	-	-
1389518_at	Tomm5	translocase of outer mitochondrial membrane 5 homolog (yeast)	680080	Rn.7385	AI009763	7.98	8.01	8.06	7.80	8.14	1.01	up	9.21E-01	9.77E-01	-	-
1383486_at	---	---	---	Rn.35842	AA926109	2.39	2.36	2.38	2.37	2.43	2.36	1.01	up	6.61E-01	8.98E-01	-	-
1393487_at	Cenpa	Centromere protein A	298850	Rn.16165	AI045420	2.46	2.45	2.50	2.46	2.49	2.43	1.01	down	6.59E-01	8.98E-01	-	-
1385110_at	---	---	---	Rn.203923	AI029476	2.40	2.41	2.44	2.41	2.41	2.39	1.01	down	4.72E-01	8.95E-01	-	-
1376427_a_at	Gldc	glycine dehydrogenase (decarboxylating)	309312	Rn.17101	AI029729	2.30	2.29	2.33	2.30	2.30	2.29	1.01	down	4.73E-01	8.95E-01	-	-
1376794_at	---	---	---	Rn.11637	BF548418	4.52	4.07	3.70	4.11	4.08	4.06	1.01	down	9.65E-01	9.90E-01	-	-
1396392_at	Dctn6	Dynactin 6	290798	Rn.3642	BF403099	2.48	2.45	2.48	2.46	2.54	2.44	1.01	up	7.46E-01	9.18E-01	-	-
1396456_at	---	---	---	Rn.209568	BF398860	2.55	2.50	2.57	2.52	2.58	2.48	1.01	down	7.63E-01	9.22E-01	-	-
1371083_at	LOC299282	Serine protease inhibitor	299282	Rn.97597	D00752	2.39	2.37	2.39	2.37	2.38	2.36	1.01	down	2.38E-01	8.95E-01	-	-
1380134_at	Vtcn1	V-set domain containing T cell activation inhibitor 1	295322	Rn.160956	AI639163	2.46	2.43	2.47	2.43	2.46	2.43	1.01	down	4.44E-01	8.95E-01	-	-
1397542_at	---	---	---	Rn.27433	AI137472	2.42	2.41	2.43	2.41	2.43	2.39	1.01	down	4.41E-01	8.95E-01	-	-
1386935_at	Nr4a1	nuclear receptor subfamily 4, group A, member 1	79240	Rn.10000	NM_024388	2.46	2.41	2.44	2.42	2.46	2.39	1.01	down	6.71E-01	9.00E-01	-	-
1389826_at	Sox2	SRY (sex determining region Y)-box 2	499593	Rn.219221	AI102567	2.26	2.25	2.26	2.25	2.30	2.25	1.01	up	5.60E-01	8.95E-01	-	-
1395908_at	Mier2	mesoderm induction early response 1, family member 2	362841	Rn.41306	AW920951	2.27	2.27	2.30	2.27	2.28	2.26	1.01	down	3.95E-01	8.95E-01	-	-
1372639_at	Trim54	tripartite motif-containing 54	362708	Rn.6303	AA800245	2.43	2.42	2.45	2.41	2.44	2.42	1.01	down	3.34E-01	8.95E-01	-	-
1395834_at	---	---	---	Rn.190502	H34267	2.55	2.54	2.57	2.53	2.56	2.53	1.01	down	4.65E-01	8.95E-01	-	-
1370033_at	Myf1	myosin, light polypeptide 1	56781	Rn.84920	NM_020104	2.41	2.39	2.41	2.39	2.41	2.38	1.01	down	3.68E-01	8.95E-01	-	-
1394640_at	---	---	---	Rn.204882	AI777100	2.46	2.45	2.46	2.45	2.47	2.42	1.01	down	4.83E-01	8.95E-01	-	-
1373415_at	---	---	---	Rn.165854	AI407050	6.58	5.69	5.73	6.09	6.51	5.43	1.01	up	9.81E-01	9.94E-01	-	-
1379682_at	---	---	---	Rn.166497	BI281668	2.48	2.48	2.51	2.48	2.49	2.47	1

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)				REG	MTC
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval		
1396554_at	---	---	---	Rn.62839	BF405511	2.48	2.46	2.50	2.46	2.49	2.45	1.01	down	6.00E-01	8.95E-01	-	-
1395546_at	---	---	---	Rn.172248	AW529685	2.52	2.51	2.54	2.51	2.52	2.50	1.01	down	3.91E-01	8.95E-01	-	-
1377912_at	---	---	---	Rn.17964	AI013104	2.32	2.30	2.32	2.30	2.32	2.29	1.01	down	3.60E-01	8.95E-01	-	-
1378025_at	---	---	---	---	AI598498	2.45	2.44	2.46	2.44	2.45	2.43	1.01	down	3.36E-01	8.95E-01	-	-
1375264_at	---	---	---	Rn.51480	BF416264	2.57	2.55	2.58	2.62	2.57	2.54	1.01	up	6.83E-01	9.03E-01	-	-
1371065_at	/C688090 /// RT1-A	similar to RT1 class II histocompatibility antigen, B-1 beta chain precursor (RT1	309622 /// 688090	Rn.202964	BM389513	2.63	2.61	2.67	2.62	2.66	2.59	1.01	down	7.19E-01	9.11E-01	-	-
1376451_at	Krit1	KRIT1, ankyrin repeat containing	362317	Rn.162726	BG377849	3.19	3.35	3.53	3.39	3.33	3.38	1.01	up	9.19E-01	9.76E-01	-	-
1390299_at	---	---	---	Rn.210552	BF405880	2.36	2.35	2.38	2.35	2.36	2.34	1.01	down	3.79E-01	8.95E-01	-	-
1375619_at	---	---	---	Rn.210161	BF417982	2.54	2.53	2.53	2.53	2.55	2.49	1.01	down	5.77E-01	8.95E-01	-	-
1379338_at	Pgm2l1	phosphoglucomutase 2-like 1	685076	Rn.24187	AI044115	2.41	2.51	2.42	2.40	2.44	2.46	1.01	down	7.72E-01	9.26E-01	-	-
1371801_at	Myoz2	myozenin 2	295426	Rn.12931	AI104354	2.41	2.40	2.42	2.39	2.42	2.39	1.01	down	4.25E-01	8.95E-01	-	-
1386162_at	Txk	TXK tyrosine kinase	305311	Rn.163245	AI009944	2.39	2.36	2.38	2.36	2.37	2.36	1.01	down	3.12E-01	8.95E-01	-	-
1395909_at	---	---	---	Rn.35489	BE105118	2.68	2.65	2.77	2.81	2.68	2.64	1.01	up	8.73E-01	9.61E-01	-	-
1376395_at	---	---	---	Rn.161460	AI145359	2.35	2.35	2.36	2.35	2.36	2.33	1.01	down	2.30E-01	8.95E-01	-	-
1397754_at	---	---	---	Rn.41663	BG373236	2.35	2.34	2.35	2.34	2.36	2.30	1.01	down	6.16E-01	8.95E-01	-	-
1394187_at	Lmod3	leiomodin 3 (fetal)	500267	Rn.91424	AI639267	2.40	2.38	2.43	2.40	2.40	2.37	1.01	down	5.27E-01	8.95E-01	-	-
1371895_at	Krt14	keratin 14	287701	Rn.153972	BI279646	2.50	2.49	2.53	2.50	2.50	2.49	1.01	down	3.80E-01	8.95E-01	-	-
1397422_at	---	---	---	Rn.57323	BF390904	2.47	2.45	2.50	2.45	2.48	2.46	1.01	down	5.83E-01	8.95E-01	-	-
1369205_at	Neurog1	neurogenin 1	29410	Rn.10606	NM_019207	2.47	2.46	2.51	2.47	2.50	2.44	1.01	down	6.67E-01	8.99E-01	-	-
1387248_at	Kcnj5	potassium inwardly-rectifying channel, subfamily J, member 5	29713	Rn.10047	D50136	2.30	2.28	2.33	2.29	2.30	2.29	1.01	down	4.84E-01	8.95E-01	-	-
1375984_at	Zfhx4	zinc finger homeobox 4	310250	Rn.133363	BE103689	2.45	2.42	2.43	2.42	2.45	2.40	1.01	down	5.94E-01	8.95E-01	-	-
1369790_at	Tat	tyrosine aminotransferase	24813	Rn.9947	M18340	2.37	2.37	2.40	2.37	2.38	2.36	1.01	down	4.05E-01	8.95E-01	-	-
1387880_at	Cugbp2	CUG triplet repeat, RNA binding protein 2	29428	Rn.162247	AI237598	2.48	2.47	2.51	2.47	2.49	2.46	1.01	down	4.99E-01	8.95E-01	-	-
1393405_at	Xrcc2	X-ray repair complementing defective repair in Chinese hamster cells 2	499966	Rn.8224	AA825444	2.35	2.34	2.36	2.32	2.35	2.34	1.01	down	3.19E-01	8.95E-01	-	-
1392447_at	---	---	---	Rn.148210	AI073058	2.29	2.29	2.31	2.36	2.30	2.27	1.01	up	7.10E-01	9.09E-01	-	-
1391242_at	---	---	---	Rn.146230	AI112229	2.54	2.51	2.55	2.51	2.56	2.49	1.01	down	6.69E-01	9.00E-01	-	-
1388637_at	Fgl2	fibrinogen-like 2	84586	Rn.64635	BF561454	2.46	2.45	2.48	2.45	2.47	2.43	1.01	down	4.91E-01	8.95E-01	-	-
1381634_at	---	---	---	Rn.147937	BF386493	2.50	2.43	2.48	2.47	2.51	2.40	1.01	down	7.88E-01	9.31E-01	-	-
1391647_at	---	---	---	Rn.24665	AI232625	2.57	2.57	2.60	2.57	2.57	2.57	1.01	down	3.77E-01	8.95E-01	-	-
1375100_at	Cgnbp1	gametogenetin-binding protein 1	494520	Rn.51883	AI400662	2.43	2.42	2.44	2.42	2.42	2.41	1.01	down	2.45E-01	8.95E-01	-	-
1396188_at	Rhoj	ras homolog gene family, member J	299145	Rn.6890	BE127432	2.40	2.38	2.41	2.39	2.40	2.37	1.01	down	4.25E-01	8.95E-01	-	-
1381186_at	---	---	---	Rn.156145	AW527770	2.74	2.66	2.88	2.71	2.84	2.71	1.01	down	8.97E-01	9.68E-01	-	-
1379106_at	---	---	---	Rn.208634	BF400615	2.42	2.41	2.46	2.41	2.44	2.40	1.01	down	6.22E-01	8.95E-01	-	-
1368783_at	Icos	inducible T-cell co-stimulator	64545	Rn.168816	NM_022610	2.40	2.37	2.39	2.38	2.39	2.36	1.01	down	4.32E-01	8.95E-01	-	-
1397602_at	---	---	---	Rn.205994	BF419930	2.30	2.30	2.29	2.32	2.30	2.30	1.01	up	2.57E-01	8.95E-01	-	-
1385027_at	---	---	---	Rn.148207	BG380549	2.41	2.40	2.42	2.41	2.41	2.38	1.01	down	4.07E-01	8.95E-01	-	-
1385803_at	Gtf2h2	general transcription factor IIH, polypeptide 2	294693	Rn.14260	BM388555	2.54	2.57	2.72	2.64	2.59	2.57	1.01	down	8.65E-01	9.58E-01	-	-
1393747_at	Spink4	serine peptidase inhibitor, Kazal type 4	408233	Rn.13875	AI090659	2.47	2.46	2.47	2.51	2.47	2.45	1.01	up	5.86E-01	8.95E-01	-	-
1382560_at	---	---	---	---	AI176676	2.41	2.40	2.43	2.40	2.41	2.39	1.01	down	3.97E-01	8.95E-01	-	-
1391388_at	LOC679811	Similar to RIKEN cDNA D930015E06	679811	Rn.160937	BF403622	2.32	2.31	2.34	2.31	2.32	2.30	1.01	down	3.11E-01	8.95E-01	-	-
1381238_at	---	---	---	Rn.207489	BE102046	2.54	2.51	2.59	2.54	2.58	2.49	1.01	down	7.78E-01	9.28E-01	-	-
1369657_at	Cpa1	carboxypeptidase A1	24269	Rn.9576	NM_016998	2.42	2.40	2.42	2.40	2.42	2.39	1.01	down	4.28E-01	8.95E-01	-	-
1396795_at	---	---	---	Rn.210613	BF399428	2.44	2.43	2.48	2.44	2.46	2.42	1.01	down	5.71E-01	8.95E-01	-	-
1374590_at	Pld2	phospholipase C-like 2	301173	Rn.204118	BF420110	2.48	2.47	2.51	2.50	2.48	2.45	1.01	down	6.26E-01	8.95E-01	-	-
1379193_at	---	---	---	Rn.212025	BG375472	2.31	2.32	2.32	2.30	2.32	2.30	1.01	down	1.36E-01	8.95E-01	-	-
1395330_at	---	---	---	Rn.170273	BF283126	2.28	2.26	2.26	2.26	2.26	2.25	1.01	down	2.72E-01	8.95E-01	-	-
1394722_at	Mrpl17	mitochondrial ribosomal protein L17	171061	Rn.40354	AA964121	2.48	2.53	2.48	2.47	2.48	2.58	1.01	up	7.99E-01	9.35E-01	-	-
1385023_at	Rasgrf1	RAS protein-specific guanine nucleotide-releasing factor 1	192213	Rn.135776	AI144787	2.31	2.33	2.32	2.31	2.32	2.30	1.01	down	1.85E-01	8.95E-01	-	-
1380442_at	oxc9 /// rCG_5075	homeobox C9 /// homeo box C8	24460 /// 368178	Rn.101733	AI235507	2.37	2.36	2.39	2.41	2.38	2.36	1.01	up	5.68E-01	8.95E-01	-	-
1372459_at	Vasp	vasodilator-stimulated phosphoprotein	361517	Rn.98750	AW520792	10.16	9.48	9.71	10.03	9.70	9.65	1.01	up	9.66E-01	9.90E-01	-	-
1373000_at	Srpx2	sushi-repeat-containing protein, X-linked 2	317181	Rn.33831	AA818334	2.42	2.41	2.44	2.41	2.43	2.40	1.01	down	3.88E-01	8.95E-01	-	-
1399126_at	Klc1	kinesin light chain 1	171041	Rn.106230	AA964114	5.56	5.36	5.17	5.31	5.52	5.22	1.01	down	9.44E-01	9.84E-01	-	-
1383692_at	C683855 /// Prelid	hypothetical protein LOC683855 /// PRELI domain containing 2	681037 /// 683855	Rn.15238	BG377830	2.44	2.66	2.46	2.43	2.64	2.45	1.01	down	9.17E-01	9.75E-01	-	-
1396966_at	---	---	---	Rn.210987	BF404367	2.38	2.37	2.39	2.37	2.38	2.35	1.01	down	3.38E-01	8.95E-01	-	-
1385282_at	Nat14	N-acetyltransferase 14	361500	Rn.140257	BE097029	2.57	2.54	2.57	2.56	2.59	2.49	1.01	down	7.47E-01	9.18E-01	-	-
1381812_at	---	---	---	Rn.168116	AF416550	2.42	2.39	2.44	2.40	2.43	2.39	1.01	down	6.03E-01	8.95E-01	-	-
1393670_at	Ptpn14	protein tyrosine phosphatase, non-receptor type 14	305064	Rn.61089	BM386651	2.37	2.36	2.39	2.36	2.37	2.35	1.01	down	4.34E-01	8.95E-01	-	-
1372771_at	---	---	---	Rn.3109	BI279659	2.35	2.33	2.35	2.33	2.35	2.32	1.01	down	3.47E-01	8.95E-01	-	-
1381582_at	---	---	---	Rn.169151	AI548608	2.41	2.39	2.45	2.41	2.42	2.38	1.01	down	6.39E-01	8.95E-01	-	-
1367957_at	Rgs3	regulator of G-protein signaling 3	54293	Rn.53900	NM_019340	2.32	2.27	2.29	2.28	2.29	2.28	1.01	down	5.29E-01	8.95E-01	-	-
1396873_at	---	---	---	Rn.205170	AI501537	2.29	2.27	2.30	2.29	2.32	2.28	1.01	up	5.14E-01	8.95E-01	-	-
1370101_at	Crx	cone-rod homeobox	60446	Rn.44287	NM_021855	2.38	2.36	2.38	2.37	2.38	2.35	1.01	down	3.47E-01	8.95E-01	-	-
1394835_at	---	---	---	---	AI176861	2.45	2.43	2.55	2.45	2.46	2.57	1.01	up	8.50E-01	9.53E-01	-	-
1378525_at	---	---	---	Rn.172778	BF394459	2.36	2.35	2.37	2.35	2.37	2.33	1.01	down	4.69E-01	8.95E-01	-	-
1396505_at	---	---	---	---	BE113909	2.55	2.50	2.53	2.51	2.56	2.47	1.01	down	7.36E-01	9.15E-01	-	-
1379931_at	---	---	---	Rn.199388	BF398819	2.35	2.34	2.36	2.34	2.36	2.33	1.01	down	3.54E-01	8.95E-01	-	-
1382869_at	Ado	2-aminoethanethiol (cysteamine) dioxygenase	309732	Rn.106483	BF419182	2.42	2.41	2.42	2.41	2.42	2.39	1.01	down	2.83E-01	8.95E-01	-	-
1397538_at	Tbc1d30	TBC1 domain family, member 30	299824	Rn.30342	BF407593	2.48	2.46	2.51	2.47	2.50	2.44	1.01	down	6.68E-01	9.00E-01	-	-
1388033_at	Cxcl3	chemokine (C-X-C motif) ligand 3	171551	Rn.10525	D21095	2.41	2.40	2.43	2.40	2.42	2.38	1.01	down	4.99E-01	8.95E-01	-	-
1374220_at	Ccny	cyclin Y	361261	Rn.17533	AI599176	7.68	8.36	8.66	8.24	8.14	8.28	1.01	down	9.73E-01	9.92E-01	-	-
1392279_at	Dnai1	dynein, axonemal, intermediate chain 1	500442	Rn.198718	BI291154	2.33	2.33	2.36	2.32	2.34	2.32	1.01	down	4.14E-01	8.95E-01	-	-
1394449_at	---	---	---	Rn.169463	AW524715	2.57	2.55	2.64	2.56	2.64	2.52	1.01	down	8.15E-01	9.40E-01	-	-
1383726_at	RGD1309360	hypothetical LOC294715	294715	Rn.198108	BG669800	2.37	2.37	2.41	2.37	2.38	2.36	1.01	down	4.73E-01	8.95E-01	-	-
1371010_at	Nkx2-1	NK2 homeobox 1	25628	Rn.34265	BF389361	2.34	2.32	2.37	2.33	2.41	2.32	1.01	up	7.57E-01	9.21E-01	-	-
1391587_at	---	---	---	Rn.16809	AI170450	2.40	2.38	2.42	2.39	2.40	2.37	1.01	down	4.77E-01	8.95E-01	-	-
1378849_at	LOC501422	similar to glutamate receptor, ionotropic, N-methyl D-aspartate-like 1A	501422	---	AF414619	2.41	2.40	2.44	2.40	2.43	2.38	1.01	down	6.26E-01	8.95E-01	-	-
1396708_at	Tmem151a	transmembrane protein 151A	309158	Rn.100997	BF404975	2.36	2.35	2.36	2.38	2.37	2.35	1.01	up	3.50E-01	8.95E-01	-	-
1396428_at	---	---	---	Rn.173340	BF410381	2.51	2.50	2.52	2.51	2.52	2.48	1.01	down	4.42E-01	8.95E-01	-	-
1373629_at	Slc7a6	solute carrier family 7 (cationic amino acid transporter, y+ system), member 6	307811	Rn.8066	BE108272	2.37	2.36	2.38	2.36	2.38	2.40	1.01	up	4.49E-01	8.95E-01	-	-
1389680_at	Ell2	elongation factor RNA polymerase II 2	309918	Rn.105837	BI291626	4.77	4.95	5.03	4.82	4.56	5.33	1.01	down	9.67E-01	9.90E-01	-	-
1392878_at	---	---	---	Rn.33662	AI231319	2.50	2.50	2.53	2.50	2.54	2.45	1.01	down	7.04E-01	9.07E-01	-	-
1369486_at	Ank1	ankyrin repeat, SAM and basic leucine zipper domain containing 1	170578	Rn.81233	NM_130750	2.39	2.38	2.41	2.38	2.40	2.37	1.01	down	3.65E-01	8.95E-01	-	-
1373458_at	Bex4	brain expressed gene 4	501624	Rn.9287	BI289546	2.89	2.38	2.40	2.40	2.92	2.38	1.01	up	9.67E-01	9.90E-01	-	-
1397240_at	---	---	---	---	AA926273	2.49	2.50	2.51	2.50	2.52	2.45	1.01	down	6.27E-01	8.95E-01	-	-
1385434_at	Ptger2	Prostaglandin E receptor 2, subtype EP2	81752	Rn.10264	AI705087	2.28	2.26	2.28	2.28	2.30	2.28	1.01	up	3.63E-01	8.95E-01	-	-
1386359_x_at	---	---	---	---	AI639222	2.22	2.22	2.25	2.22	2.22	2.21	1.01	down	3.85E-01	8.95E-01	-	-
1395867_at	---	---	---	Rn.212005	BI296703	2.54	2.53	2.55	2.53	2.59	2.52	1.01	up	6.64E-01	8.99E-01	-	-
1369299_at	Ptafr	platelet-activating factor receptor	58949	Rn.10137	NM_053321	2.53	2.52	2.54	2.52	2.53	2.50	1.01	down	4.32E-01	8.95E-01	-	-
1382519_at	Lrp	limb and neural patterns	362151	Rn.50581	BE103940	2.75	2.76	2.81	2.77	2.78	2.75	1.01	down	6.36E-01	8.95E-01	-	-
1397559_at	Ppp1r3a	protein phosphatase 1, regulatory (inhibitor) subunit 3A	500036	Rn.29809	BI287330	2.39	2.37	2.39	2.37	2.39	2.36	1.01	down	4.14E-01	8.95E-01	-	-
1379708_at	---	---	---	Rn.205235	BG381298	2.31	2.31	2.34	2.31	2.31	2.30	1.01	down	3.43E-01	8.95E-01	-	-
1381491_at	---	---	---	Rn.206177	BE097634	2.37	2.36	2.39	2.37	2.38	2.35	1.01	down	4.19E-01	8.95E-01	-	-
1378963_at	Tgfb2	Transforming growth factor, beta 2	81809	Rn.24539	AA863004	2.50	2.48	2.52	2.48	2.51	2.46	1.01	down	5.84E-01	8.95E-01	-	-
1396432_at	---	---	---	Rn.61716	BF410473	2.30	2.29	2.34	2.29	2.32	2.29	1.01	down	6.15E-01	8.95E-01	-	-
1382607_at	---	---	---	Rn.15497	AA925323	2.39	2.38	2.41	2.38	2.39	2.37	1.01	down	4.02E-01	8.95E-01	-	-
1370795_at	Foxc2	forkhead box C2	171356	Rn.216723	L13193	2.32	2.31	2.32	2.37	2.32	2.30	1.01	up	6.13E-01	8.95E-01	-	-
1391030_at	LOC500591	similar to calmodulin-binding transcription activator 1	500591	---	AW524694	2.39	2.38	2.42	2.39	2.40	2.37	1.01	down	5.46E-01	8.95E-01	-	-
1394673_at	LOC687856	similar to Myeloid cell surface antigen CD33 precursor (Siglec-3)	687856	---	AI454014	2.46	2.45	2.48	2.45	2.47	2.43	1.01	down	4.56E-01	8.95E-01	-	-
1396740_at	LOC311352	Similar to Adenosine deaminase CG11994-PA	311352	Rn.204498	AI556643	2.40	2.38	2.41	2.39	2.41	2.37	1.01	down	4.66E-01	8.95E-01	-	-
1397598_at	---	---	---	Rn.164807	BF290562	2.39	2.53	2.41	2.38	2.39	2.58	1.01	up	8.97E-01	9.68E-01	-	-
1392746_x_at	Larp1	La ribonucleoprotein domain family, member 1	303158	Rn.98804	BF394189	5.60	5.36	5.49	5.36	5.64	5.48	1.01	up	9.27E-01	9.79E-01	-	-
1387832_at	Bche	butyrylcholinesterase	65036	Rn.48791	NM_022942	2.32	2.31	2.34	2.32	2.33	2.30	1.01	down	4.18E-01	8.95E-01	-	-
1394751_at	---	---	---	Rn.203415	AI577528	2.51	2.51	2.51	2.52	2.58	2.40	1.01	down	8.56E-01	9.55E-01	-	-
1381921_at	---	---	---	Rn.120425	BE110228	2.39	2.39	2.41	2.38	2.39	2.38	1.01	down	2.61E-01	8.95E-01	-	-
1391790_at	---	---	---	Rn.199280	AI044233	2.30	2.30	2.32	2.30	2.31	2.28	1.01	down	3.01E-01	8.95E-01	-	-
1396257_at	---	---	---	Rn.209617	BF389756	2.44	2.42	2.47	2.44	2.46	2.41	1.01	down	5.96E-01	8.95E-01	-	-
1381151_at	---	---	---	Rn.209189	BF386697	2.44	2.43	2.45	2.43	2.46	2.40	1.01	down	6.08E-01	8.95E-01	-	-
1373151_at	Lhfp	lipoma HMGIC fusion partner	499615	Rn.6635	AW252169	2.35	2.34	2.36	2.35	2.34	2.34	1.01	down	1.15E-01	8.95E-01	-	-
1375635_at	---	---	---	Rn.164695	AI406410	7.45	7.70	7.81	7.89	7.25	7.79	1.01	down	9.65E-01	9.90E-01	-	-
1380043_at	---	---	---	---	BF288242	2.31	2.30	2.33	2.31	2.37	2.30	1.01	up	6.55E-01	8.98E-01	-	-
1371152_a_at	Oas1a	2'-5' oligoadenylate synthetase 1A	192281	Rn.10383	Z18877	2.39	2.38	2.40	2.38	2.38	2.37	1.01	down	2.01E-01	8.95E-01	-	-
1382590_at	Rftn1	raftlin lipid raft linker 1	501095	Rn.204423	BI277914	2.61	2.57	2.67	2.58	2.65	2.58	1.01	down	7.96E-01	9.34E-01	-	-
1379738_at	---	---	---	Rn.21509	AI007726	2.44	2.43	2.47	2.44	2.44	2.43	1.01	down	4.05E-01	8.95E-01	-	-
1383858_at	Tfyh1	tweety homolog 1 (Drosophila)	292597	Rn.14889	BF548326	2.34	2.31	2.32	2.31	2.32	2.30	1.01	down	2.99E-01	8.95E-01	-	-
1391345_at	Bmper	BMP-binding endothelial regulator	300455	Rn.62611	BI293047	2.50	2.48	2.53	2.49	2.52	2.47	1.01	down	6.59E-01	8.98E-01	-	-
1384609_a_at	Fam63b	family with sequence similarity 63, member B	363089	Rn.15746	AI045965	6.58	4.37	3.88	5.51	5.64	3.71	1.01	up	9.92E-01	9.98E-01	-	-
1369905_at	Gabra4	gamma-aminobutyric acid (GABA) A receptor, alpha 4	140675	Rn.81205	NM_080587	2.32	2.31	2.35	2.32	2.38	2.31	1.01	up	7.04E-01	9.07E-01	-	-
1379416_at	---	---	---	Rn.169950	AW535897	2.38	2.36	2.37	2.43	2.36	2.34	1.01	up	7.27E-01	9.13E-01	-	-
1390230_at	Mip	major intrinsic protein of lens fiber	25480	Rn.23532	BG374588	2.53	2.50	2.53	2.51	2.61	2.47	1.01	up	8.21E-01	9.43E-01	-	-
1369593_at	Utp11l	UTP11-like, U3 small nucleolar ribonucleoprotein, (yeast)	170669	Rn.127806	NM_130825	2.55	2.52	2.60	2.53	2.58	2.53	1.01	down	7.53E-01	9.20E-01	-	-
1369357_at	Phka1	phosphorylase kinase alpha 1	64561	Rn.48743	NM_022626	2.30	2.29	2.34	2.31	2.30	2.29	1.01	down	5.20E-01	8.95E-01	-	-
1395195_at	---	---	---	Rn.167976	AI502884	2.45	2.47	2.46	2.44	2.46	2.44	1.01	down	2.16E-01	8.95E-01	-	-
1394745_at	Fam46a	Family with sequence similarity 46, member A	300870	Rn.788	AA850950	2.54	2.58	2.48	2.54	2.58	2.48	1.01	down	7.92E-01	9.33E-01	-	-
1377610_at	Lmod2	leiomodin 2 (cardiac)	299935	Rn.16210	AI453854	2.39	2.38	2.41	2.38	2.39	2.40	2.36	1.01	down	5.27E-01	8.95E-01	-	-
1381109_at	---	---	---	Rn.209207	BF412395	2.35	2.34	2.35	2.34	2.35	2.32	1.01	down	4.23E-01	8.95E-01	-	-
1392771_at	LOC689769	hypothetical protein LOC689769	689769	---	AI511314	2.52	2.51	2.48	2.51	2.52	2.51	1.01	up	4.92E-01	8.95E-01	-	-
1385542_at	---	---	---	Rn.153877	BF402259	2.48	2.47	2.48	2.47	2.53	2.46	1.01	up	6.47E-01	8.95E-01	-	-
1386409_at	---	---	---	Rn.157028	AI178343	2.44	2.42	2.44	2.43	2.43	2.41	1.01	down	3.38E-01	8.95E-01	-	-
1368240_a_at	Prkcb	protein kinase C, beta	25023	Rn.91118	X04440	2.37	2.36	2.38	2.36	2.38	2.34	1.01	down	4.33E-01	8.95E-01	-	-
1381041_at	---	---	---	Rn.211030	BF416665	2.43	2.41	2.45	2.42	2.43	2.40	1.01	down	5.04E-01	8.95E-01	-	-
1394284_at	---	---	---	Rn.171541	AW143904	2.43	2.42	2.45	2.43	2.45	2.40	1.01	down	5.69E-01	8.95E-01	-	-
1395590_at	LOC501485	hypothetical LOC501485	501485	---	BF391746	2.49	2.41	2.42	2.39	2.41	2.55	1.01	up	8.61E-01	9.57E-01	-	-
1367841_a_at	Pri8a9	prolactin family 8, subfamily a, member 9	171406	Rn.56124	NM_134385	2.43	2.41	2.46	2.42	2.45	2.40	1.01	down	6.39E-01	8.95E-01	-	-
1380176_at	---	---	---	---	BE097867	2.39	2.37	2.39	2.38	2.38	2.36	1.01	down	3.37E-01	8.95E-01	-	-
1380440_at	---	---	---	Rn.155425	BF549478	2.34	2.32	2.39	2.34	2.35	2.34	1.01	down	6.06E-01	8.95E-01	-	-
1374659_at	rCG_25854	cyclic AMP-regulated phosphoprotein	363153	Rn.7511	AI227983	2.39	2.37	2.42	2.38	2.39	2.37	1.01	down	5.31E-01	8.95E-01	-	-
1385235_at	AZbp1	ataxin 2 binding protein 1	302920	Rn.92540	AA818804	2.40	2.39	2.40	2.39	2.40	2.37	1.01	down	3.53E-01	8.95E-01	-	-
1380390_at	---	---	---	Rn.41929	AW523643	2.47	2.48	2.54	2.49	2.48	2.48	1.01	down	6.67E-01	8.99E-01	-	-
1397661_at	---	---	---	Rn.60089	BF390492	2.41	2.39	2.45	2.41	2.42	2.39	1.01	down	5.75E-01	8.95E-01	-	-
1384922_at	---	---	---	Rn.199647	AW527642	2.47	2.45	2.49	2.46	2.48	2.44	1.01	down	5.38E-01	8.95E-01	-	-
1368513_at	Enpep	glutamyl aminopeptidase	64017	Rn.162610	AW144216	3.97	5.00	3.60	4.85	3.89	3.86	1.01	up	9.85E-01	9.96E-01	-	-
1378859_at	Alx3	aristaless-like homeobox 3	365900	Rn.18878	AI058446	2.41	2.39	2.44	2.41	2.42	2.39	1.01	down	5.96E-01	8.95E-01	-	-
1385018_at	Dsg1b	desmoglein 1 beta	291755	Rn.35296	BM385089	2.36	2.35	2.39	2.36	2.36	2.34	1.01	down	4.74E-01	8.95E-01	-	-
1386265_at	---	---	---	Rn.125774	AI177183	2.33	2.32	2.35	2.32	2.33	2.31	1.01	down	4.12E-01	8.95E-01	-	-
1368649_at	Dkc1	dyskeratosis congenita 1, dyskerin	170944	Rn.4223	NM_133419	6.20	5.80	6.33	6.19	6.30	5.87	1.01

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicats)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1372893_at	Yipf1	Yip1 domain family, member 1	298312	Rn.98698	BI284198	5.29	5.53	4.89	4.87	5.36	5.44	1.01	down	9.70E-01	9.91E-01	-	-
1390511_at	---	---	---	---	BI285801	2.38	2.36	2.40	2.37	2.38	2.36	1.01	down	4.72E-01	8.95E-01	-	-
1397843_at	Wdr44	WD repeat domain 44	246152	Rn.79380	BG663841	2.48	2.48	2.54	2.48	2.55	2.45	1.01	down	7.92E-01	9.33E-01	-	-
1383777_at	---	---	---	---	BG666391	2.39	2.39	2.39	2.38	2.39	2.37	1.01	down	2.10E-01	8.95E-01	-	-
1396689_at	---	---	---	Rn.207541	BF413213	2.29	2.29	2.31	2.29	2.31	2.27	1.01	down	4.84E-01	8.95E-01	-	-
1394976_at	---	---	---	---	AI008980	2.49	2.47	2.49	2.48	2.50	2.45	1.01	down	5.72E-01	8.95E-01	-	-
1398201_at	---	---	---	Rn.59657	BF400860	2.45	2.44	2.47	2.46	2.46	2.40	1.01	down	6.40E-01	8.95E-01	-	-
1391927_at	---	---	---	Rn.201875	BE100100	2.53	2.46	2.48	2.56	2.48	2.47	1.01	up	7.93E-01	9.34E-01	-	-
1384941_at	Shf	Src homology 2 domain containing F	362205	Rn.205773	AI548100	2.79	2.80	2.80	2.78	2.85	2.78	1.01	up	6.66E-01	8.99E-01	-	-
1391058_at	RGD1310958	similar to RIKEN cDNA C130090K23	360307	Rn.40896	BE328934	2.54	2.49	2.51	2.56	2.50	2.45	1.01	down	7.80E-01	9.28E-01	-	-
1384723_at	Fut11	fucosyltransferase 11 (alpha (1,3) fucosyltransferase)	286971	Rn.24040	AI172124	2.37	2.61	2.38	2.36	2.37	2.59	1.01	down	9.30E-01	9.80E-01	-	-
1390446_at	---	---	---	Rn.137455	BI296080	2.36	2.35	2.37	2.40	2.37	2.35	1.01	up	5.57E-01	8.95E-01	-	-
1386392_at	Anapc10	anaphase promoting complex subunit 10	361389	Rn.9619	AI104638	2.45	2.42	2.47	2.44	2.46	2.41	1.01	down	6.14E-01	8.95E-01	-	-
1371690_at	Arl1	ADP-ribosylation factor-like 1	64187	Rn.3065	AA849825	9.86	9.59	10.10	9.88	9.62	10.08	1.01	up	9.61E-01	9.89E-01	-	-
1381681_at	---	---	---	Rn.176446	BE110205	2.79	2.77	2.81	2.78	2.80	2.76	1.01	down	5.95E-01	8.95E-01	-	-
1385044_at	Csrnp3	cysteine-serine-rich nuclear protein 3	311093	Rn.51147	BE107277	2.38	2.39	2.44	2.40	2.40	2.39	1.01	down	6.05E-01	8.95E-01	-	-
1398655_at	Myod1	myogenic differentiation 1	337868	Rn.9493	AA955902	2.33	2.32	2.35	2.32	2.34	2.31	1.01	down	4.77E-01	8.95E-01	-	-
1375437_at	---	---	---	Rn.22718	BI298111	8.82	8.95	8.78	8.81	8.78	8.92	1.01	down	8.82E-01	9.64E-01	-	-
1398654_at	---	---	---	Rn.33257	AI501129	2.64	2.65	2.66	2.63	2.69	2.60	1.01	down	7.36E-01	9.15E-01	-	-
1398209_at	---	---	---	Rn.210743	BF413358	2.73	2.56	2.85	2.70	2.80	2.67	1.01	up	9.19E-01	9.76E-01	-	-
1379458_at	---	---	---	Rn.40956	BE114418	2.36	2.35	2.37	2.36	2.37	2.32	1.01	down	5.06E-01	8.95E-01	-	-
1384137_at	---	---	---	Rn.134334	AI030318	2.48	2.47	2.50	2.47	2.48	2.46	1.01	down	4.24E-01	8.95E-01	-	-
1369373_at	Fgfr3	fibroblast growth factor receptor 3	84489	Rn.23671	NM_053429	2.40	2.38	2.41	2.39	2.39	2.38	1.01	down	3.23E-01	8.95E-01	-	-
1382498_x_at	Gdap1l1	ganglioside-induced differentiation-associated protein 1-like 1	311616	Rn.7542	BF408710	2.30	2.27	2.28	2.28	2.28	2.27	1.01	down	3.12E-01	8.95E-01	-	-
1368473_at	Gja5	gap junction protein, alpha 5	50563	Rn.88300	M83092	2.31	2.30	2.31	2.30	2.35	2.30	1.01	up	6.05E-01	8.95E-01	-	-
1369719_at	Phex	phosphate regulating endopeptidase homolog, X-linked	25512	Rn.37861	NM_013004	2.40	2.38	2.42	2.39	2.41	2.37	1.01	down	5.23E-01	8.95E-01	-	-
1383707_at	Gria4	glutamate receptor, ionotropic, AMPA4	29629	Rn.10938	BE101725	2.43	2.41	2.45	2.42	2.44	2.40	1.01	down	5.66E-01	8.95E-01	-	-
1396384_at	---	---	---	Rn.216630	AW521197	2.49	2.46	2.47	2.46	2.47	2.46	1.01	down	2.86E-01	8.95E-01	-	-
1394956_at	---	---	---	Rn.145170	AA859238	2.38	2.37	2.40	2.37	2.39	2.36	1.01	down	4.35E-01	8.95E-01	-	-
1382700_at	---	---	---	Rn.25420	AI237227	2.40	2.39	2.43	2.39	2.41	2.39	1.01	down	4.94E-01	8.95E-01	-	-
1385752_at	---	---	---	Rn.219500	BF394136	2.53	2.51	2.53	2.51	2.58	2.51	1.01	up	7.07E-01	9.08E-01	-	-
1369821_a_at	Cngb1	cyclic nucleotide gated channel beta 1	83686	Rn.10733	AF068572	2.42	2.41	2.43	2.41	2.43	2.39	1.01	down	4.62E-01	8.95E-01	-	-
1380540_at	---	---	---	Rn.211770	AI547392	2.49	2.46	2.50	2.48	2.49	2.44	1.01	down	6.51E-01	8.97E-01	-	-
1380669_at	---	---	---	---	BI292034	2.44	2.41	2.45	2.42	2.46	2.38	1.01	down	7.06E-01	9.08E-01	-	-
1378699_at	Pkhd1l1	polycystic kidney and hepatic disease 1-like 1	314917	Rn.3365	AI176379	2.43	2.41	2.45	2.42	2.44	2.40	1.01	down	5.69E-01	8.95E-01	-	-
1373179_at	LOC689994	similar to H43E16.1	689994	Rn.34800	BI300727	2.40	2.38	2.41	2.39	2.41	2.37	1.01	down	5.09E-01	8.95E-01	-	-
1374861_at	Tle2	transducin-like enhancer of split 2 (E(sp1) homolog, Drosophila)	299636	Rn.38683	AI175907	2.41	2.41	2.44	2.42	2.42	2.40	1.01	down	4.21E-01	8.95E-01	-	-
1396995_at	---	---	---	---	BG376821	2.43	2.40	2.45	2.49	2.43	2.40	1.01	up	7.53E-01	9.20E-01	-	-
1391361_at	---	---	---	Rn.153705	BF411568	2.56	2.53	2.67	2.57	2.75	2.48	1.01	up	9.12E-01	9.74E-01	-	-
1396772_at	---	---	---	Rn.171061	BE116581	2.51	2.49	2.53	2.52	2.52	2.46	1.01	down	6.79E-01	9.02E-01	-	-
1391755_at	---	---	---	Rn.204488	AI535177	2.35	2.35	2.39	2.35	2.36	2.35	1.01	down	4.90E-01	8.95E-01	-	-
1375959_at	Nkd1	naked cuticle homolog 1 (Drosophila)	364952	Rn.8826	AI007970	2.39	2.37	2.40	2.38	2.40	2.34	1.01	down	5.85E-01	8.95E-01	-	-
1388914_at	Ybx2	Y box binding protein 2	303250	Rn.40911	BI288013	2.34	2.32	2.35	2.33	2.34	2.31	1.01	down	4.68E-01	8.95E-01	-	-
1398001_at	---	---	---	Rn.93466	BF389870	2.28	2.27	2.31	2.27	2.28	2.27	1.01	down	3.92E-01	8.95E-01	-	-
1387395_at	Adora2b	adenosine A2B receptor	29316	Rn.89544	NM_017161	2.34	2.34	2.35	2.33	2.34	2.33	1.01	down	1.12E-01	8.95E-01	-	-
1369570_at	t1 /// Sult2a2 /// Ss	sulfotransferase family 2A, dehydroepiandrosterone (DHEA)-preferring, mem	02 /// 24912 /// 361	Rn.91378	NM_133616	2.53	2.49	2.58	2.52	2.58	2.47	1.01	down	8.10E-01	9.39E-01	-	-
1395242_at	---	---	---	Rn.166784	BF419005	3.17	4.57	3.26	3.25	3.99	3.79	1.01	up	9.85E-01	9.96E-01	-	-
1378490_at	---	---	---	Rn.207443	BE110558	2.41	2.40	2.44	2.40	2.42	2.39	1.01	down	5.23E-01	8.95E-01	-	-
1392096_at	RGD1308065	hypothetical LOC287935	287935	Rn.23006	BE112055	2.36	2.35	2.38	2.35	2.37	2.34	1.01	down	4.82E-01	8.95E-01	-	-
1373361_at	---	---	---	Rn.62782	BF394144	2.54	2.51	2.58	2.52	2.57	2.49	1.01	down	7.58E-01	9.21E-01	-	-
1378126_at	Dennd2a	DENN/MADD domain containing 2A	312257	Rn.50302	BE111592	2.41	2.40	2.43	2.40	2.42	2.39	1.01	down	4.83E-01	8.95E-01	-	-
1380220_at	---	---	---	Rn.205742	AW534345	2.41	2.42	2.42	2.40	2.41	2.40	1.01	down	1.56E-01	8.95E-01	-	-
1379120_at	---	---	---	Rn.172751	BF393971	2.41	2.40	2.43	2.41	2.42	2.39	1.01	down	4.46E-01	8.95E-01	-	-
1391785_at	Gldc	glycine dehydrogenase (decarboxylating)	309312	Rn.17101	BE115309	2.38	2.38	2.40	2.38	2.38	2.36	1.01	down	3.38E-01	8.95E-01	-	-
1398994_at	Tpst2	tyrosylprotein sulfotransferase 2	288719	Rn.3659	BI301193	8.63	8.62	7.91	8.73	8.02	8.38	1.01	down	9.76E-01	9.93E-01	-	-
1368931_at	Sh3gl3	SH3-domain GRB2-like 3	81921	Rn.5909	NM_031238	2.32	2.29	2.31	2.30	2.30	2.29	1.01	down	3.26E-01	8.95E-01	-	-
1390714_at	---	---	---	---	AI600086	2.36	2.34	2.36	2.35	2.35	2.33	1.01	down	2.54E-01	8.95E-01	-	-
1375077_at	---	---	---	Rn.33478	BE099881	2.74	2.70	2.74	2.71	2.81	2.64	1.01	down	8.49E-01	9.53E-01	-	-
1392728_at	---	---	---	Rn.167516	AW144027	2.30	2.29	2.32	2.29	2.30	2.28	1.01	down	3.78E-01	8.95E-01	-	-
1387643_at	Fgf21	fibroblast growth factor 21	170580	Rn.81231	NM_130752	2.44	2.43	2.46	2.43	2.44	2.42	1.01	down	4.50E-01	8.95E-01	-	-
1394821_at	---	---	---	Rn.144597	BF399731	2.38	2.37	2.40	2.36	2.40	2.36	1.01	down	5.05E-01	8.95E-01	-	-
1380772_at	---	---	---	Rn.199514	BE105726	2.39	2.38	2.41	2.39	2.39	2.38	1.01	down	3.68E-01	8.95E-01	-	-
1394776_at	Adamts6	ADAM metallopeptidase with thrombospondin type 1 motif, 6	361886	Rn.32385	AA899386	2.46	2.43	2.45	2.44	2.45	2.42	1.01	down	4.49E-01	8.95E-01	-	-
1389287_at	---	---	---	Rn.148060	BI279573	9.66	9.05	8.73	9.13	9.07	9.21	1.01	down	9.72E-01	9.92E-01	-	-
1377468_at	Dkk3	dickkopf homolog 3 (Xenopus laevis)	171548	Rn.12516	BF404521	2.45	2.44	2.46	2.44	2.45	2.43	1.01	down	2.94E-01	8.95E-01	-	-
1379118_at	---	---	---	---	AI072498	2.50	2.48	2.51	2.49	2.51	2.46	1.01	down	5.41E-01	8.95E-01	-	-
1394506_at	---	---	---	Rn.92717	AI549348	2.33	2.32	2.36	2.32	2.34	2.31	1.01	down	4.94E-01	8.95E-01	-	-
1393168_at	LOC688133	similar to mbt domain containing 1	688133	---	BF398450	5.22	5.30	5.23	5.18	5.35	5.18	1.01	down	8.72E-01	9.61E-01	-	-
1391357_at	---	---	---	Rn.208932	BF410388	2.48	2.47	2.49	2.47	2.48	2.45	1.01	down	4.70E-01	8.95E-01	-	-
1380819_at	---	---	---	Rn.212771	BF391871	2.50	2.48	2.53	2.49	2.52	2.47	1.01	down	6.67E-01	8.99E-01	-	-
1375625_at	Paqr8	progestin and adipoQ receptor family member VIII	316275	Rn.209282	BF405077	2.38	2.35	2.37	2.36	2.37	2.35	1.01	down	3.07E-01	8.95E-01	-	-
1381534_at	---	---	---	Rn.20386	BI278449	2.41	2.42	2.42	2.40	2.41	2.46	1.01	up	6.28E-01	8.95E-01	-	-
1376166_at	RGD1308544	LOC361192	361192	Rn.46881	AW528438	2.51	2.47	2.52	2.51	2.52	2.50	1.01	up	5.59E-01	8.95E-01	-	-
1380697_at	---	---	---	Rn.63336	BE107803	2.31	2.31	2.35	2.31	2.32	2.31	1.01	down	4.56E-01	8.95E-01	-	-
1372114_at	LOC682083	similar to family 53, member C protein	682083	---	BE099433	2.34	2.34	2.35	2.34	2.39	2.33	1.01	up	5.95E-01	8.95E-01	-	-
1381089_at	---	---	---	Rn.147596	BE114458	2.44	2.39	2.45	2.41	2.46	2.38	1.01	down	7.34E-01	9.15E-01	-	-
1381490_at	---	---	---	Rn.168531	AI711004	2.53	2.52	2.56	2.53	2.55	2.50	1.01	down	6.31E-01	8.95E-01	-	-
1386404_at	---	---	---	---	AI639198	2.42	2.40	2.45	2.41	2.43	2.39	1.01	down	6.04E-01	8.95E-01	-	-
1375385_at	LOC500007	similar to EF hand calcium binding domain 1	500007	Rn.198668	BF406234	2.43	2.44	2.44	2.44	2.40	2.41	1.01	down	4.96E-01	8.95E-01	-	-
1393355_at	---	---	---	Rn.23553	AI111659	2.44	2.42	2.46	2.43	2.44	2.41	1.01	down	5.25E-01	8.95E-01	-	-
1374696_at	---	---	---	Rn.76252	AI170182	6.28	5.83	6.07	6.13	5.81	6.20	1.01	down	9.57E-01	9.88E-01	-	-
1389855_at	Ppp2r2c	Protein phosphatase 2 (formerly 2A), regulatory subunit B, gamma isoform	117256	Rn.54550	BF414575	2.32	2.31	2.32	2.31	2.36	2.31	1.01	up	5.44E-01	8.95E-01	-	-
1397914_at	---	---	---	Rn.171112	BE108111	2.37	2.38	2.39	2.44	2.39	2.35	1.01	up	7.04E-01	9.07E-01	-	-
1378289_at	---	---	---	Rn.199257	BE120159	2.28	2.28	2.29	2.32	2.28	2.27	1.01	up	5.69E-01	8.95E-01	-	-
1381815_at	---	---	---	Rn.170606	BE097058	2.31	2.30	2.35	2.30	2.33	2.29	1.01	down	6.28E-01	8.95E-01	-	-
1398061_at	---	---	---	Rn.58247	BF394224	2.34	2.34	2.37	2.34	2.35	2.33	1.01	down	4.00E-01	8.95E-01	-	-
1393529_at	---	---	---	Rn.155903	AI011935	2.35	2.33	2.35	2.33	2.34	2.32	1.01	down	3.28E-01	8.95E-01	-	-
1390332_at	Znf692	zinc finger protein 692	303164	Rn.137772	BF387670	2.42	2.40	2.44	2.41	2.42	2.39	1.01	down	4.98E-01	8.95E-01	-	-
1385364_at	---	---	---	Rn.172572	BF390761	2.36	2.35	2.38	2.35	2.37	2.34	1.01	down	4.93E-01	8.95E-01	-	-
1378327_at	Dmrt2	doublesex and mab-3 related transcription factor 2	309430	Rn.11448	AA963348	2.32	2.31	2.35	2.32	2.32	2.31	1.01	down	4.34E-01	8.95E-01	-	-
1378691_at	---	---	---	Rn.8155	AA893871	3.75	4.93	3.17	3.93	3.86	4.09	1.01	up	9.86E-01	9.96E-01	-	-
1377301_at	---	---	---	Rn.161322	BF406641	2.44	2.44	2.43	2.43	2.43	2.42	1.01	down	1.07E-01	8.95E-01	-	-
1370278_at	Atp5d	ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit	245965	Rn.3879	U00926	8.62	9.32	9.24	9.08	9.24	9.09	1.01	up	9.54E-01	9.86E-01	-	-
1369606_at	Fgf20	fibroblast growth factor 20	66017	Rn.64492	NM_023961	2.53	2.50	2.58	2.53	2.55	2.50	1.01	down	7.18E-01	9.11E-01	-	-
1375771_at	---	---	---	---	BI399598	2.25	2.22	2.23	2.23	2.23	2.22	1.01	down	3.83E-01	8.95E-01	-	-
1390754_at	Cadps	Ca++-dependent secretion activator	26989	Rn.88197	BF412921	2.46	2.44	2.48	2.45	2.46	2.43	1.01	down	5.02E-01	8.95E-01	-	-
1398741_at	---	---	---	Rn.207030	BE096877	2.35	2.34	2.39	2.34	2.36	2.34	1.01	down	6.05E-01	8.95E-01	-	-
1395150_at	Kcne2	Potassium voltage-gated channel, Isk-related subfamily, gene 2	171138	Rn.48691	AI502111	2.49	2.44	2.50	2.55	2.49	2.42	1.01	up	8.17E-01	9.41E-01	-	-
1377985_at	RGD1309198	Similar to U5 snRNP-specific protein (Prp8-binding)	313056	Rn.15351	BE120398	2.46	2.44	2.46	2.45	2.46	2.43	1.01	down	3.87E-01	8.95E-01	-	-
1393885_at	---	---	---	Rn.198889	AI555628	2.52	2.44	2.45	2.42	2.51	2.44	1.01	down	7.99E-01	9.35E-01	-	-
1368771_at	Sulf1	sulfatase 1	171396	Rn.161961	NM_134378	2.38	2.38	2.40	2.38	2.39	2.36	1.01	down	3.64E-01	8.95E-01	-	-
1375159_at	---	---	---	Rn.128671	BI291443	2.44	2.41	2.44	2.43	2.44	2.40	1.01	down	5.02E-01	8.95E-01	-	-
1380469_at	---	---	---	Rn.114311	AI012603	2.33	2.32	2.36	2.32	2.33	2.32	1.01	down	4.58E-01	8.95E-01	-	-
1398266_a_at	Egr2	early growth response 2	114090	Rn.89235	D83508	2.38	2.37	2.39	2.37	2.38	2.36	1.01	down	3.49E-01	8.95E-01	-	-
1381095_at	---	---	---	Rn.154104	BI302849	2.36	2.35	2.37	2.35	2.37	2.38	1.01	up	3.74E-01	8.95E-01	-	-
1377873_at	---	---	---	Rn.137136	AW251736	2.42	2.41	2.43	2.42	2.42	2.40	1.01	down	2.26E-01	8.95E-01	-	-
1374003_at	---	---	---	Rn.32524	BM389589	3.74	3.09	3.06	3.71	3.10	3.05	1.01	down	9.75E-01	9.93E-01	-	-
1370646_at	Rmt1	mammary cancer associated protein RMT-1	246306	Rn.81216	AF308611	2.41	2.40	2.42	2.40	2.41	2.39	1.01	down	2.95E-01	8.95E-01	-	-
1392765_at	---	---	---	Rn.34696	AA965019	2.32	2.30	2.32	2.31	2.32	2.29	1.01	down	3.58E-01	8.95E-01	-	-
1379103_at	---	---	---	Rn.59850	BF406246	2.52	2.51	2.56	2.51	2.61	2.51	1.01	up	7.98E-01	9.35E-01	-	-
1370767_at	Cox6c1	cytochrome c oxidase subunit VIc-1	286962	Rn.10885	M20183	2.40	2.40	2.42	2.40	2.41	2.44	1.01	up	5.24E-01	8.95E-01	-	-
1393968_at	Scarf1	scavenger receptor class F, member 1	303313	Rn.130912	BF567034	2.59	2.61	2.55	2.57	2.64	2.51	1.01	down	8.21E-01	9.43E-01	-	-
1393685_at	Pdzrn4	PDZ domain containing RING finger 4	315250	Rn.218491	BF404962	2.36	2.35	2.39	2.35	2.37	2.34	1.01	down	4.74E-01	8.95E-01	-	-
1380234_at	---	---	---	---	BE105916	2.32	2.32	2.34	2.32	2.34	2.30	1.01	down	4.68E-01	8.95E-01	-	-
1369154_at	Nphs1	nephrosis 1 homolog, nephrin (human)	64563	Rn.48745	AF172255	2.39	2.38	2.39	2.39	2.44	2.37	1.01	up	6.61E-01	8.98E-01	-	-
1385950_at	Fam131b	family with sequence similarity 131, member B	500102	Rn.161821	AI454926	2.48	2.44	2.48	2.46	2.47	2.44	1.01	down	6.00E-01	8.95E-01	-	-
1375606_at	---	---	---	---	AI235906	2.43	2.42	2.45	2.42	2.45	2.40	1.01	down	5.74E-01	8.95E-01	-	-
1379619_at	---	---	---	Rn.27422	BE104952	2.43	2.42	2.45	2.42	2.44	2.41	1.01	down	4.44E-01	8.95E-01	-	-
1378200_at	---	---	---	---	AW434934	2.39	2.38	2.42	2.39	2.39	2.38	1.01	down	3.96E-01	8.95E-01	-	-
1396307_at	---	---	---	Rn.172895	BF522607	2.76	2.75	2.76	2.74	2.77	2.74	1.01	down	3.88E-01	8.95E-01	-	-
1381865_at	---	---	---	---	AI406463	2.56	2.53	2.55	2.53	2.61	2.52	1.01	up	7.57E-01	9.21E-01	-	-
1371050_at	Pon1	paraoxonase 1	84024	Rn.20732	AI717733	2.32	2.29	2.36	2.30	2.35	2.28	1.01	down	7.52E-01	9.20E-01	-	-
1385746_at	LOC681167	hypothetical protein LOC681167	681167	Rn.136477	BF389622	2.42	2.39	2.42	2.40	2.42	2.38	1.01	down	4.99E-01	8.95E-01	-	-
1380252_at	Psmd11	proteasome (prosome, macropain) 26S subunit, non-ATPase, 11	303353	Rn.11861	AW527866	2.49	2.44	2.48	2.45	2.50	2.43	1.01	down	7.12E-01	9.10E-01	-	-
1398086_at	---	---	---	Rn.148427	BE103205	2.38	2.37	2.39	2.37	2.38	2.35	1.01	down	3.73E-01	8.95E-01	-	-
1368876_a_at	Nrxn2	neurexin 2	116595	Rn.11282	BI111779	2.41	2.38	2.40	2.39	2.40	2.37	1.01	down	4.21E-01	8.95E-01	-	-
1397221_s_at	Fas	Fas (TNF receptor superfamily, member 6)	246097	Rn.162521	BE108106	2.41	2.39	2.43	2.40	2.42	2.38	1.01	down	4.99E-01	8.95E-01	-	-
1382418_at	---	---	---	Rn.203280	AA901131	2.38	2.37	2.39	2.37	2.38	2.36	1.01	down	3.09E-01	8.95E-01	-	-
1397299_at	Frmpd1	FERM and PDZ domain containing 1	313244	Rn.37934	AW532232	2.35	2.32	2.34	2.33	2.33	2.31	1.01	down	5.00E-01	8.95E-01	-	-
1377459_at	Ly6g6e	lymphocyte antigen 6 complex, locus G6E	406866	Rn.205716	AI764114	2.36	2.35	2.39	2.36	2.36	2.35	1.01	down	6.05E-01	8.95E-01	-	-
1381962_at	---	---	---	Rn.38164	AI548146	2.41	2.39	2.42	2.40	2.41	2.38	1.01	down	4.13E-01	8.95E-01	-	-
1382910_at	---	---	---	Rn.166505	AI072237	2.43	2.42	2.45	2.42	2.44	2.41	1.01	down	4.56E-01	8.95E-01	-	-
1368865_at	Synpr	synaptoporin	66030	Rn.211986	BG666364	2.39	2.38	2.43	2.38	2.42	2.37	1.01	down	6.82E-01	9.03E-01	-	-
1385144_at	---	---	---	Rn.136315	AW524749	2.50	2.48	2.54	2.48	2.54	2.46	1.01	down	7.71E-01	9.25E-01	-	-
1368825_at	Shox2	short stature homeobox 2	25546	Rn.11258	NM_013028	2.37	2.35	2.38	2.36	2.36	2.35	1.01	down	3.05E-01	8.95E-01	-	-
1369878_at	Olr1654	olfactory receptor 1654	60451	Rn.138118	NM_021860	2.33	2.32	2.34	2.32	2.33	2.31	1.01	down	3.35E-01	8.95E-01	-	-
1376480_at	---	---	---	Rn.59163	BF398798	2.38	2.36	2.39	2.36	2.37	2.35	1.01	down	3.66E-01	8.95E-01	-	-
1381116_at	---	---	---	Rn.200109	BF413592	2.39	2.36	2.39	2.37	2.39	2.35	1.01	down	5.37E-01	8.95E-01	-	-
1382409_at	Tsga14	testis specific, 14	500069	Rn.162740	AI072515	2.46	2.45	2.48	2.45	2.47	2.45	1.01	down	3.53E-01	8.95E-01	-	-
1396699_at	---	---	---	---	BF392736	2.39	2.38	2.41	2.39	2.40	2.37	1.01	down	4.52E-01	8.95E-01	-	-
1390737_at	---	---	---	Rn.205592	AI712996	2.36	2.35	2.37	2.35	2.40	2.35	1.01	up	6.13E-01	8.95E-01	-	-
1376562_at	RGD1561817	similar to Traf2 and NCK interacting kinase, splice variant 4	294917	Rn.220700	BI291396	2.49	2.46	2.50	2.46	2.48	2.47	1.01	down	4.67E-01	8.95E-01	-	-
1391483_at	Creb3l3	cAMP responsive element binding protein 3-like 3	314638	Rn.20059	BF282264	2.32	2.32	2.33	2.32	2.38	2.32	1.01	up	6.39E-01	8.95E-01	-	-
1398739_at	---	---	---	Rn.210538	BF400127	2.56	2.50	2.59	2.51	2.61	2.49	1.01	down	8.27E-01	9.45E-01	-	-
1370224_at	Stat3	signal transducer and activator of transcription 3	25125	Rn.10247	BE113920	6.18	7.23	7.73	6.99	7.09	7.04	1.01	down	9.84E-01	9.95E-01	-	-
1385222_at	Eomes	eomesodermin homolog (Xenopus laevis)	316052	Rn.208436	BE116545	2.39	2.39	2.46	2.39	2.50	2.38	1.01	up	8.34E-01	9.48E-01	-	-
1395002_at	---	---	---	Rn.124019	BF404368	2.36	2.35	2.36	2.35	2.36	2.33	1.01	down	2.93E-01	8.95E-01	-	-
1384682_at	---	---	---	---	AA864690	2.

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1391465_at	Otud3	OTU domain containing 3	500572	Rn.98341	BE112623	2.34	2.34	2.34	2.33	2.34	2.32	1.01	down	1.91E-01	8.95E-01	-	-
1384731_at	---	---	---	Rn.165989	AI043907	2.31	2.30	2.33	2.30	2.31	2.29	1.01	down	3.82E-01	8.95E-01	-	-
1396371_at	---	---	---	Rn.135293	BF412674	2.43	2.41	2.45	2.42	2.45	2.40	1.01	down	6.19E-01	8.95E-01	-	-
1369245_at	Chrm2	cholinergic receptor, muscarinic 2	81645	Rn.10752	NM_031016	2.39	2.38	2.41	2.38	2.40	2.37	1.01	down	4.65E-01	8.95E-01	-	-
1381108_at	363737 /// RGD136	hypothetical LOC363737 /// similar to hypothetical protein FLJ20436	300206 /// 363737	Rn.884	BF387399	2.43	2.43	2.44	2.42	2.43	2.41	1.01	down	2.37E-01	8.95E-01	-	-
1367782_at	Cox6a2	cytochrome c oxidase, subunit VIa, polypeptide 2	25278	Rn.5119	NM_012812	2.36	2.35	2.37	2.35	2.37	2.34	1.01	down	4.03E-01	8.95E-01	-	-
1393748_at	Tlll1	tubulin tyrosine ligase-like family, member 11	689746	Rn.56586	BF387694	2.48	2.47	2.50	2.47	2.49	2.46	1.01	down	4.96E-01	8.95E-01	-	-
1380241_a_at	Lrp5	low density lipoprotein receptor-related protein 5	293649	Rn.12698	AW435376	2.48	2.90	2.49	2.90	2.48	2.46	1.01	down	9.63E-01	9.90E-01	-	-
1386115_at	---	---	---	Rn.136212	BF290493	2.48	2.45	2.49	2.46	2.49	2.43	1.01	down	6.55E-01	8.98E-01	-	-
1393429_at	---	---	---	Rn.20719	AI044048	2.34	2.34	2.36	2.34	2.34	2.33	1.01	down	3.54E-01	8.95E-01	-	-
1394983_at	---	---	---	Rn.149143	BE108223	2.47	2.46	2.48	2.46	2.48	2.45	1.01	down	4.87E-01	8.95E-01	-	-
1392164_at	---	---	---	Rn.161442	BG374714	2.32	2.31	2.33	2.31	2.32	2.30	1.01	down	2.56E-01	8.95E-01	-	-
1374274_at	---	---	---	Rn.50697	AW434998	2.38	2.38	2.39	2.38	2.42	2.37	1.01	up	6.00E-01	8.95E-01	-	-
1395469_at	---	---	---	---	AW251983	2.30	2.29	2.32	2.30	2.31	2.28	1.01	down	4.64E-01	8.95E-01	-	-
1396231_at	Cdca4	cell division cycle associated 4	500727	Rn.32426	BI293502	2.54	2.48	2.50	2.57	2.50	2.48	1.01	up	7.88E-01	9.31E-01	-	-
1391871_at	Stard13	StAR-related lipid transfer (START) domain containing 13	498130	Rn.26672	AI763550	2.58	2.74	2.65	2.57	2.62	2.74	1.01	down	8.95E-01	9.67E-01	-	-
1371182_at	Tpo	Thyroid peroxidase	54314	Rn.91199	M57705	2.55	2.53	2.59	2.54	2.58	2.52	1.01	down	7.08E-01	9.08E-01	-	-
1385107_at	Slc6a14	solute carrier family 6 (neurotransmitter transporter), member 14	298340	Rn.103683	AI137961	2.57	2.53	2.64	2.54	2.67	2.50	1.01	down	8.77E-01	9.62E-01	-	-
1380302_at	---	---	---	Rn.206035	BE121073	2.39	2.39	2.41	2.43	2.40	2.38	1.01	up	6.01E-01	8.95E-01	-	-
1383565_at	---	---	---	Rn.48491	BE120852	2.41	2.42	2.43	2.42	2.42	2.39	1.01	down	4.23E-01	8.95E-01	-	-
1381553_at	---	---	---	Rn.207786	BG371725	2.43	2.41	2.44	2.41	2.43	2.41	1.01	down	2.83E-01	8.95E-01	-	-
1395414_at	Agl	amylo-1,6-glucosidase, 4-alpha-glucanotransferase	362029	Rn.34559	BI296064	2.44	2.42	2.46	2.43	2.45	2.42	1.01	down	4.83E-01	8.95E-01	-	-
1392026_at	---	---	---	Rn.146760	BF391823	2.38	2.37	2.39	2.38	2.43	2.37	1.01	up	6.61E-01	8.98E-01	-	-
1385073_at	---	---	---	---	AI145639	2.47	2.45	2.48	2.45	2.47	2.45	1.01	down	4.60E-01	8.95E-01	-	-
1397007_at	---	---	---	Rn.147943	BI278529	2.49	2.47	2.51	2.48	2.50	2.46	1.01	down	5.89E-01	8.95E-01	-	-
1374928_at	---	---	---	---	BF406240	2.39	2.43	2.40	2.40	2.41	2.39	1.01	down	4.93E-01	8.95E-01	-	-
1395008_at	Itsn1	intersectin 1 (SH3 domain protein)	29491	Rn.48657	BF406892	2.33	2.32	2.35	2.33	2.36	2.29	1.01	down	6.61E-01	8.98E-01	-	-
1382531_at	Tlr7	toll-like receptor 7	317468	Rn.219862	AI408425	2.43	2.41	2.44	2.42	2.43	2.40	1.01	down	4.87E-01	8.95E-01	-	-
1367592_at	Tnnt2	troponin T type 2 (cardiac)	24837	Rn.9965	NM_012676	2.50	2.47	2.53	2.51	2.52	2.45	1.01	down	7.48E-01	9.19E-01	-	-
1387617_at	Tpm3	tropomyosin 3, gamma	117557	Rn.37575	NM_057208	12.26	12.14	12.27	12.15	12.25	12.30	1.01	up	8.79E-01	9.63E-01	-	-
1388963_at	Astn1	astrotactin 1	304900	Rn.28132	AI102087	2.38	2.37	2.40	2.37	2.39	2.36	1.01	down	4.98E-01	8.95E-01	-	-
1378918_at	---	---	---	Rn.33489	AI071712	2.31	2.30	2.32	2.30	2.32	2.29	1.01	down	4.42E-01	8.95E-01	-	-
1384711_at	---	---	---	Rn.166886	AI144960	2.40	2.37	2.44	2.39	2.40	2.38	1.01	down	6.44E-01	8.95E-01	-	-
1368294_at	Dnase1l3	deoxyribonuclease 1-like 3	116687	Rn.29996	NM_053907	2.33	2.32	2.35	2.32	2.34	2.31	1.01	down	4.32E-01	8.95E-01	-	-
1394693_at	---	---	---	,200086 /// Rn.201	AW919728	2.57	2.52	2.61	2.53	2.67	2.48	1.01	down	8.84E-01	9.64E-01	-	-
1393124_at	---	---	---	Rn.60676	AI145807	2.42	2.41	2.44	2.41	2.42	2.40	1.01	down	3.73E-01	8.95E-01	-	-
1384547_at	RY2G5	potential ligand-binding protein	499925	---	AI070639	2.38	2.36	2.38	2.36	2.45	2.34	1.01	up	7.97E-01	9.35E-01	-	-
1395868_at	---	---	---	---	BF287970	2.35	2.34	2.36	2.34	2.36	2.33	1.01	down	3.80E-01	8.95E-01	-	-
1395446_at	---	---	---	---	AW916813	2.53	2.47	2.53	2.50	2.52	2.48	1.01	down	6.96E-01	9.06E-01	-	-
1379257_at	Epb4.1l4a	erythrocyte protein band 4.1-like 4a	307514	Rn.107191	BE100811	5.31	3.98	3.71	3.79	4.72	4.53	1.01	up	9.87E-01	9.96E-01	-	-
1378212_at	---	---	---	Rn.206837	BI003251	2.34	2.30	2.31	2.31	2.31	2.30	1.01	down	3.94E-01	8.95E-01	-	-
1397903_at	---	---	---	Rn.146838	BI280014	2.44	2.43	2.47	2.44	2.45	2.43	1.01	down	4.81E-01	8.95E-01	-	-
1381583_at	---	---	---	Rn.45525	AW522965	2.39	2.37	2.40	2.38	2.39	2.36	1.01	down	4.46E-01	8.95E-01	-	-
1390528_at	---	---	---	Rn.205575	AW251953	2.35	2.35	2.36	2.35	2.40	2.34	1.01	up	6.74E-01	9.01E-01	-	-
1392929_at	RGD1565616	RGD1565616	499891	Rn.6943	BF416678	7.28	6.05	5.35	5.70	6.41	6.54	1.01	down	9.88E-01	9.96E-01	-	-
1391306_at	---	---	---	Rn.220420	AI070952	6.79	6.44	7.76	6.87	7.57	6.57	1.01	up	9.85E-01	9.96E-01	-	-
1387647_at	Tff1	trefoil factor 1	117270	Rn.10715	NM_057129	2.44	2.41	2.44	2.42	2.50	2.40	1.01	up	7.88E-01	9.24E-01	-	-
1379705_at	---	---	---	---	AI511060	2.45	2.43	2.48	2.45	2.46	2.43	1.01	down	5.43E-01	8.95E-01	-	-
1367621_at	Dapk3	death-associated protein kinase 3	64391	Rn.60353	NM_022546	3.10	3.08	3.03	3.10	3.06	3.09	1.01	up	7.02E-01	9.07E-01	-	-
1379080_at	---	---	---	Rn.133105	AI412555	2.31	2.29	2.32	2.29	2.31	2.29	1.01	down	3.83E-01	8.95E-01	-	-
1381236_at	---	---	---	---	AI578104	2.50	2.49	2.52	2.49	2.50	2.48	1.01	down	4.24E-01	8.95E-01	-	-
1375433_at	Disp2	Dispatched homolog 2 (Drosophila)	311324	Rn.19932	AI412473	2.36	2.36	2.38	2.36	2.37	2.35	1.01	down	3.77E-01	8.95E-01	-	-
1370900_at	Myh4	myosin, heavy chain 4, skeletal muscle	360543	Rn.202948	BM391169	2.50	2.46	2.59	2.49	2.64	2.44	1.01	up	8.96E-01	9.67E-01	-	-
1373801_at	---	---	---	Rn.63570	BF404819	2.44	2.41	2.44	2.42	2.44	2.41	1.01	down	4.93E-01	8.95E-01	-	-
1386407_at	---	---	---	---	AI137911	2.56	2.53	2.62	2.54	2.68	2.51	1.01	up	8.80E-01	9.63E-01	-	-
1376111_at	---	---	---	Rn.139017	BG371699	2.44	2.43	2.45	2.43	2.44	2.42	1.01	down	3.11E-01	8.95E-01	-	-
1391247_at	---	---	---	Rn.140746	BF403208	2.40	2.39	2.42	2.39	2.41	2.38	1.01	down	5.21E-01	8.95E-01	-	-
1389712_at	Ebf3	early B-cell factor 3	361668	Rn.64435	BE117335	2.38	2.36	2.39	2.37	2.38	2.36	1.01	down	4.06E-01	8.95E-01	-	-
1395006_at	---	---	---	Rn.171802	BE121319	2.50	2.44	2.50	2.47	2.47	2.47	1.01	down	6.23E-01	8.95E-01	-	-
1387850_at	Tmeff1	transmembrane protein with EGF-like and two follistatin-like domains 1	63845	Rn.162809	NM_023020	2.37	2.36	2.39	2.36	2.38	2.35	1.01	down	4.29E-01	8.95E-01	-	-
1376311_at	Ntng1	netrin G1	295382	Rn.162628	BM391312	2.41	2.40	2.43	2.40	2.42	2.39	1.01	down	5.00E-01	8.95E-01	-	-
1385559_at	RGD1563441	similar to RIKEN cDNA A030009H04	497935	Rn.148168	BF562977	2.51	2.44	2.46	2.45	2.51	2.43	1.01	down	7.84E-01	9.30E-01	-	-
1378712_at	Icam5	intercellular adhesion molecule 5, telencephalin	313785	Rn.59765	BM382822	2.38	2.35	2.42	2.41	2.39	2.33	1.01	down	7.71E-01	9.25E-01	-	-
1387377_a_at	Pak1	p21 protein (Cdc42/Rac)-activated kinase 1	29431	Rn.9149	U23443	5.26	5.68	5.00	4.73	6.09	5.14	1.01	up	9.84E-01	9.95E-01	-	-
1398020_at	---	---	---	---	BF393027	2.35	2.36	2.35	2.35	2.35	2.33	1.01	down	2.29E-01	8.95E-01	-	-
1396386_at	Bace2	Beta-site APP-cleaving enzyme 2	288227	Rn.38581	BF408665	2.51	2.48	2.54	2.50	2.53	2.47	1.01	down	7.15E-01	9.10E-01	-	-
1376750_at	---	---	---	Rn.13859	AA963477	2.36	2.35	2.37	2.35	2.36	2.33	1.01	down	4.13E-01	8.95E-01	-	-
1394736_at	Popdc2	popeye domain containing 2	360718	Rn.145147	BE106093	2.35	2.33	2.37	2.34	2.35	2.33	1.01	down	5.24E-01	8.95E-01	-	-
1389471_at	Tomm34	translocase of outer mitochondrial membrane 34	311621	Rn.16749	AI412736	4.53	5.04	4.31	4.82	4.52	4.51	1.01	down	9.89E-01	9.91E-01	-	-
1374122_at	Myo5c	myosin VC	315820	Rn.2304	BM386808	2.34	2.34	2.36	2.34	2.35	2.33	1.01	down	3.90E-01	8.95E-01	-	-
1381339_at	Eif3k	eukaryotic translation initiation factor 3, subunit K	292762	Rn.1706	AI113218	2.53	2.93	2.54	2.53	2.54	2.96	1.01	up	9.62E-01	9.89E-01	-	-
1398505_at	Rasip1	Ras interacting protein 1	292912	Rn.23451	BE112418	2.36	2.35	2.37	2.35	2.36	2.34	1.01	down	2.92E-01	8.95E-01	-	-
1389813_at	---	---	---	Rn.20324	AI070324	2.41	2.41	2.42	2.40	2.48	2.40	1.01	up	7.42E-01	9.17E-01	-	-
1390971_at	---	---	---	Rn.16009	AI171284	2.49	2.49	2.53	2.49	2.51	2.48	1.01	down	5.73E-01	8.95E-01	-	-
1394911_at	Zc3hav1l	zinc finger CCCH-type, antiviral 1-like	362341	Rn.23445	AI235676	2.31	2.31	2.32	2.30	2.31	2.29	1.01	down	2.61E-01	8.95E-01	-	-
1382465_at	Lipe	lipase, hormone sensitive	25330	Rn.10566	AW533397	2.22	2.19	2.19	2.19	2.19	2.19	1.01	down	3.19E-01	8.95E-01	-	-
1375016_at	---	---	---	Rn.24461	AI408912	6.61	6.77	7.19	6.95	6.47	7.18	1.01	up	9.73E-01	9.92E-01	-	-
1381162_at	10-Sep	Septin 10	309891	Rn.27246	AI136863	2.93	2.59	2.98	2.81	2.86	2.80	1.01	down	9.41E-01	9.83E-01	-	-
1379478_at	Stac2	SH3 and cysteine rich domain 2	363674	Rn.153636	BF406342	2.32	2.32	2.34	2.32	2.33	2.31	1.01	down	2.35E-01	8.95E-01	-	-
1386584_x_at	---	---	---	Rn.148318	AI045356	2.42	2.41	2.42	2.42	2.45	2.41	1.01	up	5.44E-01	8.95E-01	-	-
1398519_at	---	---	---	---	AI549576	2.40	2.39	2.41	2.39	2.40	2.38	1.01	down	3.61E-01	8.95E-01	-	-
1394141_at	---	---	---	Rn.130142	AI638976	2.41	2.39	2.42	2.40	2.41	2.38	1.01	down	5.08E-01	8.95E-01	-	-
1380817_at	Depdc2	DEP domain containing 2	312912	Rn.219440	BF394055	2.40	2.38	2.41	2.39	2.40	2.37	1.01	down	5.10E-01	8.95E-01	-	-
1370742_at	Clph	casein-like phosphoprotein	64029	Rn.54001	AF271155	2.42	2.39	2.41	2.40	2.41	2.39	1.01	down	3.53E-01	8.95E-01	-	-
1376338_at	Garnl1	GTPase activating Rap/RanGAP domain-like 1	56785	Rn.86984	BE111650	2.34	2.32	2.34	2.33	2.33	2.31	1.01	down	3.86E-01	8.95E-01	-	-
1385419_at	Gpr143	G protein-coupled receptor 143	302619	Rn.141649	AI070365	2.39	2.53	2.41	2.60	2.40	2.36	1.01	up	9.17E-01	9.75E-01	-	-
1397223_at	---	---	---	---	AI231513	2.35	2.34	2.37	2.34	2.35	2.33	1.01	down	4.30E-01	8.95E-01	-	-
1396389_at	LOC687758	similar to phosphatidylinositol-4-phosphate 5-kinase-like 1	687758	---	AW522358	2.45	2.44	2.48	2.45	2.46	2.44	1.01	down	4.94E-01	8.95E-01	-	-
1397716_at	Klhdc2	Kelch domain containing 2	299113	Rn.129179	AI547852	2.49	2.49	2.53	2.49	2.51	2.48	1.01	down	5.99E-01	8.95E-01	-	-
1397291_at	RGD1310185	Similar to RIKEN cDNA 9030625A04	313790	Rn.168042	AI535254	2.37	2.36	2.38	2.36	2.37	2.35	1.01	down	3.08E-01	8.95E-01	-	-
1372917_at	Ptrh2	peptidyl-tRNA hydrolase 2	287593	Rn.13456	AI111992	2.82	2.38	2.37	2.36	2.36	2.88	1.01	up	9.68E-01	9.91E-01	-	-
1369599_at	Galp	galanin-like peptide	64568	Rn.48754	NM_022633	2.37	2.34	2.36	2.35	2.36	2.33	1.01	down	3.86E-01	8.95E-01	-	-
1386555_at	Csnk2a2	casein kinase 2, alpha prime polypeptide	307641	Rn.24013	BF563960	2.48	2.47	2.49	2.48	2.49	2.44	1.01	down	5.81E-01	8.95E-01	-	-
1379547_at	---	---	---	Rn.175173	AA964652	2.49	2.46	2.53	2.48	2.53	2.45	1.01	down	7.75E-01	9.27E-01	-	-
1374684_at	---	---	---	Rn.16704	AI228978	2.40	2.38	2.42	2.39	2.40	2.38	1.01	down	5.15E-01	8.95E-01	-	-
1374691_at	Sult5a1	sulfotransferase family 5A, member 1	292077	Rn.107747	BF283670	2.36	2.42	2.38	2.36	2.43	2.34	1.01	down	7.73E-01	9.26E-01	-	-
1377358_at	---	---	---	Rn.16196	AW253361	2.33	2.34	2.35	2.34	2.32	2.32	1.01	down	2.98E-01	8.95E-01	-	-
1378060_at	---	---	---	Rn.202450	BF399121	2.25	2.23	2.26	2.24	2.25	2.23	1.01	down	4.08E-01	8.95E-01	-	-
1367778_at	Furin	furin (paired basic amino acid cleaving enzyme)	54281	Rn.3220	NM_019331	9.51	9.29	9.35	9.45	9.46	9.23	1.01	down	9.26E-01	9.79E-01	-	-
1395076_at	Runx1t1	runt-related transcription factor 1; translocated to, 1 (cyclin D-related)	362489	Rn.218117	BE117804	2.45	2.44	2.46	2.44	2.45	2.42	1.01	down	4.18E-01	8.95E-01	-	-
1394008_x_at	Cntfr	ciliary neurotrophic factor receptor	313173	Rn.55036	BF562455	2.62	2.61	2.62	2.61	2.65	2.61	1.01	up	4.92E-01	8.95E-01	-	-
1377915_at	---	---	---	Rn.203626	BE120674	2.41	2.40	2.43	2.41	2.42	2.38	1.01	down	5.06E-01	8.95E-01	-	-
1370623_at	Fgl2	fibrinogen-like 2	84586	Rn.64635	AF323608	2.30	2.29	2.33	2.30	2.31	2.29	1.01	down	4.40E-01	8.95E-01	-	-
1378516_at	---	---	---	Rn.209147	BF409076	2.50	2.47	2.51	2.49	2.51	2.45	1.01	down	7.03E-01	9.07E-01	-	-
1384875_at	---	---	---	Rn.127009	AW529951	3.29	2.70	2.88	2.70	3.60	2.53	1.01	down	9.81E-01	9.94E-01	-	-
1383768_at	Elavl2	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 2 (Hu antigen B)	286973	Rn.12662	BF563441	2.44	2.42	2.46	2.43	2.45	2.41	1.01	down	5.79E-01	8.95E-01	-	-
1385955_at	rCG_58138	Hypothetical protein LOC100125362	100125362	Rn.18127	AI029023	2.46	2.44	2.49	2.45	2.48	2.43	1.01	down	6.74E-01	9.01E-01	-	-
1380348_at	Wnt9a	wingless-type MMTV integration site family, member 9A	287357	Rn.40411	AI601956	2.39	2.38	2.41	2.38	2.39	2.38	1.01	down	2.65E-01	8.95E-01	-	-
1380757_at	---	---	---	Rn.211051	BF404991	2.67	2.59	2.62	2.58	2.61	2.65	1.01	down	7.74E-01	9.26E-01	-	-
1393418_at	Rasal1	RAS protein activator like 1 (GAP1 like)	360814	Rn.63791	AI717045	2.38	2.37	2.38	2.37	2.43	2.36	1.01	up	6.82E-01	9.03E-01	-	-
1378077_at	---	---	---	Rn.206529	BF412632	2.36	2.35	2.37	2.35	2.36	2.34	1.01	down	3.02E-01	8.95E-01	-	-
1390327_at	---	---	---	Rn.46349	BF418351	2.44	2.42	2.46	2.43	2.45	2.41	1.01	down	6.21E-01	8.95E-01	-	-
1394295_at	---	---	---	Rn.33045	BG672252	2.50	2.48	2.52	2.48	2.54	2.45	1.01	down	7.50E-01	9.19E-01	-	-
1397247_at	Cdcp1	CUB domain containing protein 1	301082	Rn.7729	BI276505	2.36	2.36	2.37	2.36	2.41	2.35	1.01	up	6.35E-01	8.95E-01	-	-
1387677_at	Pou3f4	POU class 3 homeobox 4	29589	Rn.33030	M84645	2.30	2.29	2.32	2.29	2.30	2.29	1.01	down	4.27E-01	8.95E-01	-	-
1378647_at	RGD1306959	similar to C11orf17 protein	361624	Rn.106344	AI235274	2.44	2.43	2.50	2.44	2.47	2.43	1.01	down	7.15E-01	9.10E-01	-	-
1385725_at	LOC684444	similar to H3Stone family member (his-41)	684444	---	BE107780	2.39	2.37	2.40	2.38	2.39	2.37	1.01	down	3.73E-01	8.95E-01	-	-
1384619_at	---	---	---	---	AA858492	2.32	2.30	2.31	2.30	2.31	2.29	1.01	down	3.04E-01	8.95E-01	-	-
1373628_at	---	---	---	Rn.1026	AA818342	2.42	2.40	2.44	2.40	2.44	2.39	1.01	down	6.18E-01	8.95E-01	-	-
1377246_at	LOC685652	similar to keratin 6L	685652	Rn.201702	BI282860	2.47	2.44	2.45	2.43	2.46	2.44	1.01	down	4.60E-01	8.95E-01	-	-
1384961_at	Lce1c	late cornified envelope 1C	685998	---	BI285650	2.53	2.50	2.62	2.52	2.59	2.51	1.01	down	8.38E-01	9.49E-01	-	-
1385511_at	RGD1563628	similar to Seizure 6-like protein precursor	304554	Rn.207591	BE103003	2.28	2.27	2.29	2.27	2.28	2.26	1.01	down	3.23E-01	8.95E-01	-	-
1393497_at	---	---	---	Rn.165015	AA964476	2.38	2.38	2.39	2.38	2.38	2.36	1.01	down	3.88E-01	8.95E-01	-	-
1380779_at	---	---	---	---	BF395839	2.35	2.33	2.34	2.33	2.34	2.32	1.01	down	3.62E-01	8.95E-01	-	-
1395384_at	Usp31	ubiquitin specific peptidase 31	308959	Rn.64320	BG664969	2.30	2.30	2.33	2.30	2.31	2.30	1.01	down	4.41E-01	8.95E-01	-	-
1391878_at	D1560020_predic	similar to Myb proto-oncogene protein (C-myb) (predicted)	498982	---	AI234125	2.39	2.38	2.41	2.39	2.40	2.37	1.01	down	4.71E-01	8.95E-01	-	-
1375132_at	Lypd2	Ly6/Plaur domain containing 2	300017	Rn.19695	BG373030	2.28	2.29	2.29	2.28	2.29	2.27	1.01	down	1.77E-01	8.95E-01	-	-
1388234_at	Ifna1	interferon-alpha 1	298210	Rn.196548	X00336	2.30	2.29	2.32	2.29	2.30	2.28	1.01	down	4.26E-01	8.95E-01	-	-
1380338_at	---	---	---	Rn.147619	BF562910	2.45	2.44	2.46	2.44	2.46	2.42	1.01	down	4.58E-01	8.95E-01	-	-
1379958_at	---	---	---	Rn.203505	BE102434	2.41	2.38	2.42	2.40	2.46	2.37	1.01	up	7.56E-01	9.20E-01	-	-
1382716_at	---	---	---	Rn.199434	AI235527	2.33	2.32	2.35	2.33	2.34	2.32	1.01	down	4.33E-01	8.95E-01	-	-
1389758_at	Tada2l	transcriptional adaptor 2 (ADA2 homolog, yeast)-like	360581	Rn.8027	AA946332	2.39	2.35	2.37	2.36	2.37	2.35	1.01	down	5.01E-01	8.95E-01	-	-
1397630_at	Hecw2	HECT, C2 and WW domain containing E3 ubiquitin protein ligase 2	316395	Rn.198842	BE119116	2.64	2.61	2.67	2.63	2.66	2.65	1.01	up	6.61E-01	8.98E-01	-	-
1369173_at	C3ar1	complement component 3a receptor 1	84007	Rn.9772	NM_030960	2.68	2.65	2.71	2.67	2.69	2.65	1.01	down	6.61E-01	8.98E-01	-	-
1370647_at	Impg2	interphotoreceptor matrix proteoglycan 2	245919	Rn.10612	U76717	2.40	2.38	2.41	2.39	2.40	2.37	1.01	down	5.04E-01	8.95E-01	-	-
1370227_at	Prlla7	prolactin family 8, subfamily a, member 7	64368	Rn.202970	AI013851	2.50	2.47	2.54	2.48	2.59	2.47	1.01	up	8.30E-01	9.46E-01	-	-
1394226_at	---	---	---	---	AI639396	2.42	2.41	2.44	2.41	2.43	2.41	1.01	down	4.27E-01	8.95E-01	-	-
1376586_at	Rdh10	Retinol dehydrogenase 10 (all-trans)	353252	Rn.16968	AI137314	2.28	2.28	2.29	2.31	2.28	2.28	1.01	up	4.37E-01	8.95E-01	-	-
1389223_at	---	---	---	Rn.204883	AI177186	2.31	2.30	2.32	2.30	2.31	2.28	1.01	down	3.81E-01	8.95E-01	-	-
1392567_at	---	---	---	Rn.205382	AI556652	2.45	2.45	2.45	2.48	2.46	2.44	1.01	up	4.26E-01	8.95E-01	-	-
1392218_at	RGD1560556	Similar to C14orf25 protein	366631	Rn.95516	BF405138	2.33	2.33	2.34	2.31	2.33	2.33	1.01	down	2.97E-01	8.95E-01	-	-
1385411_at	rCG_32844	ubiquitin specific protease 43	100147704	Rn.219475	BE120893	2.34	2.33	2.38	2.34	2.36	2.32	1.01	down	6.35E-01	8.95E-01	-	-
1381348_at	---	---	---	Rn.19788	AI070572	2.61	2.59	2.61	2.60	2.63	2.56	1.01	down	6.64E-01	8.99E-01	-	-
1394485_at	---	---	---	Rn.204780	AW532781	2.41	2.39	2.42	2.40	2.41	2.38	1.01	down	3.87E-01	8.95E-01	-	-
1367706_at	Vdac1	voltage-dependent anion channel 1	83529	Rn.54594	AF268467	12.93	12.89	12.81	12.91	12.85	12.90	1.01	up	8.13E-01	9.40E-01	-	-

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicats)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1380093_at	RGD1563996	similar to Protein UNQ9166/PRO28631 precursor	315163	Rn.141004	AA901309	2.22	2.19	2.20	2.19	2.20	2.19	1.01	down	3.72E-01	8.95E-01	-	-
1380557_at	Bckdha	branched chain ketoacid dehydrogenase E1, alpha polypeptide	25244	Rn.49145	BE119497	2.38	2.36	2.39	2.37	2.38	2.37	1.01	down	3.54E-01	8.95E-01	-	-
1377161_at	---	---	---	Rn.34711	BG378317	2.42	2.40	2.44	2.41	2.43	2.39	1.01	down	6.07E-01	8.95E-01	-	-
1378904_at	LOC499587	similar to solute carrier family 7, member 14	499587	Rn.162570	AW529244	2.46	2.46	2.52	2.48	2.51	2.44	1.01	down	7.49E-01	9.19E-01	-	-
1398639_at	---	---	---	Rn.216637	AI146049	2.39	2.37	2.39	2.38	2.39	2.36	1.01	down	3.84E-01	8.95E-01	-	-
1392209_at	Gcnt3	glucosaminyl (N-acetyl) transferase 3, mucin type	286976	Rn.43518	AI639436	2.40	2.39	2.41	2.39	2.40	2.38	1.01	down	3.96E-01	8.95E-01	-	-
1374280_at	Cbln2	cerebellin 2 precursor	291388	Rn.16398	AA817812	2.48	2.48	2.52	2.48	2.50	2.47	1.01	down	6.05E-01	8.95E-01	-	-
1398073_at	---	---	---	Rn.216872	BF400712	2.42	2.40	2.45	2.42	2.46	2.41	1.01	up	6.82E-01	9.03E-01	-	-
1382900_at	---	---	---	---	BF566547	2.42	2.42	2.43	2.42	2.43	2.39	1.01	down	4.75E-01	8.95E-01	-	-
1396779_at	---	---	---	Rn.208699	BF402702	2.57	2.53	2.64	2.55	2.63	2.53	1.01	down	8.45E-01	9.52E-01	-	-
1369675_at	Itpr2	inositol 1,4,5-triphosphate receptor, type 2	81678	Rn.89152	X61677	2.39	2.37	2.40	2.38	2.39	2.36	1.01	down	4.65E-01	8.95E-01	-	-
1394011_at	Bbs7	Bardet-Biedl syndrome 7	361930	Rn.28442	BF543825	2.67	2.66	2.67	2.65	2.66	2.65	1.01	down	1.54E-01	8.95E-01	-	-
1393649_at	---	---	---	Rn.208004	BE108758	2.43	2.41	2.44	2.42	2.44	2.40	1.01	down	5.62E-01	8.95E-01	-	-
1393187_at	---	---	---	Rn.199308	BF417625	2.38	2.37	2.39	2.37	2.39	2.36	1.01	down	4.08E-01	8.95E-01	-	-
1384809_at	Gpr123	G protein-coupled receptor 123	309097	Rn.169427	AW526563	2.38	2.37	2.39	2.37	2.38	2.36	1.01	down	3.80E-01	8.95E-01	-	-
1368970_at	Cdh23	cadherin 23 (otocadherin)	114102	Rn.208796	NM_053644	2.44	2.42	2.45	2.43	2.44	2.40	1.01	down	5.46E-01	8.95E-01	-	-
1392264_s_at	Serpine1	serine (or cysteine) peptidase inhibitor, clade E, member 1	24617	Rn.29367	AI500951	2.39	2.38	2.41	2.38	2.40	2.37	1.01	down	4.85E-01	8.95E-01	-	-
1398051_at	---	---	---	Rn.172696	BF392993	2.39	2.38	2.41	2.38	2.40	2.37	1.01	down	5.04E-01	8.95E-01	-	-
1369072_at	Adh7	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide	171178	Rn.42935	NM_134329	2.67	2.64	2.78	2.68	2.70	2.68	1.01	down	8.37E-01	9.49E-01	-	-
1382456_at	---	---	---	Rn.53927	AA801402	2.44	2.43	2.44	2.43	2.44	2.41	1.01	down	4.49E-01	8.95E-01	-	-
1395310_at	Asb1	ankyrin repeat and SOCS box-containing 1	316628	Rn.220453	AW534041	2.39	2.39	2.41	2.39	2.40	2.37	1.01	down	4.68E-01	8.95E-01	-	-
1369009_at	Serpinh1	serine (or cysteine) peptidase inhibitor, clade H, member 1	29345	Rn.98199	NM_017173	2.42	2.39	2.40	2.40	2.38	2.38	1.01	down	4.00E-01	8.95E-01	-	-
1374449_at	Cdca3	cell division cycle associated 3	297594	Rn.129078	BF417638	2.33	2.32	2.35	2.32	2.33	2.32	1.01	down	3.66E-01	8.95E-01	-	-
1368594_at	Pla2g2c	phospholipase A2, group IIC	29387	Rn.216343	NM_019202	2.45	2.43	2.47	2.43	2.45	2.43	1.01	down	5.48E-01	8.95E-01	-	-
1378436_at	---	---	---	Rn.161171	BM384580	2.36	2.35	2.38	2.36	2.37	2.34	1.01	down	4.12E-01	8.95E-01	-	-
1367460_at	Gdi2	GDP dissociation inhibitor 2	29662	Rn.1441	BM387347	11.69	11.62	11.61	11.52	11.73	11.71	1.01	up	8.98E-01	9.68E-01	-	-
1375558_at	Rab34	RAB34, member RAS oncogene family	360571	Rn.98493	BM387339	2.28	2.28	2.32	2.28	2.29	2.28	1.01	down	4.97E-01	8.95E-01	-	-
1382992_at	---	---	---	---	AI179314	2.41	2.41	2.42	2.41	2.42	2.39	1.01	down	4.04E-01	8.95E-01	-	-
1395319_at	---	---	---	---	BM383557	2.44	2.44	2.45	2.43	2.47	2.40	1.01	down	6.65E-01	8.99E-01	-	-
1381470_at	---	---	---	Rn.163608	AI454052	5.20	4.43	5.24	4.73	6.02	4.09	1.01	down	9.89E-01	9.96E-01	-	-
1389578_at	Yrdc	yrdC domain containing (E.coli)	319113	Rn.9476	AA850740	5.27	4.55	5.37	4.85	4.92	5.40	1.01	down	9.77E-01	9.93E-01	-	-
1381575_at	Neb	nebulin	311029	Rn.134031	AI638986	2.49	2.45	2.51	2.47	2.53	2.42	1.01	down	8.13E-01	9.40E-01	-	-
1387543_at	Slc5a7	solute carrier family 5 (choline transporter), member 7	85426	Rn.44872	NM_053521	2.41	2.40	2.43	2.40	2.42	2.38	1.01	down	5.36E-01	8.95E-01	-	-
1370555_at	Nalcn	sodium leak channel, non-selective	266760	Rn.18624	AF078779	2.35	2.35	2.36	2.35	2.35	2.33	1.01	down	4.04E-01	8.95E-01	-	-
1384203_at	---	---	---	Rn.163591	AA818664	2.41	2.40	2.43	2.40	2.42	2.39	1.01	down	4.88E-01	8.95E-01	-	-
1385973_at	---	---	---	Rn.213014	AI717265	2.31	2.31	2.32	2.31	2.32	2.34	1.01	up	4.48E-01	8.95E-01	-	-
1372280_at	Ankz2	ankyrin repeat and SOCS box-containing 2	299266	Rn.98677	BI295982	2.38	2.37	2.39	2.37	2.38	2.36	1.01	down	3.31E-01	8.95E-01	-	-
1370664_a_at	C286980 /// Vom2	putative pheromone receptor (Go-VN13B) /// vomeronasal 2 receptor, 75	286980 /// 286986	Rn.10874	AF016185	2.43	2.41	2.44	2.42	2.43	2.40	1.01	down	4.81E-01	8.95E-01	-	-
1394832_at	---	---	---	Rn.166727	AI136675	2.44	2.43	2.46	2.43	2.46	2.41	1.01	down	6.19E-01	8.95E-01	-	-
1397114_at	---	---	---	Rn.209433	BF388191	2.46	2.44	2.48	2.49	2.46	2.41	1.01	down	7.40E-01	9.16E-01	-	-
1387181_at	Myf6	myogenic factor 6	25714	Rn.2236	NM_013172	2.38	2.37	2.40	2.38	2.39	2.36	1.01	down	4.55E-01	8.95E-01	-	-
1393664_at	---	---	---	Rn.151589	BE097138	2.37	2.35	2.37	2.35	2.36	2.35	1.01	down	3.09E-01	8.95E-01	-	-
1391749_a_at	Nxnl2	nucleoredoxin-like 2	689232	Rn.15096	AW535122	2.35	2.34	2.36	2.37	2.35	2.35	1.01	up	3.29E-01	8.95E-01	-	-
1389283_at	---	---	---	Rn.216932	BF402613	2.39	2.38	2.42	2.39	2.40	2.38	1.01	down	4.66E-01	8.95E-01	-	-
1384721_at	---	---	---	---	BI286077	2.40	2.39	2.41	2.39	2.40	2.37	1.01	down	4.02E-01	8.95E-01	-	-
1390652_at	---	---	---	Rn.111443	BF390059	2.43	2.42	2.44	2.42	2.43	2.41	1.01	down	2.75E-01	8.95E-01	-	-
1375719_s_at	Cdh13	cadherin 13	192248	Rn.23806	BG381748	2.34	2.34	2.35	2.33	2.40	2.33	1.01	up	6.97E-01	9.07E-01	-	-
1386245_at	---	---	---	---	BG153343	2.37	2.36	2.39	2.36	2.37	2.35	1.01	down	4.93E-01	8.95E-01	-	-
1376545_at	---	---	---	Rn.209371	BF394077	2.34	2.33	2.35	2.33	2.34	2.31	1.01	down	4.75E-01	8.95E-01	-	-
1372345_at	---	---	---	---	AA894210	2.44	2.42	2.46	2.43	2.45	2.41	1.01	down	5.50E-01	8.95E-01	-	-
1384977_at	LOC689911	similar to Msx2-interacting protein (SPEN homolog) (SMART/HDAC1-associa	689911	Rn.25022	BI295169	2.32	2.32	2.33	2.31	2.32	2.31	1.01	down	1.56E-01	8.95E-01	-	-
1375165_at	LOC678843	similar to paternally expressed 10	678843	---	AI179460	2.43	2.35	2.37	2.42	2.37	2.34	1.01	down	7.74E-01	9.26E-01	-	-
1379702_at	Ankmy2	ankyrin repeat and MYND domain containing 2	314046	Rn.17274	AI410993	2.43	2.42	2.45	2.42	2.44	2.41	1.01	down	5.12E-01	8.95E-01	-	-
1379437_at	---	---	---	Rn.87868	AW918480	2.39	2.38	2.42	2.39	2.40	2.37	1.01	down	5.61E-01	8.95E-01	-	-
1398688_at	Spink5	serine peptidase inhibitor, Kazal type 5	361319	Rn.106870	BM390176	2.44	2.42	2.47	2.44	2.46	2.41	1.01	down	6.63E-01	8.98E-01	-	-
1396940_at	---	---	---	---	AA956161	2.40	2.39	2.41	2.39	2.40	2.39	1.01	down	2.77E-01	8.95E-01	-	-
1396833_at	---	---	---	Rn.206615	AW528601	2.39	2.38	2.40	2.38	2.39	2.37	1.01	down	4.18E-01	8.95E-01	-	-
1373357_at	---	---	---	Rn.200288	BI291467	2.43	2.40	2.43	2.42	2.48	2.40	1.01	up	7.34E-01	9.15E-01	-	-
1387493_at	Akap5	A kinase (PRKA) anchor protein 5	171026	Rn.122003	NM_133515	2.39	2.37	2.39	2.37	2.39	2.36	1.01	down	4.61E-01	8.95E-01	-	-
1368144_at	Rgs2	regulator of G-protein signaling 2	84583	Rn.1892	AY043246	2.43	2.38	2.37	2.38	2.39	2.37	1.01	down	6.33E-01	8.95E-01	-	-
1385448_at	Adamtsl5	ADAMTS-like 5	314626	Rn.219460	BE112763	2.50	2.49	2.51	2.50	2.50	2.48	1.01	down	3.25E-01	8.95E-01	-	-
1389411_at	---	---	---	Rn.19686	AW435329	2.43	2.41	2.45	2.43	2.44	2.40	1.01	down	5.97E-01	8.95E-01	-	-
1370783_a_at	Ms4a2	membrane-spanning 4-domains, subfamily A, member 2 (Fc fragment of IgE,	25316	Rn.10922	M22924	2.43	2.42	2.43	2.42	2.43	2.40	1.01	down	4.53E-01	8.95E-01	-	-
1369778_at	Dio2	deiodinase, iodothyronine, type II	65162	Rn.88380	NM_031720	2.39	2.38	2.42	2.39	2.40	2.37	1.01	down	5.20E-01	8.95E-01	-	-
1370069_at	Slc12a5	solute carrier family 12 (potassium-chloride transporter), member 5	171373	Rn.10513	NM_134363	2.32	2.30	2.34	2.31	2.32	2.30	1.01	down	4.67E-01	8.95E-01	-	-
1385029_at	---	---	---	Rn.124278	BE110921	2.46	2.41	2.46	2.41	2.47	2.41	1.01	down	7.44E-01	9.17E-01	-	-
1397237_at	Rpl28	ribosomal protein L28	64638	Rn.36614	AW534329	2.53	2.53	2.58	2.54	2.55	2.53	1.01	down	6.05E-01	8.95E-01	-	-
1369032_at	Blcap	bladder cancer associated protein homolog (human)	171113	Rn.127812	NM_133582	2.43	2.45	2.46	2.45	2.47	2.44	1.01	up	4.79E-01	8.95E-01	-	-
1384713_at	Tesp2	testicular serine protease 2	170939	Rn.220373	BF399647	2.39	2.37	2.40	2.38	2.39	2.37	1.01	down	4.61E-01	8.95E-01	-	-
1390580_at	---	---	---	---	BG378657	2.28	2.30	2.28	2.28	2.29	2.27	1.01	down	3.99E-01	8.95E-01	-	-
1393403_at	Angptl3	angiopoietin-like 3	502970	Rn.11755	AI058911	2.41	2.40	2.43	2.40	2.42	2.38	1.01	down	5.48E-01	8.95E-01	-	-
1395845_at	---	---	---	Rn.205753	AW534087	2.52	2.45	2.49	2.47	2.49	2.48	1.01	down	7.00E-01	9.07E-01	-	-
1367822_at	Cacna1a	calcium channel, voltage-dependent, P/Q type, alpha 1A subunit	25398	Rn.87769	BF400631	2.38	2.38	2.41	2.38	2.39	2.37	1.01	down	5.08E-01	8.95E-01	-	-
1376056_at	---	---	---	---	BF291214	2.76	2.76	2.78	2.76	2.77	2.76	1.01	down	2.53E-01	8.95E-01	-	-
1391165_at	Sost	Sclerosteosis	80722	Rn.95369	BF407514	2.43	2.41	2.45	2.42	2.44	2.40	1.01	down	5.91E-01	8.95E-01	-	-
1377138_at	---	---	---	Rn.204276	AI709547	2.38	2.37	2.39	2.38	2.40	2.40	1.01	up	4.27E-01	8.95E-01	-	-
1398532_at	---	---	---	Rn.107953	BF524297	2.36	2.35	2.37	2.35	2.36	2.34	1.01	down	3.93E-01	8.95E-01	-	-
1369603_at	Kcnip1	Kv channel-interacting protein 1	65023	Rn.20530	NM_022929	2.51	2.48	2.53	2.50	2.52	2.47	1.01	down	6.71E-01	9.00E-01	-	-
1379035_at	---	---	---	Rn.209211	BF413511	2.47	2.45	2.49	2.46	2.48	2.44	1.01	down	5.67E-01	8.95E-01	-	-
1384991_a_at	Hdac10	histone deacetylase 10	362981	Rn.107028	AI236142	2.42	2.41	2.42	2.41	2.43	2.39	1.01	down	4.76E-01	8.95E-01	-	-
1376438_at	---	---	---	Rn.207474	BF416513	2.41	2.39	2.44	2.39	2.43	2.39	1.01	down	6.57E-01	8.98E-01	-	-
1377867_at	RGD1562284	similar to Glutaminyl-peptide cyclotransferase precursor (QC)	313837	Rn.7474	BM390001	2.42	2.41	2.44	2.41	2.43	2.40	1.01	down	5.13E-01	8.95E-01	-	-
1392129_at	---	---	---	Rn.153927	AI013033	2.74	2.72	2.78	2.74	2.74	2.73	1.01	down	6.13E-01	8.95E-01	-	-
1384594_at	Ltk	leukocyte receptor tyrosine kinase	311337	Rn.47513	BE106366	2.28	2.26	2.29	2.27	2.27	2.26	1.01	down	2.89E-01	8.95E-01	-	-
1369074_at	Slc38a4	solute carrier family 38, member 4	170573	Rn.17990	NM_130748	2.41	2.41	2.43	2.41	2.42	2.39	1.01	down	4.99E-01	8.95E-01	-	-
1380558_at	Dlx3	distal-less homeobox 3	287638	Rn.104800	BM391243	2.48	2.48	2.49	2.48	2.52	2.48	1.01	up	5.92E-01	8.95E-01	-	-
1367819_at	Got2	glutamic-oxaloacetic transaminase 2, mitochondrial (aspartate aminotransfera	25721	Rn.98650	NM_013177	8.72	8.47	8.74	8.70	8.79	8.41	1.01	down	9.52E-01	9.86E-01	-	-
1395889_at	---	---	---	Rn.56956	AA956651	2.41	2.39	2.42	2.40	2.42	2.38	1.01	down	5.37E-01	8.95E-01	-	-
1369191_at	Il6	interleukin 6	24498	Rn.9873	NM_012589	2.39	2.38	2.40	2.38	2.40	2.37	1.01	down	4.60E-01	8.95E-01	-	-
1390860_at	Igf2bp3	insulin-like growth factor 2 mRNA binding protein 3	312320	Rn.100446	AI230709	2.46	2.44	2.49	2.45	2.48	2.44	1.01	down	6.57E-01	8.98E-01	-	-
1394594_at	---	---	---	Rn.169422	BM383974	3.22	3.16	3.17	3.14	3.18	3.20	1.01	down	7.48E-01	9.19E-01	-	-
1380822_at	---	---	---	Rn.170646	BE097945	2.43	2.42	2.45	2.42	2.44	2.41	1.01	down	5.53E-01	8.95E-01	-	-
1387569_at	Sv2c	synaptic vesicle glycoprotein 2c	29643	Rn.161757	NM_031593	2.26	2.26	2.29	2.25	2.27	2.26	1.01	down	4.01E-01	8.95E-01	-	-
1377541_at	---	---	---	Rn.210898	BF405546	2.36	2.35	2.38	2.36	2.37	2.34	1.01	down	4.58E-01	8.95E-01	-	-
1378165_at	Twist1	twist homolog 1 (Drosophila)	85489	Rn.161904	BF420349	2.45	2.42	2.45	2.43	2.47	2.39	1.01	down	7.10E-01	9.09E-01	-	-
1394766_at	---	---	---	Rn.177382	AW534610	2.44	2.42	2.51	2.43	2.49	2.42	1.01	down	8.10E-01	9.39E-01	-	-
1372695_at	---	---	---	Rn.216578	AI172165	2.37	2.37	2.38	2.36	2.37	2.35	1.01	down	2.18E-01	8.95E-01	-	-
1397190_at	---	---	---	Rn.168263	AI576518	2.40	2.38	2.42	2.39	2.40	2.37	1.01	down	5.49E-01	8.95E-01	-	-
1378873_at	Hils1	histone linker H1 domain, spermatid-specific 1	690026	Rn.166800	AI145933	2.48	2.44	2.48	2.45	2.47	2.45	1.01	down	4.95E-01	8.95E-01	-	-
1371279_at	RGD1564767	Histone H2a	498753	Rn.196555	U95113	2.46	2.44	2.46	2.45	2.48	2.45	1.01	up	4.96E-01	8.95E-01	-	-
1378087_at	---	---	---	Rn.45036	BM387164	2.34	2.70	3.06	2.70	2.72	2.70	1.01	up	9.67E-01	9.90E-01	-	-
1394914_at	---	---	---	Rn.206548	AW528092	2.34	2.33	2.34	2.34	2.37	2.32	1.01	up	5.81E-01	8.95E-01	-	-
1383469_at	Aldh1a3	aldehyde dehydrogenase 1 family, member A3	266603	Rn.8297	BG372269	2.50	2.49	2.52	2.49	2.51	2.48	1.01	down	5.16E-01	8.95E-01	-	-
1379921_at	Fsd2	fibronectin type III and SPRY domain containing 2	308779	Rn.41372	AA799521	2.25	2.24	2.28	2.25	2.25	2.24	1.01	down	4.55E-01	8.95E-01	-	-
1382687_at	Six6	SIX homeobox 6	314221	Rn.21301	BE096599	2.41	2.41	2.42	2.41	2.42	2.39	1.01	down	3.94E-01	8.95E-01	-	-
1383872_at	---	---	---	---	AW142811	2.26	2.25	2.28	2.26	2.26	2.25	1.01	down	4.10E-01	8.95E-01	-	-
1395078_at	Sema3g	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (se	290562	Rn.32183	AI547430	2.29	2.30	2.30	2.29	2.30	2.28	1.01	down	1.33E-01	8.95E-01	-	-
1377282_at	---	---	---	Rn.209735	BF390569	2.46	2.46	2.48	2.45	2.47	2.46	1.01	down	3.39E-01	8.95E-01	-	-
1394277_at	RGD1311783	similar to RIKEN cDNA 2010012O05	294012	Rn.25364	BF287357	2.40	2.38	2.42	2.39	2.39	2.39	1.01	down	4.20E-01	8.95E-01	-	-
1396783_at	---	---	---	Rn.146552	BF417894	2.37	2.36	2.38	2.36	2.38	2.35	1.01	down	4.66E-01	8.95E-01	-	-
1378948_at	Zcchc24	zinc finger, CCHC domain containing 24	361104	Rn.219261	AI406365	2.41	2.41	2.42	2.41	2.41	2.44	1.01	up	4.98E-01	8.95E-01	-	-
1375834_at	Hrasls5	HRAS-like suppressor family, member 5	293711	Rn.136627	BF409874	2.55	2.53	2.55	2.54	2.55	2.51	1.01	down	4.87E-01	8.95E-01	-	-
1394943_at	RGD1565584	Similar to tyrosine kinase-associated leucine zipper protein LAZIpII	293112	Rn.35776	AA893197	3.13	3.61	4.49	3.62	3.97	3.66	1.01	up	9.83E-01	9.95E-01	-	-
1372071_at	Cd320	CD320 molecule	362851	---	AI102320	7.44	7.43	7.70	7.61	7.23	7.71	1.01	down	9.59E-01	9.89E-01	-	-
1397905_at	---	---	---	Rn.79933	BI273836	2.37	2.37	2.37	2.36	2.37	2.34	1.01	down	3.33E-01	8.95E-01	-	-
1384329_at	Prss22	protease, serine, 22	302971	Rn.13172	BM389391	2.49	2.49	2.50	2.49	2.50	2.46	1.01	down	4.22E-01	8.95E-01	-	-
1377962_at	Myst2	myeloblastosis oncogene-like 2	296344	Rn.20824	AI549424	2.31	2.30	2.32	2.31	2.35	2.30	1.01	up	6.36E-01	8.95E-01	-	-
1384633_at	---	---	---	Rn.23138	AI146097	2.38	2.38	2.40	2.38	2.39	2.36	1.01	down	4.87E-01	8.95E-01	-	-
1376215_at	11-Mar	membrane-associated ring finger (C3HC4) 11	499558	Rn.206431	AW528861	2.41	2.40	2.44	2.40	2.43	2.39	1.01	down	6.46E-01	8.95E-01	-	-
1394230_at	---	---	---	Rn.130707	H33516	2.41	2.40	2.43	2.41	2.42	2.40	1.01	down	4.46E-01	8.95E-01	-	-
1397499_at	Tnnt3	Troponin T type 3 (skeletal, fast)	24838	Rn.15488	AI170878	2.34	2.33	2.35	2.33	2.34	2.32	1.01	down	3.33E-01	8.95E-01	-	-
1396625_at	---	---	---	Rn.58216	BF394114	2.41	2.39	2.43	2.40	2.42	2.39	1.01	down	5.30E-01	8.95E-01	-	-
1370787_at	Bcl2l11	Bcl2-like 11 (apoptosis facilitator)	64547	Rn.82709	AF065433	2.32	2.32	2.33	2.32	2.33	2.35	1.01	up	3.87E-01	8.95E-01	-	-
1385636_at	Cd5l	Cd5 molecule-like	310693	Rn.43804	AI029143	2.39	2.37	2.40	2.38	2.39	2.37	1.01	down	4.86E-01	8.95E-01	-	-
1386300_at	---	---	---	Rn.133826	AI638962	2.48	2.46	2.50	2.47	2.47	2.47	1.01	down	4.70E-01	8.95E-01	-	-
1371700_at	Mtap4	microfibrillar-associated protein 4	287382	Rn.12328	AI177059	2.33	2.32	2.33	2.35	2.34	2.32	1.01	up	4.53E-01	8.95E-01	-	-
1396938_at	---	---	---	Rn.148745	AW529349	2.36	2.35	2.37	2.35	2.36	2.34	1.01	down	3.94E-01	8.95E-01	-	-
1385209_at	Myst3	MYST histone acetyltransferase (monocytic leukemia) 3	306571	Rn.33802	BE105313	3.56	3.53	4.25	4.68	2.93	3.69	1.01	down	9.88E-01	9.96E-01	-	-
1396461_at	---	---	---	---	BE117448	2.43	2.41	2.43	2.42	2.42	2.40	1.01	down	3.12E-01	8.95E-01	-	-
1394633_at	Ttse2 /// LOC10019	CDC42 small effector 2 /// hypothetical LOC100191012	0191012 /// 69102	Rn.7470	AI709770	2.70	2.68	2.70	2.73	2.71	2.68	1.01	up	6.45E-01	8.95E-01	-	-
1379990_at	---	---	---	Rn.206922	BG380925	2.35	2.34	2.35	2.34	2.35	2.38	1.01	up	5.22E-01	8.95E-01	-	-
1378809_at	---	---	---	Rn.46429	BF416647	2.40	2.38	2.41	2.38	2.40	2.38	1.01	down	4.88E-01	8.95E-01	-	-
1385216_at	---	---	---	Rn.202000	BI290864	2.36	2.36	2.37	2.35	2.36	2.35	1.01	down	1.48E-01	8.95E-01	-	-
1392513_at	RGD1307041	similar to hypothetical protein FLJ11305	361182	Rn.43960	AI171879	2.38	2.40	2.38	2.38	2.37	2.38	1.01	down	2.13E-01	8.95E-01	-	-
1383419_at	Lhfpl3	lipoma HMGIC fusion partner-like 3	499977	Rn.22819	BE106398	2.57	2.53	2.61	2.55	2.62	2.52	1.01	down	8.17E-01	9.41E-01	-	-
1398167_at	---	---	---	Rn.207873	BE107816	2.35	2.33	2.35	2.33	2.34	2.32	1.01	down	3.21E-01	8.95E-01	-	-
1397724_at	---	---	---	Rn.139138	BF418817	2.35	2.37	2.36	2.35	2.36	2.34	1.01	down	2.50E-01	8.95E-01	-	-
1391096_at	Foxd3	forkhead box D3	29203	Rn.92964	AI764493	2.56	2.56	2.57	2.56	2.56	2.54	1.01	down	2.10E-01	8.95E-01	-	-
1377800_at	---	---	---	Rn.205017	BF400895	2.41	2.40	2.43	2.40	2.42	2.39	1.01	down	5.16E-01	8.95E-01	-	-
1377518_at	Camk1g	calcium/calmodulin-dependent protein kinase IG	171358	Rn.91453	AW251224	2.46	2.44	2.49	2.45	2.48	2.43	1.01	down	6.61E-01	8.98E-01	-	-
1398048_at	Ints10	integrator complex subunit 10	290679	Rn.2385	BF402809	2.30	2.28	2.29	2.28	2.28	2.27	1.01	down	2.37E-01	8.95E-01	-	-
1395545_at	---	---	---	Rn.170180	BF284554	2.48	2.48	2.51	2.48	2.50	2.46	1.01	down	5.97E-01	8.95E-01	-	-
1379712_at	---	---	---	Rn.165342	BF408872	2.39	2.38	2.41	2.39	2.40	2.37	1.01	down	4.91E-01	8.95E-01	-	-
1389852_at	Cenpm	centromere protein M	315164	Rn.11654	AI598316	2.37	2.36	2.38	2.37	2.40	2.36	1.01	up

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1385605_at	Gpr84	G protein-coupled receptor 84	688730	Rn.171137	BF401793	2.31	2.30	2.33	2.30	2.31	2.29	1.01	down	3.69E-01	8.95E-01	-	-
1392633_at	---	---	---	Rn.33382	AI045724	2.36	2.35	2.37	2.35	2.36	2.34	1.01	down	3.32E-01	8.95E-01	-	-
1378109_at	---	---	---	Rn.160504	BF285325	2.45	2.43	2.46	2.44	2.49	2.44	1.01	up	6.74E-01	9.01E-01	-	-
1398457_at	---	---	---	Rn.146912	AI146156	2.39	2.37	2.41	2.38	2.39	2.37	1.01	down	4.89E-01	8.95E-01	-	-
1398129_at	---	---	---	---	BF524983	2.35	2.35	2.38	2.35	2.36	2.35	1.01	down	3.81E-01	8.95E-01	-	-
1382548_at	---	---	---	Rn.203294	AI011760	2.37	2.35	2.37	2.35	2.42	2.34	1.01	up	7.33E-01	9.14E-01	-	-
1378296_at	Ncaph	non-SMC condensin I complex, subunit H	680089	Rn.138041	AI012651	2.31	2.30	2.32	2.29	2.31	2.30	1.01	down	3.03E-01	8.95E-01	-	-
1395940_at	Agpat5	1-acylglycerol-3-phosphate O-acyltransferase 5 (lysophosphatidic acid acyltra	306582	Rn.199010	AA956595	2.23	2.22	2.24	2.27	2.23	2.22	1.01	up	6.11E-01	8.95E-01	-	-
1390111_at	Fam91a1	family with sequence similarity 91, member A1	689997	Rn.8212	BI285224	5.33	5.78	5.24	5.48	5.23	5.61	1.01	down	9.66E-01	9.90E-01	-	-
1368146_at	---	---	---	Rn.25080	AW523578	2.43	2.42	2.46	2.42	2.44	2.42	1.01	down	5.41E-01	8.95E-01	-	-
1380230_at	---	---	---	Rn.204182	AI639457	2.35	2.34	2.36	2.35	2.35	2.33	1.01	down	2.84E-01	8.95E-01	-	-
1380712_at	---	---	---	Rn.147840	AI406475	2.41	2.39	2.41	2.40	2.41	2.38	1.01	down	4.37E-01	8.95E-01	-	-
1395284_at	---	---	---	Rn.210375	BF397576	2.43	2.40	2.41	2.40	2.42	2.39	1.01	down	4.62E-01	8.95E-01	-	-
1384777_at	Fam158a	Family with sequence similarity 158, member A	290224	Rn.163298	AI136182	2.43	2.41	2.58	2.43	2.54	2.43	1.01	down	8.97E-01	9.68E-01	-	-
1387150_at	Padi1	peptidyl arginine deiminase, type I	54282	Rn.30030	NM_019332	2.32	2.33	2.33	2.32	2.32	2.31	1.01	down	4.96E-02	8.95E-01	-	-
1390670_at	---	---	---	---	BF405447	2.30	2.30	2.32	2.30	2.31	2.29	1.01	down	3.89E-01	8.95E-01	-	-
1390250_x_at	LOC685152	similar to Probable phospholipid-transporting ATPase ID (ATPase class I type	685152	Rn.164557	BI273855	2.44	2.40	2.41	2.41	2.43	2.39	1.01	down	6.32E-01	8.95E-01	-	-
1380737_at	Elmo2	engulfment and cell motility 2	362271	Rn.2097	BF415834	2.40	2.40	2.43	2.40	2.41	2.39	1.01	down	4.89E-01	8.95E-01	-	-
1380965_at	---	---	---	Rn.209332	BF387640	2.33	2.32	2.35	2.32	2.33	2.32	1.01	down	4.56E-01	8.95E-01	-	-
1385392_at	---	---	---	---	BE101795	2.34	2.33	2.36	2.33	2.34	2.32	1.01	down	4.14E-01	8.95E-01	-	-
1369822_at	Kit	v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog	64030	Rn.54004	NM_022264	2.37	2.35	2.37	2.36	2.42	2.35	1.01	up	7.10E-01	9.09E-01	-	-
1391203_at	---	---	---	---	BF415296	2.41	2.39	2.42	2.40	2.42	2.38	1.01	down	5.39E-01	8.95E-01	-	-
1381154_at	---	---	---	Rn.209831	BF403058	2.36	2.36	2.40	2.36	2.37	2.36	1.01	down	5.14E-01	8.95E-01	-	-
1369337_at	Adcy10	adenylate cyclase 10 (soluble)	59320	Rn.42892	NM_021684	2.39	2.38	2.42	2.39	2.40	2.38	1.01	down	5.36E-01	8.95E-01	-	-
1376741_at	Hook3	hook homolog 3 (Drosophila)	306548	Rn.203282	AI413004	2.40	2.38	2.39	2.38	2.39	2.37	1.01	down	3.50E-01	8.95E-01	-	-
1376237_at	---	---	---	Rn.36521	AI145040	5.10	4.85	4.30	3.72	6.09	4.41	1.01	down	9.91E-01	9.97E-01	-	-
1397400_at	---	---	---	Rn.148867	BM391846	2.38	2.37	2.39	2.37	2.38	2.36	1.01	down	3.79E-01	8.95E-01	-	-
1385151_at	---	---	---	Rn.49533	BE097096	2.49	2.46	2.46	2.46	2.47	2.45	1.01	down	3.94E-01	8.95E-01	-	-
1369842_at	Accn5	amiloride-sensitive cation channel 5, intestinal	63866	Rn.44631	NM_022227	2.44	2.42	2.45	2.42	2.44	2.42	1.01	down	3.89E-01	8.95E-01	-	-
1396487_at	---	---	---	Rn.209919	BF404419	2.33	2.32	2.34	2.31	2.33	2.32	1.01	down	2.71E-01	8.95E-01	-	-
1383582_at	Tmem54	transmembrane protein 54	362605	Rn.162106	BG377582	2.31	2.30	2.33	2.30	2.31	2.29	1.01	down	4.47E-01	8.95E-01	-	-
1369652_at	Thy1	Thy-1 cell surface antigen	24832	Rn.108198	AI145313	2.38	2.38	2.39	2.38	2.39	2.36	1.01	down	4.21E-01	8.95E-01	-	-
1396563_at	---	---	---	Rn.211057	BF405036	2.42	2.42	2.44	2.41	2.45	2.38	1.01	down	6.72E-01	9.01E-01	-	-
1397527_at	Trim47	tripartite motif-containing 47	690374	Rn.198921	AI578294	2.34	2.33	2.35	2.33	2.35	2.31	1.01	down	4.19E-01	8.95E-01	-	-
1394533_at	---	---	---	Rn.133105	BI291166	2.40	2.38	2.42	2.38	2.41	2.37	1.01	down	5.64E-01	8.95E-01	-	-
1379192_at	Asf1a	ASF1 anti-silencing function 1 homolog A (S. cerevisiae)	294408	Rn.163427	AW528096	4.70	4.48	4.45	3.91	4.68	5.08	1.01	up	9.81E-01	9.94E-01	-	-
1389457_at	Mybl2	myeloblastosis oncogene-like 2	296344	Rn.20824	BF281184	2.35	2.34	2.37	2.34	2.36	2.33	1.01	down	4.24E-01	8.95E-01	-	-
1380047_at	---	---	---	Rn.35231	AI600979	2.46	2.43	2.48	2.45	2.47	2.42	1.01	down	6.85E-01	9.03E-01	-	-
1391889_at	---	---	---	Rn.204596	BG671963	3.26	3.56	3.48	3.78	3.24	3.31	1.01	up	9.65E-01	9.90E-01	-	-
1395277_at	---	---	---	Rn.148501	BF396535	2.31	2.30	2.31	2.31	2.31	2.27	1.01	down	5.26E-01	8.95E-01	-	-
1385576_at	Smtnl1	smoothelin-like 1	311167	Rn.34843	AI535506	2.37	2.35	2.38	2.36	2.37	2.35	1.01	down	4.65E-01	8.95E-01	-	-
1376413_at	---	---	---	Rn.205021	BF410366	2.36	2.34	2.38	2.36	2.37	2.33	1.01	down	5.98E-01	8.95E-01	-	-
1390079_at	Rdh10	Retinol dehydrogenase 10 (all-trans)	353252	Rn.16968	AI555453	2.50	2.50	2.51	2.50	2.50	2.49	1.01	down	2.69E-01	8.95E-01	-	-
1393999_at	LOC100192314	Hypothetical protein LOC100192314	100192314	Rn.217950	AI060127	2.33	2.33	2.36	2.33	2.34	2.32	1.01	down	4.66E-01	8.95E-01	-	-
1390978_at	---	---	---	Rn.48887	BF406177	2.36	2.34	2.39	2.36	2.36	2.34	1.01	down	5.87E-01	8.95E-01	-	-
1396886_at	---	---	---	Rn.57644	BF387869	2.41	2.40	2.42	2.43	2.42	2.40	1.01	up	4.79E-01	8.95E-01	-	-
1383902_at	Cep97	centrosomal protein 97kDa	304007	Rn.46231	BI295406	2.43	2.42	2.45	2.42	2.44	2.41	1.01	down	5.17E-01	8.95E-01	-	-
1371196_at	---	---	---	Rn.129675	M23890	2.33	2.32	2.35	2.33	2.33	2.32	1.01	down	4.05E-01	8.95E-01	-	-
1370198_at	Trdn	triadin	59299	Rn.41863	AJ243304	2.33	2.32	2.36	2.33	2.34	2.32	1.01	down	5.07E-01	8.95E-01	-	-
1379976_at	---	---	---	---	AI013509	2.32	2.30	2.31	2.30	2.31	2.29	1.01	down	2.99E-01	8.95E-01	-	-
1387332_at	Nmur2	neuromedin U receptor 2	64042	Rn.160579	NM_022275	2.34	2.33	2.36	2.34	2.34	2.32	1.01	down	3.70E-01	8.95E-01	-	-
1383398_at	RGD1564327	similar to integrin alpha 8	364786	Rn.69726	AI059150	2.37	2.37	2.39	2.37	2.38	2.35	1.01	down	4.65E-01	8.95E-01	-	-
1396902_at	---	---	---	Rn.147282	BF399037	2.43	2.42	2.45	2.42	2.45	2.41	1.01	down	5.87E-01	8.95E-01	-	-
1377122_at	---	---	---	Rn.24207	AI454840	2.35	2.33	2.38	2.35	2.36	2.34	1.01	down	5.99E-01	8.95E-01	-	-
1387980_at	Ctsq	cathepsin Q	246147	Rn.34875	AF187323	2.42	2.39	2.42	2.41	2.47	2.38	1.01	up	7.60E-01	9.22E-01	-	-
1392873_at	---	---	---	Rn.165084	AA957014	2.59	2.54	2.60	2.59	2.63	2.55	1.01	up	7.77E-01	9.28E-01	-	-
1368728_at	P2ry12	purinergic receptor P2Y, G-protein coupled 12	64803	Rn.64592	NM_022800	2.35	2.35	2.43	2.41	2.36	2.34	1.01	down	8.02E-01	9.36E-01	-	-
1392950_at	Myot	myotilin	291605	Rn.163370	BF562973	2.41	2.40	2.42	2.40	2.42	2.39	1.01	down	4.93E-01	8.95E-01	-	-
1381743_at	---	---	---	Rn.138483	BF412250	2.77	2.76	2.77	2.79	2.77	2.72	1.01	down	6.80E-01	9.03E-01	-	-
1387241_at	Gpr88	G-protein coupled receptor 88	64443	Rn.59513	NM_031696	2.41	2.40	2.43	2.40	2.42	2.39	1.01	down	4.74E-01	8.95E-01	-	-
1395795_at	---	---	---	Rn.206623	AW528651	2.38	2.37	2.40	2.37	2.39	2.36	1.01	down	4.49E-01	8.95E-01	-	-
1396233_at	---	---	---	Rn.169772	AW529318	2.36	2.36	2.38	2.36	2.37	2.34	1.01	down	4.86E-01	8.95E-01	-	-
1380388_at	---	---	---	Rn.63363	BF418094	2.32	2.31	2.33	2.32	2.32	2.30	1.01	down	4.37E-01	8.95E-01	-	-
1375013_at	---	---	---	Rn.205619	AW533445	2.46	2.53	2.46	2.43	2.57	2.43	1.01	down	8.71E-01	9.60E-01	-	-
1396877_at	---	---	---	Rn.204402	AI715187	2.34	2.33	2.36	2.34	2.35	2.33	1.01	down	4.73E-01	8.95E-01	-	-
1384025_at	---	---	---	Rn.7560	AA943432	2.40	2.39	2.40	2.39	2.41	2.37	1.01	down	5.10E-01	8.95E-01	-	-
1382888_at	---	---	---	Rn.151960	AA858981	2.35	2.34	2.35	2.36	2.36	2.34	1.01	up	2.66E-01	8.95E-01	-	-
1370431_at	Syn2	synapsin II	29179	Rn.506	M27925	2.37	2.36	2.38	2.36	2.37	2.35	1.01	down	3.85E-01	8.95E-01	-	-
1394671_at	---	---	---	Rn.19452	AI454769	2.37	2.34	2.38	2.38	2.37	2.36	1.01	up	5.12E-01	8.95E-01	-	-
1378917_at	Rexo1	REX1, RNA exonuclease 1 homolog (S. cerevisiae)	314630	Rn.12613	BF406470	2.39	2.40	2.39	2.39	2.39	2.38	1.01	down	1.66E-01	8.95E-01	-	-
1397263_at	---	---	---	Rn.34352	AI045741	2.41	2.40	2.42	2.40	2.41	2.40	1.01	down	2.90E-01	8.95E-01	-	-
1378893_at	---	---	---	---	BF410387	2.59	2.58	2.59	2.62	2.59	2.58	1.01	up	4.39E-01	8.95E-01	-	-
1391033_s_at	Nrg2	neuregulin 2	432361	Rn.22434	AI412659	2.27	2.23	2.25	2.24	2.24	2.24	1.01	down	4.70E-01	8.95E-01	-	-
1384021_at	Commd7	COMM domain containing 7	296285	Rn.92689	BF406950	2.32	2.31	2.34	2.32	2.33	2.30	1.01	down	4.32E-01	8.95E-01	-	-
1392880_at	---	---	---	---	AA900508	2.43	2.43	2.44	2.43	2.44	2.41	1.01	down	4.40E-01	8.95E-01	-	-
1372307_at	---	---	---	Rn.203274	BI275234	2.31	2.32	2.32	2.30	2.32	2.30	1.01	down	1.52E-01	8.95E-01	-	-
1382279_at	Rhobtb2	Rho-related BTB domain containing 2	306004	Rn.163307	BE097598	2.38	2.38	2.39	2.38	2.39	2.36	1.01	down	3.91E-01	8.95E-01	-	-
1368027_at	Tbxas1	thromboxane A synthase 1, platelet	24886	Rn.16283	NM_012687	2.30	2.28	2.31	2.31	2.32	2.29	1.01	up	5.02E-01	8.95E-01	-	-
1382252_at	---	---	---	Rn.161419	BE099808	2.78	2.79	2.85	2.77	2.87	2.74	1.01	down	8.50E-01	9.53E-01	-	-
1378064_at	---	---	---	Rn.204634	AI144892	2.38	2.36	2.38	2.36	2.37	2.36	1.01	down	2.64E-01	8.95E-01	-	-
1391736_at	Lmbr1l	limb region 1-like homolog (mouse)	300215	Rn.162025	BG376666	2.42	2.42	2.42	2.45	2.42	2.41	1.01	up	5.20E-01	8.95E-01	-	-
1372590_at	---	---	---	Rn.53880	BM386449	2.38	2.37	2.38	2.40	2.40	2.36	1.01	up	4.94E-01	8.95E-01	-	-
1385643_at	---	---	---	Rn.149042	AI045069	2.33	2.32	2.33	2.32	2.33	2.31	1.01	down	2.06E-01	8.95E-01	-	-
1381270_at	---	---	---	Rn.206139	AW522565	2.37	2.36	2.39	2.37	2.38	2.35	1.01	down	4.87E-01	8.95E-01	-	-
1368883_at	Nov	nephroblastoma overexpressed gene	81526	Rn.162955	NM_030868	2.35	2.32	2.33	2.32	2.34	2.32	1.01	down	3.91E-01	8.95E-01	-	-
1368522_at	Timeless	timeless homolog (Drosophila)	83508	Rn.31755	NM_031340	2.41	2.40	2.42	2.41	2.43	2.39	1.01	down	4.05E-01	8.95E-01	-	-
1387754_at	Tacr2	tachykinin receptor 2	25007	Rn.202846	NM_080768	2.40	2.39	2.42	2.39	2.41	2.38	1.01	down	5.42E-01	8.95E-01	-	-
1384998_at	---	---	---	Rn.152656	BF399981	2.46	2.44	2.47	2.45	2.46	2.44	1.01	down	4.75E-01	8.95E-01	-	-
1368003_at	Add2	adducin 2 (beta)	24171	Rn.11353	NM_012491	2.33	2.33	2.37	2.33	2.34	2.33	1.01	down	5.32E-01	8.95E-01	-	-
1378048_at	LOC683733	similar to Transcription factor 7-like 2 (HMG box transcription factor 4) (T-cell-	683733	---	BE116976	2.36	2.34	2.36	2.35	2.36	2.33	1.01	down	3.92E-01	8.95E-01	-	-
1380528_at	---	---	---	Rn.43715	AI407573	2.39	2.38	2.40	2.39	2.40	2.42	1.01	up	4.97E-01	8.95E-01	-	-
1398664_at	Gramd3	GRAM domain containing 3	307288	Rn.53932	C06752	2.36	2.36	2.37	2.36	2.36	2.34	1.01	down	3.12E-01	8.95E-01	-	-
1379965_at	---	---	---	Rn.204874	BE113082	2.62	2.70	2.57	2.72	2.62	2.53	1.01	down	9.00E-01	9.69E-01	-	-
1390143_at	Sbf1	SET binding factor 1	300147	Rn.7632	AW141172	2.34	2.33	2.35	2.33	2.34	2.32	1.01	down	3.22E-01	8.95E-01	-	-
1396547_at	---	---	---	Rn.200279	BI299163	2.38	2.37	2.40	2.38	2.39	2.36	1.01	down	4.93E-01	8.95E-01	-	-
1395245_at	---	---	---	Rn.168304	AI578413	2.41	2.40	2.42	2.40	2.41	2.38	1.01	down	4.69E-01	8.95E-01	-	-
1392946_at	---	---	---	Rn.121260	AI029194	2.45	2.44	2.47	2.44	2.46	2.43	1.01	down	5.76E-01	8.95E-01	-	-
1376988_at	Grip1	glutamate receptor interacting protein 1	84016	Rn.74240	AW527989	2.46	2.45	2.47	2.45	2.46	2.44	1.01	down	3.55E-01	8.95E-01	-	-
1396958_at	---	---	---	---	BI286502	2.37	2.36	2.38	2.37	2.38	2.35	1.01	down	3.96E-01	8.95E-01	-	-
1397476_at	Tlk	Tlk protein kinase	315852	Rn.107533	BM383386	2.44	2.42	2.47	2.44	2.46	2.41	1.01	down	6.73E-01	9.01E-01	-	-
1377589_at	---	---	---	Rn.209103	BF386215	2.50	2.48	2.52	2.48	2.52	2.48	1.01	down	6.37E-01	8.95E-01	-	-
1391916_at	---	---	---	Rn.146945	BE116043	4.25	4.22	4.29	4.23	4.36	4.20	1.01	up	8.72E-01	9.61E-01	-	-
1385888_at	---	---	---	Rn.203624	AA863272	8.94	8.33	7.79	7.91	9.01	8.11	1.01	down	9.86E-01	9.98E-01	-	-
1393518_at	Wfdc5	WAP four-disulfide core domain 5	296352	Rn.47294	AW529736	2.33	2.34	2.34	2.32	2.33	2.32	1.01	down	9.59E-02	8.95E-01	-	-
1386993_at	Myh7	myosin, heavy chain 7, cardiac muscle, beta	29557	---	BF395647	2.38	2.35	2.38	2.37	2.38	2.34	1.01	down	5.51E-01	8.95E-01	-	-
1385120_at	Pof1b	premature ovarian failure 1B	302328	Rn.141102	BG375052	2.40	2.39	2.42	2.39	2.41	2.38	1.01	down	5.36E-01	8.95E-01	-	-
1390691_at	RGD1561551	Similar to Hypothetical protein MGC75664	500359	Rn.41466	AW252626	2.50	2.46	2.51	2.47	2.51	2.47	1.01	down	6.94E-01	9.05E-01	-	-
1393714_at	---	---	---	Rn.206204	AW523488	2.43	2.42	2.45	2.43	2.44	2.41	1.01	down	5.54E-01	8.95E-01	-	-
1380049_at	---	---	---	Rn.154329	BM382847	2.42	2.40	2.42	2.41	2.42	2.39	1.01	down	3.89E-01	8.95E-01	-	-
1387397_at	Aqp4	aquaporin 4	25293	Rn.90091	NM_012825	2.41	2.40	2.42	2.40	2.41	2.39	1.01	down	3.64E-01	8.95E-01	-	-
1395762_at	---	---	---	Rn.205380	BG670091	2.60	2.59	2.64	2.59	2.61	2.59	1.01	down	6.14E-01	8.95E-01	-	-
1375698_at	---	---	---	Rn.23254	BG372400	2.38	2.38	2.40	2.38	2.43	2.37	1.01	up	6.79E-01	9.02E-01	-	-
1380589_at	---	---	---	Rn.204061	AI045025	2.41	2.39	2.42	2.40	2.41	2.38	1.01	down	5.16E-01	8.95E-01	-	-
1395859_at	---	---	---	Rn.130301	BI293415	2.38	2.37	2.40	2.37	2.38	2.36	1.01	down	5.24E-01	8.95E-01	-	-
1395492_at	Zc4h2	Zinc finger, C4H2 domain containing	367838	Rn.12889	AF406131	2.45	2.44	2.47	2.45	2.46	2.43	1.01	down	5.59E-01	8.95E-01	-	-
1397403_at	---	---	---	---	AI105130	2.63	2.62	2.65	2.62	2.71	2.54	1.01	down	8.67E-01	9.58E-01	-	-
1380463_at	---	---	---	Rn.133864	AA892945	2.79	2.77	2.84	2.84	2.83	2.70	1.01	down	8.61E-01	9.57E-01	-	-
1384076_at	Cachd1	Cache domain containing 1	298267	Rn.64271	BF567204	5.65	4.69	4.12	4.94	4.58	4.92	1.01	down	9.86E-01	9.96E-01	-	-
1395299_at	Krt24	keratin 24	287675	Rn.61799	BF415218	2.38	2.37	2.40	2.38	2.39	2.36	1.01	down	4.88E-01	8.95E-01	-	-
1381505_at	---	---	---	---	BE106836	2.36	2.36	2.37	2.36	2.34	2.34	1.01	down	3.60E-01	8.95E-01	-	-
1397849_at	---	---	---	Rn.130863	BF564083	2.39	2.37	2.40	2.38	2.39	2.37	1.01	down	4.91E-01	8.95E-01	-	-
1391508_at	---	---	---	---	AI011730	2.39	2.37	2.39	2.37	2.39	2.36	1.01	down	4.85E-01	8.95E-01	-	-
1394805_at	---	---	---	Rn.210848	BF402425	2.38	2.37	2.40	2.38	2.43	2.37	1.01	up	6.87E-01	9.04E-01	-	-
1394703_at	---	---	---	Rn.172087	BF288414	2.34	2.33	2.37	2.34	2.35	2.33	1.01	down	5.66E-01	8.95E-01	-	-
1383804_at	Dnrtb1	DMRT-like family B with proline-rich C-terminal, 1	313484	Rn.198286	BI287409	2.35	2.34	2.37	2.34	2.35	2.34	1.01	down	4.19E-01	8.95E-01	-	-
1371119_at	LOC360231	MHC class I RT1.O type 149 processed pseudogene	360231	---	L40364	2.23	2.22	2.24	2.22	2.22	2.22	1.01	down	2.74E-01	8.95E-01	-	-
1372086_at	Fhdc1	FH2 domain containing 1	295161	Rn.4218	BM387251	2.38	2.36	2.39	2.37	2.38	2.36	1.01	down	4.46E-01	8.95E-01	-	-
1370347_at	Pdlim7	PDZ and LIM domain 7	286908	Rn.7274	AF095585	3.02	2.98	3.00	3.17	3.05	2.75	1.01	down	9.48E-01	9.85E-01	-	-
1397816_at	---	---	---	---	AW921129	2.39	2.37	2.40	2.38	2.39	2.37	1.01	down	4.44E-01	8.95E-01	-	-
1393433_at	Egflam	EGF-like, fibronectin type III and laminin G domains	365691	Rn.27713	AI144872	2.43	2.42	2.44	2.42	2.43	2.40	1.01	down	4.43E-01	8.95E-01	-	-
1375777_at	---	---	---	Rn.202475	BF402633	2.29	2.29	2.31	2.29	2.30	2.28	1.01	down	3.42E-01	8.95E-01	-	-
1395202_at	---	---	---	Rn.207718	BE106256	2.36	2.35	2.38	2.35	2.37	2.34	1.01	down	5.12E-01	8.95E-01	-	-
1378698_at	Myh8	myosin, heavy chain 8, skeletal muscle, perinatal	252942	---	AI555163	2.41	2.40	2.43	2.40	2.43	2.38	1.01	down	5.82E-01	8.95E-01	-	-
1394453_at	---	---	---	Rn.146512	BE121160	2.39	2.38	2.41	2.38	2.40	2.37	1.01	down	4.90E-01	8.95E-01	-	-
1398202_at	---	---	---	Rn.147579	BF394499	2.41	2.40	2.43	2.41	2.42	2.39	1.01	down	5.42E-01	8.95E-01	-	-
1383853_at	Dyrk3	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 3	304775	Rn.162390	BE103067	2.45	2.43	2.46	2.44	2.45	2.43	1.01	down	5.00E-01	8.95E-01	-	-
1377467_at	Smad6	SMAD family member 6	367100	Rn.42472	AA997044	2.26	2.26	2.28	2.26	2.26	2.25	1.01	down	2.82E-01	8.95E-01	-	-
1397253_at	---	---	---	Rn.167312	AI178349	2.46	2.45	2.46	2.45	2.46	2.43	1.01	down	3.24E-01	8.95E-01	-	-
1396891_at	---	---	---	Rn.207002	AW533248	2.71	2.69	2.84	2.65	2.88	2.68	1.01	down	9.25E-01	9.78E-01	-	-
1370908_at	Hdac2	histone deacetylase 2	84577	Rn.1797	AA892297	8.83	8.56	8.91	8.74	8.70	8.89	1.01	up	9.45E-01	9.84E-01	-	-
1373314_at	---	---	---	Rn.173029	BF399075	2.30	2.29	2.31	2.30	2.34	2.29	1.01	up	6.19E-01	8.95E-01	-	-
1368422_at	Meox2	mesenchyme homeobox 2	29279	Rn.34890	NM_017149	2.37	2.36	2.39	2.37	2.38	2.35	1.01	down	4.86E-01	8.95E-01	-	-
1394259_at	Cldn15	claudin 15	304388	Rn.202600	AW920342	2.48	2.46	2.50	2.48	2.51	2.48	1.01	up	5.64E-01	8.95E-01	-	-
1370021_at	Rho	rhodopsin	24717	Rn.92530	NM_033441	2.44	2.42	2.48	2.43	2.46	2.42	1.01	down	6.74E-01	9.01E-01	-	-
1384886_at	RGD1560157	similar to hypothetical protein LOC168850	500057	Rn.219941	AW523423	2.76	2.71	2.75	2.72	2.89	2.64	1.01	up	9.14E-01	9.74E-01	-	-
1395561_at	pa2b1 /// RGD156	heterogeneous nuclear ribonucleoprotein A2/B1 /// similar to heterogeneous r	362361 /// 500008	Rn.4057	BG666358	7.77	7.77	7.71	7.50	7.96	7.75	1.01	down	9.51E-01	9.86E-01	-	-
1384045_at	---	---	---	---	BF288380	2.42	2.40	2.44	2.41	2.43	2.39	1.01	down	6.10E-01	8.95E-01	-	-
1396507_at	---	---	---	---	BE102411	2.29	2.28	2.31	2.29	2.29	2.28	1.01	down	4.07E-01	8.95E-01	-	-
1374277_at	Ccnjl	cyclin J-like	303059	Rn.34782	BI289615	2.79

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1378729_at	Tomm34	translocase of outer mitochondrial membrane 34	311621	Rn.16749	AW251636	2.62	2.60	2.61	2.60	2.61	2.60	1.01	down	2.48E-01	8.95E-01	-	-
1392104_at	---	---	---	Rn.200163	BF419583	2.29	2.28	2.33	2.28	2.31	2.28	1.01	down	6.42E-01	8.95E-01	-	-
1397940_at	Hspb11	Heat shock protein family B (small), member 11	685284	Rn.98778	BF406368	2.55	2.51	2.56	2.55	2.57	2.48	1.01	down	7.97E-01	9.34E-01	-	-
1398715_at	Nmt2	N-myristoyltransferase 2	291318	Rn.162255	BF563806	2.42	2.40	2.45	2.41	2.45	2.39	1.01	down	7.38E-01	9.16E-01	-	-
1397235_at	---	---	---	Rn.165245	AA963984	2.33	2.30	2.32	2.31	2.32	2.30	1.01	down	3.73E-01	8.95E-01	-	-
1369016_at	Cdon	Cdon homolog (mouse)	50938	Rn.10818	NM_017358	2.35	2.34	2.38	2.34	2.36	2.34	1.01	down	5.29E-01	8.95E-01	-	-
1391305_at	---	---	---	---	AI576233	2.57	2.53	2.61	2.53	2.73	2.48	1.01	up	9.18E-01	9.75E-01	-	-
1398274_at	Spata2	spermatogenesis associated 2	114210	Rn.201291	NM_053675	2.41	2.35	2.37	2.35	2.42	2.34	1.01	down	7.93E-01	9.34E-01	-	-
1396438_at	---	---	---	---	BF416791	2.40	2.40	2.42	2.40	2.41	2.37	1.01	down	5.56E-01	8.95E-01	-	-
1380946_at	---	---	---	Rn.2798	AW251808	2.44	2.43	2.45	2.43	2.44	2.42	1.01	down	3.85E-01	8.95E-01	-	-
1386869_at	Actg2	actin, gamma 2, smooth muscle, enteric	25365	Rn.958	NM_012893	2.55	2.49	2.58	2.53	2.56	2.50	1.01	down	7.81E-01	9.29E-01	-	-
1380838_at	---	---	---	Rn.146526	BF400892	2.44	2.43	2.44	2.43	2.45	2.40	1.01	down	5.98E-01	8.95E-01	-	-
1396607_at	---	---	---	Rn.77150	BI301860	2.33	2.30	2.32	2.31	2.32	2.29	1.01	down	4.76E-01	8.95E-01	-	-
1370424_at	Prb1	proline-rich protein BstNI subfamily 1	257651	Rn.29950	L17318	2.40	2.39	2.42	2.40	2.41	2.38	1.01	down	5.10E-01	8.95E-01	-	-
1396603_at	---	---	---	Rn.173364	BF406214	2.38	2.37	2.40	2.37	2.39	2.36	1.01	down	5.16E-01	8.95E-01	-	-
1374234_at	Hkr3	GLI-Kruppel family member HKR3	362668	Rn.20379	AI073183	2.46	2.46	2.48	2.45	2.47	2.46	1.01	down	4.53E-01	8.95E-01	-	-
1368812_at	Lmnb1	lamin B1	116685	Rn.11362	AI407364	2.47	2.44	2.45	2.44	2.45	2.44	1.01	down	4.06E-01	8.95E-01	-	-
1369282_at	Tnfsf11	tumor necrosis factor (ligand) superfamily, member 11	117516	Rn.217570	NM_057149	2.43	2.41	2.45	2.43	2.44	2.40	1.01	down	6.45E-01	8.95E-01	-	-
1396637_at	---	---	---	Rn.170713	BE099828	2.34	2.34	2.36	2.34	2.36	2.32	1.01	down	5.27E-01	8.95E-01	-	-
1384662_at	---	---	---	Rn.12289	AI030739	2.44	2.43	2.46	2.44	2.45	2.42	1.01	down	4.75E-01	8.95E-01	-	-
1396697_at	---	---	---	Rn.63580	BF419773	2.47	2.46	2.50	2.47	2.48	2.45	1.01	down	6.09E-01	8.95E-01	-	-
1375780_at	---	---	---	Rn.153674	BM386309	2.57	2.53	2.60	2.55	2.57	2.54	1.01	down	7.19E-01	9.11E-01	-	-
1388503_at	Eid1	EP300 interacting inhibitor of differentiation 1	499882	Rn.22737	BE107430	9.91	10.10	9.86	9.98	9.82	10.09	1.01	up	9.41E-01	9.83E-01	-	-
1384687_at	Enc1	ectodermal-neural cortex 1	294674	Rn.3039	AI071307	2.40	2.42	2.41	2.40	2.41	2.40	1.01	down	2.76E-01	8.95E-01	-	-
1375875_at	---	---	---	Rn.218792	BF415701	2.28	2.27	2.28	2.27	2.27	2.26	1.01	down	2.52E-01	8.95E-01	-	-
1383220_at	---	---	---	Rn.67079	BE114231	2.40	2.38	2.42	2.40	2.41	2.38	1.01	down	5.57E-01	8.95E-01	-	-
1393256_at	Sephs1	selenophosphate synthetase 1	291314	Rn.100803	AI137711	7.56	7.48	8.07	7.34	7.97	7.79	1.01	down	9.75E-01	9.92E-01	-	-
1390713_at	---	---	---	Rn.47100	BF410051	2.45	2.44	2.47	2.46	2.46	2.41	1.01	down	6.75E-01	9.01E-01	-	-
1373437_at	Ppp1r8	protein phosphatase 1, regulatory (inhibitor) subunit 8	313030	Rn.16580	BI286565	7.02	6.82	8.10	7.64	7.12	7.21	1.01	up	9.85E-01	9.96E-01	-	-
1369365_at	Pde3a	phosphodiesterase 3A, cGMP inhibited	50678	Rn.44403	NM_017337	2.33	2.33	2.33	2.32	2.33	2.31	1.01	down	1.87E-01	8.95E-01	-	-
1392996_at	Cpeb1	cytoplasmic polyadenylation element binding protein 1	293056	Rn.14572	BG668435	2.34	2.32	2.34	2.33	2.36	2.33	1.01	up	5.24E-01	8.95E-01	-	-
1387133_at	Calb2	calbindin 2	117059	Rn.10321	NM_053988	2.27	2.26	2.29	2.27	2.27	2.26	1.01	down	3.49E-01	8.95E-01	-	-
1396045_at	---	---	---	Rn.176345	BI299536	2.43	2.40	2.43	2.41	2.44	2.39	1.01	down	6.15E-01	8.95E-01	-	-
1398245_at	Sncg	synuclein, gamma (breast cancer-specific protein 1)	64347	Rn.2883	NM_031688	2.40	2.39	2.41	2.40	2.40	2.38	1.01	down	3.46E-01	8.95E-01	-	-
1372967_at	Geft	Rho/ARAC/CDC42 exchange factor	314904	Rn.104028	BI280323	2.35	2.34	2.35	2.34	2.35	2.32	1.01	down	3.59E-01	8.95E-01	-	-
1395732_at	---	---	---	Rn.169627	BF567236	2.47	2.46	2.49	2.47	2.48	2.45	1.01	down	4.79E-01	8.95E-01	-	-
1375651_at	ND1	NADH dehydrogenase subunit 1	26193	---	AI230164	12.61	12.37	12.71	12.55	12.69	12.49	1.01	up	9.46E-01	9.84E-01	-	-
1392762_at	Rad18	RAD18 homolog (S. cerevisiae)	362412	Rn.22793	BF559727	2.52	2.50	2.52	2.51	2.52	2.49	1.01	down	5.66E-01	8.95E-01	-	-
1391237_at	---	---	---	Rn.207758	BE119564	2.40	2.39	2.44	2.39	2.42	2.38	1.01	down	6.70E-01	9.00E-01	-	-
1395233_at	---	---	---	Rn.171068	BE107671	2.70	2.82	2.81	2.68	2.72	2.96	1.01	up	9.31E-01	9.81E-01	-	-
1391047_at	---	---	---	Rn.30592	AI009553	2.56	2.56	2.75	2.71	2.60	2.53	1.01	down	9.22E-01	9.77E-01	-	-
1396590_at	---	---	---	Rn.60488	BF404407	2.37	2.37	2.39	2.37	2.43	2.36	1.01	up	7.21E-01	9.11E-01	-	-
1383590_at	Csgalnact1	chondroitin sulfate N-acetylgalactosaminyltransferase 1	306375	Rn.162264	AA963863	2.41	2.40	2.42	2.40	2.42	2.39	1.01	down	3.73E-01	8.95E-01	-	-
1379304_at	Prkrip1	Prkr interacting protein 1 (IL11 inducible)	498171	Rn.44767	BM388446	2.33	2.31	2.36	2.32	2.34	2.32	1.01	down	6.13E-01	8.95E-01	-	-
1379722_at	---	---	---	Rn.205893	BF387136	2.40	2.39	2.42	2.39	2.39	2.41	1.01	down	4.51E-01	8.95E-01	-	-
1385183_at	---	---	---	Rn.219230	AI549021	2.43	2.41	2.42	2.41	2.45	2.36	1.01	down	7.59E-01	9.21E-01	-	-
1385895_at	---	---	---	Rn.17279	AA859889	2.50	2.43	2.57	2.45	2.60	2.43	1.01	down	9.04E-01	9.70E-01	-	-
1397397_at	Pof1b	premature ovarian failure 1B	302328	Rn.141102	BI291859	2.34	2.32	2.34	2.33	2.34	2.31	1.01	down	5.17E-01	8.95E-01	-	-
1368554_at	Pnlip	pancreatic lipase	25702	Rn.10130	NM_013161	2.37	2.38	2.38	2.37	2.38	2.36	1.01	down	1.90E-01	8.95E-01	-	-
1391547_at	---	---	---	Rn.190653	AI045689	2.43	2.42	2.45	2.43	2.44	2.41	1.01	down	4.82E-01	8.95E-01	-	-
1395739_at	Efr3a	EFR3 homolog A (S. cerevisiae)	362923	Rn.21009	BG672302	2.53	2.61	2.78	2.47	2.52	2.92	1.01	down	9.60E-01	9.89E-01	-	-
1380040_at	LOC689933	hypothetical protein LOC689933	689933	Rn.33202	BE120695	2.38	2.37	2.40	2.37	2.38	2.36	1.01	down	4.73E-01	8.95E-01	-	-
1397553_s_at	Prdm2	PR domain containing 2, with ZNF domain	313678	Rn.202632	AI101637	2.43	2.42	2.44	2.42	2.43	2.41	1.01	down	2.42E-01	8.95E-01	-	-
1383048_at	Arhgap10	Rho GTPase activating protein 10	688429	Rn.40465	AI013384	2.38	2.36	2.38	2.36	2.38	2.35	1.01	down	4.49E-01	8.95E-01	-	-
1369872_a_at	Fcer2	Fc fragment of IgE, low affinity II, receptor for (CD23)	171075	Rn.10326	AF381978	2.33	2.33	2.35	2.33	2.33	2.32	1.01	down	3.16E-01	8.95E-01	-	-
1370076_at	Kcnj16	potassium inwardly-rectifying channel, subfamily J, member 16	29719	Rn.1989	NM_053314	7.37	7.77	7.23	7.53	7.26	7.61	1.01	up	9.67E-01	9.90E-01	-	-
1369770_at	Sstr1	somatostatin receptor 1	25033	Rn.42915	M97656	2.35	2.33	2.35	2.34	2.34	2.32	1.01	down	3.30E-01	8.95E-01	-	-
1393389_at	Nr4a3	nuclear receptor subfamily 4, group A, member 3	58853	Rn.62694	BF396297	2.35	2.33	2.35	2.34	2.34	2.33	1.01	down	3.48E-01	8.95E-01	-	-
1377395_at	---	---	---	Rn.199710	AW535261	2.46	2.44	2.49	2.45	2.50	2.42	1.01	down	7.58E-01	9.21E-01	-	-
1397879_at	---	---	---	Rn.209459	BF388414	2.40	2.38	2.41	2.39	2.40	2.38	1.01	down	4.45E-01	8.95E-01	-	-
1375070_at	---	---	---	Rn.216899	BG376853	2.38	2.37	2.39	2.37	2.38	2.36	1.01	down	3.84E-01	8.95E-01	-	-
1396583_at	---	---	---	Rn.206913	AW531808	2.30	2.29	2.32	2.29	2.30	2.29	1.01	down	3.64E-01	8.95E-01	-	-
1390065_at	Kcnv2	potassium channel, subfamily V, member 2	294065	Rn.168638	BE096685	2.36	2.35	2.38	2.35	2.36	2.34	1.01	down	4.53E-01	8.95E-01	-	-
1369806_at	Adrb1	adrenergic, beta-1-, receptor	24925	Rn.87064	NM_012701	2.34	2.33	2.34	2.36	2.34	2.33	1.01	up	4.20E-01	8.95E-01	-	-
1395132_at	Utrn	Utrophin	25600	Rn.9901	BE115432	2.53	2.58	2.68	2.58	2.58	2.59	1.01	down	8.58E-01	9.56E-01	-	-
1380242_at	Lrp5	low density lipoprotein receptor-related protein 5	293649	Rn.12698	AW435376	2.32	2.32	2.32	2.31	2.32	2.31	1.01	down	5.18E-02	8.95E-01	-	-
1395089_at	---	---	---	Rn.40956	BF390878	2.31	2.32	2.32	2.31	2.32	2.30	1.01	down	9.64E-02	8.95E-01	-	-
1389819_at	---	---	---	Rn.51390	BF409843	2.28	2.29	2.28	2.28	2.28	2.27	1.01	down	1.51E-01	8.95E-01	-	-
1381132_at	---	---	---	Rn.145684	AI501937	2.43	2.42	2.48	2.43	2.47	2.40	1.01	down	7.60E-01	9.22E-01	-	-
1379923_at	---	---	---	Rn.49073	AW525902	2.34	2.33	2.37	2.34	2.34	2.32	1.01	down	5.46E-01	8.95E-01	-	-
1397034_at	---	---	---	Rn.208740	BE121170	2.51	2.50	2.55	2.51	2.52	2.50	1.01	down	5.78E-01	8.95E-01	-	-
1385170_at	Fstl5	follistatin-like 5	365823	Rn.151470	BE120758	2.49	2.48	2.50	2.48	2.50	2.47	1.01	down	4.93E-01	8.95E-01	-	-
1374334_at	OC366772 /// LOC	immunoglobulin heavy chain, alpha /// similar to immunoglobulin heavy chain 87 /// 366772 /// 67	---	Rn.219258	AI412189	2.34	2.34	2.36	2.34	2.35	2.33	1.01	down	4.04E-01	8.95E-01	-	-
1376637_at	---	---	---	Rn.25154	AI102401	2.49	2.48	2.52	2.49	2.51	2.48	1.01	down	6.03E-01	8.95E-01	-	-
1385295_at	Ccdc151	coiled-coil domain containing 151	315465	Rn.218536	AI144607	2.39	2.36	2.38	2.37	2.38	2.36	1.01	down	4.28E-01	8.95E-01	-	-
1398466_at	Calr4	calreticulin 4	689537	Rn.156271	BG375382	2.45	2.43	2.48	2.44	2.45	2.44	1.01	down	5.65E-01	8.95E-01	-	-
1378270_at	Ppp1r3d	Protein phosphatase 1, regulatory subunit 3D	689995	Rn.93537	BF418935	2.40	2.35	2.44	2.39	2.46	2.38	1.01	up	8.23E-01	9.43E-01	-	-
1385775_at	---	---	---	---	BF416686	2.31	2.29	2.33	2.30	2.32	2.28	1.01	down	6.05E-01	8.95E-01	-	-
1387968_at	Slc6a15	solute carrier family 6 (neutral amino acid transporter), member 15	282712	Rn.9716	L22022	2.47	2.45	2.49	2.46	2.49	2.44	1.01	down	6.81E-01	9.03E-01	-	-
1370095_at	Ltb4r	leukotriene B4 receptor	59264	Rn.41003	NM_021656	2.30	2.29	2.32	2.30	2.31	2.28	1.01	down	5.46E-01	8.95E-01	-	-
1377131_at	Socs7	Suppressor of cytokine signaling 7	287659	Rn.205543	BE096220	2.24	2.21	2.21	2.21	2.21	2.21	1.01	down	4.71E-01	8.95E-01	-	-
1388871_at	---	---	---	Rn.212027	BI286086	2.29	2.29	2.31	2.29	2.30	2.28	1.01	down	2.10E-01	8.95E-01	-	-
1385827_at	Clcf1	cardiotrophin-like cytokine factor 1	365395	Rn.130193	AI575844	2.60	2.56	2.65	2.58	2.65	2.57	1.01	down	8.23E-01	9.43E-01	-	-
1392826_at	Psgb1	pregnancy-specific beta 1-glycoprotein	59313	Rn.42878	AW921174	2.35	2.34	2.35	2.34	2.35	2.33	1.01	down	3.30E-01	8.95E-01	-	-
1384616_at	Fkbp15	FK506 binding protein 15	362528	Rn.162820	AW523666	2.47	2.45	2.46	2.46	2.46	2.43	1.01	down	5.26E-01	8.95E-01	-	-
1368983_at	Hbegf	heparin-binding EGF-like growth factor	25433	Rn.10148	NM_012945	2.37	2.36	2.38	2.37	2.42	2.35	1.01	up	6.98E-01	9.07E-01	-	-
1381706_at	---	---	---	---	BE096841	2.63	2.63	2.64	2.63	2.63	2.61	1.01	down	3.90E-01	8.95E-01	-	-
1385618_at	---	---	---	Rn.754	AA858570	2.56	2.53	2.57	2.54	2.59	2.50	1.01	down	7.78E-01	9.28E-01	-	-
1377795_at	---	---	---	Rn.25383	AI578745	2.39	2.37	2.40	2.38	2.40	2.36	1.01	down	5.53E-01	8.95E-01	-	-
1378895_at	Ccdc155	coiled-coil domain containing 155	308581	Rn.21840	AI073050	2.32	2.31	2.34	2.32	2.32	2.31	1.01	down	3.89E-01	8.95E-01	-	-
1395450_at	RGD1561558 /// I	similar to RIKEN cDNA 1700001F22 /// similar to RIKEN cDNA 1700001F22 /84 /// 367928 /// 68	---	Rn.206713	BE102568	2.52	2.51	2.54	2.51	2.55	2.49	1.01	down	6.69E-01	9.00E-01	-	-
1395227_at	---	---	---	---	BF386208	2.37	2.36	2.39	2.36	2.37	2.36	1.01	down	4.89E-01	8.95E-01	-	-
1374866_at	---	---	---	---	BF404936	2.67	2.66	2.68	2.66	2.67	2.65	1.01	down	2.85E-01	8.95E-01	-	-
1385380_at	---	---	---	Rn.150534	AI044983	2.40	2.39	2.41	2.39	2.40	2.38	1.01	down	4.11E-01	8.95E-01	-	-
1396174_at	---	---	---	Rn.207320	BM383970	2.32	2.35	2.33	2.33	2.33	2.31	1.01	down	4.14E-01	8.95E-01	-	-
1381321_at	---	---	---	Rn.208209	BE113257	2.46	2.43	2.45	2.44	2.45	2.43	1.01	down	4.62E-01	8.95E-01	-	-
1385022_at	RGD1563309	similar to diacylglycerol kinase, delta 130Kda isoform 1	368088	Rn.17832	BE120566	2.46	2.47	2.47	2.45	2.45	2.52	1.01	up	7.37E-01	9.16E-01	-	-
1394213_at	RGD1308139	similar to RIKEN cDNA 1200014J11	360563	Rn.13279	AI030380	2.44	2.44	2.47	2.44	2.45	2.44	1.01	down	3.98E-01	8.95E-01	-	-
1396951_at	LOC500908	similar to hypothetical protein FLJ23584	500908	---	BI286016	2.33	2.33	2.34	2.32	2.33	2.31	1.01	down	2.78E-01	8.95E-01	-	-
1376369_at	Troap	trophinin associated protein	300219	Rn.18273	BM392307	2.30	2.30	2.30	2.29	2.34	2.29	1.01	up	6.46E-01	8.95E-01	-	-
1369046_at	Syt6	synaptotagmin VI	60565	Rn.48074	NM_022191	2.36	2.36	2.38	2.35	2.36	2.35	1.01	down	3.09E-01	8.95E-01	-	-
1391336_at	---	---	---	Rn.168587	AI763749	2.19	2.18	2.19	2.18	2.22	2.18	1.01	up	5.78E-01	8.95E-01	-	-
1387745_at	Cd200r1	CD200 receptor 1	64357	Rn.12439	NM_023953	2.34	2.32	2.34	2.32	2.33	2.31	1.01	down	3.25E-01	8.95E-01	-	-
1398131_at	---	---	---	Rn.207238	BE096035	2.32	2.32	2.33	2.32	2.30	2.31	1.01	down	4.18E-01	8.95E-01	-	-
1382627_at	---	---	---	Rn.203559	AA956525	2.50	2.47	2.50	2.50	2.49	2.45	1.01	down	6.62E-01	8.98E-01	-	-
1381511_at	---	---	---	Rn.206376	AW524625	2.46	2.44	2.47	2.46	2.46	2.42	1.01	down	6.16E-01	8.95E-01	-	-
1381265_at	Rbm27	RNA binding motif protein 27	361317	Rn.218050	BE099149	2.89	2.89	2.89	2.94	2.89	2.86	1.01	up	7.42E-01	9.17E-01	-	-
1380167_at	---	---	---	Rn.52691	BE116526	2.33	2.32	2.36	2.32	2.34	2.32	1.01	down	5.24E-01	8.95E-01	-	-
1383524_at	---	---	---	Rn.4172	AA955352	2.38	2.36	2.39	2.37	2.38	2.35	1.01	down	5.11E-01	8.95E-01	-	-
1376387_at	---	---	---	Rn.202021	BF416283	2.45	2.43	2.46	2.45	2.45	2.42	1.01	down	5.38E-01	8.95E-01	-	-
1384838_at	Slc34a3	solute carrier family 34 (sodium phosphate), member 3	246234	Rn.15318	AA924432	2.55	2.54	2.56	2.54	2.55	2.53	1.01	down	3.98E-01	8.95E-01	-	-
1377540_at	---	---	---	---	BF393067	2.24	2.23	2.25	2.23	2.24	2.23	1.01	down	3.10E-01	8.95E-01	-	-
1396319_at	Dennd4b	DENN/MADD domain containing 4B	361987	Rn.22411	AI771725	2.37	2.35	2.38	2.36	2.37	2.34	1.01	down	4.90E-01	8.95E-01	-	-
1375280_at	Pppde1	PPPDE peptidase domain containing 1	289277	Rn.9401	AW913871	8.21	7.61	6.53	7.67	7.58	7.14	1.01	up	9.88E-01	9.96E-01	-	-
1385361_at	Atp10a	ATPase, class V, type 10A	365266	Rn.208837	BE120437	2.43	2.42	2.46	2.42	2.46	2.40	1.01	down	6.70E-01	9.00E-01	-	-
1380427_at	---	---	---	---	BF413017	2.58	2.55	2.60	2.56	2.65	2.55	1.01	up	8.23E-01	9.43E-01	-	-
1384869_at	RGD1311019	similar to hypothetical protein DKFZp434H2010	298694	Rn.207816	BE107398	2.37	2.36	2.38	2.36	2.36	2.36	1.01	down	3.64E-01	8.95E-01	-	-
1378817_at	Itsn1	intersectin 1 (SH3 domain protein)	29491	Rn.48657	AW434016	2.35	2.33	2.36	2.36	2.35	2.35	1.01	up	3.60E-01	8.95E-01	-	-
1390644_at	---	---	---	Rn.208106	BE110273	2.40	2.38	2.41	2.39	2.40	2.37	1.01	down	5.21E-01	8.95E-01	-	-
1381720_at	---	---	---	Rn.147233	BE120510	2.40	2.38	2.41	2.39	2.41	2.37	1.01	down	6.18E-01	8.95E-01	-	-
1381148_at	---	---	---	Rn.200054	AF410261	2.55	2.51	2.61	2.53	2.58	2.53	1.01	down	8.13E-01	9.40E-01	-	-
1391781_at	---	---	---	Rn.206929	BE097788	2.37	2.34	2.36	2.35	2.36	2.34	1.01	down	4.64E-01	8.95E-01	-	-
1382616_at	Epb4.2	erythrocyte protein band 4.2	362202	Rn.23855	AI103190	2.44	2.43	2.45	2.43	2.45	2.42	1.01	down	4.95E-01	8.95E-01	-	-
1385481_at	Dsel	dermatan sulfate epimerase-like	297865	Rn.101678	AW526551	2.44	2.44	2.46	2.43	2.45	2.44	1.01	down	3.90E-01	8.95E-01	-	-
1369109_at	Oprm1	opioid receptor, mu 1	25601	Rn.10118	L20684	2.33	2.32	2.33	2.32	2.33	2.31	1.01	down	2.35E-01	8.95E-01	-	-
1369470_at	Akap14	A kinase (PRKA) anchor protein 14	60332	Rn.42933	NM_021703	2.38	2.35	2.37	2.36	2.38	2.35	1.01	down	5.13E-01	8.95E-01	-	-
1388040_a_at	Myo1e	myosin IVI	192253	Rn.207204	AF209114	2.56	2.50	2.53	2.53	2.55	2.52	1.01	up	6.46E-01	8.95E-01	-	-
1370981_at	Rxrg	retinoid X receptor gamma	83574	Rn.40816	BE118450	2.28	2.28	2.31	2.29	2.29	2.28	1.01	down	4.21E-01	8.95E-01	-	-
1371418_at	Cct2	chaperonin containing TCP1, subunit 2 (beta)	299809	Rn.2392	BG665035	10.07	10.35	10.11	10.09	9.98	10.49	1.01	up	9.64E-01	9.90E-01	-	-
1377207_at	---	---	---	Rn.211048	BF404972	2.33	2.32	2.35	2.32	2.33	2.32	1.01	down	4.21E-01	8.95E-01	-	-
1369801_at	Sell	selectin, lymphocyte	29259	Rn.10461	D10831	2.36	2.35	2.37	2.36	2.36	2.34	1.01	down	3.59E-01	8.95E-01	-	-
1377097_at	Cox6b2	cytochrome c oxidase subunit VIb polypeptide 2	654441	Rn.97699	BF545080	2.34	2.33	2.35	2.33	2.34	2.32	1.01	down	2.71E-01	8.95E-01	-	-
1369143_at	Chrnb3	cholinergic receptor, nicotinic, beta 3	171131	Rn.9694	NM_133597	2.41	2.40	2.43	2.41	2.42	2.39	1.01	down	5.13E-01	8.95E-01	-	-
1396226_at	---	---	---	Rn.27297	BI276258	2.46	2.44	2.48	2.44	2.47	2.44	1.01	down	6.46E-01	8.95E-01	-	-
1395814_at	---	---	---	Rn.47307	AW529817	2.34	2.34	2.35	2.34	2.34	2.32	1.01	down	2.64E-01	8.95E-01	-	-
1370488_a_at	Ptprs	protein tyrosine phosphatase, receptor type, S	25529	Rn.91202	L19181	2.40	2.40	2.41	2.39	2.41	2.38	1.01	down	3.82E-01	8.95E-01	-	-
1377841_at	---	---	---	Rn.201609	AW142828	2.38	2.37	2.39	2.38	2.38	2.36	1.01	down	4.52E-01	8.95E-01	-	-
1368729_a_at	Adcyap1r1	adenylate cyclase activating polypeptide 1 (pituitary) receptor type I	24167	Rn.88408	Z23279	2.41	2.40	2.42	2.40	2.42	2.39	1.01	down	5.04E-01	8.95E-01	-	-
1384695_at	Upk3a	uroplakin 3A	315190	Rn.81907	BM387108	2.33	2.32	2.35	2.32	2.33	2.32	1.01	down	4.69E-01	8.95E-01	-	-
1396571_at	---	---	---	---	BF418055	2.54	2.52	2.56	2.52	2.60	2.48	1.01	down	8.34E-01	9.48E-01	-	-
1379877_at	Zfat	zinc finger and AT hook domain containing	362925	Rn.33031	BI286191	2.36	2.36	2.37	2.35	2.36	2.34	1.01	down	2.79E-01	8.95E-01	-	-
1376091_at	Adsl	adenylosuccinate lyase	315150	Rn.23276	AA963616	5.79	5.49	6.41	5.94	5.31	6.41	1.01	down	9.85E-01	9.96E-01	-	-
1382282_at	Lix1l	Lix1 homolog (mouse)-like	499677	Rn.3632	BF390321	2.38	2.36	2.38	2.36	2.38	2.35	1.01	down	5.23E-01	8.95E-01	-	-
1389462_at	---	---	---	Rn.41650	BG373049	2.41	2.40	2.42	2.40	2.42	2.39	1.01	down	5.37E-01	8.95E-01	-	-
1398460_at	RGD1311723	similar to

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)				REG	MTC
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval		
1380264_at	---	---	---	Rn.52191	BF399532	2.44	2.43	2.46	2.43	2.45	2.43	1.01	down	4.80E-01	8.95E-01	-	-
1391879_at	---	---	---	Rn.133780	AA864161	2.59	2.55	2.70	2.58	2.67	2.56	1.01	down	8.87E-01	9.65E-01	-	-
1382378_at	Clsw	cathepsin W	293676	Rn.34406	BI279370	2.48	2.47	2.48	2.47	2.48	2.46	1.01	down	2.70E-01	8.95E-01	-	-
1390090_at	---	---	---	---	AW534085	2.30	2.29	2.30	2.29	2.30	2.28	1.01	down	2.41E-01	8.95E-01	-	-
1376354_a_at	---	---	---	Rn.43762	BI273698	2.38	2.37	2.39	2.37	2.39	2.36	1.01	down	4.67E-01	8.95E-01	-	-
1391298_at	---	---	---	Rn.209975	BF416081	2.35	2.34	2.36	2.34	2.35	2.33	1.01	down	3.64E-01	8.95E-01	-	-
1378879_at	---	---	---	Rn.154279	BI289790	2.49	2.46	2.53	2.47	2.53	2.44	1.01	down	8.16E-01	9.41E-01	-	-
1381725_at	---	---	---	Rn.147632	BF393429	2.36	2.36	2.39	2.36	2.37	2.35	1.01	down	5.23E-01	8.95E-01	-	-
1393726_at	Duxbl	double homeobox B-like	306226	Rn.21629	AI030773	2.29	2.28	2.29	2.28	2.32	2.28	1.01	up	6.00E-01	8.95E-01	-	-
1385715_at	Gpr155	G protein-coupled receptor 155	311730	Rn.2051	AA866489	2.58	2.52	2.60	2.57	2.59	2.57	1.01	up	7.71E-01	9.25E-01	-	-
1385662_at	Dnmt3b	DNA methyltransferase 3B	444985	Rn.117353	BF562135	2.33	2.31	2.31	2.30	2.31	2.30	1.01	down	2.97E-01	8.95E-01	-	-
1377291_at	Trim66	tripartite motif-containing 66	361623	Rn.198515	AW525040	2.30	2.29	2.32	2.30	2.31	2.28	1.01	down	4.63E-01	8.95E-01	-	-
1395315_at	---	---	---	Rn.191187	BF395708	2.44	2.43	2.46	2.43	2.46	2.42	1.01	down	6.21E-01	8.95E-01	-	-
1378030_at	---	---	---	Rn.167135	AW527482	2.52	2.49	2.54	2.52	2.52	2.49	1.01	down	6.92E-01	9.05E-01	-	-
1370362_at	Ptprn	protein tyrosine phosphatase, receptor type, N	116660	Rn.11097	D45414	6.44	7.93	7.31	7.25	6.90	7.51	1.01	down	9.87E-01	9.96E-01	-	-
1370628_at	Gzmb	granzyme B	171528	Rn.132115	M34097	2.32	2.31	2.34	2.32	2.32	2.31	1.01	down	3.86E-01	8.95E-01	-	-
1379235_x_at	Cdc45l	CDC45 cell division cycle 45-like (S. cerevisiae)	287961	Rn.98535	AI179539	2.32	2.31	2.33	2.31	2.32	2.35	1.01	up	5.74E-01	8.95E-01	-	-
1392027_at	---	---	---	Rn.172865	BF396714	2.39	2.38	2.40	2.37	2.39	2.38	1.01	down	2.57E-01	8.95E-01	-	-
1377516_at	---	---	---	Rn.210640	BF399641	2.39	2.37	2.40	2.38	2.39	2.36	1.01	down	5.14E-01	8.95E-01	-	-
1370255_at	Sftpc	surfactant protein C	50683	Rn.3926	AI009659	2.36	2.35	2.37	2.35	2.36	2.34	1.01	down	3.98E-01	8.95E-01	-	-
1369090_at	Prkg2	protein kinase, cGMP-dependent, type II	25523	Rn.87721	NM_013012	2.42	2.40	2.44	2.42	2.43	2.39	1.01	down	5.97E-01	8.95E-01	-	-
1394128_at	---	---	---	Rn.206010	AI639276	2.46	2.45	2.48	2.45	2.48	2.44	1.01	down	5.97E-01	8.95E-01	-	-
1376987_at	Lrrc49	leucine rich repeat containing 49	300763	Rn.26984	AW523375	2.45	2.44	2.46	2.44	2.45	2.43	1.01	down	3.70E-01	8.95E-01	-	-
1396492_at	Nfatm1	NFAT activating protein with ITAM motif 1	362666	Rn.209796	BF399099	2.31	2.31	2.32	2.30	2.32	2.29	1.01	down	3.81E-01	8.95E-01	-	-
1374363_at	Aifm3	apoptosis-inducing factor, mitochondrion-associated 3	303786	Rn.138718	AI232693	2.33	2.32	2.35	2.32	2.33	2.32	1.01	down	3.34E-01	8.95E-01	-	-
1398940_at	Strm2	serine/arginine repetitive matrix 2	302969	Rn.162027	AW532525	10.88	10.90	11.08	11.30	11.00	10.54	1.01	down	9.73E-01	9.92E-01	-	-
1381279_at	Ripk2	receptor-interacting serine-threonine kinase 2	362491	Rn.102179	BF412519	2.40	2.38	2.40	2.38	2.39	2.38	1.01	down	4.22E-01	8.95E-01	-	-
1369706_at	Cacng1	calcium channel, voltage-dependent, gamma subunit 1	29658	Rn.24079	NM_019255	2.37	2.36	2.38	2.37	2.40	2.36	1.01	up	5.02E-01	8.95E-01	-	-
1369751_at	Trhr	thyrotropin releasing hormone receptor	25570	Rn.9962	M90308	2.32	2.31	2.33	2.31	2.32	2.30	1.01	down	4.38E-01	8.95E-01	-	-
1376302_at	---	---	---	Rn.203515	AA955175	2.35	2.35	2.37	2.36	2.35	2.33	1.01	down	5.07E-01	8.95E-01	-	-
1395833_at	Zfp259	zinc finger protein 259	500989	Rn.102011	BF563535	2.35	2.34	2.35	2.35	2.32	2.32	1.01	down	4.40E-01	8.95E-01	-	-
1375798_at	---	---	---	Rn.200091	BF410097	2.40	2.39	2.41	2.39	2.45	2.38	1.01	up	7.24E-01	9.13E-01	-	-
1392321_at	---	---	---	Rn.146798	BE120641	2.44	2.42	2.46	2.44	2.45	2.40	1.01	down	6.62E-01	8.98E-01	-	-
1370989_at	Ret	ret proto-oncogene	24716	Rn.93200	AI639318	2.41	2.40	2.43	2.40	2.43	2.38	1.01	down	6.36E-01	8.95E-01	-	-
1379137_at	---	---	---	Rn.56489	BF387378	2.38	2.39	2.39	2.38	2.40	2.36	1.01	down	5.16E-01	8.95E-01	-	-
1376286_at	RGD1566083	similar to hypothetical protein MGC24047	298602	Rn.46026	AF413225	2.40	2.39	2.42	2.40	2.41	2.38	1.01	down	5.59E-01	8.95E-01	-	-
1397555_at	RGD1563838	similar to leucine zipper protein 2	361583	---	BG668744	2.37	2.36	2.38	2.36	2.37	2.35	1.01	down	3.26E-01	8.95E-01	-	-
1381972_at	Crbn	cereblon	297498	Rn.195259	BG673626	7.19	7.55	7.55	7.31	7.44	7.56	1.01	up	9.56E-01	9.87E-01	-	-
1367489_at	---	---	---	---	BE114147	2.36	2.35	2.34	2.37	2.36	2.35	1.01	up	2.67E-01	8.95E-01	-	-
1390859_at	N4bp1	Nedd4 binding protein 1	291921	Rn.137980	BI280968	2.49	2.48	2.55	2.49	2.53	2.48	1.01	down	7.60E-01	9.22E-01	-	-
1395421_at	Punc	putative neuronal cell adhesion molecule	315759	Rn.19376	BF390052	2.35	2.34	2.36	2.34	2.35	2.33	1.01	down	2.59E-01	8.95E-01	-	-
1393532_at	Ubqln3	ubiquilin 3	308905	Rn.66649	BG379163	2.52	2.48	2.56	2.50	2.58	2.46	1.01	down	8.49E-01	9.53E-01	-	-
1393460_at	Lrrc33	leucine rich repeat containing 33	303875	Rn.138732	BM388665	2.22	2.24	2.23	2.22	2.22	2.22	1.01	down	1.32E-01	8.95E-01	-	-
1383323_at	Dsn1	DSN1, MIND kinetochore complex component, homolog (S. cerevisiae)	499933	Rn.117385	AW435234	2.41	2.41	2.43	2.41	2.43	2.38	1.01	down	5.97E-01	8.95E-01	-	-
1376223_at	RGD1309079	similar to Ab2-095	315891	Rn.15757	BE120464	2.24	2.26	2.24	2.23	2.24	2.24	1.01	down	3.59E-01	8.95E-01	-	-
1381538_at	---	---	---	Rn.146812	BF391531	2.42	2.40	2.44	2.41	2.43	2.39	1.01	down	6.09E-01	8.95E-01	-	-
1393599_at	LOC690020	similar to killer cell lectin-like receptor, subfamily A, member 17	690020	Rn.211887	AA926241	2.47	2.41	2.42	2.42	2.45	2.41	1.01	down	7.26E-01	9.13E-01	-	-
1396889_at	---	---	---	---	BF419391	2.31	2.30	2.32	2.30	2.31	2.29	1.01	down	4.09E-01	8.95E-01	-	-
1370771_at	Cacng7	calcium channel, voltage-dependent, gamma subunit 7	140728	Rn.81218	AF361345	2.37	2.37	2.39	2.37	2.38	2.36	1.01	down	4.16E-01	8.95E-01	-	-
1378192_at	Tmem42	Transmembrane protein 42	363171	Rn.161976	BE100915	2.36	2.35	2.38	2.36	2.37	2.35	1.01	down	4.87E-01	8.95E-01	-	-
1378813_at	---	---	---	Rn.62907	BF398841	2.35	2.35	2.36	2.35	2.35	2.33	1.01	down	3.62E-01	8.95E-01	-	-
1374587_at	Tmtc3	transmembrane and tetratricopeptide repeat containing 3	314785	Rn.3901	AI009750	3.20	3.00	3.02	3.03	3.15	3.01	1.01	down	9.19E-01	9.76E-01	-	-
1387622_at	Rfng	RFNG O-fucosylpeptide 3-beta-N-acetylglucosaminyltransferase	60433	Rn.168817	NM_021849	2.38	2.37	2.38	2.38	2.38	2.35	1.01	down	4.23E-01	8.95E-01	-	-
1377464_at	---	---	---	Rn.205945	BF402138	2.35	2.34	2.37	2.35	2.36	2.33	1.01	down	5.55E-01	8.95E-01	-	-
1379170_at	---	---	---	Rn.200045	BF393059	2.36	2.34	2.36	2.34	2.35	2.35	1.01	down	2.60E-01	8.95E-01	-	-
1370053_at	Dlgap1	Discs, large (Drosophila) homolog-associated protein 1	65040	Rn.90059	NM_022946	2.44	2.43	2.45	2.44	2.44	2.42	1.01	down	3.92E-01	8.95E-01	-	-
1383889_at	---	---	---	Rn.34659	AI511225	3.14	2.75	3.81	3.45	2.83	3.39	1.01	down	9.83E-01	9.95E-01	-	-
1387138_at	Tac2	tachykinin 2	29191	Rn.9708	NM_019162	2.37	2.36	2.38	2.36	2.37	2.35	1.01	down	4.09E-01	8.95E-01	-	-
1370092_at	Mas1	MAS1 oncogene	25153	Rn.21943	NM_012757	2.38	2.36	2.39	2.37	2.38	2.35	1.01	down	5.38E-01	8.95E-01	-	-
1396032_at	---	---	---	---	BF409507	2.24	2.23	2.30	2.24	2.27	2.24	1.01	down	7.50E-01	9.19E-01	-	-
1370627_at	Rhov	ras homolog gene family, member V	171581	Rn.30047	AF097887	2.42	2.41	2.43	2.41	2.42	2.40	1.01	down	4.16E-01	8.95E-01	-	-
1376027_at	---	---	---	---	AI101673	2.49	2.48	2.53	2.48	2.52	2.47	1.01	down	7.29E-01	9.14E-01	-	-
1370754_at	Tas2r123	taste receptor, type 2, member 123	287003	Rn.48792	AF240765	2.39	2.39	2.40	2.38	2.41	2.37	1.01	down	5.60E-01	8.95E-01	-	-
1369907_at	Alpi	alkaline phosphatase, intestinal	24197	Rn.48774	NM_022665	2.34	2.34	2.35	2.34	2.35	2.32	1.01	down	3.13E-01	8.95E-01	-	-
1392863_at	---	---	---	Rn.95324	AA817953	2.39	2.37	2.38	2.37	2.38	2.35	1.01	down	4.78E-01	8.95E-01	-	-
1377101_at	---	---	---	---	AI045635	2.43	2.37	2.40	2.40	2.39	2.39	1.01	down	6.52E-01	8.97E-01	-	-
1391753_at	---	---	---	Rn.204984	BI288825	2.43	2.43	2.46	2.44	2.44	2.47	1.01	up	5.77E-01	8.95E-01	-	-
1393829_at	Fgfr1op2	FGFR1 oncogene partner 2	362463	Rn.68658	AI639475	5.11	4.79	4.44	4.70	4.72	4.90	1.01	down	9.70E-01	9.91E-01	-	-
1392163_at	---	---	---	Rn.63147	BF391452	2.62	2.57	2.62	2.57	2.68	2.53	1.01	down	8.76E-01	9.61E-01	-	-
1376090_at	Thumpd2	THUMP domain containing 2	313851	Rn.204569	AW252828	2.89	2.79	2.79	2.78	2.81	2.86	1.01	down	8.53E-01	9.55E-01	-	-
1367590_at	Ran	RAN, member RAS oncogene family	84509	Rn.107698	NM_053439	9.41	9.33	9.44	9.30	9.41	9.46	1.01	down	8.93E-01	9.67E-01	-	-
1379995_at	---	---	---	Rn.205488	BE113173	2.36	2.35	2.37	2.36	2.36	2.34	1.01	down	4.12E-01	8.95E-01	-	-
1387738_at	Mycs	myc-like oncogene, s-myc protein	24581	Rn.138106	NM_021837	2.38	2.37	2.39	2.37	2.38	2.36	1.01	down	4.55E-01	8.95E-01	-	-
1385519_at	Runx1t1	runt-related transcription factor 1; translocated to, 1 (cyclin D-related)	362489	Rn.218117	BE105678	2.34	2.32	2.34	2.33	2.34	2.32	1.01	down	3.61E-01	8.95E-01	-	-
1385759_at	Serpinb10	serine (or cysteine) peptidase inhibitor, clade B (ovalbumin), member 10	266775	Rn.59484	BF399855	2.51	2.46	2.52	2.50	2.53	2.49	1.01	up	7.28E-01	9.13E-01	-	-
1374238_at	---	---	---	Rn.147161	BI296639	2.41	2.40	2.42	2.41	2.41	2.39	1.01	down	4.61E-01	8.95E-01	-	-
1384526_at	Tex15	testis expressed 15	290803	Rn.46623	BF419582	2.36	2.33	2.35	2.34	2.34	2.33	1.01	down	4.61E-01	8.95E-01	-	-
1376734_at	---	---	---	Rn.29042	BI279030	2.40	2.39	2.42	2.39	2.40	2.38	1.01	down	4.62E-01	8.95E-01	-	-
1395811_at	---	---	---	Rn.28171	BI385611	2.43	2.41	2.45	2.42	2.44	2.40	1.01	down	6.11E-01	8.95E-01	-	-
1378793_at	---	---	---	Rn.205134	BE121233	2.47	2.42	2.52	2.47	2.47	2.43	1.01	down	8.04E-01	9.37E-01	-	-
1398613_at	---	---	---	Rn.169951	AW532063	2.46	2.44	2.48	2.45	2.47	2.43	1.01	down	6.21E-01	8.95E-01	-	-
1379510_at	---	---	---	Rn.37950	BF546306	2.41	2.40	2.43	2.40	2.42	2.39	1.01	down	5.65E-01	8.95E-01	-	-
1389802_at	---	---	---	Rn.172641	BF403989	2.34	2.34	2.36	2.34	2.35	2.33	1.01	down	4.98E-01	8.95E-01	-	-
1377973_at	---	---	---	---	BF402062	2.47	2.46	2.50	2.46	2.51	2.44	1.01	down	7.55E-01	9.20E-01	-	-
1380113_at	---	---	---	Rn.146277	BI289454	2.37	2.35	2.37	2.36	2.36	2.34	1.01	down	4.17E-01	8.95E-01	-	-
1370857_at	Acta2	smooth muscle alpha-actin	81633	Rn.196319	BI282702	2.42	2.42	2.46	2.42	2.44	2.42	1.01	down	6.11E-01	8.95E-01	-	-
1385602_at	RGD1306233	similar to hypothetical protein MGC29761	296608	Rn.94715	BF561593	2.45	2.42	2.50	2.44	2.50	2.41	1.01	down	8.21E-01	9.42E-01	-	-
1382499_at	---	---	---	Rn.148165	AA819839	2.33	2.32	2.34	2.32	2.33	2.31	1.01	down	3.51E-01	8.95E-01	-	-
1376677_a_at	---	---	---	Rn.53921	BF282021	3.05	3.96	3.10	3.54	3.39	3.22	1.01	up	9.80E-01	9.94E-01	-	-
1370849_at	Hapln2	hyaluronan and proteoglycan link protein 2	64057	Rn.76545	AI145465	2.35	2.34	2.35	2.32	2.35	2.34	1.01	down	4.21E-01	8.95E-01	-	-
1374556_at	Smox	spermine oxidase	308652	Rn.100278	BI289700	2.36	2.34	2.36	2.35	2.36	2.33	1.01	down	3.55E-01	8.95E-01	-	-
1397436_at	---	---	---	Rn.61492	BF409822	2.44	2.42	2.46	2.43	2.46	2.41	1.01	down	6.74E-01	9.01E-01	-	-
1398878_at	---	---	---	---	BF565720	2.37	2.36	2.39	2.37	2.39	2.35	1.01	down	6.18E-01	8.95E-01	-	-
1396952_at	---	---	---	Rn.60505	BF404446	2.41	2.41	2.43	2.41	2.43	2.39	1.01	down	5.39E-01	8.95E-01	-	-
1384986_at	Ankrd35	ankyrin repeat domain 35	365881	Rn.42986	BM387490	2.38	2.37	2.39	2.37	2.38	2.37	1.01	down	2.93E-01	8.95E-01	-	-
1367982_at	Alas1	aminolevulinate, delta-, synthase 1	85155	Rn.97126	NM_024484	8.13	7.96	8.31	8.16	7.96	8.25	1.01	down	9.55E-01	9.87E-01	-	-
1370758_at	Rab15	RAB15, member RAS oncogene family	299156	Rn.24234	M83679	2.27	2.27	2.32	2.30	2.28	2.26	1.01	down	7.02E-01	9.07E-01	-	-
1376358_at	---	---	---	---	BF397657	2.43	2.42	2.45	2.43	2.44	2.41	1.01	down	5.42E-01	8.95E-01	-	-
1379563_at	Ifit5	interferon regulatory factor 5	296953	Rn.203787	AA998071	2.85	2.71	2.55	2.71	2.71	2.70	1.01	up	9.29E-01	9.80E-01	-	-
1398961_at	LOC681578	similar to ring finger protein 13	681578	Rn.17153	AI232296	7.30	6.98	7.01	6.79	6.99	7.53	1.01	up	9.75E-01	9.92E-01	-	-
1389662_at	Wnk4	WNK lysine deficient protein kinase 4	287715	Rn.162189	AI406290	5.31	4.74	5.41	5.41	5.20	4.87	1.01	up	9.77E-01	9.93E-01	-	-
1392722_at	Dapp1	dual adaptor of phosphotyrosine and 3-phosphoinositides	362046	Rn.16615	AA819134	2.46	2.45	2.51	2.46	2.50	2.44	1.01	down	7.60E-01	9.22E-01	-	-
1369812_at	P2ry4	pyrimidinergic receptor P2Y, G-protein coupled, 4	63843	Rn.30068	NM_031680	2.35	2.34	2.37	2.35	2.36	2.33	1.01	down	4.88E-01	8.95E-01	-	-
1394278_at	RGD1560812	RGD1560812	500640	Rn.16708	AW143811	2.35	2.36	2.35	2.34	2.35	2.33	1.01	down	3.34E-01	8.95E-01	-	-
1384843_at	Spaca3	sperm acrosome associated 3	287557	Rn.47764	AW531575	2.40	2.39	2.54	2.40	2.54	2.37	1.01	down	9.13E-01	9.74E-01	-	-
1369115_at	Adrb2	adrenergic, beta-2-, receptor, surface	24176	Rn.10206	AY057895	2.30	2.30	2.32	2.30	2.31	2.29	1.01	down	4.59E-01	8.95E-01	-	-
1390734_at	---	---	---	Rn.176363	BI291369	2.45	2.43	2.48	2.44	2.47	2.43	1.01	down	6.90E-01	9.05E-01	-	-
1381333_at	---	---	---	Rn.148860	BI294382	2.45	2.44	2.47	2.45	2.51	2.43	1.01	up	7.69E-01	9.24E-01	-	-
1391562_at	---	---	---	Rn.204609	AI598473	2.37	2.36	2.37	2.36	2.37	2.35	1.01	down	3.56E-01	8.95E-01	-	-
1396108_at	RGD1309821	Similar to KIAA1161 protein	366360	Rn.106115	BF389026	2.44	2.44	2.46	2.44	2.45	2.42	1.01	down	5.14E-01	8.95E-01	-	-
1380385_at	Ccdc136	coiled-coil domain containing 136	362331	Rn.117708	BF410322	2.38	2.37	2.40	2.38	2.38	2.37	1.01	down	3.89E-01	8.95E-01	-	-
1376901_a_at	Elfn2	extracellular leucine-rich repeat and fibronectin type III domain containing 2	315117	Rn.93288	AA864675	2.35	2.35	2.36	2.34	2.36	2.33	1.01	down	3.93E-01	8.95E-01	-	-
1375199_at	Kctd13	potassium channel tetramerisation domain containing 13	293497	Rn.103144	AI045333	2.37	2.36	2.37	2.36	2.40	2.36	1.01	up	5.39E-01	8.95E-01	-	-
1371753_at	LOC296235	similar to Cystatin S precursor (LM protein)	296235	Rn.79319	BI285082	2.40	2.39	2.42	2.39	2.41	2.38	1.01	down	5.87E-01	8.95E-01	-	-
1383079_at	RGD1566155	similar to 2610030H06Rik protein	501658	Rn.108094	AW916826	5.61	6.66	5.83	5.78	5.74	6.55	1.01	down	9.85E-01	9.96E-01	-	-
1395009_at	---	---	---	Rn.58082	BE097120	2.36	2.35	2.36	2.35	2.36	2.33	1.01	down	4.75E-01	8.95E-01	-	-
1395606_at	---	---	---	Rn.173596	BF412220	2.62	2.39	2.44	2.38	2.67	2.67	1.01	down	9.49E-01	9.85E-01	-	-
1388554_at	Bzw1	basic leucine zipper and W2 domains 1	363232	Rn.96215	AI229287	7.90	7.43	8.47	7.73	7.96	8.07	1.01	down	9.81E-01	9.94E-01	-	-
1397111_at	---	---	---	Rn.211235	BF409107	2.36	2.34	2.36	2.34	2.35	2.34	1.01	down	3.09E-01	8.95E-01	-	-
1384325_at	Plunc	palate, lung, and nasal epithelium associated	246238	Rn.19272	BF546645	2.29	2.29	2.32	2.29	2.30	2.28	1.01	down	4.73E-01	8.95E-01	-	-
1377682_at	---	---	---	Rn.93512	AW522708	2.44	2.38	2.39	2.48	2.39	2.37	1.01	up	8.44E-01	9.52E-01	-	-
1380273_at	---	---	---	Rn.166672	AA944386	2.41	2.40	2.42	2.41	2.42	2.38	1.01	down	5.19E-01	8.95E-01	-	-
1396160_at	---	---	---	---	BF419307	2.31	2.30	2.32	2.31	2.31	2.32	1.01	up	3.50E-01	8.95E-01	-	-
1396154_at	Klf5c	kinesin family member 5C	311024	Rn.50843	BF559198	2.36	2.35	2.37	2.35	2.36	2.34	1.01	down	4.73E-01	8.95E-01	-	-
1394843_at	---	---	---	Rn.168505	BI276823	3.12	2.58	2.48	2.94	2.77	2.51	1.01	up	9.74E-01	9.92E-01	-	-
1394551_at	Car3	Carbonic anhydrase 3	54232	Rn.1647	AW144120	2.44	2.42	2.45	2.43	2.46	2.41	1.01	down	6.68E-01	9.00E-01	-	-
1377752_at	Emp2	epithelial membrane protein 2	360468	Rn.21730	BE112998	2.39	2.38	2.42	2.38	2.41	2.37	1.01	down	6.56E-01	8.98E-01	-	-
1381554_at	---	---	---	Rn.134603	BE097095	2.36	2.35	2.38	2.35	2.36	2.34	1.01	down	5.35E-01	8.95E-01	-	-
1380891_at	---	---	---	Rn.206412	BF391693	2.40	2.39	2.42	2.40	2.41	2.38	1.01	down	5.88E-01	8.95E-01	-	-
1391367_at	---	---	---	---	BF419542	2.39	2.38	2.42	2.39	2.41	2.37	1.01	down	6.56E-01	8.98E-01	-	-
1374805_at	Dscc1	defective in sister chromatid cohesion 1 homolog (S. cerevisiae)	299933	Rn.8559	AW251849	2.53	2.52	2.55	2.52	2.56	2.49	1.01	down	7.31E-01	9.14E-01	-	-
1369889_at	Ifnb1	interferon beta 1, fibroblast	24481	Rn.138105	NM_019127	2.33	2.32	2.35	2.33	2.34	2.32	1.01	down	4.52E-01	8.95E-01	-	-
1398544_at	---	---	---	Rn.200087	BF398673	2.50	2.50	2.51	2.48	2.51	2.50	1.01	down	4.47E-01	8.95E-01	-	-
1390903_at	---	---	---	Rn.23861	AI105410	2.44	2.43	2.47	2.43	2.47	2.41	1.01	down	7.21E-01	9.11E-01	-	-
1370346_at	Ccnb1	cyclin B1	25203	Rn.9232	X64589	2.34	2.33	2.35	2.34	2.34	2.32	1.01	down	3.72E-01	8.95E-01	-	-
1391243_at	---	---	---	Rn.216717	AI575416	2.40	2.38	2.41	2.39	2.41	2.37	1.01	down	6.10E-01	8.95E-01	-	-
1380218_at	RGD1306603	similar to RIKEN cDNA D330022A01 gene	363144	Rn.159436	BI296630	2.36	2.35	2.37	2.36	2.37	2.34	1.01	down	4.12E-01	8.95E-01	-	-
1381338_at	---	---	---	---	AI008973	2.43	2.41	2.43	2.41	2.44	2.39	1.01	down	6.37E-01	8.95E-01	-	-
1397326_at	---	---	---	Rn.208647	BE119158	2.36	2.36	2.37	2.36	2.37	2.34	1.01	down	4.15E-01	8.95E-01	-	-
1380996_at	---	---	---	Rn.44070	BE112025	2.32	2.31	2.33	2.31	2.32	2.30	1.01	down	3.87E-01	8.95E-01	-	-
1396176_at	Dbndd1	dysbindin (dystrobrevin binding protein 1) domain containing 1	361437	Rn.163416	BF552028	2.41	2.44	2.41	2.43	2.40	2.41	1.01	down	5.88E-01	8.95E-01	-	-
1369780_at	Rasgrf2	RAS protein-specific guanine nucleotide-releasing factor 2	114513	Rn.210995	NM_053721	2.34	2.33	2.35	2.33	2.34	2.32	1.01	down	3.97E-01	8.95E-01	-	-
1370293_at	Gata4	GATA binding protein 4	54254	Rn.26251	L22761	2.38	2.38	2.40	2.37	2.38	2.37	1.01	down	2.60E-01	8.95E-01	-	-
1373777_at	---	---	---	Rn.1141	BF391820	2.29	2.27	2.28	2.27	2.28	2.27	1.01	down	3.60E-01	8.95E-01	-	-
1392284_at	---	---	---	Rn.172764	BF405779	2.37	2.36	2.39	2.37	2.38	2.36	1.01	down	4.84E-01	8.95E-01	-	-
1391659_at	---	---	---	Rn.7883	BF283697	2.40	2.39

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1369695_at	Wt1	Wilms tumor 1	24883	Rn.92531	NM_031534	2.32	2.31	2.34	2.32	2.33	2.31	1.01	down	4.40E-01	8.95E-01	-	-
1396624_at	---	---	---	Rn.59238	BF403301	2.36	2.35	2.37	2.35	2.36	2.34	1.01	down	4.47E-01	8.95E-01	-	-
1373904_at	Lysmd2	LysM, putative peptidoglycan-binding, domain containing 2	300839	Rn.7432	AI103948	2.45	2.45	2.47	2.45	2.47	2.43	1.01	down	5.60E-01	8.95E-01	-	-
1397160_at	---	---	---	Rn.147802	BE108549	2.50	2.49	2.51	2.49	2.52	2.47	1.01	down	6.70E-01	9.00E-01	-	-
1392035_at	---	---	---	Rn.136250	AI010107	2.37	2.36	2.38	2.36	2.37	2.35	1.01	down	4.63E-01	8.95E-01	-	-
1379009_at	---	---	---	---	AI548331	2.36	2.35	2.40	2.36	2.37	2.36	1.01	down	6.15E-01	8.95E-01	-	-
1394464_at	900830 /// RGD15	hypothetical protein LOC690830 /// RGD1560652	500352 /// 690830	Rn.47043	AW528921	2.49	2.46	2.50	2.47	2.49	2.45	1.01	down	6.37E-01	8.95E-01	-	-
1395239_at	---	---	---	Rn.211868	BI302053	2.33	2.33	2.34	2.33	2.34	2.35	1.01	up	3.93E-01	8.95E-01	-	-
1396130_at	Scyl3	SCY1-like 3 (S. cerevisiae)	360866	Rn.15991	AW915869	2.40	2.39	2.40	2.40	2.44	2.39	1.01	up	6.58E-01	8.98E-01	-	-
1391725_at	---	---	---	Rn.18260	BI289277	2.36	2.34	2.37	2.35	2.35	2.35	1.01	down	3.44E-01	8.95E-01	-	-
1375402_at	---	---	---	Rn.209804	BF391604	2.33	2.33	2.38	2.33	2.36	2.32	1.01	down	7.29E-01	9.14E-01	-	-
1395481_at	---	---	---	Rn.211996	BI296456	2.37	2.36	2.39	2.36	2.37	2.35	1.01	down	4.68E-01	8.95E-01	-	-
1367535_at	Irf2bp1	interferon regulatory factor 2 binding protein 1	308404	Rn.9129	BG373523	2.86	2.95	3.07	2.99	2.96	2.95	1.01	up	9.06E-01	9.71E-01	-	-
1396628_at	---	---	---	Rn.209150	BF403338	2.47	2.46	2.51	2.61	2.48	2.33	1.01	down	9.27E-01	9.79E-01	-	-
1382130_at	Pcdh19	protocadherin 19	317183	Rn.24970	AA997710	2.43	2.43	2.45	2.38	2.43	2.47	1.01	down	7.95E-01	9.34E-01	-	-
1380821_a_at	---	---	---	Rn.204366	AI072678	2.33	2.58	2.33	2.32	2.33	2.62	1.01	up	9.54E-01	9.87E-01	-	-
1377314_at	Gfpt1	glutamine fructose-6-phosphate transaminase 1	297417	Rn.161844	BE104391	2.30	2.29	2.32	2.30	2.30	2.29	1.01	down	4.12E-01	8.95E-01	-	-
1393791_at	Trat1	T cell receptor associated transmembrane adaptor 1	498075	Rn.131204	AI044622	2.38	2.36	2.39	2.36	2.39	2.35	1.01	down	6.12E-01	8.95E-01	-	-
1392622_at	Spata2L	spermatogenesis associated 2-like	498963	Rn.91547	AI145454	2.28	2.27	2.29	2.27	2.27	2.26	1.01	down	3.42E-01	8.95E-01	-	-
1396205_at	---	---	---	Rn.42361	BI303419	2.33	2.33	2.35	2.33	2.34	2.32	1.01	down	4.41E-01	8.95E-01	-	-
1392943_at	Mboat2	membrane bound O-acyltransferase domain containing 2	313997	Rn.35322	BG663534	2.42	2.41	2.44	2.41	2.43	2.39	1.01	down	6.23E-01	8.95E-01	-	-
1387422_at	Pglyrp1	peptidoglycan recognition protein 1	84387	Rn.2834	NM_053373	2.33	2.31	2.33	2.32	2.33	2.31	1.01	down	3.59E-01	8.95E-01	-	-
1382619_at	---	---	---	Rn.166520	AI072460	2.36	2.35	2.38	2.36	2.37	2.35	1.01	down	4.56E-01	8.95E-01	-	-
1391208_at	Pcdh20	protocadherin 20	306081	Rn.99314	BG379836	2.33	2.33	2.35	2.33	2.34	2.32	1.01	down	5.05E-01	8.95E-01	-	-
1385410_at	LOC680503	hypothetical protein LOC680503	680503	Rn.153036	BF406439	2.36	2.36	2.37	2.35	2.39	2.37	1.01	up	5.19E-01	8.95E-01	-	-
1387706_at	Gabrg1	gamma-aminobutyric acid (GABA) A receptor, gamma 1	140674	Rn.10366	NM_080586	2.29	2.28	2.31	2.28	2.30	2.27	1.01	down	5.69E-01	8.95E-01	-	-
1393808_at	---	---	---	Rn.76361	AW524185	2.45	2.43	2.48	2.44	2.47	2.43	1.01	down	6.94E-01	9.05E-01	-	-
1387094_at	Slco1a4	solute carrier organic anion transporter family, member 1a4	170698	Rn.5641	U95011	2.31	2.30	2.33	2.31	2.32	2.30	1.01	down	4.50E-01	8.95E-01	-	-
1391982_at	---	---	---	Rn.146685	BF403851	2.41	2.40	2.43	2.41	2.41	2.40	1.01	down	3.88E-01	8.95E-01	-	-
1381307_at	---	---	---	Rn.32754	AI412008	2.34	2.34	2.36	2.34	2.35	2.33	1.01	down	4.83E-01	8.95E-01	-	-
1368421_at	Ptpn5	protein tyrosine phosphatase, non-receptor type 5	29644	Rn.10618	NM_019253	2.37	2.36	2.39	2.36	2.38	2.35	1.01	down	5.47E-01	8.95E-01	-	-
1368976_at	Cd38	CD38 molecule	25668	Rn.11414	D30795	2.39	2.38	2.40	2.38	2.40	2.37	1.01	down	5.39E-01	8.95E-01	-	-
1384781_at	Zfhx4	zinc finger homeobox 4	310250	Rn.133363	AA965176	2.35	2.33	2.35	2.34	2.35	2.32	1.01	down	4.09E-01	8.95E-01	-	-
1398365_at	Tppp3	tubulin polymerization-promoting protein family member 3	291966	Rn.196028	AI714466	2.32	2.31	2.34	2.31	2.33	2.30	1.01	down	5.49E-01	8.95E-01	-	-
1389404_at	Foxs1	forkhead box S1	311547	Rn.3227	AI008883	2.32	2.31	2.34	2.32	2.32	2.30	1.01	down	4.77E-01	8.95E-01	-	-
1379233_at	---	---	---	Rn.161208	BF394087	2.34	2.31	2.32	2.32	2.32	2.31	1.01	down	3.73E-01	8.95E-01	-	-
1370712_at	Vnr2	vomeronasal receptor 2	286957	Rn.10145	U36899	2.37	2.36	2.37	2.36	2.37	2.34	1.01	down	4.47E-01	8.95E-01	-	-
1390258_at	---	---	---	Rn.14807	AA893505	2.68	2.58	2.59	2.58	2.67	2.58	1.01	down	8.72E-01	9.60E-01	-	-
1385007_at	Zcchc9	zinc finger, CCHC domain containing 9	309986	Rn.94285	BI303672	7.80	8.57	8.70	8.14	8.38	8.57	1.01	up	9.81E-01	9.94E-01	-	-
1390675_at	---	---	---	Rn.146534	BE119856	2.36	2.35	2.38	2.36	2.37	2.34	1.01	down	4.75E-01	8.95E-01	-	-
1376289_at	---	---	---	---	AW252092	2.37	2.36	2.39	2.36	2.38	2.35	1.01	down	5.78E-01	8.95E-01	-	-
1395664_at	---	---	---	Rn.51186	BE118148	2.41	2.39	2.42	2.40	2.41	2.38	1.01	down	6.09E-01	8.95E-01	-	-
1384510_at	---	---	---	Rn.199264	BI288603	2.34	2.32	2.36	2.33	2.35	2.32	1.01	down	6.28E-01	8.95E-01	-	-
1378349_at	---	---	---	---	AI706429	2.33	2.32	2.34	2.38	2.33	2.31	1.01	up	7.10E-01	9.09E-01	-	-
1367552_at	Svs4	seminal vesicle secretory protein 4	24802	Rn.9942	M25590	2.36	2.35	2.39	2.36	2.37	2.34	1.01	down	5.87E-01	8.95E-01	-	-
1393081_at	Rasgef1a	RasGEF domain family, member 1A	312664	Rn.29825	AI145237	2.33	2.31	2.33	2.32	2.32	2.31	1.01	down	2.86E-01	8.95E-01	-	-
1370737_at	Casp9	caspase 9, apoptosis-related cysteine peptidase	58918	Rn.32199	AF293333	2.38	2.36	2.39	2.37	2.38	2.35	1.01	down	5.39E-01	8.95E-01	-	-
1369866_at	LOC56825	prochymosin	56825	Rn.48676	NM_020091	2.40	2.39	2.40	2.40	2.40	2.37	1.01	down	5.65E-01	8.95E-01	-	-
1383937_at	Tcfap2c	transcription factor AP-2, gamma	362280	Rn.16142	BI284495	2.31	2.30	2.30	2.30	2.29	2.31	1.01	down	2.80E-01	8.95E-01	-	-
1382257_at	---	---	---	Rn.204048	AI044813	2.39	2.38	2.40	2.38	2.40	2.37	1.01	down	4.72E-01	8.95E-01	-	-
1396657_at	---	---	---	Rn.173049	BF396545	2.36	2.34	2.37	2.35	2.36	2.34	1.01	down	4.34E-01	8.95E-01	-	-
1397805_at	Ank1	ankyrin 1, erythrocytic	306570	Rn.20868	BF392600	2.50	2.47	2.52	2.49	2.52	2.45	1.01	down	7.75E-01	9.27E-01	-	-
1397796_at	---	---	---	Rn.201915	AW526956	2.71	2.62	2.77	2.63	2.67	2.77	1.01	down	9.01E-01	9.69E-01	-	-
1397896_at	RGD1566400	similar to hypothetical protein FLJ23074	289001	Rn.146612	BI296980	2.38	2.34	2.37	2.36	2.37	2.34	1.01	down	5.50E-01	8.95E-01	-	-
1398275_at	Mmp9	matrix metallopeptidase 9	81687	Rn.10209	NM_031055	2.32	2.31	2.32	2.31	2.36	2.30	1.01	up	6.97E-01	9.07E-01	-	-
1394928_at	Xkr4	XK, Kell blood group complex subunit-related family, member 4	297801	Rn.206440	BG669146	2.47	2.39	2.41	2.39	2.40	2.45	1.01	down	8.11E-01	9.39E-01	-	-
1380830_at	---	---	---	Rn.18288	AI412331	2.44	2.43	2.46	2.43	2.45	2.43	1.01	down	5.54E-01	8.95E-01	-	-
1380912_at	---	---	---	Rn.207935	BE108142	2.47	2.46	2.50	2.47	2.51	2.43	1.01	down	7.61E-01	9.22E-01	-	-
1384734_at	Ncam2	neural cell adhesion molecule 2	288280	Rn.138756	BE121383	2.35	2.34	2.37	2.35	2.36	2.33	1.01	down	4.94E-01	8.95E-01	-	-
1390986_at	---	---	---	Rn.46076	AW526072	2.33	2.32	2.34	2.32	2.34	2.31	1.01	down	4.49E-01	8.95E-01	-	-
1369682_at	Scn2a1	sodium channel, voltage-gated, type II, alpha 1	24766	Rn.89192	NM_012647	2.38	2.37	2.39	2.41	2.38	2.36	1.01	up	6.35E-01	8.95E-01	-	-
1392300_at	---	---	---	Rn.51094	BE110178	2.38	2.36	2.39	2.37	2.38	2.36	1.01	down	4.07E-01	8.95E-01	-	-
1398064_at	---	---	---	Rn.210792	BF405538	2.32	2.31	2.34	2.32	2.33	2.31	1.01	down	4.34E-01	8.95E-01	-	-
1377242_at	---	---	---	Rn.28275	BF400656	2.37	2.36	2.38	2.36	2.37	2.35	1.01	down	4.82E-01	8.95E-01	-	-
1385491_at	Pnma2	PNMA-like 2	308393	Rn.98225	BF403514	2.63	2.61	2.66	2.59	2.67	2.65	1.01	up	7.92E-01	9.33E-01	-	-
1378651_at	---	---	---	Rn.171258	BF403339	2.36	2.35	2.37	2.35	2.36	2.34	1.01	down	4.08E-01	8.95E-01	-	-
1383546_at	Gdpd2	glycerophosphodiester phosphodiesterase domain containing 2	302421	Rn.26777	BE097393	2.33	2.31	2.36	2.32	2.34	2.32	1.01	down	5.85E-01	8.95E-01	-	-
1387418_a_at	Slc6a2	solute carrier family 6 (neurotransmitter transporter, noradrenalin), member 2	83511	Rn.14579	AB021970	2.38	2.39	2.38	2.37	2.38	2.37	1.01	down	1.03E-01	8.95E-01	-	-
1385327_at	Pcdh13	protocadherin beta 13	307489	Rn.45529	AW522979	2.52	2.51	2.54	2.52	2.53	2.50	1.01	down	4.90E-01	8.95E-01	-	-
1395312_at	#1e1 /// RGD15644	eukaryotic translation elongation factor 1 epsilon 1 /// similar to eukaryotic tran	291057 /// 502882	Rn.98308	BE121118	2.40	2.39	2.41	2.39	2.40	2.38	1.01	down	4.47E-01	8.95E-01	-	-
1398298_at	Htr1d	5-hydroxytryptamine (serotonin) receptor 1D	25323	Rn.34834	NM_012852	2.30	2.29	2.31	2.30	2.30	2.28	1.01	down	3.28E-01	8.95E-01	-	-
1368919_at	Pgf	placental growth factor	94203	Rn.6960	BF281271	2.36	2.34	2.36	2.35	2.39	2.35	1.01	up	6.15E-01	8.95E-01	-	-
1380778_at	Tmem200a	transmembrane protein 200A	498987	Rn.162404	BE114005	2.29	2.28	2.30	2.28	2.29	2.28	1.01	down	3.81E-01	8.95E-01	-	-
1387326_at	Spam1	sperm adhesion molecule 1 (PH-20 hyaluronidase, zona pellucida binding)	117037	Rn.87544	NM_053967	2.36	2.35	2.37	2.36	2.39	2.36	1.01	up	5.54E-01	8.95E-01	-	-
1378767_at	Atxn7l2	Ataxin 7-like 2	310781	Rn.46019	BE104003	2.35	2.34	2.36	2.34	2.35	2.33	1.01	down	4.02E-01	8.95E-01	-	-
1386412_at	---	---	---	---	AI639458	2.36	2.35	2.37	2.36	2.36	2.34	1.01	down	4.35E-01	8.95E-01	-	-
1381438_at	Tns1	Tensin 1	301509	Rn.3793	AI059928	2.26	2.25	2.28	2.26	2.26	2.25	1.01	down	3.05E-01	8.95E-01	-	-
1375797_at	---	---	---	Rn.209329	BF416482	2.38	2.37	2.38	2.37	2.38	2.36	1.01	down	3.99E-01	8.95E-01	-	-
1383645_at	---	---	---	Rn.6609	BF411062	2.45	2.45	2.49	2.44	2.48	2.49	1.01	up	6.89E-01	9.04E-01	-	-
1368811_at	Lmnb1	lamin B1	116685	Rn.11362	AI407364	2.36	2.35	2.38	2.36	2.37	2.34	1.01	down	5.04E-01	8.95E-01	-	-
1387720_at	Clstn2	calsyntenin 2	171394	Rn.212755	NM_134377	2.35	2.34	2.36	2.34	2.35	2.33	1.01	down	3.73E-01	8.95E-01	-	-
1384655_at	Kirrel3	kin of IRRE like 3 (Drosophila)	315546	Rn.7602	AW142820	2.50	2.49	2.50	2.49	2.49	2.48	1.01	down	1.66E-01	8.95E-01	-	-
1375495_at	---	---	---	Rn.199541	BG376193	2.40	2.38	2.41	2.39	2.41	2.37	1.01	down	5.74E-01	8.95E-01	-	-
1385012_at	Ccdc105	coiled-coil domain containing 105	500800	Rn.145678	BF389534	2.32	2.30	2.32	2.31	2.31	2.30	1.01	down	3.48E-01	8.95E-01	-	-
1369335_at	Spef2	sperm flagellar 2	64555	Rn.48731	NM_022620	2.37	2.36	2.38	2.36	2.38	2.35	1.01	down	4.91E-01	8.95E-01	-	-
1394696_at	---	---	---	---	BF287122	2.37	2.36	2.38	2.37	2.38	2.35	1.01	down	5.49E-01	8.95E-01	-	-
1383418_at	Adam11	ADAM metallopeptidase domain 11	360638	Rn.20276	BG377805	2.32	2.31	2.33	2.31	2.36	2.31	1.01	up	6.77E-01	9.02E-01	-	-
1381594_at	---	---	---	Rn.160243	AW526802	2.37	2.36	2.38	2.37	2.37	2.36	1.01	down	3.53E-01	8.95E-01	-	-
1393554_at	RGD1562657	similar to hypothetical protein DKFZp761E198	361709	Rn.214948	AI043914	4.54	4.77	4.54	4.61	4.53	4.73	1.01	up	9.38E-01	9.83E-01	-	-
1392520_at	Dlc1	deleted in liver cancer 1	58834	Rn.7255	AI136944	2.33	2.32	2.34	2.32	2.33	2.31	1.01	down	3.49E-01	8.95E-01	-	-
1387949_at	Cyp2c22	cytochrome P450, family 2, subfamily c, polypeptide 22	171518	Rn.88025	M58041	2.36	2.34	2.37	2.35	2.36	2.34	1.01	down	5.16E-01	8.95E-01	-	-
1379522_at	---	---	---	Rn.8996	AA956480	2.28	2.28	2.30	2.28	2.28	2.27	1.01	down	4.12E-01	8.95E-01	-	-
1395488_at	Msh3	mutS homolog 3 (E. coli)	499505	Rn.162551	BF390807	5.61	4.20	4.33	4.53	5.51	4.12	1.01	up	9.90E-01	9.97E-01	-	-
1374282_at	---	---	---	Rn.172238	BF404878	2.42	2.40	2.43	2.40	2.42	2.39	1.01	down	5.32E-01	8.95E-01	-	-
1395092_at	---	---	---	Rn.212959	BM388276	2.41	2.41	2.43	2.40	2.43	2.40	1.01	down	5.43E-01	8.95E-01	-	-
1369416_at	Ibsp	integrin binding sialoprotein	24477	Rn.9721	NM_012587	2.39	2.38	2.40	2.38	2.40	2.36	1.01	down	5.45E-01	8.95E-01	-	-
1371376_at	H1fx	H1 histone family, member X	500252	Rn.2931	AI072448	2.41	2.40	2.42	2.40	2.41	2.40	1.01	down	2.94E-01	8.95E-01	-	-
1393404_at	Rtn4rl1	reticulon 4 receptor-like 1	303311	Rn.22361	BF554746	2.41	2.39	2.41	2.40	2.41	2.38	1.01	down	5.50E-01	8.95E-01	-	-
1397938_at	---	---	---	Rn.200170	BF419712	2.31	2.30	2.31	2.30	2.34	2.29	1.01	up	6.51E-01	8.97E-01	-	-
1387197_at	Omd	osteomodulin	83717	Rn.30124	NM_031817	2.51	2.49	2.50	2.49	2.56	2.48	1.01	up	7.64E-01	9.23E-01	-	-
1380140_at	---	---	---	Rn.204825	BF284487	2.41	2.40	2.43	2.41	2.42	2.39	1.01	down	5.57E-01	8.95E-01	-	-
1396218_at	---	---	---	---	BF389585	2.45	2.43	2.46	2.44	2.46	2.43	1.01	down	5.45E-01	8.95E-01	-	-
1380679_at	---	---	---	Rn.155051	BI289402	2.41	2.39	2.42	2.40	2.42	2.38	1.01	down	5.92E-01	8.95E-01	-	-
1371067_at	Adam6	a disintegrin and metallopeptidase domain 6	192271	Rn.24189	Y09111	2.30	2.29	2.32	2.29	2.31	2.29	1.01	down	5.07E-01	8.95E-01	-	-
1377175_at	---	---	---	Rn.19499	BF408588	2.36	2.35	2.37	2.36	2.36	2.34	1.01	down	3.99E-01	8.95E-01	-	-
1378775_at	RGD1562339	RGD1562339	498107	Rn.95097	BG374753	2.50	2.48	2.49	2.48	2.49	2.47	1.01	down	3.51E-01	8.95E-01	-	-
1373349_at	LOC683295	similar to keratin complex 2, basic, gene 6a	683295	---	AI764437	2.29	2.28	2.31	2.28	2.29	2.28	1.01	down	4.51E-01	8.95E-01	-	-
1377828_at	Tmem16c	transmembrane protein 16C	311287	Rn.216624	BG672090	2.36	2.35	2.37	2.35	2.36	2.34	1.01	down	4.90E-01	8.95E-01	-	-
1370517_at	Npbx1	neuronal pentraxin 1	266777	Rn.54707	U18772	2.37	2.36	2.38	2.36	2.38	2.35	1.01	down	5.26E-01	8.95E-01	-	-
1378803_at	Nkx6-2	NK6 homeobox 2	309095	Rn.221953	BF400968	2.44	2.42	2.47	2.43	2.47	2.41	1.01	down	7.29E-01	9.14E-01	-	-
1394712_at	---	---	---	Rn.206692	AW529312	2.39	2.37	2.41	2.38	2.39	2.37	1.01	down	6.46E-01	8.95E-01	-	-
1370736_s_at	Trhr	thyrotropin releasing hormone receptor	25570	Rn.9962	S69160	2.35	2.34	2.36	2.34	2.36	2.33	1.01	down	4.73E-01	8.95E-01	-	-
1389718_at	---	---	---	Rn.16079	AA956417	2.38	2.37	2.40	2.38	2.39	2.37	1.01	down	4.38E-01	8.95E-01	-	-
1387715_at	Expi	extracellular proteinase inhibitor	171059	Rn.10437	NM_133537	2.37	2.36	2.38	2.37	2.38	2.35	1.01	down	4.57E-01	8.95E-01	-	-
1391741_a_at	---	---	---	Rn.15212	AA901290	2.39	2.37	2.40	2.39	2.39	2.36	1.01	down	5.74E-01	8.95E-01	-	-
1392091_at	---	---	---	Rn.165888	AI043891	2.42	2.40	2.43	2.40	2.48	2.39	1.01	up	8.12E-01	9.39E-01	-	-
1396075_at	---	---	---	Rn.151837	BF567479	2.38	2.37	2.39	2.38	2.39	2.36	1.01	down	4.78E-01	8.95E-01	-	-
1392403_at	---	---	---	Rn.34662	BF386907	2.41	2.40	2.43	2.40	2.42	2.39	1.01	down	5.38E-01	8.95E-01	-	-
1370116_at	03-Sep	septin 3	56003	Rn.48803	NM_019375	2.39	2.37	2.39	2.38	2.43	2.37	1.01	up	7.18E-01	9.11E-01	-	-
1396208_at	Ggt5	gamma-glutamyltransferase 5	29566	Rn.44367	BM389807	2.73	2.64	2.68	2.65	2.79	2.62	1.01	up	8.98E-01	9.68E-01	-	-
1395777_at	---	---	---	---	BF409664	2.40	2.38	2.39	2.39	2.40	2.36	1.01	down	5.99E-01	8.95E-01	-	-
1385079_at	Gadma1	gasdermin A1	360619	Rn.82083	BM387797	2.53	2.50	2.59	2.52	2.59	2.48	1.01	down	8.60E-01	9.57E-01	-	-
1387583_at	Cyp26a1	cytochrome P450, family 26, subfamily A, polypeptide 1	154985	Rn.81072	NM_130408	2.41	2.39	2.43	2.39	2.43	2.38	1.01	down	7.04E-01	9.07E-01	-	-
1389470_at	Clb	calbindin 2	294257	Rn.109148	AI839117	2.43	2.40	2.48	2.45	2.43	2.40	1.01	down	7.92E-01	9.33E-01	-	-
1398215_at	Rlbp1l2	retinaldehyde binding protein 1-like 2	361459	Rn.61331	BF409369	2.44	2.43	2.46	2.44	2.45	2.42	1.01	down	5.23E-01	8.95E-01	-	-
1395679_at	LOC681924	hypothetical protein LOC681924	681924	---	BF399249	2.36	2.35	2.37	2.35	2.36	2.35	1.01	down	3.48E-01	8.95E-01	-	-
1384583_at	Smgc	submandibular gland protein C	446171	Rn.81962	BM389858	2.39	2.38	2.41	2.38	2.40	2.37	1.01	down	5.65E-01	8.95E-01	-	-
1369602_at	Fgf17	fibroblast growth factor 17	29368	Rn.44353	NM_019198	2.34	2.33	2.35	2.33	2.34	2.32	1.01	down	4.35E-01	8.95E-01	-	-
1378365_at	---	---	---	Rn.154314	AW529483	2.35	2.34	2.36	2.35	2.36	2.33	1.01	down	4.89E-01	8.95E-01	-	-
1383970_at	---	---	---	Rn.217023	BI291647	2.27	2.27	2.28	2.27	2.27	2.26	1.01	down	3.46E-01	8.95E-01	-	-
1392404_at	---	---	---	Rn.177386	H33111	2.32	2.31	2.32	2.31	2.32	2.30	1.01	down	3.62E-01	8.95E-01	-	-
1395770_at	---	---	---	Rn.176376	BM391695	2.44	2.45	2.47	2.43	2.46	2.44	1.01	down	5.31E-01	8.95E-01	-	-
1390044_at	Nrg2	Neuregulin 2	432361	Rn.22434	AI501288	2.32	2.31	2.38	2.32	2.36	2.31	1.01	down	7.78E-01	9.28E-01	-	-
1374375_at	RGD1560925	similar to 2610034M16Rik protein	501196	Rn.13689	AI406903	2.37	2.36	2.38	2.36	2.38	2.35	1.01	down	5.07E-01	8.95E-01	-	-
1389701_at	---	---	---	Rn.202995	AI599419	2.36	2.34	2.38	2.35	2.37	2.34	1.01	down	5.73E-01	8.95E-01	-	-
1389160_at	Eraf	erythroid associated factor	293522	Rn.136569	AI230287	2.44	2.43	2.46	2.44	2.44	2.42	1.01	down	4.67E-01	8.95E-01	-	-
1393426_at	Pde8a	phosphodiesterase 8A, cGMP-specific, rod, alpha	307401	Rn.211725	BG374465	2.47	2.46	2.48	2.47	2.48	2.46	1.01	down	3.84E-01	8.95E-01	-	-
1383613_at	---	---	---	Rn.47415	AW530263	2.43	2.44	2.48	2.47	2.45	2.42	1.01	down	7.14E-01	9.10E-01	-	-
1373698_at	S100vp	S100 calcium-binding protein, ventral prostate	295176	Rn.54023	BI278681	2.43	2.41	2.45	2.42	2.44	2.40	1.01	down	6.78E-01	9.02E-01	-	-
1377288_at	Hsf4	heat shock transcription factor 4	291960	Rn.163399	BI275801	2.35	2.33	2.35	2.34	2.35	2.32	1.01	down	4.34E-01	8.95E-01	-	-
1388602_at	Cfd	complement factor D (adipsin)	54249	Rn.16172	AI237358	2.32	2.31	2.33	2.31	2.32	2.30	1.01	down	4.46E-01	8.95E-01	-	-
1378489_at	---	---	---	Rn.209755	BF390687	2.39	2.38	2.40	2.38	2.39	2.37	1.01	down	5.09E-01	8.95E-01	-	-
1373886_at	Reep1	receptor accessory protein 1	362384	Rn.11891	BF284692	2.34	2.34	2.35	2.34	2.34	2.32	1.01	down	3.19E-01	8.95E-01	-	-
1394167_at	---	---	---	---	AI639302	2.33	2.33	2.34	2.33	2.34	2.32	1.01	down	3.30E-01	8.95E-01	-	-
1395754_at	Frem2	Fras1 related extracellular matrix protein 2	310418	Rn.63994	AA998594	2.47	2.44	2.47

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicats)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1391146_at	Cdh11	cadherin 11	84407	Rn.8900	BE111632	2.38	2.36	2.39	2.37	2.38	2.36	1.01	down	4.92E-01	8.95E-01	-	-
1388035_a_at	Scn5a	sodium channel, voltage-gated, type V, alpha subunit	25665	Rn.32074	AF353637	2.33	2.33	2.34	2.33	2.33	2.32	1.01	down	2.28E-01	8.95E-01	-	-
1396658_at	---	---	---	Rn.200000	BF403875	2.39	2.37	2.39	2.38	2.39	2.35	1.01	down	6.08E-01	8.95E-01	-	-
1393190_at	---	---	---	---	AA900732	2.35	2.35	2.36	2.35	2.36	2.33	1.01	down	4.29E-01	8.95E-01	-	-
1392325_at	---	---	---	Rn.210458	BF398187	2.55	2.48	2.51	2.48	2.60	2.44	1.01	down	8.85E-01	9.64E-01	-	-
1379697_at	---	---	---	Rn.46561	AW531088	2.32	2.34	2.32	2.32	2.32	2.31	1.01	down	2.83E-01	8.95E-01	-	-
1381293_at	---	---	---	---	BE097087	2.39	2.38	2.41	2.38	2.40	2.37	1.01	down	5.86E-01	8.95E-01	-	-
1375361_at	Snx18	sorting nexin 18	310097	Rn.8090	BE100014	2.28	2.27	2.28	2.28	2.31	2.27	1.01	up	5.29E-01	8.95E-01	-	-
1376271_at	AA926063	AA926063gene	294284	---	AI178914	2.50	2.45	2.52	2.49	2.58	2.43	1.01	up	8.84E-01	9.64E-01	-	-
1385665_at	Adam19	a disintegrin and metalloppeptidase domain 19 (meltrin beta)	303068	Rn.163114	AI454778	2.48	2.46	2.48	2.46	2.47	2.46	1.01	down	2.86E-01	8.95E-01	-	-
1396580_at	---	---	---	Rn.207033	AW533943	2.32	2.32	2.33	2.32	2.33	2.30	1.01	down	3.46E-01	8.95E-01	-	-
1393973_at	LOC687399	hypothetical protein LOC687399	687399	Rn.202679	BI289001	2.41	2.40	2.44	2.43	2.41	2.40	1.01	down	6.46E-01	8.95E-01	-	-
1381037_at	---	---	---	Rn.204730	AI146059	2.33	2.32	2.34	2.32	2.33	2.31	1.01	down	2.83E-01	8.95E-01	-	-
1387211_at	Barhl1	BarH-like homeobox 1	117232	Rn.162655	NM_057109	2.35	2.35	2.36	2.35	2.36	2.33	1.01	down	5.23E-01	8.95E-01	-	-
1386200_at	---	---	---	Rn.132981	AA799883	2.29	2.28	2.30	2.29	2.29	2.28	1.01	down	3.56E-01	8.95E-01	-	-
1396768_at	---	---	---	Rn.210813	BF404627	2.36	2.35	2.37	2.35	2.37	2.33	1.01	down	5.77E-01	8.95E-01	-	-
1381686_at	Clec16a	C-type lectin domain family 16, member A	287044	Rn.12453	BI276419	2.37	2.34	2.35	2.34	2.36	2.34	1.01	down	4.99E-01	8.95E-01	-	-
1392463_at	Map7d2	MAP7 domain containing 2	317508	Rn.92968	AI576058	2.37	2.36	2.37	2.36	2.41	2.36	1.01	up	6.65E-01	8.99E-01	-	-
1378258_at	---	---	---	Rn.27106	AI716449	2.35	2.34	2.36	2.34	2.35	2.33	1.01	down	3.97E-01	8.95E-01	-	-
1397065_at	---	---	---	Rn.148139	BF399120	2.34	2.33	2.34	2.33	2.34	2.31	1.01	down	4.04E-01	8.95E-01	-	-
1368625_at	Prap1	proline-rich acidic protein 1	60574	Rn.43329	NM_031669	2.32	2.31	2.33	2.31	2.32	2.30	1.01	down	2.64E-01	8.95E-01	-	-
1394947_at	Noxo1	NADPH oxidase organizer 1	302976	Rn.137764	BF392512	2.36	2.35	2.38	2.36	2.36	2.35	1.01	down	4.34E-01	8.95E-01	-	-
1372577_at	Arpc4	actin related protein 2/3 complex, subunit 4	297518	Rn.198683	AI411582	9.65	9.45	9.37	9.77	9.29	9.39	1.01	down	9.66E-01	9.90E-01	-	-
1393917_at	Cd163	CD163 molecule	312701	Rn.221900	BF555488	2.47	2.46	2.47	2.46	2.47	2.44	1.01	down	4.41E-01	8.95E-01	-	-
1375049_at	Ltbp3	latent transforming growth factor beta binding protein 3	83838	Rn.202129	AI711132	2.74	2.51	2.60	2.80	2.53	2.50	1.01	down	9.50E-01	9.85E-01	-	-
1397817_at	---	---	---	Rn.212283	BI299276	2.37	2.36	2.38	2.36	2.37	2.36	1.01	down	4.25E-01	8.95E-01	-	-
1395769_at	---	---	---	Rn.19734	BE105421	2.35	2.33	2.36	2.34	2.35	2.33	1.01	down	5.68E-01	8.95E-01	-	-
1395902_at	---	---	---	Rn.45132	AW521205	2.38	2.38	2.41	2.38	2.39	2.37	1.01	down	4.96E-01	8.95E-01	-	-
1369342_at	Atp7a	ATPase, Cu++ transporting, alpha polypeptide	24941	Rn.10554	NM_052803	2.49	2.47	2.52	2.48	2.50	2.48	1.01	down	6.36E-01	8.95E-01	-	-
1395088_at	---	---	---	Rn.43587	AI406814	2.40	2.37	2.38	2.38	2.39	2.36	1.01	down	5.05E-01	8.95E-01	-	-
1371134_at	Atp2c1	ATPase, Ca++ transporting, type 2C, member 1	170699	Rn.5805	M93018	2.33	2.32	2.35	2.33	2.34	2.31	1.01	down	5.04E-01	8.95E-01	-	-
1387161_at	Slc1a6	solute carrier family 1 (high affinity aspartate/glutamate transporter), member	84012	Rn.10827	NM_032065	2.42	2.41	2.44	2.41	2.43	2.41	1.01	down	5.70E-01	8.95E-01	-	-
1370490_at	Pcdhb12	protocadherin beta 12	25133	Rn.10166	L43592	2.31	2.29	2.30	2.29	2.30	2.28	1.01	down	4.22E-01	8.95E-01	-	-
1397543_at	---	---	---	Rn.33718	AW526679	2.34	2.34	2.37	2.34	2.36	2.33	1.01	down	5.52E-01	8.95E-01	-	-
1377708_at	LOC499339	hypothetical protein LOC499339	499339	Rn.127943	BF281491	7.97	8.32	8.54	7.90	7.89	9.02	1.01	down	9.86E-01	9.86E-01	-	-
1377317_at	---	---	---	Rn.209701	BF390379	2.38	2.37	2.39	2.37	2.39	2.36	1.01	down	4.68E-01	8.95E-01	-	-
1376282_at	---	---	---	Rn.46489	BM392087	2.34	2.33	2.36	2.34	2.35	2.33	1.01	down	4.34E-01	8.95E-01	-	-
1389497_at	---	---	---	Rn.206030	AI639184	2.40	2.38	2.41	2.39	2.41	2.37	1.01	down	6.14E-01	8.95E-01	-	-
1388078_a_at	Accn2	amiloride-sensitive cation channel 2, neuronal	79123	Rn.37385	ABD49451	2.43	2.42	2.44	2.42	2.44	2.41	1.01	down	4.91E-01	8.95E-01	-	-
1391735_at	---	---	---	Rn.146938	AW528011	2.40	2.38	2.41	2.38	2.41	2.37	1.01	down	6.13E-01	8.95E-01	-	-
1381165_at	---	---	---	Rn.200122	BF403479	2.41	2.39	2.43	2.40	2.41	2.40	1.01	down	5.79E-01	8.95E-01	-	-
1368646_at	Cox4i2	cytochrome c oxidase subunit IV isoform 2	84683	Rn.7214	NM_053472	2.33	2.32	2.34	2.33	2.33	2.31	1.01	down	3.33E-01	8.95E-01	-	-
1378602_at	---	---	---	Rn.147328	BE098753	2.48	2.47	2.52	2.47	2.50	2.48	1.01	down	6.84E-01	9.03E-01	-	-
1368457_at	Gabrr1	gamma-aminobutyric acid (GABA) receptor, rho 1	29694	Rn.33552	U21070	2.40	2.39	2.41	2.40	2.40	2.38	1.01	down	4.85E-01	8.95E-01	-	-
1390536_at	---	---	---	Rn.18139	BF551311	2.29	2.29	2.30	2.29	2.33	2.28	1.01	up	6.54E-01	8.97E-01	-	-
1369284_at	Barhl2	BarH-like homeobox 2	65050	Rn.30005	NM_022956	2.35	2.34	2.35	2.34	2.35	2.33	1.01	down	4.01E-01	8.95E-01	-	-
1371731_at	RGD1566215	Similar to Coatomer gamma-2 subunit (Gamma-2 coat protein) (Gamma-2 CO	301742	Rn.216502	AI408151	2.43	2.41	2.46	2.42	2.44	2.41	1.01	down	6.49E-01	8.96E-01	-	-
1398251_a_at	Camk2b	calcium/calmodulin-dependent protein kinase II beta	24245	Rn.9743	NM_021739	2.39	2.38	2.40	2.38	2.40	2.37	1.01	down	4.38E-01	8.95E-01	-	-
1377956_at	---	---	---	---	AI548035	2.42	2.41	2.45	2.42	2.43	2.41	1.01	down	5.61E-01	8.95E-01	-	-
1380483_at	Pde8b	phosphodiesterase 8B	309962	Rn.208889	BI300942	2.41	2.39	2.41	2.40	2.41	2.37	1.01	down	6.13E-01	8.95E-01	-	-
1391832_at	---	---	---	Rn.177183	AI709522	2.37	2.36	2.39	2.36	2.38	2.35	1.01	down	5.70E-01	8.95E-01	-	-
1382025_at	Mtm1	X-linked myotubular myopathy gene 1	288762	Rn.23921	BG668084	2.41	2.40	2.42	2.42	2.41	2.41	1.01	up	3.61E-01	8.95E-01	-	-
1398727_at	---	---	---	Rn.32838	BF398091	5.53	5.05	4.78	4.94	5.38	5.02	1.01	down	9.78E-01	9.93E-01	-	-
1369124_at	Htr2a	5-hydroxytryptamine (serotonin) receptor 2A	29595	Rn.10294	NM_017254	2.27	2.26	2.29	2.26	2.27	2.26	1.01	down	3.96E-01	8.95E-01	-	-
1382387_at	Tmem16a	transmembrane protein 16A	309135	Rn.162509	BF288508	2.33	2.32	2.33	2.32	2.32	2.31	1.01	down	7.80E-02	8.95E-01	-	-
1379932_at	Clcn4-2	chloride channel 4-2	60586	Rn.44406	BG378827	2.32	2.30	2.34	2.31	2.32	2.31	1.01	down	5.14E-01	8.95E-01	-	-
1373599_at	---	---	---	Rn.13322	AI599525	2.34	2.35	2.35	2.33	2.34	2.38	1.01	up	6.15E-01	8.95E-01	-	-
1396139_at	---	---	---	---	BE120196	2.41	2.40	2.43	2.41	2.41	2.40	1.01	down	4.70E-01	8.95E-01	-	-
1397864_at	---	---	---	---	BF412601	2.42	2.40	2.43	2.41	2.43	2.39	1.01	down	6.09E-01	8.95E-01	-	-
1381369_at	Lgi3	leucine-rich repeat LGI family, member 3	306013	Rn.50862	AI412508	2.32	2.33	2.33	2.32	2.32	2.32	1.01	down	1.09E-01	8.95E-01	-	-
1378339_at	Fam124a	family with sequence similarity 124A	691938	Rn.208278	BM390636	2.38	2.37	2.39	2.37	2.39	2.36	1.01	down	5.33E-01	8.95E-01	-	-
1398124_at	Jazf1	JAZF zinc finger 1	685879	Rn.204296	AI071356	2.49	2.47	2.50	2.48	2.50	2.46	1.01	down	6.02E-01	8.95E-01	-	-
1394398_at	---	---	---	Rn.199435	AI556697	2.47	2.46	2.48	2.47	2.48	2.48	1.01	up	3.78E-01	8.95E-01	-	-
1393671_at	Pcdha12	protocadherin alpha 12	116779	---	BE107491	2.34	2.33	2.34	2.33	2.34	2.32	1.01	down	3.41E-01	8.95E-01	-	-
1368396_at	Cel	carboxyl ester lipase	24254	Rn.91234	NM_016997	2.40	2.41	2.41	2.40	2.41	2.40	1.01	down	2.51E-01	8.95E-01	-	-
1390881_at	Abra	actin-binding Rho activating protein	286965	Rn.21198	AI172339	2.42	2.40	2.43	2.41	2.43	2.39	1.01	down	6.05E-01	8.95E-01	-	-
1393064_at	---	---	---	Rn.22807	AI709766	2.40	2.39	2.42	2.39	2.41	2.38	1.01	down	5.93E-01	8.95E-01	-	-
1386361_at	Teddm1	transmembrane epididymal protein 1	664710	Rn.195123	AI639391	2.46	2.43	2.44	2.43	2.47	2.40	1.01	down	7.44E-01	9.17E-01	-	-
1395267_at	---	---	---	Rn.8110	BM391972	2.36	2.35	2.37	2.35	2.37	2.34	1.01	down	4.19E-01	8.95E-01	-	-
1376530_at	---	---	---	Rn.160009	BF403095	2.50	2.47	2.50	2.47	2.50	2.46	1.01	down	6.67E-01	8.99E-01	-	-
1376993_at	Amotl1	angiomotin-like 1	315430	Rn.24081	AW553490	2.35	2.34	2.36	2.35	2.36	2.33	1.01	down	4.12E-01	8.95E-01	-	-
1392822_at	Nf1	Neurofibromin 1	24592	Rn.10686	AA857509	2.37	2.36	2.40	2.37	2.39	2.36	1.01	down	6.10E-01	8.95E-01	-	-
1392249_at	---	---	---	Rn.204707	AI145746	2.37	2.36	2.38	2.36	2.39	2.34	1.01	down	6.17E-01	8.95E-01	-	-
1381881_at	Panx1	Pannexin 1	315435	Rn.204521	BF392037	2.59	2.62	2.64	2.61	2.62	2.58	1.01	down	7.21E-01	9.11E-01	-	-
1378419_at	Rnase2	ribonuclease, RNase A family, 2 (liver, eosinophil-derived neurotoxin)	474169	Rn.87496	AI177934	2.39	2.37	2.40	2.38	2.39	2.36	1.01	down	5.56E-01	8.95E-01	-	-
1375838_at	---	---	---	---	BF399901	2.47	2.46	2.48	2.46	2.50	2.43	1.01	down	7.58E-01	9.21E-01	-	-
1391032_at	Sez6	seizure related 6 homolog (mouse)	192247	Rn.52541	AI112194	2.40	2.39	2.41	2.40	2.40	2.38	1.01	down	4.95E-01	8.95E-01	-	-
1396939_at	---	---	---	Rn.204685	AI145547	2.37	2.37	2.38	2.37	2.38	2.35	1.01	down	4.76E-01	8.95E-01	-	-
1384038_at	---	---	---	Rn.122028	BF563211	2.42	2.37	2.37	2.38	2.39	2.37	1.01	down	6.54E-01	8.97E-01	-	-
1397348_at	---	---	---	Rn.152724	BE118444	2.35	2.34	2.36	2.34	2.35	2.33	1.01	down	4.22E-01	8.95E-01	-	-
1376542_at	Golim4	Golgi integral membrane protein 4	310526	Rn.24186	BF394843	2.41	2.39	2.43	2.40	2.42	2.39	1.01	down	6.00E-01	8.95E-01	-	-
1384561_at	RGD1561983	similar to Muc5b protein	309114	Rn.209074	BM390809	2.37	2.35	2.37	2.36	2.39	2.36	1.01	up	5.70E-01	8.95E-01	-	-
1372270_at	Dpagt1	dolichyl-phosphate (UDP-N-acetylglucosamine) N-acetylglucosaminephospho	300668	Rn.129301	BM391270	5.63	4.81	4.98	5.03	4.68	5.73	1.01	up	9.86E-01	9.96E-01	-	-
1396253_at	---	---	---	Rn.52653	BE116294	2.89	2.66	3.31	2.89	2.91	3.10	1.01	up	9.72E-01	9.92E-01	-	-
1377193_at	---	---	---	Rn.210730	BF405021	2.40	2.39	2.41	2.39	2.40	2.38	1.01	down	4.25E-01	8.95E-01	-	-
1369489_at	Aif1	allograft inflammatory factor 1	29427	Rn.32080	NM_022283	2.26	2.25	2.26	2.25	2.29	2.25	1.01	up	6.00E-01	8.95E-01	-	-
1396613_at	---	---	---	Rn.210828	BF403417	2.51	2.50	2.52	2.51	2.53	2.46	1.01	down	7.50E-01	9.19E-01	-	-
1392168_at	Vrk1	vaccinia related kinase 1	362779	Rn.92083	BE102668	2.77	2.75	2.77	2.78	2.77	2.77	1.01	up	3.71E-01	8.95E-01	-	-
1387868_at	Lbp	lipopolysaccharide binding protein	29469	Rn.48863	BF280368	2.44	2.43	2.45	2.43	2.44	2.42	1.01	down	4.32E-01	8.95E-01	-	-
1392905_at	Gng2	Guanine nucleotide binding protein (G protein), gamma 2	80850	Rn.179365	BF552733	2.39	2.37	2.44	2.39	2.40	2.39	1.01	down	7.43E-01	9.17E-01	-	-
1395541_at	---	---	---	Rn.152108	BF568017	2.33	2.32	2.35	2.33	2.33	2.31	1.01	down	4.97E-01	8.95E-01	-	-
1395037_at	RGD1563444	similar to RIKEN cDNA 2900090M10	500577	Rn.61245	AI232989	2.36	2.35	2.36	2.36	2.36	2.34	1.01	down	3.96E-01	8.95E-01	-	-
1393424_at	---	---	---	Rn.173461	BF560755	2.34	2.32	2.35	2.33	2.35	2.36	1.01	up	5.67E-01	8.95E-01	-	-
1379855_at	---	---	---	---	BF413298	2.40	2.39	2.41	2.39	2.41	2.38	1.01	down	5.77E-01	8.95E-01	-	-
1380345_at	---	---	---	Rn.47079	AW529036	2.35	2.34	2.35	2.34	2.35	2.33	1.01	down	3.50E-01	8.95E-01	-	-
1381073_at	Spred3	sprouty-related, EVH1 domain containing 3	308478	Rn.137062	BF418395	2.28	2.28	2.30	2.28	2.29	2.27	1.01	down	3.91E-01	8.95E-01	-	-
1384374_at	---	---	---	Rn.199877	BF523755	6.73	6.10	6.35	7.49	6.33	5.34	1.01	down	9.91E-01	9.97E-01	-	-
1377520_at	---	---	---	---	BF418916	2.25	2.24	2.28	2.24	2.28	2.23	1.01	down	7.13E-01	9.10E-01	-	-
1395942_at	---	---	---	---	BF564798	2.41	2.40	2.43	2.41	2.42	2.39	1.01	down	5.76E-01	8.95E-01	-	-
1398052_at	---	---	---	Rn.209272	BF387269	2.33	2.33	2.36	2.33	2.34	2.33	1.01	down	4.65E-01	8.95E-01	-	-
1394337_at	Gbx2	gastrulation brain homeobox 2	114500	Rn.92363	BF562141	2.32	2.30	2.32	2.31	2.35	2.30	1.01	up	6.81E-01	9.03E-01	-	-
1370852_at	LOC171573	spleen protein 1 precursor	171573	Rn.8438	AA851958	2.32	2.31	2.33	2.32	2.32	2.31	1.01	down	3.95E-01	8.95E-01	-	-
1369225_at	Kng2	kininogen 2	25087	Rn.44576	NM_012741	2.34	2.34	2.35	2.34	2.34	2.32	1.01	down	3.35E-01	8.95E-01	-	-
1394847_at	Syde1	synapse defective 1, Rho GTPase, homolog 1 (C. elegans)	362842	Rn.54315	BF566756	2.37	2.36	2.37	2.36	2.37	2.35	1.01	down	3.31E-01	8.95E-01	-	-
1390984_at	RGD1560470	Similar to Gene model 996	362083	Rn.44904	AI576736	2.49	2.33	2.34	2.33	2.47	2.33	1.01	down	9.20E-01	9.76E-01	-	-
1391764_at	---	---	---	Rn.53284	BE119571	2.40	2.39	2.42	2.40	2.42	2.38	1.01	down	6.28E-01	8.95E-01	-	-
1376872_at	Plxnc1	plexin C1	362873	Rn.7829	BF283556	2.39	2.37	2.39	2.38	2.40	2.35	1.01	down	6.32E-01	8.95E-01	-	-
1375465_at	Otx2	orthodenticle homolog 2 (Drosophila)	305858	Rn.35222	BG374268	2.41	2.39	2.42	2.40	2.41	2.39	1.01	down	5.61E-01	8.95E-01	-	-
1369546_at	Bbox1	butyrobetaine (gamma), 2-oxoglutarate dioxygenase (gamma-butyrobetaine h	64564	Rn.16333	NM_022629	2.36	2.35	2.37	2.35	2.36	2.34	1.01	down	3.28E-01	8.95E-01	-	-
1396873_at	---	---	---	Rn.41924	AI548900	2.31	2.31	2.33	2.31	2.32	2.30	1.01	down	4.63E-01	8.95E-01	-	-
1393963_at	Nthl1	nth (endonuclease III)-like 1 (E.coli)	29541	Rn.14632	BF542548	2.35	2.35	2.36	2.35	2.36	2.34	1.01	down	3.86E-01	8.95E-01	-	-
1398323_at	---	---	---	---	L81136	2.50	2.49	2.51	2.49	2.51	2.48	1.01	down	5.39E-01	8.95E-01	-	-
1392240_at	---	---	---	Rn.154071	AI704093	2.25	2.25	2.28	2.26	2.25	2.25	1.01	down	4.34E-01	8.95E-01	-	-
1396974_at	---	---	---	Rn.160283	BF406150	2.40	2.37	2.41	2.44	2.41	2.36	1.01	up	7.92E-01	9.33E-01	-	-
1378340_at	---	---	---	---	AI639305	2.60	2.60	2.61	2.60	2.62	2.57	1.01	down	5.91E-01	8.95E-01	-	-
1375176_at	Fam172a	family with sequence similarity 172, member A	294606	Rn.203242	BF409908	2.36	2.35	2.37	2.35	2.36	2.34	1.01	down	4.57E-01	8.95E-01	-	-
1375193_at	Lrp11	low density lipoprotein receptor-related protein 11	292462	Rn.40930	BE095528	2.26	2.26	2.29	2.26	2.26	2.26	1.01	down	4.62E-01	8.95E-01	-	-
1394753_at	LOC689621	hypothetical protein LOC689621	689621	Rn.220904	BF288394	2.38	2.37	2.39	2.37	2.39	2.36	1.01	down	5.22E-01	8.95E-01	-	-
1390095_at	---	---	---	Rn.171138	BE120144	2.32	2.31	2.32	2.31	2.36	2.30	1.01	up	6.83E-01	9.03E-01	-	-
1378538_at	---	---	---	Rn.43573	AW251819	2.29	2.28	2.31	2.28	2.30	2.28	1.01	down	3.54E-01	8.95E-01	-	-
1375733_at	---	---	---	Rn.45062	AW520755	2.33	2.31	2.32	2.31	2.32	2.30	1.01	down	4.15E-01	8.95E-01	-	-
1387814_at	Cav3	caveolin 3	29161	Rn.98191	NM_019155	2.40	2.38	2.40	2.39	2.40	2.37	1.01	down	4.79E-01	8.95E-01	-	-
1379448_at	Tik	Tik protein kinase	315852	Rn.107533	BE110883	2.39	2.38	2.41	2.39	2.40	2.37	1.01	down	5.95E-01	8.95E-01	-	-
1396295_at	LOC685576	hypothetical protein LOC685576	685576	Rn.217024	BG371608	2.37	2.35	2.38	2.36	2.38	2.35	1.01	down	5.44E-01	8.95E-01	-	-
1396651_at	---	---	---	Rn.203822	BE120496	2.39	2.37	2.40	2.38	2.40	2.36	1.01	down	5.79E-01	8.95E-01	-	-
1388224_at	Sec14l3	SEC14-like 3 (S. cerevisiae)	64543	Rn.42868	AJ132352	2.38	2.36	2.40	2.37	2.38	2.36	1.01	down	5.85E-01	8.95E-01	-	-
1369625_at	Aqp1	aquaporin 1	25240	Rn.1618	L07268	11.20	11.52	11.24	11.18	11.22	11.57	1.01	up	9.65E-01	9.90E-01	-	-
1395529_at	---	---	---	---	BF286905	2.35	2.33	2.35	2.34	2.35	2.33	1.01	down	4.08E-01	8.95E-01	-	-
1387335_s_at	Abo	ABO blood group (transferase A, alpha 1-3-N-acetylgalactosaminyltransferase	65270	Rn.112591	NM_023094	2.34	2.34	2.36	2.34	2.35	2.33	1.01	down	4.42E-01	8.95E-01	-	-
1392245_at	---	---	---	Rn.146953	AI030231	2.34	2.33	2.34	2.33	2.34	2.32	1.01	down	3.53E-01	8.95E-01	-	-
1397885_at	---	---	---	Rn.207418	BF552583	2.25	2.27	2.26	2.25	2.26	2.24	1.01	down	2.41E-01	8.95E-01	-	-
1379733_at	---	---	---	Rn.161444	BF396474	2.36	2.35	2.37	2.35	2.37	2.34	1.01	down	5.53E-01	8.95E-01	-	-
1394451_at	Anxa1	annexin A1	25380	Rn.1792	AI236455	2.33	2.37	2.33	2.32	2.33	2.35	1.01	down	6.22E-01	8.95E-01	-	-
1388237_s_at	Atp2b3	ATPase, Ca++ transporting, plasma membrane 3	29599	Rn.11053	M96626	2.39	2.37	2.42	2.38	2.47	2.35	1.01	up	8.52E-01	9.54E-01	-	-
1385285_at	---	---	---	Rn.148797	AI145977	2.36	2.35	2.38	2.35	2.38	2.34	1.01	down	6.48E-01	8.95E-01	-	-
1395066_at	Nol4	nucleolar protein 4	307553	Rn.148516	BF416024	2.30	2.29	2.30	2.29	2.30	2.28	1.01	down	3.09E-01	8.95E-01	-	-
1380354_at	Zscan10	zinc finger and SCAN domain containing 10	302962	Rn.106364	BF388963	2.37	2.36	2.37	2.39	2.37	2.36	1.01	up	4.40E-01	8.95E-01	-	-
1392915_at	Col11a1	collagen, type XI, alpha 1	25654	Rn.260	BM389291	2.33	2.31	2.34	2.32	2.34	2.31	1.01	down	5.79E-01	8.95E-01	-	-
1398145_at	---	---	---	---	BF406348	2.32	2.31	2.34	2.32	2.33	2.31	1.01	down	4.57E-01	8.95E-01	-	-
1391311_at	Sox21	SRY (sex determining region Y)-box 21	306168	Rn.44876	AA965274	2.51	2.47	2.53	2.50	2.51	2.47	1.01	down	7.57E-01	9.21E-01	-	-
1368998_at	Nkx6-1	NK6 homeobox 1	65193	Rn.11387	NM_031737	2.38	2.37	2.40	2.38	2.39	2.37	1.01	down	5.55E-01	8.95E-01	-	-
1398742_at	---	---	---	Rn.205348	AI555222	2.39	2.38	2.40	2.38	2.40	2.37	1.01	down	5.31E-01	8.95E-01	-	-
1391182_at	---	---	---	Rn.210190	BI295606	2.36	2.35	2.38	2.36	2.37	2.35	1.01	down	5.13E-01	8.95E-01	-	-
1367700_at	Fmod	Fibromodulin	64507	Rn.8778	NM_080698	2.33	2.32	2.34	2.32	2.33	2.31	1.01	down	4.09E-01	8.95E-01	-	-
1387722_at	Cyp2b12	cytochrome P450, family 2, subfamily b, polypeptide 12	29295	Rn.144570	NM_017156	2.38	2.37	2.39	2.37	2.38	2.36	1.01	down	5.02E-01	8.95E-01	-	-
1380918_at	---	---	---	Rn.171564	BM383889	2.31	2.30	2

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1371144_at	Treh	trehalase (brush-border membrane glycoprotein)	60576	Rn.163015	AF038043	2.35	2.35	2.36	2.35	2.36	2.34	1.01	down	3.47E-01	8.95E-01	-	-
1383224_at	Pard6b	par-6 (partitioning defective 6) homolog beta (C. elegans)	362279	Rn.21123	BF525012	7.74	8.26	7.88	7.70	7.90	8.26	1.01	down	9.76E-01	9.93E-01	-	-
1398521_at	---	---	---	Rn.22483	AI101583	2.46	2.44	2.48	2.45	2.47	2.44	1.01	down	6.34E-01	8.95E-01	-	-
1393201_at	Lrmp	lymphoid-restricted membrane protein	500361	Rn.154961	BI283679	2.47	2.47	2.50	2.47	2.48	2.46	1.01	down	4.95E-01	8.95E-01	-	-
1382932_at	Lrrc50	leucine rich repeat containing 50	361419	Rn.160929	AI145291	2.31	2.31	2.33	2.31	2.31	2.30	1.01	down	4.04E-01	8.95E-01	-	-
1398629_at	---	---	---	Rn.16819	AA817985	2.39	2.37	2.40	2.38	2.39	2.37	1.01	down	5.39E-01	8.95E-01	-	-
1386212_at	Spta1	spectrin, alpha, erythrocytic 1 (elliptocytosis 2)	289257	Rn.44157	AI639523	2.47	2.46	2.49	2.46	2.47	2.45	1.01	down	4.98E-01	8.95E-01	-	-
1381834_at	---	---	---	---	AI112905	2.45	2.44	2.47	2.44	2.47	2.43	1.01	down	6.51E-01	8.97E-01	-	-
1377847_at	---	---	---	Rn.21429	BE098450	2.37	2.36	2.39	2.37	2.38	2.35	1.01	down	5.50E-01	8.95E-01	-	-
1392682_at	---	---	---	---	AA897283	2.41	2.40	2.43	2.41	2.42	2.40	1.01	down	4.24E-01	8.95E-01	-	-
1383511_at	---	---	---	Rn.24826	BF409024	2.35	2.34	2.36	2.34	2.35	2.33	1.01	down	4.49E-01	8.95E-01	-	-
1368631_at	Dbil5	diazepam binding inhibitor-like 5	59116	Rn.35510	NM_021596	2.45	2.43	2.48	2.44	2.47	2.44	1.01	down	7.02E-01	9.07E-01	-	-
1390239_at	---	---	---	Rn.15594	BE112417	2.33	2.32	2.34	2.33	2.36	2.32	1.01	up	6.67E-01	8.99E-01	-	-
1376026_at	Donson	downstream neighbor of SON	288257	Rn.17226	AI178243	2.39	2.37	2.40	2.38	2.39	2.37	1.01	down	5.32E-01	8.95E-01	-	-
1380196_at	---	---	---	---	AW526395	2.40	2.38	2.41	2.39	2.39	2.38	1.01	down	3.72E-01	8.95E-01	-	-
1368479_at	Drd1a	dopamine receptor D1A	24316	Rn.24039	M35077	2.43	2.41	2.43	2.45	2.44	2.40	1.01	up	7.00E-01	9.07E-01	-	-
1378834_at	Xrcc5	X-ray repair complementing defective repair in Chinese hamster cells 5	363247	Rn.52078	BE112496	2.38	2.38	2.41	2.39	2.39	2.38	1.01	down	4.04E-01	8.95E-01	-	-
1394015_at	---	---	---	Rn.219428	AA965157	2.43	2.42	2.44	2.42	2.43	2.41	1.01	down	5.08E-01	8.95E-01	-	-
1379727_at	---	---	---	Rn.199099	AI598320	3.63	2.52	2.53	2.61	2.84	3.21	1.01	down	9.87E-01	9.96E-01	-	-
1396746_at	---	---	---	Rn.132445	BF405991	2.40	2.39	2.41	2.39	2.40	2.38	1.01	down	4.92E-01	8.95E-01	-	-
1380781_at	---	---	---	Rn.205519	BE106259	2.33	2.34	2.34	2.33	2.36	2.32	1.01	up	6.11E-01	8.95E-01	-	-
1369604_at	Fgf10	fibroblast growth factor 10	25443	Rn.44439	NM_012951	2.39	2.38	2.40	2.38	2.40	2.37	1.01	down	5.10E-01	8.95E-01	-	-
1391612_at	Il22ra2	interleukin 22 receptor, alpha 2	444986	Rn.13127	BF282190	2.42	2.41	2.44	2.42	2.44	2.39	1.01	down	6.97E-01	9.07E-01	-	-
1382454_at	Cxcl9	chemokine (C-X-C motif) ligand 9	246759	Rn.7391	AI044222	2.36	2.34	2.35	2.34	2.35	2.34	1.01	down	3.78E-01	8.95E-01	-	-
1378673_at	---	---	---	Rn.21948	AI071509	2.41	2.39	2.42	2.40	2.42	2.37	1.01	down	6.82E-01	9.03E-01	-	-
1397382_at	---	---	---	Rn.207904	BE107990	2.44	2.43	2.45	2.43	2.44	2.42	1.01	down	5.01E-01	8.95E-01	-	-
1374365_at	---	---	---	Rn.212199	BI300732	2.37	2.36	2.37	2.36	2.37	2.34	1.01	down	4.58E-01	8.95E-01	-	-
1369658_at	Cebpa	CCAAT/enhancer binding protein (C/EBP), alpha	24252	Rn.204833	NM_012524	2.36	2.35	2.37	2.35	2.37	2.34	1.01	down	5.09E-01	8.95E-01	-	-
1375383_at	---	---	---	Rn.205588	AW251217	2.39	2.37	2.40	2.38	2.39	2.37	1.01	down	5.32E-01	8.95E-01	-	-
1371224_a_at	Drp2	dystrophin related protein 2	66027	Rn.162341	AF195789	2.36	2.35	2.37	2.35	2.36	2.34	1.01	down	5.10E-01	8.95E-01	-	-
1395644_at	Abca8	ATP-binding cassette, sub-family A (ABC1), member 8	303637	Rn.15354	BF386852	2.41	2.42	2.41	2.39	2.42	2.40	1.01	down	4.39E-01	8.95E-01	-	-
1370768_at	LOC286992	peptide HP (rs14)	286992	Rn.127832	AF012282	2.35	2.34	2.36	2.35	2.36	2.33	1.01	down	4.37E-01	8.95E-01	-	-
1381022_at	Clip2	cartilage intermediate layer protein 2	306356	Rn.140751	BI276121	2.59	2.56	2.56	2.52	2.61	2.55	1.01	down	8.10E-01	9.39E-01	-	-
1384081_at	---	---	---	Rn.218988	BG372643	2.46	2.45	2.50	2.45	2.53	2.44	1.01	up	8.22E-01	9.43E-01	-	-
1372846_at	Cybasc3	cytochrome b, ascorbate dependent 3	361729	Rn.203831	AI179227	5.42	5.38	5.59	5.37	5.34	5.65	1.01	down	9.53E-01	9.86E-01	-	-
1383765_at	Dmrtc1a	DMRT-like family C1a	501668	Rn.80016	BI274834	2.34	2.33	2.35	2.33	2.35	2.32	1.01	down	4.53E-01	8.95E-01	-	-
1393905_at	Sec31	SEC3-like 1 (S. cerevisiae)	305287	Rn.204678	AI145446	2.58	2.57	2.58	2.67	2.58	2.51	1.01	up	8.84E-01	9.64E-01	-	-
1394622_at	---	---	---	Rn.149038	BE097185	2.39	2.37	2.39	2.38	2.39	2.36	1.01	down	4.36E-01	8.95E-01	-	-
1378451_at	Cyba	cytochrome b-245, alpha polypeptide	79129	Rn.5856	AI411767	2.44	2.43	2.45	2.43	2.44	2.42	1.01	down	4.21E-01	8.95E-01	-	-
1390744_at	---	---	---	---	BF399664	2.42	2.41	2.43	2.40	2.42	2.41	1.01	down	3.57E-01	8.95E-01	-	-
1397171_at	Rnf2	ring finger protein, transmembrane 2	304521	Rn.28670	BF413241	2.34	2.32	2.34	2.33	2.33	2.31	1.01	down	3.26E-01	8.95E-01	-	-
1368959_at	Pacsin1	protein kinase C and casein kinase substrate in neurons 1	29704	Rn.161729	NM_017294	2.51	2.56	2.45	2.50	2.51	2.48	1.01	down	8.37E-01	9.49E-01	-	-
1388043_at	Atp4a	ATPase, H+/K+ exchanging, alpha polypeptide	24216	Rn.214529	J02649	2.30	2.29	2.32	2.30	2.30	2.29	1.01	down	4.18E-01	8.95E-01	-	-
1396504_at	---	---	---	Rn.208227	BE120185	2.40	2.40	2.42	2.39	2.41	2.39	1.01	down	4.61E-01	8.95E-01	-	-
1367555_at	Alb	albumin	24186	Rn.202968	NM_134326	2.37	2.36	2.39	2.37	2.38	2.36	1.01	down	5.59E-01	8.95E-01	-	-
1389046_at	---	---	---	Rn.178741	AA860015	2.39	2.38	2.41	2.39	2.39	2.37	1.01	down	5.25E-01	8.95E-01	-	-
1386604_at	Mpp3	membrane protein, palmitoylated 3 (MAGUK p55 subfamily member 3)	114202	Rn.144626	AW141549	2.37	2.36	2.38	2.36	2.38	2.34	1.01	down	5.83E-01	8.95E-01	-	-
1384628_at	---	---	---	Rn.21855	AI716819	2.37	2.36	2.37	2.36	2.37	2.35	1.01	down	4.42E-01	8.95E-01	-	-
1398241_a_at	LOC685608 /// Spt	hypothetical protein LOC685608 /// salivary protein 1	29229 /// 685608	Rn.109733	NM_019171	2.36	2.35	2.37	2.35	2.36	2.35	1.01	down	3.39E-01	8.95E-01	-	-
1398288_at	Agtr2	angiotensin II receptor, type 2	24182	Rn.162367	BF552873	2.39	2.38	2.40	2.38	2.39	2.37	1.01	down	5.09E-01	8.95E-01	-	-
1385506_at	---	---	---	Rn.153184	AW530507	2.40	2.38	2.40	2.38	2.40	2.37	1.01	down	4.45E-01	8.95E-01	-	-
1380630_at	---	---	---	Rn.67377	BM389720	2.34	2.33	2.35	2.36	2.35	2.33	1.01	up	5.04E-01	8.95E-01	-	-
1394542_at	---	---	---	Rn.156552	AW919060	2.42	2.41	2.42	2.40	2.42	2.41	1.01	down	3.71E-01	8.95E-01	-	-
1378599_at	---	---	---	Rn.130971	BF412298	2.38	2.37	2.39	2.37	2.38	2.36	1.01	down	5.32E-01	8.95E-01	-	-
1369325_at	Lyst	lysosomal trafficking regulator	85419	Rn.44274	NM_053518	2.47	2.48	2.48	2.47	2.48	2.46	1.01	down	3.22E-01	8.95E-01	-	-
1376434_at	---	---	---	Rn.15539	AI101016	2.35	2.32	2.37	2.33	2.36	2.32	1.01	down	6.92E-01	9.05E-01	-	-
1382472_at	---	---	---	---	AI502459	2.32	2.31	2.33	2.31	2.32	2.30	1.01	down	3.95E-01	8.95E-01	-	-
1396418_at	---	---	---	---	BF394629	2.43	2.42	2.45	2.42	2.43	2.42	1.01	down	4.81E-01	8.95E-01	-	-
1391246_at	Dtna	dystrobrevin alpha	307548	---	BF390318	2.40	2.39	2.41	2.39	2.41	2.39	1.01	down	4.37E-01	8.95E-01	-	-
1393588_at	Cldn14	claudin 14	304073	Rn.11783	AA964346	2.31	2.31	2.34	2.31	2.34	2.29	1.01	down	7.09E-01	9.09E-01	-	-
1395462_at	Nkx3-1	NK3 homeobox 1	305999	Rn.43468	BM386415	2.38	2.37	2.39	2.37	2.38	2.36	1.01	down	4.84E-01	8.95E-01	-	-
1369612_at	LOC60591	calcium-activated potassium channel beta subunit	60591	Rn.127785	NM_022203	2.33	2.31	2.33	2.32	2.33	2.31	1.01	down	4.47E-01	8.95E-01	-	-
1374200_at	Slc29a3	solute carrier family 29 (nucleoside transporters), member 3	353307	Rn.15870	BM392280	7.55	8.55	8.57	8.20	8.33	8.11	1.01	down	9.84E-01	9.95E-01	-	-
1382743_at	LOC641315	Similar to mouse LOC212632	641315	Rn.222020	AI578576	2.31	2.44	2.87	2.55	2.54	1.01	up	9.68E-01	9.91E-01	-	-
1385429_at	---	---	---	Rn.146323	AA957452	6.77	6.83	7.64	7.43	6.82	6.98	1.01	down	9.84E-01	9.95E-01	-	-
1381418_at	---	---	---	Rn.146555	AI145015	2.44	2.42	2.46	2.43	2.47	2.40	1.01	down	7.79E-01	9.28E-01	-	-
1396270_at	---	---	---	Rn.209313	BI290209	2.37	2.36	2.40	2.37	2.38	2.36	1.01	down	6.00E-01	8.95E-01	-	-
1385516_at	---	---	---	Rn.43725	AI030975	2.32	2.31	2.34	2.32	2.32	2.30	1.01	down	4.85E-01	8.95E-01	-	-
1385570_at	---	---	---	---	AI717105	2.29	2.28	2.30	2.29	2.29	2.28	1.01	down	3.86E-01	8.95E-01	-	-
1382495_x_at	---	---	---	Rn.24030	AA926196	2.33	2.30	2.51	2.31	2.51	2.29	1.01	down	9.42E-01	9.84E-01	-	-
1398029_at	RGD1561849	similar to RIKEN cDNA 3110035E14	500393	Rn.18085	BF394260	2.42	2.41	2.45	2.41	2.44	2.41	1.01	down	6.11E-01	8.95E-01	-	-
1385178_at	---	---	---	Rn.135405	BE121180	2.34	2.34	2.36	2.34	2.35	2.34	1.01	down	4.07E-01	8.95E-01	-	-
1396339_at	---	---	---	Rn.50757	BF411257	2.41	2.39	2.42	2.40	2.41	2.38	1.01	down	6.13E-01	8.95E-01	-	-
1376968_at	Mybpc2	myosin binding protein C, fast-type	292879	Rn.137668	AW533848	2.41	2.39	2.44	2.40	2.41	2.40	1.01	down	6.75E-01	9.01E-01	-	-
1384634_at	---	---	---	---	AI235340	2.33	2.32	2.34	2.33	2.33	2.31	1.01	down	4.89E-01	8.95E-01	-	-
1368616_at	Fancc	Fanconi anemia, complementation group C	24361	Rn.10798	NM_012557	2.63	2.64	2.64	2.62	2.64	2.63	1.01	down	3.44E-01	8.95E-01	-	-
1392377_at	---	---	---	---	BF409415	2.33	2.32	2.33	2.36	2.33	2.32	1.01	up	5.36E-01	8.95E-01	-	-
1389900_at	Grin1	glutamate receptor, ionotropic, N-methyl D-aspartate 1	24408	Rn.9840	BF394115	2.40	2.39	2.41	2.39	2.40	2.38	1.01	down	3.21E-01	8.95E-01	-	-
1387269_s_at	Plaur	plasminogen activator, urokinase receptor	50692	Rn.82711	AF007789	2.33	2.32	2.33	2.32	2.33	2.31	1.01	down	3.19E-01	8.95E-01	-	-
1387812_at	Pcsk6	proprotein convertase subtilisin/kexin type 6	25507	Rn.950	NM_012999	2.45	2.42	2.44	2.43	2.43	2.42	1.01	down	3.86E-01	8.95E-01	-	-
1391124_at	---	---	---	Rn.147521	BF403846	2.41	2.40	2.44	2.41	2.43	2.39	1.01	down	6.79E-01	9.02E-01	-	-
1382960_at	---	---	---	Rn.63294	BE108047	2.43	2.41	2.45	2.42	2.46	2.40	1.01	down	7.42E-01	9.17E-01	-	-
1371589_at	Ubl5	ubiquitin-like 5	500954	Rn.91722	BM386159	10.35	10.12	9.80	9.86	10.37	10.07	1.01	up	9.75E-01	9.92E-01	-	-
1398747_at	---	---	---	Rn.107216	AI071171	2.44	2.42	2.45	2.43	2.48	2.43	1.01	up	7.33E-01	9.14E-01	-	-
1390548_at	---	---	---	Rn.57184	BI295738	2.36	2.35	2.36	2.36	2.36	2.34	1.01	down	4.06E-01	8.95E-01	-	-
1379992_at	Gdpd3	glycerophosphodiester phosphodiesterase domain containing 3	293490	Rn.27295	BM389800	2.40	2.41	2.41	2.40	2.41	2.40	1.01	down	2.32E-01	8.95E-01	-	-
1377525_at	---	---	---	---	BF408794	2.46	2.43	2.45	2.44	2.45	2.44	1.01	down	4.65E-01	8.95E-01	-	-
1384623_at	Abca8	ATP-binding cassette, sub-family A (ABC1), member 8	303637	Rn.15354	AA924613	2.39	2.37	2.40	2.38	2.39	2.37	1.01	down	5.69E-01	8.95E-01	-	-
1375101_at	---	---	---	Rn.79335	BI292651	2.39	2.37	2.40	2.38	2.39	2.36	1.01	down	5.67E-01	8.95E-01	-	-
1390605_at	---	---	---	Rn.209962	BF405113	2.37	2.36	2.38	2.36	2.37	2.35	1.01	down	5.48E-01	8.95E-01	-	-
1368910_at	Ppm2c	protein phosphatase 2C, magnesium dependent, catalytic subunit	54705	Rn.31799	NM_019372	2.38	2.36	2.36	2.36	2.37	2.35	1.01	down	3.86E-01	8.95E-01	-	-
1396839_at	---	---	---	Rn.206896	BE101807	2.22	2.24	2.22	2.22	2.23	2.21	1.01	down	3.96E-01	8.95E-01	-	-
1378323_at	Nol4	nucleolar protein 4	307553	Rn.148516	AW524892	2.43	2.41	2.44	2.42	2.44	2.40	1.01	down	6.56E-01	8.98E-01	-	-
1376702_at	Mlc1	megalencephalic leukoencephalopathy with subcortical cysts 1 homolog (hum	315215	Rn.219347	AI228307	4.59	6.42	5.50	5.69	4.63	6.17	1.01	down	9.92E-01	9.97E-01	-	-
1377504_at	---	---	---	Rn.170770	BG376478	2.41	2.41	2.41	2.41	2.42	2.39	1.01	down	4.90E-01	8.95E-01	-	-
1369624_at	Prlh	prolactin releasing hormone	63850	Rn.91303	NM_022222	2.34	2.33	2.35	2.33	2.34	2.32	1.01	down	3.85E-01	8.95E-01	-	-
1397927_at	---	---	---	Rn.208191	BE112811	2.37	2.37	2.39	2.37	2.38	2.35	1.01	down	5.18E-01	8.95E-01	-	-
1370621_at	Cd247	Cd247 molecule	25300	Rn.9997	L08447	2.45	2.50	2.45	2.49	2.45	2.43	1.01	down	7.78E-01	9.28E-01	-	-
1374769_at	---	---	---	Rn.17146	BF405313	2.39	2.37	2.40	2.38	2.44	2.37	1.00	up	7.71E-01	9.25E-01	-	-
1384762_at	---	---	---	Rn.147915	BE103873	2.37	2.36	2.38	2.36	2.37	2.35	1.00	down	4.42E-01	8.95E-01	-	-
1392553_at	Adamtsl5	ADAMTS-like 5	314626	Rn.219460	BF412281	2.35	2.34	2.38	2.34	2.37	2.33	1.00	down	7.06E-01	9.08E-01	-	-
1392843_at	---	---	---	Rn.201823	AI008432	2.41	2.40	2.43	2.40	2.42	2.39	1.00	down	6.14E-01	8.95E-01	-	-
1397963_x_at	Nans	N-acetylneuraminic acid synthase	298071	Rn.17006	BE106401	2.59	2.58	2.95	2.69	2.70	2.71	1.00	down	9.56E-01	9.87E-01	-	-
1398026_at	---	---	---	Rn.149739	BF393070	2.28	2.27	2.31	2.28	2.28	2.28	1.00	down	5.42E-01	8.95E-01	-	-
1384010_at	Ganc	glucosidase, alpha; neutral C	24382	Rn.23744	AW920178	2.46	2.44	2.48	2.56	2.40	2.41	1.00	down	8.99E-01	9.69E-01	-	-
1388290_at	---	---	---	---	X72759	2.23	2.23	2.26	2.23	2.23	2.23	1.00	down	4.73E-01	8.95E-01	-	-
1387014_at	Muc10	mucin 10, submandibular gland salivary mucin	65182	Rn.10113	NM_133513	2.40	2.39	2.42	2.40	2.41	2.38	1.00	down	6.20E-01	8.95E-01	-	-
1389955_at	---	---	---	Rn.206351	BE104483	2.54	2.50	2.56	2.51	2.55	2.52	1.00	down	7.37E-01	9.15E-01	-	-
1378702_at	---	---	---	Rn.62443	AF413730	2.30	2.29	2.32	2.30	2.31	2.29	1.00	down	5.17E-01	8.95E-01	-	-
1379230_at	---	---	---	---	AI556682	2.26	2.26	2.26	2.26	2.29	2.26	1.00	up	5.02E-01	8.95E-01	-	-
1377164_at	---	---	---	---	BE100632	2.50	2.49	2.51	2.49	2.50	2.48	1.00	down	4.32E-01	8.95E-01	-	-
1394641_at	---	---	---	Rn.30210	BF288295	2.40	2.38	2.42	2.40	2.41	2.38	1.00	down	6.18E-01	8.95E-01	-	-
1369512_at	Chst3	carbohydrate sulfotransferase 3	84468	Rn.64646	NM_053408	2.35	2.34	2.36	2.34	2.35	2.34	1.00	down	4.25E-01	8.95E-01	-	-
1380868_at	---	---	---	Rn.204976	BF418138	2.48	2.46	2.48	2.49	2.48	2.47	1.00	up	4.97E-01	8.95E-01	-	-
1382554_at	C8a	complement component 8, alpha polypeptide	298288	Rn.105718	AA998638	2.56	2.53	2.61	2.55	2.59	2.53	1.00	down	8.14E-01	9.40E-01	-	-
1370097_a_at	Cxcr4	chemokine (C-X-C motif) receptor 4	60628	Rn.44431	U54791	2.39	2.37	2.40	2.37	2.39	2.37	1.00	down	5.51E-01	8.95E-01	-	-
1368299_at	Gpr83	G protein-coupled receptor 83	140595	Rn.63079	NM_080411	2.33	2.32	2.34	2.32	2.33	2.32	1.00	down	3.18E-01	8.95E-01	-	-
1395389_at	---	---	---	Rn.210115	BG663624	2.46	2.44	2.46	2.46	2.47	2.45	1.00	up	5.53E-01	8.95E-01	-	-
1397316_at	---	---	---	---	AI179830	2.78	2.66	2.86	2.77	2.82	2.73	1.00	up	9.18E-01	9.76E-01	-	-
1380641_at	Pcdhb6	protocadherin beta 6	291853	Rn.173366	BF406179	2.37	2.36	2.39	2.37	2.39	2.35	1.00	down	6.87E-01	9.04E-01	-	-
1380127_at	---	---	---	Rn.13916	AI009500	2.35	2.34	2.36	2.34	2.35	2.33	1.00	down	4.00E-01	8.95E-01	-	-
1368398_at	Cacna1h	calcium channel, voltage-dependent, T type, alpha 1H subunit	114862	Rn.49178	NM_031601	2.32	2.31	2.33	2.31	2.32	2.31	1.00	down	4.34E-01	8.95E-01	-	-
1376386_at	---	---	---	Rn.62758	BF393799	2.35	2.33	2.35	2.33	2.35	2.32	1.00	down	4.93E-01	8.95E-01	-	-
1387527_at	Syngr1	synaptogyrin 1	29205	Rn.88235	NM_019166	2.32	2.32	2.34	2.32	2.33	2.31	1.00	down	4.38E-01	8.95E-01	-	-
1398133_at	---	---	---	Rn.168048	AI548652	2.35	2.34	2.37	2.35	2.36	2.34	1.00	down	5.08E-01	8.95E-01	-	-
1382523_at	Dpm1	dolichyl-phosphate mannosyltransferase polypeptide 1, catalytic subunit	296394	Rn.7840	BF282274	2.47	2.44	2.45	2.44	2.47	2.44	1.00	down	6.31E-01	8.95E-01	-	-
1370284_at	Atp5e	ATP synthase, H+ transporting, mitochondrial F1 complex, epsilon subunit	245958	Rn.3454	AF010323	12.51	12.24	12.21	12.24	12.44	12.26	1.00	down	9.54E-01	9.86E-01	-	-
1369272_at	Adora3	adenosine A3 receptor	25370	Rn.10457	NM_012896	2.27	2.26	2.28	2.27	2.30	2.26	1.00	up	6.38E-01	8.95E-01	-	-
1369920_at	Hist1h1t	histone cluster 1, H1t	24438	Rn.138104	NM_012579	2.39	2.38	2.40	2.38	2.40	2.38	1.00	down	4.89E-01	8.95E-01	-	-
1396567_at	---	---	---	---	BE119808	2.58	2.52	2.59	2.58	2.56	2.52	1.00	down	8.05E-01	9.37E-01	-	-
1370732_at	V1ra12	vomeronasal 1 receptor, A12	297439	Rn.10141	U36895	2.54	2.54	2.58	2.54	2.61	2.54	1.00	up	8.08E-01	9.38E-01	-	-
1368487_at	Serpinb2	serine (or cysteine) peptidase inhibitor, clade B, member 2	60325	Rn.42912	NM_021696	2.39	2.38	2.40	2.38	2.40	2.37	1.00	down	5.69E-01	8.95E-01	-	-
1385774_at	Rshl1	radial spokehead-like 1	292684	Rn.55304	BF416401	2.42	2.40	2.44	2.41	2.44	2.39	1.00	down	7.58E-01	9.21E-01	-	-
1397010_at	---	---	---	---	BE109584	2.44	2.44	2.45	2.43	2.45	2.42	1.00	down	5.54E-01	8.95E-01	-	-
1396428_at	---	---	---	Rn.147145	BF409243	2.30	2.29	2.31	2.29	2.30	2.28	1.00	down	4.75E-01	8.95E-01	-	-
1396125_at	---	---	---	Rn.220632	BG672693	2.35	2.32	2.33	2.34	2.33	2.32	1.00	down	5.46E-01	8.95E-01	-	-
1370896_at	---	---	---	---	U154525	2.39	2.38	2.41	2.38	2.40	2.37	1.00	down	5.39E-01	8.95E-01	-	-
1396701_at	Kalrn	Kalirin, RhoGEF kinase	84009	Rn.87882	BE110052	2.46	2.44	2.48	2.44	2.49	2.43	1.00	down	7.53E-01	9.20E-01	-	-
1396561_x_at	Piga	phosphatidylinositol glycan anchor biosynthesis, class A	363464	Rn.124358	BF409296	2.45	2.44	2.48	2.45	2.47	2.42	1.00	down	7.29E-01	9.14E-01	-	-
1390215_at	---	---	---	Rn.25184	AI235499	2.39	2.34	2.36	2.35	2.38	2.34	1.00	down	7.31E-01	9.14E-01	-	-
1368598_at	Sstr3	somatostatin receptor 3	171044	Rn.10458	NM_133522	2.31	2.30	2.31	2.30	2.31	2.29	1.00	down	3.21E-01	8.95E-01	-	-
1392100_at	---	---	---	Rn.153926	BF412475	2.36	2.39	2.36	2.35	2.36	2.38	1.00	down	6.50E-01	8.96E-01	-	-
1380466_at	---	---	---	Rn.14723	BG670778	3.40	3.74	4.03	3.70	3.10	4.40	1.00	up	9.87E-01	9.96E-01	-	-
1395716_at	---	---	---	---	AW919386	2.41	2.40	2.42	2.40	2.42	2.39	1.00	down	5.45E-01	8.95E-01	-	-
1391292_at	---	---	---	Rn.153619	AI556811	2.37	2.36	2.38	2.36	2.42	2.35	1.00	up	7.56E-01	9.21E-01	-	-
1397337_at	---	---	---	---	BE119980	2.33	2.32	2.33	2.33	2.33	2.31	1.00	down	3.99E-01	8.95E-01	-	-
1376032_at	---	---	---	Rn.147189	BF283840	2.45	2.44	2.45	2.44	2.44	2

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1369050_at	Plk3c2g	phosphoinositide-3-kinase, class 2, gamma polypeptide	116720	Rn.14870	NM_053923	2.36	2.35	2.39	2.36	2.38	2.34	1.00	down	6.52E-01	8.97E-01	-	-
1395075_at	---	---	---	Rn.60530	BF404541	2.37	2.35	2.37	2.36	2.37	2.35	1.00	down	4.87E-01	8.95E-01	-	-
1386231_at	RGD1306474	similar to RIKEN cDNA 9530003J23	362881	Rn.43053	AI639105	2.27	2.26	2.29	2.27	2.27	2.26	1.00	down	4.02E-01	8.95E-01	-	-
1386543_at	Fbxl8	F-box and leucine-rich repeat protein 8	498941	Rn.144768	BF559650	2.32	2.32	2.33	2.32	2.32	2.31	1.00	down	3.83E-01	8.95E-01	-	-
1394186_at	---	---	---	---	BG153276	2.47	2.46	2.48	2.47	2.49	2.43	1.00	down	7.32E-01	9.14E-01	-	-
1392700_at	Gmnn	Geminin	291137	Rn.15438	AA900604	2.33	2.31	2.33	2.31	2.32	2.31	1.00	down	3.77E-01	8.95E-01	-	-
1387189_at	Slc22a3	solute carrier family 22 (extraneuronal monoamine transporter), member 3	29504	Rn.24231	NM_019230	2.44	2.43	2.45	2.44	2.45	2.42	1.00	down	5.76E-01	8.95E-01	-	-
1396511_at	---	---	---	Rn.41386	AI763815	2.36	2.36	2.37	2.36	2.37	2.35	1.00	down	3.01E-01	8.95E-01	-	-
1376908_at	Ifit3	interferon-induced protein with tetratricopeptide repeats 3	309526	Rn.35775	AW531805	2.44	2.43	2.45	2.44	2.47	2.44	1.00	up	5.85E-01	8.95E-01	-	-
1397506_at	Fxn	frataxin	499335	Rn.13133	AI101200	2.36	2.35	2.38	2.36	2.37	2.35	1.00	down	4.54E-01	8.95E-01	-	-
1391505_x_at	---	---	---	---	BI275261	2.51	2.55	2.51	2.51	2.54	2.50	1.00	down	7.50E-01	9.19E-01	-	-
1396757_at	---	---	---	Rn.56609	BF387154	2.45	2.44	2.45	2.45	2.45	2.42	1.00	down	4.49E-01	8.95E-01	-	-
1380718_at	---	---	---	Rn.40495	AI600021	2.39	2.38	2.41	2.38	2.40	2.37	1.00	down	5.77E-01	8.95E-01	-	-
1392731_at	Tnfrsf1b	tumor necrosis factor receptor superfamily, member 1b	156767	Rn.83633	BM390522	2.52	2.50	2.51	2.50	2.50	2.51	1.00	down	3.49E-01	8.95E-01	-	-
1385664_at	---	---	---	Rn.34745	AI535113	2.38	2.36	2.40	2.37	2.39	2.36	1.00	down	7.06E-01	9.08E-01	-	-
1394926_at	---	---	---	Rn.206451	AW527214	2.38	2.37	2.39	2.37	2.38	2.36	1.00	down	4.22E-01	8.95E-01	-	-
1398560_at	---	---	---	Rn.206826	AW530670	2.40	2.38	2.41	2.39	2.40	2.37	1.00	down	5.80E-01	8.95E-01	-	-
1382912_at	Usp44	ubiquitin specific protease 44	314746	Rn.64954	BE103768	2.36	2.35	2.38	2.36	2.37	2.35	1.00	down	4.76E-01	8.95E-01	-	-
1378981_at	---	---	---	Rn.207984	BE108620	2.43	2.41	2.44	2.43	2.42	2.41	1.00	down	4.67E-01	8.95E-01	-	-
1377094_at	---	---	---	Rn.61109	BF393685	2.46	2.45	2.48	2.46	2.48	2.43	1.00	down	7.15E-01	9.10E-01	-	-
1393778_at	RGD1562010	similar to Fls485 protein	500286	---	BE120676	2.36	2.36	2.37	2.36	2.34	2.34	1.00	down	4.44E-01	8.95E-01	-	-
1394096_at	Cr1l	complement component (3b/4b) receptor 1-like	54243	Rn.5825	AI555027	6.31	4.76	3.30	4.91	5.14	4.29	1.00	down	9.94E-01	9.98E-01	-	-
1391167_at	---	---	---	Rn.47980	AW532567	2.41	2.40	2.41	2.40	2.44	2.40	1.00	up	6.19E-01	8.95E-01	-	-
1396817_at	---	---	---	Rn.178370	AI599545	2.33	2.32	2.34	2.32	2.33	2.31	1.00	down	4.45E-01	8.95E-01	-	-
1386728_at	Kcnd2	Potassium voltage gated channel, Shal-related family, member 2	65180	Rn.87841	BF545849	2.35	2.34	2.36	2.34	2.36	2.33	1.00	down	4.66E-01	8.95E-01	-	-
1397156_at	---	---	---	Rn.171236	BE110322	2.34	2.33	2.35	2.33	2.34	2.32	1.00	down	4.38E-01	8.95E-01	-	-
1396096_at	Mgat4a	mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase	367252	Rn.145359	BF405016	2.44	2.40	2.39	2.41	2.42	2.38	1.00	down	7.26E-01	9.13E-01	-	-
1367965_at	Slc9a1	solute carrier family 9 (sodium/hydrogen exchanger), member 1	24782	Rn.5025	NM_012652	2.40	2.39	2.41	2.44	2.39	2.39	1.00	up	7.10E-01	9.09E-01	-	-
1388133_at	Cadc2	cold shock domain containing C2, RNA binding	266600	Rn.1171	AA800228	2.36	2.34	2.36	2.35	2.36	2.33	1.00	down	5.20E-01	8.95E-01	-	-
1386337_at	RGD1565210	RGD1565210	499072	Rn.12584	AI548910	6.16	3.70	4.09	5.46	4.28	4.24	1.00	up	9.94E-01	9.98E-01	-	-
1380421_s_at	Gfi1	growth factor independent 1 transcription repressor	24388	Rn.10935	AW532194	2.30	2.29	2.31	2.29	2.30	2.29	1.00	down	3.43E-01	8.95E-01	-	-
1371970_at	Fam111a	family with sequence similarity 111, member A	499322	Rn.112856	AA799328	2.34	2.33	2.35	2.34	2.34	2.33	1.00	down	3.24E-01	8.95E-01	-	-
1377195_at	---	---	---	Rn.210777	BF406252	2.64	2.59	2.69	2.64	2.66	2.63	1.00	up	8.23E-01	9.43E-01	-	-
1373098_at	Bcas1	breast carcinoma amplified sequence 1	246755	Rn.154429	BF394321	2.34	2.36	2.34	2.34	2.35	2.33	1.00	down	4.36E-01	8.95E-01	-	-
1368887_at	RGD1566401	similar to GTL2, imprinted maternally expressed untranslated	500717	Rn.202990	NM_019161	2.37	2.35	2.38	2.36	2.37	2.35	1.00	down	5.38E-01	8.95E-01	-	-
1382776_at	Mboat1	membrane bound O-acyltransferase domain containing 1	498741	Rn.14994	AI716936	2.43	2.41	2.44	2.42	2.45	2.39	1.00	down	7.29E-01	9.14E-01	-	-
1393756_at	Dmp1	dentin matrix acidic phosphoprotein 1	25312	Rn.19340	AI060002	2.37	2.36	2.39	2.37	2.37	2.36	1.00	down	4.56E-01	8.95E-01	-	-
1398190_at	---	---	---	Rn.170099	BF564894	2.60	2.57	2.61	2.60	2.61	2.56	1.00	down	7.28E-01	9.13E-01	-	-
1381557_at	Gna14	guanine nucleotide binding protein, alpha 14	309242	Rn.35127	BI289045	2.62	2.62	2.63	2.64	2.63	2.62	1.00	up	5.02E-01	8.95E-01	-	-
1398540_at	Rgs1	regulator of G-protein signaling 1	54289	Rn.14787	BM386789	2.39	2.38	2.41	2.38	2.40	2.37	1.00	down	5.56E-01	8.95E-01	-	-
1379621_at	MGC108974	similar to replication protein-binding trans-activator RBT1	499108	Rn.22759	AI136896	2.49	2.49	2.50	2.47	2.50	2.49	1.00	down	5.00E-01	8.95E-01	-	-
1382697_at	---	---	---	---	BF289134	2.38	2.36	2.39	2.37	2.38	2.35	1.00	down	5.60E-01	8.95E-01	-	-
1396040_at	Shank1	SH3 and multiple ankyrin repeat domains 1	78957	Rn.144602	BE108568	2.42	2.40	2.46	2.42	2.43	2.42	1.00	down	6.86E-01	9.04E-01	-	-
1384524_at	---	---	---	---	BM385707	2.40	2.39	2.42	2.39	2.42	2.38	1.00	down	6.60E-01	8.98E-01	-	-
1379648_at	---	---	---	Rn.203348	AA800610	2.38	2.40	2.40	2.37	2.40	2.37	1.00	down	5.42E-01	8.95E-01	-	-
1385675_at	RGD1308775	similar to RIKEN cDNA 4921536K21	305476	Rn.163259	BG376858	2.47	2.46	2.49	2.47	2.48	2.46	1.00	down	4.81E-01	8.95E-01	-	-
1377335_at	Abo	ABO blood group (transferase A, alpha 1-3-N-acetylgalactosaminyltransferase	65270	Rn.54025	BM386404	2.32	2.31	2.33	2.31	2.32	2.30	1.00	down	4.67E-01	8.95E-01	-	-
1387445_at	Phkg1	phosphorylase kinase gamma 1	29353	Rn.10399	NM_031573	2.34	2.33	2.35	2.34	2.36	2.31	1.00	down	7.03E-01	9.07E-01	-	-
1370480_at	Prl5a1	prolactin family 5, subfamily a, member 1	171556	Rn.18140	AF226607	2.37	2.36	2.38	2.36	2.37	2.35	1.00	down	4.36E-01	8.95E-01	-	-
1360938_at	Itgad	integrin, alpha D	64350	Rn.34728	NM_031691	2.40	2.40	2.42	2.40	2.42	2.39	1.00	down	5.49E-01	8.95E-01	-	-
1370669_a_at	Pde10a	phosphodiesterase 10A	63885	Rn.44869	AB027156	2.43	2.43	2.44	2.43	2.43	2.46	1.00	up	4.53E-01	8.95E-01	-	-
1389165_at	Wdr26	WD repeat domain 26	498301	Rn.23078	AI178292	6.89	7.43	7.74	7.23	7.24	7.56	1.00	down	9.81E-01	9.94E-01	-	-
1390233_at	Gli2	GLI family zinc finger 2	304729	Rn.38778	BE107321	2.38	2.37	2.39	2.38	2.38	2.37	1.00	down	4.29E-01	8.95E-01	-	-
1392781_at	Spinlw1	serine peptidase inhibitor-like, with Kunitz and WAP domains 1 (eppin)	685161	Rn.201691	BF289062	2.31	2.30	2.33	2.31	2.32	2.30	1.00	down	4.79E-01	8.95E-01	-	-
1377857_at	---	---	---	Rn.41806	BF291163	2.44	2.42	2.45	2.43	2.45	2.41	1.00	down	7.00E-01	9.07E-01	-	-
1375877_at	Syt4	synaptotagmin IV	64440	Rn.126675	AI454612	2.38	2.37	2.40	2.37	2.39	2.37	1.00	down	5.20E-01	8.95E-01	-	-
1391686_at	---	---	---	Rn.203651	BF397224	2.37	2.36	2.38	2.37	2.37	2.35	1.00	down	4.00E-01	8.95E-01	-	-
1375827_at	Znf292	Zinc finger protein 292	50552	Rn.106753	BF404349	2.40	2.39	2.42	2.40	2.41	2.38	1.00	down	6.39E-01	8.95E-01	-	-
1387718_at	P2rx7	purinergic receptor P2X, ligand-gated ion channel, 7	29665	Rn.10510	NM_019256	2.49	2.47	2.49	2.49	2.48	2.47	1.00	down	4.56E-01	8.95E-01	-	-
1378471_at	Raver2	ribonucleoprotein, PTB-binding 2	362551	Rn.98798	BE111819	2.39	2.38	2.41	2.39	2.40	2.37	1.00	down	5.73E-01	8.95E-01	-	-
1381663_at	---	---	---	Rn.210062	BF410329	2.39	2.38	2.39	2.38	2.40	2.36	1.00	down	5.81E-01	8.95E-01	-	-
1385048_at	---	---	---	Rn.210470	BF398257	2.41	2.39	2.42	2.41	2.42	2.38	1.00	down	5.88E-01	8.95E-01	-	-
1387425_at	Apba1	amyloid beta (A4) precursor protein-binding, family A, member 1	83589	Rn.54819	NM_031779	2.37	2.36	2.37	2.36	2.37	2.35	1.00	down	4.32E-01	8.95E-01	-	-
1376756_at	---	---	---	Rn.64188	BI289630	2.39	2.39	2.41	2.39	2.40	2.38	1.00	down	3.74E-01	8.95E-01	-	-
1384853_at	---	---	---	Rn.160041	AW531612	2.39	2.37	2.40	2.38	2.39	2.37	1.00	down	5.20E-01	8.95E-01	-	-
1397037_at	RGD1564195	similar to hypothetical protein	361651	Rn.145190	BE111735	2.35	2.34	2.36	2.34	2.35	2.33	1.00	down	4.20E-01	8.95E-01	-	-
1396352_at	RGD1562127	similar to chromosome 11 open reading frame 9	362879	---	BF414264	2.35	2.34	2.35	2.35	2.38	2.34	1.00	up	6.17E-01	8.95E-01	-	-
1368962_at	Nxph3	neurexophilin 3	59315	Rn.19736	NM_021679	2.37	2.36	2.38	2.36	2.37	2.35	1.00	down	4.86E-01	8.95E-01	-	-
1397773_at	Cldn18	claudin 18	315953	Rn.105888	AI136670	2.36	2.35	2.37	2.35	2.36	2.34	1.00	down	4.50E-01	8.95E-01	-	-
1392217_at	---	---	---	Rn.23063	AI172126	2.37	2.36	2.38	2.36	2.38	2.35	1.00	down	5.42E-01	8.95E-01	-	-
1369744_at	Tg	thyroglobulin	24826	Rn.10429	AF221622	2.31	2.30	2.32	2.30	2.32	2.29	1.00	down	5.03E-01	8.95E-01	-	-
1377186_at	Art4c	ADP-ribosylation factor-like 4C	367311	Rn.198947	BF405017	2.31	2.29	2.31	2.30	2.31	2.29	1.00	down	3.92E-01	8.95E-01	-	-
1397286_at	---	---	---	Rn.204588	AW435211	2.39	2.38	2.41	2.38	2.40	2.37	1.00	down	5.62E-01	8.95E-01	-	-
1397399_at	Parp11	poly (ADP-ribose) polymerase family, member 11	500323	Rn.205037	AW528372	2.30	2.30	2.32	2.30	2.30	2.29	1.00	down	4.15E-01	8.95E-01	-	-
1372843_at	Epb4.1l2	erythrocyte membrane protein band 4.1-like 2	309557	Rn.1362	BE110569	2.39	2.38	2.39	2.41	2.38	2.38	1.00	up	5.59E-01	8.95E-01	-	-
1395800_at	---	---	---	---	BE120374	2.34	2.33	2.35	2.34	2.35	2.32	1.00	down	5.08E-01	8.95E-01	-	-
1376484_at	---	---	---	Rn.212017	BG375060	2.37	2.36	2.38	2.36	2.37	2.35	1.00	down	3.79E-01	8.95E-01	-	-
1375051_at	---	---	---	Rn.20417	BE104792	2.29	2.28	2.31	2.29	2.29	2.27	1.00	down	4.89E-01	8.95E-01	-	-
1384371_at	Tead3	TEA domain family member 3	294299	Rn.198086	AW521429	2.36	2.35	2.37	2.36	2.39	2.36	1.00	up	4.96E-01	8.95E-01	-	-
1369487_a_at	Kcnj4	potassium inwardly-rectifying channel, subfamily J, member 4	116649	Rn.10197	NM_053870	2.38	2.37	2.39	2.38	2.39	2.36	1.00	down	5.37E-01	8.95E-01	-	-
1371425_at	Srrm1	serine/arginine repetitive matrix 1	313620	Rn.39266	BF396399	6.23	6.62	6.25	5.89	6.10	7.10	1.00	down	9.87E-01	9.96E-01	-	-
1396277_at	Klhl21	kelch-like 21 (Drosophila)	313743	Rn.87583	AW251627	2.35	2.34	2.36	2.34	2.35	2.33	1.00	down	3.51E-01	8.95E-01	-	-
1392617_at	RGD1306151	similar to hypothetical protein DKFZp761D0211	362455	Rn.147512	BI289715	2.36	2.35	2.37	2.35	2.35	2.34	1.00	down	4.11E-01	8.95E-01	-	-
1369535_at	Gpr175	G protein-coupled receptor 175	85494	Rn.3566	NM_053534	2.45	2.44	2.46	2.44	2.46	2.44	1.00	down	5.26E-01	8.95E-01	-	-
1398624_x_at	Tubb4	tubulin, beta 4	29213	Rn.195342	AA957044	2.31	2.28	2.30	2.29	2.35	2.28	1.00	up	7.74E-01	9.26E-01	-	-
1397569_at	---	---	---	Rn.45255	BF546710	2.36	2.35	2.37	2.35	2.36	2.34	1.00	down	4.45E-01	8.95E-01	-	-
1379070_at	---	---	---	Rn.148421	BI297797	2.38	2.37	2.39	2.37	2.39	2.36	1.00	down	4.94E-01	8.95E-01	-	-
1367791_at	Ramp1	receptor (G protein-coupled) activity modifying protein 1	58965	Rn.12265	NM_031645	2.43	2.42	2.45	2.43	2.43	2.42	1.00	down	4.49E-01	8.95E-01	-	-
1370058_at	Nefl	neurofilament, light polypeptide	83613	Rn.18568	BF394545	2.37	2.36	2.38	2.37	2.38	2.35	1.00	down	5.32E-01	8.95E-01	-	-
1374236_at	---	---	---	Rn.26644	BI295858	2.35	2.34	2.36	2.35	2.36	2.33	1.00	down	5.06E-01	8.95E-01	-	-
1374816_at	Gcom1	GRINL1A complex locus	363091	Rn.2307	AI103939	2.36	2.35	2.37	2.35	2.37	2.34	1.00	down	5.11E-01	8.95E-01	-	-
1384483_at	---	---	---	Rn.103651	BI274216	2.60	2.60	2.61	2.61	2.63	2.60	1.00	up	4.85E-01	8.95E-01	-	-
1393307_at	---	---	---	---	AI136599	2.44	2.43	2.44	2.43	2.46	2.41	1.00	down	6.16E-01	8.95E-01	-	-
1395082_at	Cpsf6	cleavage and polyadenylation specific factor 6	299811	Rn.164480	AI763982	2.47	2.44	2.45	2.45	2.47	2.42	1.00	down	6.80E-01	9.03E-01	-	-
1369311_at	Scn2b	sodium channel, voltage-gated, type II, beta	25349	Rn.88636	NM_012877	2.38	2.37	2.39	2.36	2.38	2.38	1.00	down	3.84E-01	8.95E-01	-	-
1377058_at	Slc37a2	solute carrier family 37 (glycerol-3-phosphate transporter), member 2	500973	Rn.41938	BI291872	2.46	2.38	2.39	2.48	2.40	2.38	1.00	up	8.66E-01	9.58E-01	-	-
1371501_at	LOC687517	hypothetical protein LOC687517	687517	---	BI291351	2.34	2.33	2.35	2.33	2.34	2.32	1.00	down	4.94E-01	8.95E-01	-	-
1368740_at	P2rx6	purinergic receptor P2X, ligand-gated ion channel, 6	25041	Rn.10258	NM_012721	2.36	2.36	2.37	2.36	2.37	2.35	1.00	down	4.25E-01	8.95E-01	-	-
1396758_at	---	---	---	Rn.57563	BF406200	2.35	2.34	2.37	2.35	2.36	2.34	1.00	down	4.66E-01	8.95E-01	-	-
1397520_at	Eif4g2	eukaryotic translation initiation factor 4, gamma 2	361628	Rn.121213	BG672378	11.44	11.42	11.29	11.43	11.19	11.52	1.00	down	9.53E-01	9.86E-01	-	-
1373623_at	Itpkc	inositol 1,4,5-trisphosphate 3-kinase C	308451	Rn.85907	BI278809	2.57	2.53	2.55	2.54	2.62	2.46	1.00	down	8.93E-01	9.67E-01	-	-
1393044_at	Cmpk2	cytidine monophosphate (UMP-CMP) kinase 2, mitochondrial	314004	Rn.100440	BF282370	2.59	2.70	2.64	2.68	2.69	2.58	1.00	up	8.91E-01	9.66E-01	-	-
1371274_at	Cyss	cystatin S	296234	Rn.214033	M75281	2.34	2.33	2.36	2.34	2.35	2.32	1.00	down	5.00E-01	8.95E-01	-	-
1381059_at	---	---	---	Rn.20811	AI044885	2.33	2.32	2.34	2.32	2.33	2.32	1.00	down	3.44E-01	8.95E-01	-	-
1381442_x_at	---	---	---	---	AI579112	2.32	2.32	2.32	2.32	2.37	2.30	1.00	up	7.59E-01	9.21E-01	-	-
1386270_at	---	---	---	---	AI274756	2.36	2.35	2.38	2.36	2.37	2.35	1.00	down	5.03E-01	8.95E-01	-	-
1381355_at	Mks1	Meckel syndrome, type 1	287612	Rn.198890	BG377715	2.45	2.42	2.45	2.44	2.45	2.44	1.00	up	4.44E-01	8.95E-01	-	-
1394446_at	---	---	---	Rn.35743	AW523015	2.27	2.26	2.29	2.26	2.28	2.26	1.00	down	6.16E-01	8.95E-01	-	-
1382702_at	---	---	---	Rn.13303	AA998276	2.35	2.34	2.36	2.35	2.39	2.34	1.00	up	6.68E-01	9.00E-01	-	-
1395080_at	---	---	---	Rn.209552	BF389061	2.47	2.45	2.47	2.46	2.46	2.45	1.00	down	5.01E-01	8.95E-01	-	-
1395424_at	---	---	---	Rn.49346	BG380571	2.37	2.36	2.38	2.37	2.38	2.36	1.00	down	4.39E-01	8.95E-01	-	-
1375731_at	---	---	---	Rn.205442	BI296637	2.39	2.38	2.40	2.38	2.39	2.37	1.00	down	4.86E-01	8.95E-01	-	-
1379874_at	Man2a2	mannosidase 2, alpha 2	308757	Rn.41796	BI274940	3.23	3.41	3.28	3.23	3.24	3.44	1.00	down	9.42E-01	9.84E-01	-	-
1379462_at	Ksr1	kinase suppressor of ras 1	360573	Rn.179021	BM389136	2.34	2.33	2.35	2.33	2.34	2.33	1.00	down	4.67E-01	8.95E-01	-	-
1385552_at	---	---	---	Rn.176691	BG668477	2.36	2.35	2.36	2.35	2.36	2.33	1.00	down	5.26E-01	8.95E-01	-	-
1369661_at	Dnm2	dynamin 2	25751	Rn.11231	L24562	2.38	2.38	2.39	2.40	2.39	2.39	1.00	up	3.13E-01	8.95E-01	-	-
1374977_at	---	---	---	---	BG373340	2.35	2.34	2.36	2.34	2.35	2.33	1.00	down	4.59E-01	8.95E-01	-	-
1394704_at	Casc3	cancer susceptibility candidate 3	259170	Rn.162194	AI409615	2.47	2.47	2.48	2.51	2.48	2.46	1.00	up	6.48E-01	8.96E-01	-	-
1381643_at	---	---	---	---	AW536050	2.29	2.28	2.30	2.28	2.29	2.27	1.00	down	4.95E-01	8.95E-01	-	-
1367968_at	LOC171161	neurmon salivary protein 1	171161	Rn.9752	NM_133622	2.39	2.37	2.41	2.38	2.40	2.37	1.00	down	6.12E-01	8.95E-01	-	-
1398506_at	Ppp3ca	Protein phosphatase 3 (formerly 2B), catalytic subunit, alpha isoform	24674	Rn.6866	AI146158	2.49	2.48	2.49	2.48	2.54	2.42	1.00	down	8.44E-01	9.51E-01	-	-
1379701_at	---	---	---	---	AW143987	2.32	2.31	2.33	2.32	2.33	2.30	1.00	down	4.78E-01	8.95E-01	-	-
1392081_at	---	---	---	Rn.209090	BF386148	2.38	2.37	2.39	2.37	2.38	2.37	1.00	down	4.29E-01	8.95E-01	-	-
1381581_at	---	---	---	Rn.18294	AW535025	2.87	2.89	2.88	2.93	2.85	2.90	1.00	up	7.87E-01	9.31E-01	-	-
1371166_at	Nos3	nitric oxide synthase 3, endothelial cell	24600	Rn.44265	AJ011116	2.40	2.40	2.41	2.40	2.42	2.38	1.00	down	5.92E-01	8.95E-01	-	-
1396832_at	Kb15	Type II keratin Kb15	366992	Rn.49197	BE095868	2.37	2.36	2.38	2.37	2.38	2.35	1.00	down	4.95E-01	8.95E-01	-	-
1377600_at	Znf277	zinc finger protein 777	502764	Rn.20401	BF419034	2.37	2.36	2.37	2.36	2.37	2.35	1.00	down	4.00E-01	8.95E-01	-	-
1383513_at	---	---	---	Rn.14910	AA899227	2.37	2.36	2.41	2.37	2.37	2.37	1.00	down	6.69E-01	9.00E-01	-	-
1368986_at	Slc17a7	solute carrier family 17 (sodium-dependent inorganic phosphate cotransporter	116638	Rn.10267	BF567766	2.40	2.39	2.40	2.39	2.39	2.38	1.00	down	2.13E-01	8.95E-01	-	-
1380837_at	---	---	---	Rn.207492	BE102082	2.36	2.35	2.37	2.35	2.36	2.35	1.00	down	4.29E-01	8.95E-01	-	-
1368276_at	Syp	synaptophysin	24804	Rn.11067	NM_012664	2.77	2.53	2.72	2.57	2.78	2.69	1.00	up	9.46E-01	9.84E-01	-	-
1393900_at	---	---	---	Rn.148216	AW527725	2.36	2.35	2.38	2.36	2.37	2.34	1.00	down	6.16E-01	8.95E-01	-	-
1382453_at	Zic3	Zic family member 3 (odd-paired homolog, Drosophila)	367944	Rn.64713	BE118707	2.38	2.38	2.40	2.38	2.39	2.37	1.00	down	5.58E-01	8.95E-01	-	-
1392123_at	---	---	---	Rn.208302	BE114497	2.44	2.42	2.45	2.43	2.44	2.41	1.00	down	5.86E-01	8.95E-01	-	-
1380073_at	Fry	furry homolog (Drosophila)	304244	Rn.36184	AI013629	2.29	2.28	2.30	2.29	2.29	2.28	1.00	down	3.84E-01	8.95E-01	-	-
1375466_at	---	---	---	Rn.12112	AI228650	2.61	2.28	2.39	2.37	2.39	2.50	1.00	down	9.51E-01	9.86E-01	-	-
1387091_at	Padi2	peptidyl arginine deiminase, type II	29511	Rn.98523	NM_017226	2.54	2.51	2.52	2.52	2.53	2.51	1.00	down	4.32E-01	8.95E-01	-	-
1397325_at	---	---	---	---	AW535083	2.44	2.44	2.45	2.43	2.44	2.43	1.00	down	2.14E-01	8.95E-01	-	-
1375303_at	Ldb3	LIM domain binding 3	498587	Rn.219238	BI294983	2.51	2.50	2.52	2.49	2.52	2.50	1.00	down	6.02E-01	8.95E-01	-	-
1390436_at	---	---	---	---	BF406417	2.49	2.46	2.52	2.48	2.53	2.44	1.00	down	8.41E-01	9.50E-01	-	-
1379047_at	---	---	---	Rn.166823	AW251632	2.33	2.31	2.33	2.32	2.32	2.31	1.00	down	3.41E-01	8.95E-01	-	-
1377313_at	---	---	---	Rn.153896	BI298335	2.42	2.42	2.44	2.41	2.43	2.42	1.00	down	4.04E-01	8.95E-01	-	-
1368481_at	Gipr	gastric inhibitory polypeptide receptor	25024	Rn.9676	NM_012714	2.33	2.32	2.34	2.33	2.34	2.31	1.00	down	4.68E-01	8.95E-01	-	-
1377534_at	Stk32c	serine/threonine kinase 32C	366381	Rn.

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1382974_at	---	---	---	Rn.204908	AW921315	2.35	2.34	2.35	2.34	2.35	2.33	1.00	down	4.33E-01	8.95E-01	-	-
1398717_at	---	---	---	Rn.172805	BF405493	2.36	2.35	2.38	2.36	2.37	2.35	1.00	down	5.01E-01	8.95E-01	-	-
1393420_at	---	---	---	Rn.145915	AI030027	2.38	2.36	2.38	2.37	2.42	2.36	1.00	up	7.25E-01	9.13E-01	-	-
1377429_at	Lpo	lactoperoxidase	287610	Rn.60583	BI292231	2.37	2.36	2.38	2.36	2.38	2.35	1.00	down	6.12E-01	8.95E-01	-	-
1387110_at	Nrd1	nardilysin 1 (N-arginine dibasic convertase)	25499	Rn.203027	NM_012993	7.83	7.58	7.33	7.31	7.99	7.45	1.00	up	9.80E-01	9.94E-01	-	-
1390990_at	---	---	---	Rn.168114	AI409862	5.80	5.66	5.55	5.50	5.60	5.87	1.00	down	9.62E-01	9.89E-01	-	-
1391464_at	---	---	---	Rn.165242	BE104324	2.38	2.37	2.40	2.38	2.39	2.36	1.00	down	5.51E-01	8.95E-01	-	-
1390820_at	Zcchc11	zinc finger, CCHC domain containing 11	313481	Rn.15558	BE108198	2.45	2.42	2.44	2.43	2.46	2.41	1.00	down	7.29E-01	9.14E-01	-	-
1371049_at	Dpysl4	dihydropyrimidinase-like 4	25417	Rn.10503	BF413467	2.38	2.36	2.38	2.37	2.38	2.36	1.00	down	4.12E-01	8.95E-01	-	-
1385078_at	---	---	---	Rn.131973	AI857582	2.45	2.44	2.47	2.44	2.47	2.42	1.00	down	7.06E-01	9.08E-01	-	-
1395476_at	---	---	---	Rn.66281	BI298290	2.33	2.32	2.34	2.32	2.33	2.31	1.00	down	4.70E-01	8.95E-01	-	-
1369384_at	Gria4	glutamate receptor, ionotropic, AMPA4	29629	Rn.10938	NM_017263	2.37	2.36	2.39	2.37	2.38	2.35	1.00	down	5.95E-01	8.95E-01	-	-
1390176_at	Fam84b	family with sequence similarity 84, member B	315019	Rn.10109	AA957367	2.46	2.43	2.81	2.46	2.84	2.43	1.00	up	9.72E-01	9.92E-01	-	-
1368730_a_at	Adcyap1r1	adenylate cyclase activating polypeptide 1 (pituitary) receptor type I	24167	Rn.88408	D16465	2.37	2.36	2.39	2.37	2.38	2.36	1.00	down	4.84E-01	8.95E-01	-	-
1380493_at	LOC680588 /// Tet	hypothetical protein LOC680588 /// tet oncogene family member 3	680576 /// 680588	Rn.201690	AW531643	2.52	2.35	2.36	2.19	2.36	2.70	1.00	up	9.68E-01	9.91E-01	-	-
1384231_at	LOC687121	similar to Shc SH2-domain binding protein 1	687121	---	BE108276	2.44	2.44	2.46	2.45	2.46	2.41	1.00	down	6.82E-01	9.03E-01	-	-
1372435_at	---	---	---	Rn.156153	BI297607	2.27	2.27	2.28	2.27	2.27	2.26	1.00	down	1.96E-01	8.95E-01	-	-
1377274_at	---	---	---	---	BF419624	2.47	2.47	2.49	2.47	2.48	2.47	1.00	down	4.46E-01	8.95E-01	-	-
1376147_at	---	---	---	Rn.15773	BI284316	2.34	2.33	2.35	2.33	2.35	2.32	1.00	down	5.05E-01	8.95E-01	-	-
1391911_at	---	---	---	Rn.199799	AW524678	2.37	2.35	2.38	2.36	2.37	2.35	1.00	down	5.41E-01	8.95E-01	-	-
1384909_at	LOC681205	hypothetical protein LOC681205	681205	Rn.206811	AW530537	2.47	2.45	2.49	2.46	2.48	2.45	1.00	down	6.85E-01	9.03E-01	-	-
1388254_a_at	RT1-CE5	RT1 class I, CE5	309607	---	AJ243338	2.48	2.48	2.49	2.47	2.49	2.48	1.00	down	3.62E-01	8.95E-01	-	-
1396553_at	---	---	---	---	BF409852	2.46	2.45	2.46	2.45	2.46	2.44	1.00	down	3.91E-01	8.95E-01	-	-
1377406_at	---	---	---	Rn.212706	BI276251	2.50	2.47	2.49	2.49	2.50	2.46	1.00	down	6.53E-01	8.97E-01	-	-
1369613_at	---	---	---	---	NM_022682	2.37	2.36	2.38	2.36	2.37	2.35	1.00	down	4.88E-01	8.95E-01	-	-
1388012_at	Prrxl1	paired related homeobox protein-like 1	252880	Rn.10189	U29174	2.34	2.33	2.35	2.34	2.34	2.32	1.00	down	4.70E-01	8.95E-01	-	-
1392055_at	---	---	---	Rn.209669	BF397988	2.36	2.35	2.38	2.36	2.37	2.35	1.00	down	5.55E-01	8.95E-01	-	-
1373089_at	Cdh3	cadherin 3, type 1, P-cadherin (placental)	116777	Rn.105829	AI010270	2.26	2.25	2.27	2.25	2.26	2.24	1.00	down	5.14E-01	8.95E-01	-	-
1397586_at	---	---	---	---	BI300588	2.46	2.45	2.47	2.45	2.46	2.44	1.00	down	4.36E-01	8.95E-01	-	-
1380982_at	---	---	---	Rn.210775	BF412273	2.39	2.37	2.40	2.38	2.39	2.37	1.00	down	5.70E-01	8.95E-01	-	-
1391000_at	---	---	---	---	AA852050	2.51	2.48	2.53	2.49	2.56	2.46	1.00	down	8.45E-01	9.52E-01	-	-
1369639_at	---	---	---	---	BG378227	2.32	2.30	2.32	2.31	2.31	2.30	1.00	down	3.93E-01	8.95E-01	-	-
1390476_at	Zbtb39	zinc finger and BTB domain containing 39	299510	Rn.62592	BE101472	3.74	3.30	3.28	4.14	3.36	2.84	1.00	up	9.88E-01	9.96E-01	-	-
1379788_at	---	---	---	---	AI231019	2.38	2.38	2.40	2.38	2.39	2.37	1.00	down	4.97E-01	8.95E-01	-	-
1383363_at	---	---	---	Rn.11709	BF418817	2.40	2.39	2.42	2.40	2.41	2.39	1.00	down	5.97E-01	8.95E-01	-	-
1376516_at	Flywch1	FLYWCH-type zinc finger 1	360488	Rn.49088	BG372587	2.57	2.34	2.39	2.39	2.55	2.38	1.00	up	9.45E-01	9.84E-01	-	-
1393137_at	Tctex1d1	Tctex1 domain containing 1	362553	Rn.220488	BF419468	2.34	2.33	2.35	2.34	2.34	2.32	1.00	down	4.37E-01	8.95E-01	-	-
1398016_at	Scd	stearoyl-CoA desaturase (delta-9-desaturase)	83792	Rn.83595	BI850137	2.37	2.36	2.38	2.36	2.37	2.35	1.00	down	5.22E-01	8.95E-01	-	-
1393481_at	---	---	---	---	BM390812	2.57	2.55	2.59	2.60	2.52	2.58	1.00	down	7.96E-01	9.34E-01	-	-
1395756_at	---	---	---	Rn.216657	BF288921	2.36	2.38	2.39	2.38	2.39	2.38	1.00	up	5.65E-01	8.95E-01	-	-
1370514_a_at	Syt7	synaptotagmin VII	59267	Rn.91884	AI713274	2.54	2.51	2.59	2.52	2.58	2.52	1.00	down	8.40E-01	9.50E-01	-	-
1392478_at	Rab6b	RAB6B, member RAS oncogene family	363123	Rn.13756	BG381176	2.34	2.33	2.35	2.33	2.34	2.32	1.00	down	4.30E-01	8.95E-01	-	-
1398503_at	Rax	retina and anterior neural fold homeobox	114213	Rn.87955	AI575653	2.42	2.41	2.43	2.41	2.42	2.40	1.00	down	3.64E-01	8.95E-01	-	-
1377502_at	Foxo1	forkhead box O1	84482	Rn.116108	BE111515	2.44	2.44	2.46	2.44	2.46	2.42	1.00	down	5.91E-01	8.95E-01	-	-
1380051_at	---	---	---	Rn.6580	BE106288	2.37	2.36	2.38	2.37	2.38	2.35	1.00	down	5.49E-01	8.95E-01	-	-
1394521_at	---	---	---	---	AI599567	2.37	2.36	2.38	2.36	2.38	2.35	1.00	down	5.03E-01	8.95E-01	-	-
1398723_at	---	---	---	Rn.206696	BF565515	2.36	2.34	2.35	2.34	2.35	2.34	1.00	down	3.73E-01	8.95E-01	-	-
1392215_at	Ephb1	Eph receptor B1	24338	Rn.46606	AW535067	2.51	2.50	2.52	2.49	2.53	2.49	1.00	down	6.66E-01	8.99E-01	-	-
1378252_at	Chodl	chondrolectin	288289	Rn.18313	AI029745	2.44	2.42	2.49	2.46	2.46	2.42	1.00	down	8.09E-01	9.38E-01	-	-
1368664_at	LOC56764	dnaj-like protein	56764	Rn.92862	AI138041	2.34	2.33	2.35	2.34	2.34	2.32	1.00	down	4.15E-01	8.95E-01	-	-
1373951_at	---	---	---	Rn.220377	AI407792	9.84	9.37	9.37	9.77	9.42	9.40	1.00	up	9.75E-01	9.92E-01	-	-
1370466_at	Lhx5	LIM homeobox 5	124451	Rn.54653	L35572	2.44	2.41	2.43	2.40	2.47	2.40	1.00	down	8.09E-01	9.38E-01	-	-
1374779_at	F13a1	coagulation factor XIII, A1 polypeptide	60327	Rn.42925	BM388525	2.35	2.34	2.36	2.35	2.36	2.33	1.00	down	5.16E-01	8.95E-01	-	-
1379915_at	---	---	---	Rn.209901	BF393083	2.24	2.24	2.27	2.24	2.25	2.28	1.00	up	6.98E-01	9.07E-01	-	-
1368662_at	Rnf39	ring finger protein 39	171387	Rn.144662	NM_134374	2.33	2.31	2.32	2.31	2.32	2.34	1.00	up	5.53E-01	8.95E-01	-	-
1376120_at	Fam69b	family with sequence similarity 69, member B	362090	Rn.92162	BG671875	2.34	2.33	2.34	2.33	2.34	2.32	1.00	down	3.90E-01	8.95E-01	-	-
1392003_at	---	---	---	Rn.171723	AA943753	2.33	2.32	2.34	2.33	2.34	2.32	1.00	down	4.80E-01	8.95E-01	-	-
1391492_at	---	---	---	Rn.157122	AI103493	2.44	2.46	2.45	2.45	2.44	2.43	1.00	down	5.68E-01	8.95E-01	-	-
1368352_at	Stx1b	syntaxin 1B	24923	Rn.98793	NM_012700	2.36	2.35	2.37	2.35	2.36	2.34	1.00	down	4.92E-01	8.95E-01	-	-
1392810_at	Apobec3f	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3F	315137	Rn.29180	AI178143	2.49	2.47	2.52	2.48	2.52	2.46	1.00	down	7.72E-01	9.25E-01	-	-
1372527_at	Rtn2	reticulon 2	308410	Rn.3210	BG380684	2.37	2.36	2.37	2.36	2.37	2.35	1.00	down	3.43E-01	8.95E-01	-	-
1398406_at	---	---	---	Rn.127735	AI102382	2.39	2.38	2.40	2.38	2.42	2.37	1.00	down	5.74E-01	8.95E-01	-	-
1371566_at	Fbxl22	F-box and leucine-rich repeat protein 22	363083	Rn.53443	BI296437	2.39	2.38	2.41	2.38	2.40	2.38	1.00	down	5.94E-01	8.95E-01	-	-
1374125_at	Gata5	GATA binding protein 5	499951	Rn.27175	BE113131	2.35	2.34	2.36	2.34	2.35	2.33	1.00	down	4.45E-01	8.95E-01	-	-
1394581_at	---	---	---	Rn.205547	AI709431	2.34	2.34	2.35	2.34	2.35	2.33	1.00	down	2.45E-01	8.95E-01	-	-
1393991_x_at	Ube2v1	ubiquitin-conjugating enzyme E2 variant 1	296390	Rn.220168	AW520508	2.58	2.56	2.61	2.57	2.60	2.56	1.00	down	7.42E-01	9.17E-01	-	-
1394912_at	RGD1311164	similar to DNA segment, Chr 6, Wayne State University 163, expressed	297607	Rn.125921	BG377129	2.42	2.40	2.42	2.41	2.42	2.40	1.00	down	4.32E-01	8.95E-01	-	-
1391777_at	---	---	---	Rn.204884	AI177368	2.41	2.39	2.46	2.42	2.47	2.38	1.00	up	8.51E-01	9.53E-01	-	-
1398449_at	---	---	---	Rn.203256	AA849031	2.33	2.32	2.34	2.32	2.33	2.31	1.00	down	4.93E-01	8.95E-01	-	-
1376305_at	Dnajb13	DnaJ (Hsp40) related, subfamily B, member 13	308857	Rn.45046	BF406540	2.26	2.25	2.28	2.26	2.27	2.25	1.00	down	5.64E-01	8.95E-01	-	-
1396140_at	Lrrc39	leucine rich repeat containing 39	691307	Rn.79735	AA799431	2.41	2.40	2.42	2.40	2.41	2.39	1.00	down	4.83E-01	8.95E-01	-	-
1387648_at	Cxcl6	chemokine (C-X-C motif) ligand 6 (granulocyte chemotactic protein 2)	60665	Rn.44449	NM_022214	2.35	2.34	2.36	2.34	2.35	2.33	1.00	down	4.54E-01	8.95E-01	-	-
1377248_at	Zfp324	Zinc finger protein 324	365192	Rn.39324	AI227922	2.41	2.40	2.43	2.40	2.42	2.40	1.00	down	6.02E-01	8.95E-01	-	-
1383014_at	---	---	---	Rn.64255	AI639078	2.40	2.40	2.42	2.40	2.43	2.38	1.00	down	6.95E-01	9.06E-01	-	-
1372812_at	Secisbp2l	SECIS binding protein 2-like	296115	Rn.64117	H33148	6.42	7.08	7.62	6.99	6.99	7.12	1.00	down	9.86E-01	9.98E-01	-	-
1381110_at	---	---	---	---	BE105924	2.31	2.30	2.32	2.30	2.31	2.30	1.00	down	4.46E-01	8.95E-01	-	-
1395733_at	---	---	---	Rn.205677	AI717063	2.38	2.37	2.40	2.37	2.39	2.36	1.00	down	6.46E-01	8.95E-01	-	-
1393519_at	---	---	---	Rn.149158	AI071607	2.30	2.29	2.31	2.30	2.30	2.28	1.00	down	3.99E-01	8.95E-01	-	-
1384475_at	---	---	---	Rn.40322	AW918576	2.49	2.47	2.52	2.47	2.55	2.48	1.00	up	8.26E-01	9.45E-01	-	-
1392138_at	---	---	---	Rn.136959	BF387018	2.46	2.43	2.49	2.45	2.47	2.44	1.00	down	7.49E-01	9.19E-01	-	-
1398368_at	---	---	---	Rn.16640	AI406502	2.27	2.26	2.27	2.26	2.27	2.25	1.00	down	3.37E-01	8.95E-01	-	-
1385363_at	---	---	---	---	BF388841	2.40	2.39	2.41	2.40	2.41	2.38	1.00	down	5.76E-01	8.95E-01	-	-
1394544_at	---	---	---	Rn.203227	AI500969	2.29	2.29	2.31	2.29	2.30	2.28	1.00	down	4.88E-01	8.95E-01	-	-
1382983_at	---	---	---	Rn.166678	AI136134	2.32	2.32	2.34	2.32	2.33	2.31	1.00	down	4.18E-01	8.95E-01	-	-
1380898_at	---	---	---	---	BF418099	2.39	2.38	2.40	2.39	2.40	2.37	1.00	down	5.65E-01	8.95E-01	-	-
1394767_at	LOC680643	similar to MIC2 like 1	680643	---	BF396817	2.41	2.39	2.42	2.40	2.41	2.39	1.00	down	5.84E-01	8.95E-01	-	-
1387551_at	Kcnh7	potassium voltage-gated channel, subfamily H (eag-related), member 7	170739	Rn.10874	NM_131912	2.36	2.35	2.38	2.35	2.37	2.35	1.00	down	5.48E-01	8.95E-01	-	-
1387136_at	Ptprv	protein tyrosine phosphatase, receptor type, V	64576	Rn.10048	NM_033099	2.35	2.33	2.36	2.34	2.35	2.33	1.00	down	5.99E-01	8.95E-01	-	-
1385733_at	Exo1	exonuclease 1	305000	Rn.52638	BE116198	2.43	2.42	2.45	2.43	2.44	2.41	1.00	down	6.53E-01	8.97E-01	-	-
1371156_a_at	Glra1	glycine receptor, alpha 1	25674	Rn.10109	AJ310836	2.35	2.34	2.36	2.34	2.35	2.33	1.00	down	4.64E-01	8.95E-01	-	-
1368861_a_at	Mag	myelin-associated glycoprotein	29409	Rn.87331	NM_017190	2.37	2.36	2.38	2.36	2.37	2.35	1.00	down	4.33E-01	8.95E-01	-	-
1370571_at	Slco3a1	solute carrier organic anion transporter family, member 3a1	140915	Rn.102164	AF239219	2.29	2.28	2.29	2.28	2.29	2.27	1.00	down	2.88E-01	8.95E-01	-	-
1369701_at	Lipc	lipase, hepatic	24538	Rn.1195	NM_012597	2.37	2.37	2.38	2.37	2.38	2.35	1.00	down	4.54E-01	8.95E-01	-	-
1378407_at	---	---	---	Rn.12458	BF401415	2.48	2.46	2.50	2.48	2.49	2.45	1.00	down	7.03E-01	9.07E-01	-	-
1396273_at	---	---	---	Rn.146334	AW530436	2.58	2.56	2.60	2.58	2.61	2.54	1.00	down	7.83E-01	9.30E-01	-	-
1373259_at	---	---	---	Rn.79831	BI300311	2.34	2.33	2.35	2.33	2.34	2.32	1.00	down	4.62E-01	8.95E-01	-	-
1389668_at	Spc25	SPC25, NDC80 kinetochore complex component, homolog (S. cerevisiae)	295661	Rn.16268	AI408269	2.40	2.40	2.43	2.40	2.30	2.51	1.00	down	9.21E-01	9.77E-01	-	-
1393993_at	---	---	---	---	AA866294	2.37	2.36	2.38	2.36	2.37	2.35	1.00	down	5.37E-01	8.95E-01	-	-
1381328_at	Cr2	complement receptor 2	289395	Rn.23490	AI177373	2.49	2.46	2.51	2.47	2.53	2.44	1.00	down	8.40E-01	9.50E-01	-	-
1388049_a_at	Gabre	gamma-aminobutyric acid (GABA) A receptor, epsilon	65191	Rn.54455	AF255612	2.33	2.32	2.34	2.33	2.34	2.31	1.00	down	5.42E-01	8.95E-01	-	-
1376258_at	---	---	---	Rn.164670	AI406785	2.38	2.37	2.40	2.38	2.38	2.38	1.00	down	4.97E-01	8.95E-01	-	-
1368157_at	Stmn3	stathmin-like 3	29246	Rn.14961	NM_024346	2.30	2.29	2.32	2.30	2.30	2.29	1.00	down	4.38E-01	8.95E-01	-	-
1385532_x_at	Pamb5	proteasome (prosome, macropain) subunit, beta type 5	29425	Rn.2	BI281524	2.40	2.42	2.42	2.40	2.41	2.40	1.00	down	4.67E-01	8.95E-01	-	-
1376828_at	Gprc5a	G protein-coupled receptor, family C, group 5, member A	312790	Rn.23566	BI276110	2.26	2.25	2.27	2.26	2.26	2.25	1.00	down	4.15E-01	8.95E-01	-	-
1391821_at	---	---	---	Rn.53230	BF391706	2.53	2.56	2.52	2.53	2.54	2.52	1.00	down	6.25E-01	8.95E-01	-	-
1392194_at	---	---	---	Rn.207482	BE101986	2.38	2.37	2.40	2.38	2.38	2.37	1.00	down	4.70E-01	8.95E-01	-	-
1398246_s_at	gr2a /// LOC4982	Fc fragment of IgG, low affinity IIa, receptor (CD32) /// Fc gamma receptor II b	116591 /// 498276	Rn.6050	NM_053843	2.44	2.42	2.46	2.43	2.45	2.41	1.00	down	6.87E-01	9.04E-01	-	-
1385745_at	---	---	---	Rn.216936	BF389477	2.42	2.41	2.44	2.41	2.43	2.40	1.00	down	6.07E-01	8.95E-01	-	-
1368556_at	Vegp2	von Ebners gland protein 2	94106	Rn.11217	NM_053574	2.39	2.38	2.41	2.38	2.40	2.37	1.00	down	6.08E-01	8.95E-01	-	-
1377320_at	---	---	---	Rn.210054	BF409110	2.36	2.36	2.38	2.37	2.37	2.36	1.00	down	4.59E-01	8.95E-01	-	-
1390167_at	Tfc9b	tetratricopeptide repeat domain 9B	361528	Rn.45506	BI286834	2.41	2.40	2.41	2.42	2.41	2.38	1.00	down	6.20E-01	8.95E-01	-	-
1382180_at	Cradd	CASP2 and RIPK1 domain containing adaptor with death domain	314756	Rn.162947	BI295425	2.42	2.47	2.49	2.47	2.48	2.45	1.00	up	7.87E-01	9.31E-01	-	-
1397823_at	---	---	---	Rn.207988	BE117531	2.35	2.35	2.37	2.35	2.36	2.34	1.00	down	5.25E-01	8.95E-01	-	-
1396715_at	---	---	---	Rn.147341	BF400135	2.35	2.34	2.36	2.35	2.35	2.33	1.00	down	4.26E-01	8.95E-01	-	-
1392067_at	---	---	---	Rn.62304	BF413313	2.34	2.33	2.35	2.33	2.34	2.32	1.00	down	4.99E-01	8.95E-01	-	-
1391009_a_at	---	---	---	Rn.18922	AA851338	2.71	2.69	2.71	2.70	2.72	2.67	1.00	down	7.40E-01	9.16E-01	-	-
1375050_at	Gprin1	G protein-regulated inducer of neurite outgrowth 1	364676	Rn.16362	BI284558	2.37	2.53	2.47	2.45	2.46	2.44	1.00	down	8.95E-01	9.67E-01	-	-
1387297_at	Klrg1	killer cell lectin-like receptor subfamily G, member 1	58975	Rn.10256	NM_031649	2.36	2.36	2.38	2.36	2.37	2.35	1.00	down	4.92E-01	8.95E-01	-	-
1389311_at	---	---	---	Rn.22244	AW915161	5.21	4.04	2.96	3.78	3.89	4.57	1.00	up	9.93E-01	9.98E-01	-	-
1397320_at	---	---	---	Rn.212616	BI293372	2.43	2.42	2.45	2.43	2.45	2.40	1.00	down	7.25E-01	9.13E-01	-	-
1379713_at	---	---	---	---	AI233396	2.38	2.35	2.38	2.36	2.37	2.36	1.00	down	5.78E-01	8.95E-01	-	-
1395712_at	---	---	---	Rn.168252	AI576184	2.39	2.37	2.40	2.38	2.39	2.37	1.00	down	5.90E-01	8.95E-01	-	-
1398316_at	LOC288913	similar to LEYDIG CELL TUMOR 10 KD PROTEIN	288913	Rn.11148	X62277	7.98	7.76	7.42	7.81	7.57	7.75	1.00	down	9.72E-01	9.92E-01	-	-
1376284_at	---	---	---	Rn.27890	AI406517	2.30	2.30	2.30	2.30	2.29	2.30	1.00	down	1.85E-01	8.95E-01	-	-
1387324_at	Mak	male germ cell-associated kinase	25677	Rn.9670	NM_013136	2.31	2.31	2.33	2.31	2.32	2.30	1.00	down	4.51E-01	8.95E-01	-	-
1377139_at	Ttx5	T-box 5	304514	Rn.6327	BE110811	2.40	2.39	2.40	2.39	2.40	2.38	1.00	down	4.02E-01	8.95E-01	-	-
1396129_at	Cxcl14	chemokine (C-X-C motif) ligand 14	306748	Rn.3130	AI412979	2.36	2.36	2.37	2.39	2.36	2.35	1.00	up	5.94E-01	8.95E-01	-	-
1377323_at	Pla2g4b	phospholipase A2, group IVB (cytosolic)	311341	Rn.21662	AW434922	2.83	2.82	2.84	2.82	2.83	2.86	1.00	up	6.26E-01	8.95E-01	-	-
1390216_at	---	---	---	Rn.98595	AI177512	2.43	2.42	2.44	2.42	2.44	2.41	1.00	down	5.61E-01	8.95E-01	-	-
1369281_at	Tnfsf11	tumor necrosis factor (ligand) superfamily, member 11	117516	Rn.217570	NM_057149	2.33	2.33	2.35	2.34	2.34	2.32	1.00	down	4.43E-01	8.95E-01	-	-
1380031_at	---	---	---	Rn.206945	BE098261	2.32	2.31	2.33	2.31	2.32	2.30	1.00	down	4.54E-01	8.95E-01	-	-
1392313_at	LOC688721	similar to leucine rich repeat and fibronectin type III domain containing 4	688721	Rn.219382	BG376902	2.38	2.31	2.43	2.38	2.39	2.36	1.00	up	8.60E-01	9.57E-01	-	-
1370557_a_at	Kcnc2	potassium voltage gated channel, Shaw-related subfamily, member 2	246153	Rn.9733	BF400847	2.52	2.51	2.53	2.55	2.52	2.49	1.00	up	7.51E-01	9.19E-01	-	-
1393941_at	Pon1	paraoxonase 1	84024	Rn.20732	AI716284	2.33	2.32	2.36	2.33	2.35	2.32	1.00	down	7.25E-01	9.13E-01	-	-
1381677_at	Elavl2	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 2 (Hu antigen B)	286973	Rn.12662	BF403882	2.59	2.58	2.60	2.58	2.60	2.57	1.00	down	6.01E-01	8.95E-01	-	-
1370764_a_at	Tg	thyroglobulin	24826	Rn.10429	M35965	2.44	2.43	2.45	2.43	2.44	2.42	1.00	down	4.51E-01	8.95E-01	-	-
1393874_at	Aqp12b	aquaporin 12B	367316	Rn.20532	AI071423	2.34	2.33	2.35	2.33	2.34	2.32	1.00	down	3.73E-01	8.95E-01	-	-
1372049_at	Rhbdd3	rhomboid domain containing 3	289753	Rn.9606	BM385462	2.36	2.35	2.37	2.36	2.36	2.35	1.00	down	4.79E-01	8.95E-01	-	-
1373697_at	Mybpc2	myosin binding protein C, fast-type	292879	Rn.137668	BG378588	2.56	2.38	2.40	2.59	2.39	2.38	1.00	up	9.45E-01	9.84E-01	-	-
1387613_at	Npy2r	neuropeptide Y receptor Y2	66024	Rn.64505	NM_023968	2.26	2.25	2.28	2.26	2.26	2.25	1.00	down	4.62E-01	8.95E-01	-	-
1395364_at	Ifnar1	interferon (alpha, beta and omega) receptor 1	288264	Rn.105738	BE099982	2.50	2.46	2.53	2.49	2.52	2.50	1.00	up	7.68E-01	9.24E-01	-	-
1391468_at	Myct1	Myc target 1	292264	Rn.55418	AI501673	2.33	2.32	2.34	2.33	2.33	2.31	1.00	down	4.96E-01	8.95E-01	-	-
1393533_at	---	---	---	---	AI071526	2.31	2.30	2.31	2.29	2.31	2.30	1.00	down	3.85E-01	8.95E-01	-	-
1368722_at	Lta	lymphotoxin alpha (TNF superfamily, member 1)	25008	Rn.160577	NM_080769	2.38	2.37	2.40	2.38	2.39	2.37	1.00	down	5.06E-01	8.95E-01	-	-
1384170_at	Vav2	vav 2 guanine nucleotide exchange factor	296603	Rn.98555	AA800477

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1376979_at	---	---	---	Rn.63316	BF393959	2.35	2.35	2.37	2.35	2.36	2.34	1.00	down	5.48E-01	8.95E-01	-	-
1379146_at	---	---	---	Rn.210025	BF411772	2.38	2.38	2.40	2.38	2.38	2.37	1.00	down	4.43E-01	8.95E-01	-	-
1395604_at	---	---	---	Rn.154328	BF555073	2.29	2.29	2.31	2.29	2.30	2.28	1.00	down	3.92E-01	8.95E-01	-	-
1384899_at	---	---	---	Rn.33062	AA996921	2.48	2.47	2.50	2.49	2.51	2.47	1.00	up	6.73E-01	9.01E-01	-	-
1397562_at	LOC679474	similar to spermatogenesis associated glutamate (E)-rich protein 4f	679474	---	AW534448	2.39	2.37	2.41	2.38	2.43	2.37	1.00	up	7.83E-01	9.30E-01	-	-
1389951_at	---	---	---	Rn.156388	BF399415	2.33	2.32	2.34	2.32	2.33	2.31	1.00	down	3.73E-01	8.95E-01	-	-
1387667_at	Nos2	nitric oxide synthase 2, inducible	24599	Rn.10400	L12562	2.41	2.40	2.42	2.40	2.42	2.39	1.00	down	5.50E-01	8.95E-01	-	-
1385786_at	---	---	---	---	AA860039	2.43	2.39	2.43	2.41	2.43	2.40	1.00	down	6.78E-01	9.02E-01	-	-
1369429_at	Pdha2	pyruvate dehydrogenase (lipoamide) alpha 2	117098	Rn.11126	NM_053994	2.38	2.37	2.39	2.38	2.39	2.36	1.00	down	5.64E-01	8.95E-01	-	-
1385769_at	Odf3	outer dense fiber of sperm tails 3	366387	Rn.134459	BF412992	2.34	2.32	2.33	2.33	2.37	2.32	1.00	up	6.96E-01	9.06E-01	-	-
1398644_at	Plxnc1	plexin C1	362873	Rn.7829	AI535104	2.32	2.31	2.33	2.31	2.32	2.30	1.00	down	4.04E-01	8.95E-01	-	-
1369369_at	Kcnb2	potassium voltage gated channel, Shab-related subfamily, member 2	117105	Rn.32101	NM_054000	2.38	2.35	2.38	2.36	2.37	2.35	1.00	down	5.67E-01	8.95E-01	-	-
1388090_a_at	Epor	erythropoietin receptor	24336	Rn.22394	M93509	2.32	2.31	2.32	2.31	2.31	2.31	1.00	down	2.44E-01	8.95E-01	-	-
1390318_at	---	---	---	Rn.176365	BI298087	2.31	2.30	2.32	2.30	2.31	2.29	1.00	down	3.80E-01	8.95E-01	-	-
1392430_at	---	---	---	---	AW525096	2.42	2.41	2.43	2.42	2.44	2.42	1.00	up	4.50E-01	8.95E-01	-	-
1396476_at	---	---	---	Rn.131483	BG379133	2.39	2.38	2.40	2.39	2.39	2.38	1.00	down	3.55E-01	8.95E-01	-	-
1377077_at	Plxna3	plexin A3	309280	Rn.21101	AW141867	2.28	2.27	2.29	2.28	2.28	2.26	1.00	down	5.33E-01	8.95E-01	-	-
1392250_at	Anxa2	Annexin A2	56611	Rn.90546	AI145827	2.44	2.44	2.46	2.43	2.46	2.43	1.00	down	6.73E-01	9.01E-01	-	-
1385193_at	---	---	---	---	BF395008	2.36	2.36	2.38	2.36	2.37	2.35	1.00	down	4.97E-01	8.95E-01	-	-
1395774_at	Gpr153	G protein-coupled receptor 153	619550	Rn.198305	BF566655	2.36	2.35	2.37	2.35	2.36	2.34	1.00	down	5.27E-01	8.95E-01	-	-
1380155_at	---	---	---	Rn.27384	AI373306	2.37	2.38	2.37	2.37	2.41	2.37	1.00	up	6.53E-01	8.97E-01	-	-
1397198_at	---	---	---	Rn.51964	BE111113	2.38	2.36	2.39	2.37	2.38	2.36	1.00	down	5.76E-01	8.95E-01	-	-
1378633_at	Lpxn	leupaxin	293783	Rn.29200	BE106297	2.37	2.37	2.39	2.38	2.40	2.38	1.00	up	5.48E-01	8.95E-01	-	-
1375099_at	---	---	---	Rn.172235	BF415478	2.34	2.34	2.36	2.34	2.35	2.33	1.00	down	4.37E-01	8.95E-01	-	-
1391137_at	RGD1359334	similar to hypothetical protein FLJ20519	295265	Rn.56974	BM386674	2.31	2.30	2.33	2.30	2.31	2.30	1.00	down	5.27E-01	8.95E-01	-	-
1377441_at	---	---	---	Rn.51706	BF412649	2.48	2.48	2.48	2.48	2.50	2.48	1.00	up	4.82E-01	8.95E-01	-	-
1379820_at	---	---	---	Rn.62980	BF416300	2.53	2.51	2.56	2.52	2.54	2.51	1.00	down	7.27E-01	9.13E-01	-	-
1388186_at	LOC286911	cationic trypsinogen	286911	Rn.9817	AI548979	2.38	2.37	2.39	2.37	2.39	2.36	1.00	down	5.65E-01	8.95E-01	-	-
1383904_at	Fgl1	fibrinogen-like 1	246186	Rn.15994	BM386541	2.35	2.35	2.36	2.35	2.36	2.34	1.00	down	4.72E-01	8.95E-01	-	-
1369260_a_at	Mpp4	membrane protein, palmitoylated 4 (MAGUK p55 subfamily member 4)	58808	Rn.163075	NM_021265	2.38	2.37	2.40	2.38	2.39	2.37	1.00	down	5.89E-01	8.95E-01	-	-
1372094_at	Supt5h	suppressor of Ty 5 homolog (S. cerevisiae)	308472	Rn.100021	BG380656	5.90	6.89	5.63	6.38	5.80	6.23	1.00	down	9.88E-01	9.98E-01	-	-
1385629_at	RGD1306233	similar to hypothetical protein MGC29761	296608	Rn.94715	AA998089	2.41	2.39	2.42	2.40	2.43	2.38	1.00	down	7.22E-01	9.11E-01	-	-
1384013_at	---	---	---	Rn.216828	BF524215	2.41	2.41	2.43	2.41	2.42	2.40	1.00	down	5.28E-01	8.95E-01	-	-
1368990_at	Cyp1b1	cytochrome P450, family 1, subfamily b, polypeptide 1	25426	Rn.10125	NM_012940	2.34	2.33	2.42	2.33	2.40	2.40	1.00	up	8.65E-01	9.58E-01	-	-
1396726_at	RGD1308626	Similar to 9630044O09Rik protein	361087	Rn.21577	BF409293	2.34	2.32	2.34	2.33	2.34	2.32	1.00	down	4.25E-01	8.95E-01	-	-
1397318_at	---	---	---	Rn.204226	AI070053	2.44	2.42	2.44	2.43	2.43	2.42	1.00	down	4.32E-01	8.95E-01	-	-
1393488_at	---	---	---	---	AI103612	2.51	2.50	2.52	2.51	2.51	2.49	1.00	down	3.26E-01	8.95E-01	-	-
1368922_at	Ecel1	endothelin converting enzyme-like 1	60417	Rn.45803	AB023896	2.31	2.30	2.31	2.30	2.30	2.29	1.00	down	3.35E-01	8.95E-01	-	-
1385054_at	---	---	---	Rn.149552	BE104042	3.59	2.77	4.65	3.68	4.01	3.30	1.00	down	9.92E-01	9.97E-01	-	-
1378244_at	---	---	---	Rn.20215	AI072663	2.36	2.35	2.38	2.36	2.37	2.34	1.00	down	6.00E-01	8.95E-01	-	-
1367792_at	Psg	gastrolid secretory protein	50585	Rn.9766	NM_052808	2.34	2.33	2.35	2.33	2.34	2.32	1.00	down	4.09E-01	8.95E-01	-	-
1392132_at	Polr2i	polymerase (RNA) II (DNA directed) polypeptide I, 14.5kDa	292778	Rn.6227	BE099899	2.28	2.28	2.29	2.27	2.29	2.27	1.00	down	4.22E-01	8.95E-01	-	-
1377330_at	---	---	---	Rn.154338	BF411114	2.33	2.32	2.33	2.32	2.33	2.31	1.00	down	3.89E-01	8.95E-01	-	-
1389447_at	Ph-4	hypoxia-inducible factor prolyl 4-hydroxylase	301008	Rn.10391	AA955440	2.29	2.29	2.31	2.29	2.30	2.28	1.00	down	4.35E-01	8.95E-01	-	-
1389367_at	Schip1	schwannomin interacting protein 1	295105	Rn.22213	AI409747	2.63	2.60	2.66	2.62	2.64	2.61	1.00	down	7.34E-01	9.15E-01	-	-
1396552_s_at	Odz2	odz, odd Oz/ten-m homolog 2 (Drosophila)	117242	Rn.205610	BF402505	2.32	2.31	2.33	2.32	2.32	2.31	1.00	down	4.26E-01	8.95E-01	-	-
1378310_at	Nmb	neuromedin B	499194	Rn.18763	BG669018	2.36	2.35	2.37	2.35	2.36	2.34	1.00	down	4.74E-01	8.95E-01	-	-
1374088_at	Mypn	myopalladin	309760	Rn.3872	AA800249	2.42	2.42	2.44	2.42	2.43	2.41	1.00	down	4.57E-01	8.95E-01	-	-
1370048_at	Lpar1	lysophosphatidic acid receptor 1	116744	Rn.11200	NM_053936	2.49	2.46	2.55	2.55	2.47	2.45	1.00	down	8.78E-01	9.62E-01	-	-
1394740_at	---	---	---	---	AA850678	2.30	2.29	2.30	2.29	2.33	2.28	1.00	up	6.93E-01	9.05E-01	-	-
1371163_at	Slfn3	schlafen 3	114247	Rn.80831	Y17327	2.26	2.26	2.27	2.26	2.27	2.25	1.00	down	4.35E-01	8.95E-01	-	-
1378643_at	---	---	---	---	AI600226	2.36	2.36	2.37	2.36	2.36	2.34	1.00	down	4.27E-01	8.95E-01	-	-
1378375_at	Ccar1	Cell division cycle and apoptosis regulator 1	361849	Rn.92786	AI501575	2.61	2.58	2.67	2.60	2.68	2.60	1.00	up	8.66E-01	9.58E-01	-	-
1396412_at	---	---	---	Rn.154613	BF391281	2.44	2.41	2.46	2.43	2.45	2.41	1.00	down	7.23E-01	9.12E-01	-	-
1382123_at	---	---	---	Rn.7585	AI574734	2.35	2.34	2.36	2.34	2.35	2.33	1.00	down	4.83E-01	8.95E-01	-	-
1391018_at	Myo5c	myosin VC	315820	Rn.2304	BF420807	2.39	2.37	2.41	2.38	2.39	2.37	1.00	down	5.61E-01	8.95E-01	-	-
1387555_at	---	---	---	---	NM_024154	2.34	2.33	2.35	2.33	2.35	2.32	1.00	down	5.20E-01	8.95E-01	-	-
1370556_at	Vamp1	vesicle-associated membrane protein 1	25624	Rn.31977	M24104	2.39	2.38	2.41	2.39	2.39	2.38	1.00	down	5.02E-01	8.95E-01	-	-
1394080_at	---	---	---	Rn.177124	BI277860	2.34	2.33	2.34	2.33	2.34	2.32	1.00	down	4.19E-01	8.95E-01	-	-
1393725_at	Dsg1b	desmoglein 1 beta	291755	Rn.35296	AI501187	2.31	2.30	2.32	2.30	2.31	2.29	1.00	down	4.64E-01	8.95E-01	-	-
1386517_at	Rpl30	Ribosomal protein L30	64640	Rn.161950	AI233363	2.48	2.46	2.50	2.48	2.49	2.49	1.00	up	6.27E-01	8.95E-01	-	-
1370084_at	Cpb1	carboxypeptidase B1 (tissue)	24271	Rn.12780	NM_012533	2.33	2.32	2.34	2.32	2.33	2.31	1.00	down	5.12E-01	8.95E-01	-	-
1380847_at	Zmat4	zinc finger, matrin type 4	684961	Rn.61258	BF409128	2.33	2.32	2.34	2.33	2.34	2.32	1.00	down	4.64E-01	8.95E-01	-	-
1392169_at	---	---	---	Rn.207782	BI294191	2.41	2.39	2.42	2.40	2.42	2.39	1.00	down	6.50E-01	8.96E-01	-	-
1397202_at	---	---	---	Rn.92023	BF283204	2.42	2.42	2.44	2.41	2.44	2.41	1.00	down	6.26E-01	8.95E-01	-	-
1368492_at	Ptgds2	prostaglandin D2 synthase 2, hematopoietic	58962	Rn.10837	NM_031644	2.33	2.33	2.34	2.33	2.33	2.31	1.00	down	4.09E-01	8.95E-01	-	-
1371264_at	Hbe2	hemoglobin, epsilon 2	502359	Rn.215837	X56327	2.37	2.36	2.38	2.37	2.38	2.35	1.00	down	5.66E-01	8.95E-01	-	-
1388524_at	---	---	---	Rn.9323	BF284328	5.13	5.36	4.81	4.93	4.62	5.77	1.00	up	9.87E-01	9.96E-01	-	-
1369328_at	Acacb	acetyl-Coenzyme A carboxylase beta	116719	Rn.162151	NM_053922	2.42	2.40	2.43	2.42	2.42	2.40	1.00	down	5.53E-01	8.95E-01	-	-
1387125_at	S100a9	S100 calcium binding protein A9	94195	Rn.6703	NM_053587	2.40	2.40	2.42	2.40	2.42	2.38	1.00	down	6.44E-01	8.95E-01	-	-
1383351_at	---	---	---	Rn.23654	AI136019	2.35	2.34	2.36	2.34	2.35	2.33	1.00	down	4.35E-01	8.95E-01	-	-
1387660_at	Iapp	islet amyloid polypeptide	24476	Rn.11394	M25390	2.36	2.35	2.37	2.35	2.36	2.34	1.00	down	5.02E-01	8.95E-01	-	-
1398543_at	---	---	---	Rn.211079	BF411798	2.33	2.32	2.33	2.32	2.33	2.31	1.00	down	3.74E-01	8.95E-01	-	-
1368381_at	Crtac1	cartilage acidic protein 1	171438	Rn.198566	NM_134401	2.35	2.33	2.34	2.33	2.35	2.33	1.00	down	4.55E-01	8.95E-01	-	-
1397802_at	---	---	---	Rn.156561	AI775424	2.44	2.41	2.44	2.43	2.45	2.43	1.00	up	5.66E-01	8.95E-01	-	-
1395892_at	---	---	---	---	AW920797	2.46	2.43	2.46	2.44	2.46	2.42	1.00	down	6.72E-01	9.01E-01	-	-
1372915_at	---	---	---	Rn.20332	BG375484	2.35	2.34	2.35	2.34	2.35	2.33	1.00	down	3.77E-01	8.95E-01	-	-
1384552_at	---	---	---	Rn.22811	AI104480	2.38	2.37	2.40	2.38	2.38	2.37	1.00	down	4.32E-01	8.95E-01	-	-
1392063_at	---	---	---	Rn.210185	BF395773	2.30	2.29	2.30	2.30	2.30	2.31	1.00	up	3.66E-01	8.95E-01	-	-
1395511_at	---	---	---	Rn.172801	BF543472	2.36	2.35	2.38	2.36	2.37	2.34	1.00	down	5.44E-01	8.95E-01	-	-
1370674_at	Vom2r53	vomeronasal 2 receptor, 53	286915	Rn.10806	AF016178	2.31	2.31	2.32	2.31	2.31	2.30	1.00	down	3.59E-01	8.95E-01	-	-
1390718_at	---	---	---	Rn.146433	BE096865	2.56	2.54	2.58	2.55	2.57	2.54	1.00	down	6.88E-01	9.04E-01	-	-
1387171_at	Gria2	glutamate receptor, ionotropic, AMPA 2	29627	Rn.91361	NM_017261	2.44	2.41	2.45	2.42	2.46	2.40	1.00	down	7.65E-01	9.23E-01	-	-
1397379_at	Ankrd8	ankyrin repeat domain 8	500430	Rn.45844	BE118115	2.42	2.41	2.42	2.41	2.42	2.40	1.00	down	5.03E-01	8.95E-01	-	-
1387193_a_at	Spink3	serine peptidase inhibitor, Kazal type 3	24833	Rn.9767	M27882	2.42	2.41	2.44	2.42	2.43	2.41	1.00	down	5.42E-01	8.95E-01	-	-
1398414_at	LOC691504	Similar to Zinc finger protein ZFPM1 (Zinc finger protein multitype 1) (Friend c	691504	Rn.160024	AI556031	2.29	2.28	2.30	2.28	2.29	2.28	1.00	down	3.51E-01	8.95E-01	-	-
1388087_at	V1rb9	vomeronasal 1 receptor, B9	286956	Rn.10143	U36897	2.44	2.43	2.45	2.43	2.44	2.42	1.00	down	5.25E-01	8.95E-01	-	-
1391726_at	---	---	---	---	AI012408	2.49	2.45	2.55	2.49	2.52	2.46	1.00	down	8.57E-01	9.55E-01	-	-
1396429_at	---	---	---	Rn.151520	BF409858	2.36	2.35	2.37	2.35	2.37	2.34	1.00	down	5.54E-01	8.95E-01	-	-
1396623_at	---	---	---	Rn.210633	BF399568	2.57	2.56	2.57	2.56	2.56	2.55	1.00	down	3.30E-01	8.95E-01	-	-
1384234_at	Prrx1	paired related homeobox 1	266813	Rn.203584	BE126475	2.32	2.31	2.33	2.31	2.32	2.31	1.00	down	4.92E-01	8.95E-01	-	-
1376952_at	---	---	---	Rn.11709	BF398963	2.37	2.35	2.37	2.36	2.36	2.35	1.00	down	4.82E-01	8.95E-01	-	-
1381179_at	Epm2aip1	EPM2A (laforin) interacting protein 1	316021	Rn.209819	BF415421	3.62	3.61	3.66	3.61	3.48	3.77	1.00	down	9.45E-01	9.84E-01	-	-
1392935_at	---	---	---	Rn.147598	BE115639	2.42	2.41	2.44	2.42	2.43	2.41	1.00	down	5.45E-01	8.95E-01	-	-
1389950_at	Fbxo10	F-box protein 10	362511	Rn.198471	AI009171	2.35	2.35	2.36	2.35	2.36	2.34	1.00	down	3.26E-01	8.95E-01	-	-
1392509_at	Cbl1	Cas-Br-M (murine) ecotropic retroviral transforming sequence-like 1	314028	Rn.92651	AA925469	6.26	5.98	6.28	6.12	6.24	6.15	1.00	down	9.53E-01	9.86E-01	-	-
1383578_at	Rad51	RAD51 homolog (RecA homolog, E. coli) (S. cerevisiae)	499870	Rn.20474	AI071227	2.35	2.35	2.36	2.34	2.35	2.34	1.00	down	2.49E-01	8.95E-01	-	-
1379718_at	---	---	---	Rn.129285	BE102205	2.36	2.35	2.37	2.35	2.36	2.34	1.00	down	5.39E-01	8.95E-01	-	-
1373032_at	Musk1	musculoskeletal, embryonic nuclear protein 1	290553	Rn.203378	AW251450	2.36	2.35	2.37	2.35	2.37	2.34	1.00	down	5.08E-01	8.95E-01	-	-
1393892_at	RGD1306625	LOC360508	360508	Rn.59235	BF399123	2.37	2.35	2.38	2.37	2.37	2.35	1.00	down	6.33E-01	8.95E-01	-	-
1377271_at	Unc45b	unc-45 homolog B (C. elegans)	303373	Rn.61093	BF390686	2.30	2.29	2.31	2.30	2.30	2.29	1.00	down	4.11E-01	8.95E-01	-	-
1372816_at	---	---	---	Rn.49278	BE107319	5.31	5.80	6.22	5.60	5.74	5.97	1.00	down	9.83E-01	9.95E-01	-	-
1367664_at	Ankrd1	ankyrin repeat domain 1 (cardiac muscle)	27064	Rn.3789	L81174	2.32	2.31	2.33	2.32	2.32	2.31	1.00	down	3.78E-01	8.95E-01	-	-
1385754_s_at	Lrrc4	leucine rich repeat containing 4	641521	Rn.198672	BE105879	2.50	2.48	2.53	2.49	2.58	2.45	1.00	up	8.79E-01	9.63E-01	-	-
1381266_at	---	---	---	Rn.107351	AI704633	2.35	2.34	2.35	2.34	2.35	2.33	1.00	down	4.70E-01	8.95E-01	-	-
1395295_at	Mll6	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila);	303504	Rn.25109	AI112116	2.35	2.34	2.36	2.34	2.36	2.33	1.00	down	5.01E-01	8.95E-01	-	-
1369619_at	Ucn2	urocortin 2	170896	Rn.212744	NM_133385	2.40	2.40	2.42	2.40	2.41	2.40	1.00	down	3.97E-01	8.95E-01	-	-
1370558_a_at	Kcnc2	potassium voltage gated channel, Shaw-related subfamily, member 2	246153	Rn.9733	BF400847	2.41	2.39	2.42	2.40	2.41	2.38	1.00	down	6.50E-01	8.96E-01	-	-
1390635_at	---	---	---	Rn.199844	BE110246	2.54	2.52	2.55	2.53	2.54	2.51	1.00	down	6.47E-01	8.95E-01	-	-
1371148_s_at	Ina	internexin neuronal intermediate filament protein, alpha	24503	Rn.88941	X52017	2.40	2.39	2.41	2.40	2.39	2.39	1.00	down	3.70E-01	8.95E-01	-	-
1379487_at	---	---	---	Rn.48116	BF287099	2.54	2.52	2.56	2.53	2.54	2.52	1.00	down	6.48E-01	8.96E-01	-	-
1377477_at	Kcng2	Potassium voltage-gated channel, subfamily G, member 2	307234	Rn.163389	AI704152	2.32	2.32	2.33	2.32	2.33	2.31	1.00	down	3.72E-01	8.95E-01	-	-
1396887_at	---	---	---	Rn.206527	AW527935	2.30	2.30	2.31	2.30	2.30	2.29	1.00	down	3.24E-01	8.95E-01	-	-
1391130_at	RGD1308782	similar to Zinc finger protein OZF (POZF-1)	308318	Rn.143807	BI284481	2.47	2.44	2.48	2.46	2.47	2.44	1.00	down	6.90E-01	9.05E-01	-	-
1395087_at	---	---	---	Rn.206417	BE107412	2.33	2.32	2.33	2.32	2.33	2.31	1.00	down	4.83E-01	8.95E-01	-	-
1398200_at	---	---	---	Rn.57926	BF392865	2.35	2.34	2.36	2.35	2.36	2.33	1.00	down	5.39E-01	8.95E-01	-	-
1388016_a_at	Grip2	glutamate receptor interacting protein 2	171571	Rn.15680	AF112182	2.36	2.35	2.36	2.35	2.36	2.34	1.00	down	4.25E-01	8.95E-01	-	-
1375471_at	Cdk5r2	cyclin-dependent kinase 5, regulatory subunit 2 (p39)	501164	Rn.219411	BF394018	2.24	2.24	2.26	2.24	2.25	2.23	1.00	down	5.10E-01	8.95E-01	-	-
1379695_at	---	---	---	Rn.146468	AW915505	2.33	2.32	2.34	2.32	2.33	2.31	1.00	down	5.30E-01	8.95E-01	-	-
1370508_s_at	Cacna1g	calcium channel, voltage-dependent, T type, alpha 1G subunit	29717	Rn.86982	AF290212	2.42	2.41	2.43	2.41	2.42	2.41	1.00	down	3.21E-01	8.95E-01	-	-
1382967_at	Gpr64	G protein-coupled receptor 64	266735	Rn.57243	BF388060	2.38	2.36	2.37	2.36	2.37	2.36	1.00	down	3.73E-01	8.95E-01	-	-
1397713_at	---	---	---	---	AW917120	2.52	2.50	2.52	2.50	2.55	2.46	1.00	down	8.30E-01	9.46E-01	-	-
1383456_at	---	---	---	Rn.15053	BI298788	2.39	2.38	2.41	2.39	2.40	2.37	1.00	down	6.41E-01	8.95E-01	-	-
1392808_at	---	---	---	---	BF402967	2.30	2.29	2.32	2.30	2.30	2.29	1.00	down	5.03E-01	8.95E-01	-	-
1378202_at	---	---	---	Rn.168730	BE106504	2.57	2.56	2.58	2.57	2.57	2.55	1.00	down	5.63E-01	8.95E-01	-	-
1369884_at	Fgf7	fibroblast growth factor 7	29348	Rn.98842	NM_022182	2.36	2.34	2.35	2.34	2.35	2.34	1.00	down	4.59E-01	8.95E-01	-	-
1395223_at	Klhdc8b	kelch domain containing 8B	306589	Rn.41577	AI709940	2.42	2.42	2.43	2.42	2.45	2.41	1.00	up	6.44E-01	8.95E-01	-	-
1390014_at	---	---	---	---	BF399576	2.54	2.49	2.58	2.51	2.59	2.50	1.00	down	8.82E-01	9.64E-01	-	-
1375815_at	---	---	---	Rn.209696	BF391129	2.34	2.33	2.36	2.33	2.37	2.31	1.00	down	7.56E-01	9.21E-01	-	-
1381097_at	---	---	---	Rn.203425	AI030890	2.37	2.36	2.38	2.36	2.37	2.36	1.00	down	4.00E-01	8.95E-01	-	-
1376296_at	RGD1562428	similar to C20orf95	296323	---	BF387347	2.36	2.35	2.37	2.35	2.36	2.34	1.00	down	4.54E-01	8.95E-01	-	-
1391178_at	---	---	---	Rn.208088	BE110066	2.30	2.28	2.29	2.28	2.29	2.28	1.00	down	4.51E-01	8.95E-01	-	-
1377275_at	Arl1	ADP-ribosyltransferase 1	308873	Rn.6493	AI175328	2.39	2.38	2.40	2.38	2.40	2.38	1.00	down	5.26E-01	8.95E-01	-	-
1378888_at	---	---	---	Rn.32730	BF397854	2.38	2.37	2.40	2.38	2.39	2.37	1.00	down	5.52E-01	8.95E-01	-	-
1394354_at	---	---	---	Rn.27122	BF552000	2.46	2.44	2.46	2.45	2.47	2.42	1.00	down	7.12E-01	9.10E-01	-	-
1377438_at	Diras1	DIRAS family, GTP-binding RAS-like 1	366826	Rn.91520	BE095820	2.36	2.35	2.37	2.35	2.36	2.34	1.00	down	4.57E-01	8.95E-01	-	-
1377027_at	---	---	---	Rn.221915	BI295511	2.41	2.41	2.41	2.39	2.41	2.40	1.00	down	3.11E-01	8.95E-01	-	-
1380672_at	---	---	---	---	AI406316	2.34	2.33	2.35	2.33	2.35	2.32	1.00	down	5.20E-01	8.95E-01	-	-
1398668_at	---	---	---	Rn.54114	BF290204	2.33	2.33	2.34	2.33	2.34	2.32	1.00	down	4.60E-01	8.95E-01	-	-
1381136_at	Rbp3	retinol binding protein 3, interstitial	24711	Rn.41214	BE095712	2.29	2.28	2.30	2.29	2.29	2.28	1.00	down	4.32E-01	8.95E-01	-	-
1397603_at	---	---	---	---	AW528821	2.32	2.31	2.33	2.31	2.32	2.30	1.00	down	4.53E-01	8.95E-01	-	-
1390313_at	---	---	---	---	BF390740	2.32	2.31	2.34	2.31	2.32	2.31	1.00	down	5.87E-01	8.95E-01	-	-
1380111_at	---	---	---	Rn.205471	AI578095	2.35	2.34	2.36	2.34	2.36	2.33	1.00	down	5.27E-01	8.95E-01	-	-
1368641_at	Wnt4	wingless-type MMTV integration site family, member 4	84426	Rn.34782	NM_053402	2.54	2.53	2.55	2.54	2.55	2.53	1.00	down	4.72E-01	8.95E-01	-	-
1396196_at	---	---	---	---	BF290745	2.46	2.45	2.48	2.46	2.47	2.45	1.00	down	4.99E-01	8.95E-01	-	-
1396568_at	---	---	---	Rn.60342	BF405624	2.38	2.36	2.39	2.37	2.38	2.36

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1387270_at	Hhex	hematopoietically expressed homeobox	79237	Rn.12188	NM_024385	2.40	2.39	2.42	2.39	2.43	2.38	1.00	down	7.29E-01	9.14E-01	-	-
1398147_at	Dpagt1	dolichyl-phosphate (UDP-N-acetylglucosamine) N-acetylglucosaminephosphc	300668	Rn.129301	BF404483	2.43	2.43	2.44	2.43	2.44	2.42	1.00	down	5.28E-01	8.95E-01	-	-
1384020_at	---	---	---	Rn.156585	AA944187	2.33	2.32	2.34	2.32	2.33	2.31	1.00	down	4.92E-01	8.95E-01	-	-
1398462_at	---	---	---	Rn.147435	BE120209	2.32	2.31	2.33	2.31	2.32	2.30	1.00	down	4.36E-01	8.95E-01	-	-
1381007_at	---	---	---	Rn.19649	BE117875	3.19	4.05	4.83	3.69	4.35	4.02	1.00	down	9.91E-01	9.97E-01	-	-
1369797_at	Adra1a	adrenergic, alpha-1A-, receptor	29412	Rn.9991	U07126	2.41	2.41	2.42	2.43	2.43	2.40	1.00	up	5.95E-01	8.95E-01	-	-
1370734_a_at	Dspp	dentin sialophosphoprotein	25254	Rn.21392	U63111	2.43	2.41	2.43	2.41	2.44	2.39	1.00	down	7.26E-01	9.13E-01	-	-
1395836_at	Odz2	Odz, odd Oz/ten-m homolog 2 (Drosophila)	117242	Rn.205610	BF400594	2.45	2.44	2.46	2.45	2.46	2.43	1.00	down	5.56E-01	8.95E-01	-	-
1385122_at	Dst	dystonin	316313	Rn.79807	BM386832	2.29	2.28	2.30	2.28	2.29	2.27	1.00	down	3.77E-01	8.95E-01	-	-
1387480_at	Notch2	Notch homolog 2 (Drosophila)	29492	Rn.65930	NM_024358	2.32	2.31	2.33	2.31	2.32	2.30	1.00	down	4.08E-01	8.95E-01	-	-
1380676_at	---	---	---	Rn.202015	BF390778	2.51	2.49	2.51	2.50	2.79	2.24	1.00	up	9.70E-01	9.91E-01	-	-
1368801_at	Cxxc4	CXXC finger 4	83824	Rn.209562	NM_053342	2.35	2.34	2.36	2.35	2.36	2.33	1.00	down	5.23E-01	8.95E-01	-	-
1392693_at	RGD1311224	similar to fatty acid desaturase 2; linoleoyl-CoA desaturase (delta-6-desaturas	295714	Rn.47550	AW530812	2.46	2.45	2.47	2.45	2.47	2.44	1.00	down	6.38E-01	8.95E-01	-	-
1382338_at	Tnrc4	Trinucleotide repeat containing 4	498669	Rn.220623	AA964833	2.35	2.34	2.36	2.34	2.35	2.34	1.00	down	3.78E-01	8.95E-01	-	-
1373066_at	---	---	---	Rn.40480	AI407797	2.36	2.36	2.37	2.36	2.37	2.35	1.00	down	5.10E-01	8.95E-01	-	-
1397361_x_at	---	---	---	Rn.205892	AI407549	2.42	2.40	2.43	2.41	2.42	2.39	1.00	down	6.75E-01	9.01E-01	-	-
1376614_at	---	---	---	Rn.144216	BF403180	2.33	2.32	2.34	2.32	2.33	2.31	1.00	down	5.07E-01	8.95E-01	-	-
1387849_at	Epn2	epsin 2	60443	Rn.44273	NM_021852	2.34	2.33	2.35	2.34	2.35	2.33	1.00	down	5.04E-01	8.95E-01	-	-
1377471_s_at	---	---	---	Rn.216706	AI535533	3.24	3.23	3.25	3.23	3.25	3.22	1.00	down	5.74E-01	8.95E-01	-	-
1368633_at	Crisp1	cysteine-rich secretory protein 1	64827	Rn.10102	NM_022859	2.33	2.32	2.35	2.33	2.34	2.32	1.00	down	5.38E-01	8.95E-01	-	-
1368923_at	Ece1	endothelin converting enzyme-like 1	60417	Rn.45803	AB023896	2.38	2.38	2.39	2.37	2.39	2.37	1.00	down	4.96E-01	8.95E-01	-	-
1379187_at	---	---	---	Rn.147305	BF418643	2.24	2.23	2.24	2.23	2.24	2.23	1.00	down	3.24E-01	8.95E-01	-	-
1369908_at	Crhbp	corticotropin releasing hormone binding protein	29625	Rn.34568	NM_139183	2.34	2.33	2.37	2.34	2.35	2.33	1.00	down	6.49E-01	8.96E-01	-	-
1371118_a_at	Ighe	immunoglobulin heavy chain (epsilon polypeptide)	299351	Rn.202946	K02901	2.33	2.32	2.33	2.32	2.33	2.31	1.00	down	4.09E-01	8.95E-01	-	-
1389841_at	---	---	---	Rn.204071	BI296641	2.36	2.35	2.37	2.35	2.37	2.35	1.00	down	4.73E-01	8.95E-01	-	-
1391352_at	Erp27	endoplasmic reticulum protein 27	297698	Rn.16083	BF407548	2.41	2.39	2.42	2.40	2.41	2.39	1.00	down	6.15E-01	8.95E-01	-	-
1380842_at	Qrsl1	glutaminyl-tRNA synthase (glutamine-hydrolyzing)-like 1	309911	Rn.116771	BF408281	2.41	2.39	2.41	2.40	2.43	2.40	1.00	up	6.35E-01	8.95E-01	-	-
1385181_at	---	---	---	Rn.77403	AI029337	2.45	2.39	2.45	2.41	2.49	2.40	1.00	up	8.67E-01	9.58E-01	-	-
1397402_at	---	---	---	Rn.107839	BE097073	3.51	2.46	2.50	3.01	3.04	2.45	1.00	up	9.88E-01	9.96E-01	-	-
1379954_at	Eif2	E74-like factor 2	361944	Rn.107459	BF413969	2.30	2.29	2.31	2.30	2.30	2.29	1.00	down	3.27E-01	8.95E-01	-	-
1370720_at	V1ra16	vomeronasal 1 receptor, A16	266771	Rn.83612	U36898	2.35	2.34	2.36	2.35	2.36	2.33	1.00	down	5.48E-01	8.95E-01	-	-
1397148_at	Stoml3	stomatin (Epb7.2)-like 3	295041	Rn.218487	BE120535	2.39	2.38	2.40	2.39	2.40	2.37	1.00	down	6.14E-01	8.95E-01	-	-
1369457_a_at	Syt4	synaptotagmin-like 4	140594	Rn.107417	AF419342	2.31	2.31	2.33	2.31	2.32	2.30	1.00	down	4.46E-01	8.95E-01	-	-
1395407_at	Fry	furry homolog (Drosophila)	304244	Rn.36184	BF288280	2.37	2.36	2.38	2.37	2.37	2.34	1.00	down	6.34E-01	8.95E-01	-	-
1383200_at	Ccdc81	coiled-coil domain containing 81	308810	Rn.7655	BF418327	2.29	2.29	2.30	2.29	2.30	2.28	1.00	down	4.04E-01	8.95E-01	-	-
1379352_at	Plp5k1b	phosphatidylinositol-4-phosphate 5-kinase, type I, beta	309419	Rn.203303	BF406008	2.35	2.35	2.37	2.35	2.36	2.34	1.00	down	4.36E-01	8.95E-01	-	-
1398204_at	---	---	---	Rn.207886	BE107780	2.38	2.37	2.40	2.37	2.38	2.37	1.00	down	5.54E-01	8.95E-01	-	-
1378321_at	Rassf4	Ras association (RalGDS/AF-6) domain family member 4	362423	Rn.195253	BG375029	2.36	2.35	2.37	2.35	2.36	2.35	1.00	down	3.99E-01	8.95E-01	-	-
1391824_at	---	---	---	Rn.44963	AW532835	2.40	2.40	2.42	2.40	2.41	2.39	1.00	down	5.62E-01	8.95E-01	-	-
1375476_at	Pygm	phosphorylase, glycogen, muscle	24701	Rn.11238	AI717476	2.33	2.33	2.34	2.33	2.33	2.31	1.00	down	5.18E-01	8.95E-01	-	-
1393737_at	Gkn2	gastrokine 2	297419	Rn.20773	AI044560	2.28	2.27	2.29	2.28	2.28	2.27	1.00	down	4.30E-01	8.95E-01	-	-
1390337_at	---	---	---	Rn.47579	AW526289	2.41	2.41	2.44	2.41	2.42	2.41	1.00	down	5.35E-01	8.95E-01	-	-
1370037_at	Fbn2	fibrillin 2	689008	Rn.22906	NM_031826	2.43	2.42	2.44	2.42	2.44	2.41	1.00	down	5.70E-01	8.95E-01	-	-
1378762_at	---	---	---	Rn.209312	BF419592	2.28	2.27	2.29	2.28	2.28	2.27	1.00	down	4.50E-01	8.95E-01	-	-
1390138_at	MGC72567	similar to coiled-coil domain containing 8	494320	Rn.145404	BE107413	2.47	2.46	2.48	2.47	2.48	2.45	1.00	down	5.93E-01	8.95E-01	-	-
1391923_at	---	---	---	Rn.147188	BG376838	2.31	2.31	2.32	2.31	2.31	2.30	1.00	down	3.15E-01	8.95E-01	-	-
1392977_at	---	---	---	Rn.159849	BE114491	2.36	2.35	2.37	2.36	2.36	2.34	1.00	down	5.91E-01	8.95E-01	-	-
1396117_at	RGD1563838	similar to leucine zipper protein 2	361583	---	BG665533	2.35	2.34	2.36	2.35	2.36	2.33	1.00	down	5.22E-01	8.95E-01	-	-
1384197_at	Dlgap1	Discs, large (Drosophila) homolog-associated protein 1	65040	Rn.90059	AW521536	2.50	2.48	2.58	2.48	2.64	2.45	1.00	up	9.28E-01	9.79E-01	-	-
1377415_at	---	---	---	Rn.170577	BE096334	2.35	2.34	2.37	2.34	2.36	2.34	1.00	down	5.93E-01	8.95E-01	-	-
1379890_at	---	---	---	Rn.203288	AI547434	2.33	2.32	2.34	2.33	2.34	2.32	1.00	down	4.86E-01	8.95E-01	-	-
1379479_at	Klf4	kinesin family member 4	84393	Rn.22652	AA859926	2.31	2.30	2.32	2.31	2.32	2.29	1.00	down	4.65E-01	8.95E-01	-	-
1395876_at	---	---	---	Rn.172112	AW920646	2.57	2.57	2.62	2.61	2.61	2.55	1.00	up	8.26E-01	9.45E-01	-	-
1391051_at	---	---	---	Rn.12796	AA997873	2.32	2.31	2.33	2.31	2.32	2.30	1.00	down	4.58E-01	8.95E-01	-	-
1392609_at	---	---	---	Rn.120197	AI030518	2.30	2.29	2.30	2.29	2.30	2.28	1.00	down	3.40E-01	8.95E-01	-	-
1392319_at	RGD1564983	similar to leucine rich repeat containing 10	309208	Rn.45191	BE107672	2.30	2.29	2.30	2.30	2.30	2.28	1.00	down	4.19E-01	8.95E-01	-	-
1379276_at	---	---	---	Rn.203259	AW919982	2.72	2.74	2.71	2.70	2.76	2.70	1.00	down	7.76E-01	9.27E-01	-	-
1394404_at	Stim4	stromal interaction molecule 4	308392	Rn.137083	BF390948	2.39	2.34	2.37	2.36	2.37	2.35	1.00	down	6.78E-01	9.02E-01	-	-
1373696_at	RGD1564859	RGD1564859	362536	Rn.7615	AI171656	2.42	2.41	2.44	2.43	2.44	2.42	1.00	up	6.01E-01	8.95E-01	-	-
1377927_at	---	---	---	Rn.204340	AI228258	2.32	2.31	2.32	2.31	2.32	2.30	1.00	down	3.79E-01	8.95E-01	-	-
1386956_at	Scarb1	scavenger receptor class B, member 1	25073	Rn.88169	NM_031541	2.37	2.36	2.38	2.37	2.38	2.35	1.00	down	5.43E-01	8.95E-01	-	-
1379643_at	Cyp19a1	cytochrome P450, family 19, subfamily a, polypeptide 1	25147	Rn.21402	AI407180	2.36	2.35	2.37	2.35	2.37	2.34	1.00	down	5.38E-01	8.95E-01	-	-
1379593_at	Olig2	oligodendrocyte lineage transcription factor 2	304103	Rn.22121	AI007666	2.38	2.40	2.39	2.38	2.39	2.38	1.00	down	3.90E-01	8.95E-01	-	-
1392817_at	---	---	---	Rn.78244	AI044553	2.35	2.35	2.36	2.35	2.36	2.33	1.00	down	5.52E-01	8.95E-01	-	-
1390082_at	Hip1	huntingtin interacting protein 1	192154	Rn.836	BE110671	2.27	2.29	2.27	2.27	2.28	2.26	1.00	down	5.67E-01	8.95E-01	-	-
1382988_at	---	---	---	---	AI231651	2.52	2.48	2.54	2.50	2.53	2.49	1.00	down	7.87E-01	9.31E-01	-	-
1387725_at	Gulo	gulonolactone (L-) oxidase	60671	Rn.115212	NM_022220	2.30	2.30	2.31	2.30	2.31	2.29	1.00	down	3.73E-01	8.95E-01	-	-
1376224_at	Elfn2	extracellular leucine-rich repeat and fibronectin type III domain containing 2	315117	Rn.93288	BE106971	2.34	2.33	2.35	2.34	2.34	2.33	1.00	down	3.96E-01	8.95E-01	-	-
1378676_at	---	---	---	Rn.172697	BF406322	2.38	2.37	2.39	2.41	2.38	2.36	1.00	up	7.24E-01	9.13E-01	-	-
1392646_at	Ano4	anoctamin 4	299714	Rn.23908	BE107837	2.41	2.40	2.42	2.40	2.42	2.39	1.00	down	5.91E-01	8.95E-01	-	-
1369752_a_at	Camk4	calcium/calmodulin-dependent protein kinase IV	25050	Rn.11046	J04446	2.37	2.36	2.38	2.36	2.37	2.35	1.00	down	5.34E-01	8.95E-01	-	-
1371897_at	Pyapdc3	phosphatidic acid phosphatase type 2 domain containing 3	296635	Rn.24087	AI175375	2.45	2.40	2.43	2.42	2.43	2.42	1.00	down	7.28E-01	9.13E-01	-	-
1393742_at	Smc1b	structural maintenance of chromosomes 1B	300121	Rn.56972	BF389603	2.44	2.43	2.45	2.44	2.44	2.42	1.00	down	5.26E-01	8.95E-01	-	-
1389899_at	Pvrl2	Poliovirus receptor-related 2	308417	Rn.203297	BE102426	2.36	2.35	2.36	2.35	2.36	2.34	1.00	down	4.32E-01	8.95E-01	-	-
1369802_at	Kcna3	potassium voltage-gated channel, shaker-related subfamily, member 3	29731	Rn.44292	NM_019270	2.35	2.35	2.37	2.35	2.36	2.34	1.00	down	5.32E-01	8.95E-01	-	-
1370841_a_at	Gh1	growth hormone 1	24391	Rn.146351	V01238	2.33	2.32	2.34	2.33	2.33	2.32	1.00	down	4.40E-01	8.95E-01	-	-
1391576_at	---	---	---	Rn.26820	AI112211	2.33	2.31	2.33	2.31	2.33	2.31	1.00	down	5.01E-01	8.95E-01	-	-
1382652_at	Il27ra	interleukin 27 receptor, alpha	288905	Rn.47680	BF287629	2.30	2.30	2.33	2.30	2.32	2.29	1.00	down	6.48E-01	8.95E-01	-	-
1393111_at	---	---	---	---	AW524426	2.40	2.38	2.40	2.39	2.40	2.37	1.00	down	5.43E-01	8.95E-01	-	-
1371939_at	Caprin1	cell cycle associated protein 1	362173	Rn.22572	AI171369	9.31	9.13	9.00	9.09	9.20	9.13	1.00	down	9.51E-01	9.86E-01	-	-
1396710_at	---	---	---	Rn.146744	BF417339	2.30	2.29	2.33	2.29	2.32	2.29	1.00	down	6.88E-01	9.04E-01	-	-
1398142_at	---	---	---	Rn.205463	AI783899	2.37	2.36	2.38	2.36	2.37	2.35	1.00	down	4.95E-01	8.95E-01	-	-
1392625_at	---	---	---	Rn.168303	AI578406	2.45	2.44	2.48	2.45	2.46	2.45	1.00	down	6.09E-01	8.95E-01	-	-
1380814_at	---	---	---	---	AI599431	2.44	2.45	2.44	2.44	2.45	2.43	1.00	down	2.86E-01	8.95E-01	-	-
1391992_at	---	---	---	Rn.205310	AI639517	2.37	2.37	2.38	2.37	2.37	2.36	1.00	down	3.52E-01	8.95E-01	-	-
1369326_at	Akap6	A kinase (PRKA) anchor protein 6	64553	Rn.147642	NM_022618	2.38	2.37	2.39	2.37	2.38	2.36	1.00	down	5.11E-01	8.95E-01	-	-
1396061_at	---	---	---	Rn.205229	AI511079	2.38	2.36	2.40	2.37	2.38	2.37	1.00	down	6.15E-01	8.95E-01	-	-
1392440_at	---	---	---	---	AI072122	2.37	2.37	2.39	2.40	2.41	2.34	1.00	up	7.98E-01	9.35E-01	-	-
1385115_at	Nephn	nephrocan	309775	Rn.42078	AI548039	2.35	2.34	2.36	2.35	2.36	2.33	1.00	down	5.41E-01	8.95E-01	-	-
1395200_at	---	---	---	Rn.148474	AI549281	2.45	2.45	2.47	2.45	2.46	2.44	1.00	down	5.21E-01	8.95E-01	-	-
1383041_x_at	---	---	---	Rn.155723	AI044098	6.29	6.07	6.08	6.02	6.21	6.19	1.00	down	9.50E-01	9.86E-01	-	-
1389770_at	Ttll9	tubulin tyrosine ligase-like family, member 9	311548	Rn.138049	BF405468	2.43	2.42	2.43	2.42	2.43	2.41	1.00	down	3.50E-01	8.95E-01	-	-
1378265_at	---	---	---	Rn.203730	BE103245	2.45	2.44	2.47	2.44	2.46	2.44	1.00	down	6.26E-01	8.95E-01	-	-
1380329_at	Opalin	oligodendrocytic myelin paranodal and inner loop protein	361757	Rn.25053	AI717253	2.35	2.34	2.35	2.34	2.36	2.33	1.00	down	5.22E-01	8.95E-01	-	-
1369399_at	Ms4a2	membrane-spanning 4-domains, subfamily A, member 2 (Fc fragment of IgE,	25316	Rn.10922	NM_012845	2.41	2.40	2.43	2.40	2.44	2.38	1.00	down	7.46E-01	9.18E-01	-	-
1374830_at	---	---	---	Rn.30331	AA946242	2.31	2.31	2.32	2.31	2.32	2.30	1.00	down	4.23E-01	8.95E-01	-	-
1398381_at	---	---	---	Rn.21852	BE105417	2.42	2.41	2.43	2.42	2.42	2.41	1.00	down	3.70E-01	8.95E-01	-	-
1385721_at	Spag16	sperm associated antigen 16	501158	Rn.220565	AW534366	2.32	2.31	2.33	2.31	2.32	2.30	1.00	down	5.28E-01	8.95E-01	-	-
1370182_at	Ptpn2	protein tyrosine phosphatase, receptor type, N polypeptide 2	29714	Rn.11044	AI574894	2.35	2.34	2.36	2.35	2.36	2.33	1.00	down	5.07E-01	8.95E-01	-	-
1397827_at	Nanos3	nanos homolog 3 (Drosophila)	288909	Rn.161711	BE112682	2.36	2.37	2.39	2.37	2.38	2.37	1.00	down	4.69E-01	8.95E-01	-	-
1388041_s_at	Nfasc	neurofascin	116690	Rn.3048	AY061639	2.41	2.39	2.42	2.40	2.41	2.39	1.00	down	4.87E-01	8.95E-01	-	-
1398176_at	---	---	---	Rn.200193	BF414017	2.32	2.32	2.33	2.31	2.32	2.31	1.00	down	3.10E-01	8.95E-01	-	-
1378831_at	---	---	---	Rn.207934	BE108135	2.58	2.81	2.71	2.85	2.64	2.63	1.00	up	9.53E-01	9.86E-01	-	-
1392000_at	---	---	---	Rn.205489	BF405192	2.34	2.34	2.35	2.34	2.35	2.33	1.00	down	4.94E-01	8.95E-01	-	-
1386385_at	Etv2	ets variant 2	361544	Rn.50354	BE102623	2.35	2.34	2.37	2.35	2.36	2.33	1.00	down	5.55E-01	8.95E-01	-	-
1377419_at	LOC689128	Hypothetical protein LOC689128	689128	Rn.199057	BE118459	2.47	2.46	2.44	2.47	2.48	2.45	1.00	up	6.12E-01	8.95E-01	-	-
1387309_a_at	Grik1	glutamate receptor, ionotropic, kainate 1	29559	Rn.10449	AI111480	2.35	2.34	2.37	2.34	2.35	2.34	1.00	down	5.20E-01	8.95E-01	-	-
1392755_at	Lrrc8c	leucine rich repeat containing 8 family, member C	289443	Rn.25285	AW920702	2.58	2.57	2.59	2.57	2.58	2.57	1.00	down	4.27E-01	8.95E-01	-	-
1393397_at	Cpa2	carboxypeptidase A2 (pancreatic)	296959	Rn.101694	AI576488	2.45	2.43	2.48	2.44	2.47	2.43	1.00	down	7.45E-01	9.17E-01	-	-
1396782_at	---	---	---	Rn.209860	BF404815	2.34	2.33	2.35	2.33	2.35	2.32	1.00	down	6.10E-01	8.95E-01	-	-
1393084_at	Hrasls	HRAS-like suppressor	288025	Rn.11728	AA964188	2.34	2.33	2.35	2.34	2.35	2.32	1.00	down	5.63E-01	8.95E-01	-	-
1392787_at	---	---	---	Rn.22135	AI137845	2.47	2.46	2.49	2.47	2.47	2.46	1.00	down	5.19E-01	8.95E-01	-	-
1384974_at	LOC691024	similar to Protein C9orf25 homolog	691024	Rn.158904	BI283852	2.40	2.39	2.41	2.40	2.41	2.39	1.00	down	4.64E-01	8.95E-01	-	-
1396582_at	---	---	---	Rn.216898	BE120655	2.31	2.33	2.31	2.31	2.31	2.31	1.00	down	2.74E-01	8.95E-01	-	-
1369460_at	Slc7a2	solute carrier family 7 (cationic amino acid transporter, y+ system), member 2	64554	Rn.48707	NM_022619	2.40	2.39	2.41	2.39	2.40	2.38	1.00	down	5.50E-01	8.95E-01	-	-
1379841_a_at	---	---	---	Rn.204573	AI137292	4.17	3.44	3.97	3.98	3.71	3.91	1.00	up	9.80E-01	9.94E-01	-	-
1369183_at	Mapk13	mitogen activated protein kinase 13	29513	Rn.207196	NM_019231	2.37	2.36	2.37	2.36	2.37	2.36	1.00	down	4.19E-01	8.95E-01	-	-
1381997_at	Adipoq	adiponectin, C1Q and collagen domain containing	246253	Rn.24299	BM386227	2.33	2.32	2.34	2.33	2.34	2.31	1.00	down	5.14E-01	8.95E-01	-	-
1397048_at	---	---	---	Rn.79721	BI295581	2.34	2.34	2.36	2.34	2.35	2.33	1.00	down	4.76E-01	8.95E-01	-	-
1379760_at	Tnfaip8l2	tumor necrosis factor, alpha-induced protein 8-like 2	310663	Rn.35002	AI454285	2.54	2.53	2.54	2.53	2.54	2.52	1.00	down	4.25E-01	8.95E-01	-	-
1380644_at	---	---	---	Rn.172971	AI178542	2.44	2.41	2.45	2.46	2.44	2.42	1.00	up	7.10E-01	9.09E-01	-	-
1396330_at	---	---	---	Rn.148796	AW526516	2.40	2.40	2.42	2.40	2.42	2.38	1.00	down	6.33E-01	8.95E-01	-	-
1381665_at	---	---	---	Rn.207290	BF410498	2.44	2.43	2.45	2.44	2.45	2.43	1.00	down	4.33E-01	8.95E-01	-	-
1380949_at	---	---	---	---	BF409919	2.39	2.40	2.40	2.39	2.39	2.38	1.00	down	2.77E-01	8.95E-01	-	-
1395335_at	---	---	---	Rn.199163	BF544005	2.40	2.38	2.41	2.39	2.40	2.38	1.00	down	6.25E-01	8.95E-01	-	-
1380700_at	Arhgap27	Rho GTPase activating protein 27	303583	Rn.17895	BM391868	2.30	2.30	2.31	2.30	2.30	2.29	1.00	down	4.11E-01	8.95E-01	-	-
1368773_at	Cenpi	centromere protein I	25448	Rn.10411	NM_012955	2.35	2.34	2.36	2.35	2.36	2.33	1.00	down	5.46E-01	8.95E-01	-	-
1376898_at	---	---	---	Rn.22515	AI172467	2.61	2.61	2.61	2.60	2.64	2.60	1.00	up	6.68E-01	9.00E-01	-	-
1385328_at	---	---	---	Rn.165131	AA957612	2.36	2.35	2.37	2.35	2.37	2.34	1.00	down	5.88E-01	8.95E-01	-	-
1391068_at	E030032D13Rik	E030032D13Rik gene	415052	---	AI136523	2.29	2.28	2.30	2.29	2.32	2.28	1.00	up	6.78E-01	9.02E-01	-	-
1384306_at	Elk3	ELK3, member of ETS oncogene family	362871	Rn.196088	BE110960	2.40	2.39	2.42	2.40	2.41	2.39	1.00	down	4.86E-01	8.95E-01	-	-
1376253_at	Ly6h	lymphocyte antigen 6 complex, locus H	300025	Rn.7534	AW434178	2.28	2.27	2.29	2.27	2.28	2.27	1.00	down	3.74E-01	8.95E-01	-	-
1378589_at	---	---	---	Rn.86546	BG378163	2.34	2.33	2.34	2.33	2.34	2.32	1.00	down	3.62E-01	8.95E-01	-	-
1388747_at	Lcmt1	leucine carboxyl methyltransferase 1	361643	Rn.162464	BG381002	8.97	8.58	8.42	8.50	8.55	8.91	1.00	down	9.78E-01	9.93E-01	-	-
1398489_at	---	---	---	Rn.216944	BF400830	2.35	2.34	2.37	2.35	2.35	2.34	1.00	down	5.22E-01	8.95E-01	-	-
1391244_at	---	---	---	---	BF386142	2.32	2.32	2.33	2.32	2.33	2.31	1.00	down	4.20E-01	8.95E-01	-	-
1378971_at	Mll6	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila);	303504	Rn.25100	AW435316	2.52	2.52	2.51	2.49	2.53	2.49	1.00	down	6.85E-01	9.03E-01	-	-
1368624_at	Asip	agouti signaling protein	24152	Rn.205372	NM_052979	2.31	2.31	2.32	2.31	2.32	2.30	1.00	down	4.58E-01	8.95E-01	-	-
1387471_at	Cela2a	chymotrypsin-like elastase family, member 2A	24332	Rn.10272	NM_012553	2.42	2.40	2.43	2.41	2.42	2.40	1.00	down	6.01E-01	8.95E-01	-	-
1393785_at	RGD1305311	similar to hypothetical protein FLJ22527	316616	Rn.163088	BE110326	2.37	2.36	2.38	2.36	2.37	2.36	1.00	down	4.49E-01	8.95E-01	-	-
1369390_a_at	Dpp6	dipeptidylpeptidase 6	29272	Rn.10076	NM_022850	2.30	2.29	2.31	2.30	2.30	2.29	1.00	down	4.47E-01	8.95E-01	-	-
1380359_at	---	---	---	Rn.203736	BM385856	2.33	2.32	2.34	2.33	2.33	2.31	1.00	down	4.35E-01	8.95E-01	-	-
1383761_at	---	---	---	Rn.203311	AA996729	2.41	2.40	2.41	2.40	2.41	2.39	1.00	down	3.84E-01	8.95E-01	-	-
1383923_at	---	---	---	Rn.24298	BF410662	2.40	2.39	2.41	2.39	2.40	2.38	1.00	down	4.67E-01	8.95E-01	-

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1383413_at	Hhatl	hedgehog acyltransferase-like	301073	Rn.22829	AW531481	2.45	2.43	2.46	2.44	2.46	2.43	1.00	down	6.46E-01	8.95E-01	-	-
1378341_at	---	---	---	Rn.29890	AI101125	2.49	2.45	2.51	2.47	2.52	2.47	1.00	up	8.06E-01	9.38E-01	-	-
1391531_at	LOC691729	similar to spermatogenesis associated 5-like 1	691729	Rn.151898	BF561981	2.47	2.44	2.48	2.46	2.49	2.45	1.00	up	7.15E-01	9.10E-01	-	-
1368853_at	Vsnl1	visinin-like 1	24877	Rn.105934	AI227991	2.41	2.40	2.43	2.40	2.42	2.40	1.00	down	6.50E-01	8.96E-01	-	-
1382621_at	Wdr40b	WD repeat domain 40B	313296	Rn.24270	AI454799	2.34	2.33	2.35	2.34	2.35	2.32	1.00	down	5.22E-01	8.95E-01	-	-
1387988_at	Hsd3b6	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 6	29632	Rn.109394	L17138	2.39	2.37	2.39	2.38	2.39	2.36	1.00	down	5.75E-01	8.95E-01	-	-
1391788_at	---	---	---	Rn.205182	BF406814	2.31	2.30	2.33	2.30	2.32	2.30	1.00	down	5.60E-01	8.95E-01	-	-
1395891_at	---	---	---	Rn.34008	AI535546	2.35	2.34	2.36	2.34	2.35	2.33	1.00	down	4.58E-01	8.95E-01	-	-
1369011_at	Apoa5	apolipoprotein A-V	140638	Rn.48763	AF202888	2.28	2.28	2.28	2.28	2.28	2.26	1.00	down	2.43E-01	8.95E-01	-	-
1373654_at	Anxa8	annexin A8	306283	Rn.104026	BM389254	2.28	2.28	2.29	2.28	2.28	2.27	1.00	down	3.30E-01	8.95E-01	-	-
1397374_at	---	---	---	Rn.31722	AI237634	2.35	2.33	2.35	2.34	2.35	2.32	1.00	down	5.77E-01	8.95E-01	-	-
1387984_at	Ckif	chemokine-like factor	245978	Rn.81197	AF253065	2.48	2.45	2.46	2.46	2.49	2.45	1.00	up	6.57E-01	8.98E-01	-	-
1374330_at	Kel	Kell blood group, metallo-endopeptidase	297025	Rn.163642	AI179459	2.31	2.31	2.32	2.31	2.32	2.30	1.00	down	3.62E-01	8.95E-01	-	-
1393876_at	Hoxc5	homeo box C5	315341	Rn.152771	AA956024	2.31	2.30	2.32	2.30	2.31	2.30	1.00	down	4.11E-01	8.95E-01	-	-
1395063_at	Mrpl14	Mitochondrial ribosomal protein L14	301250	Rn.35669	AA851300	2.30	2.29	2.32	2.30	2.31	2.29	1.00	down	5.67E-01	8.95E-01	-	-
1396911_at	---	---	---	Rn.41314	AI715502	2.32	2.31	2.33	2.32	2.33	2.30	1.00	down	5.74E-01	8.95E-01	-	-
1388179_at	Acvr2b	activin A receptor, type IIB	25366	Rn.24240	AI548799	2.41	2.73	2.36	2.46	2.47	2.59	1.00	up	9.84E-01	9.90E-01	-	-
1384105_at	Znf830	Zinc finger protein 830	497967	Rn.137587	BE109571	2.44	2.41	2.43	2.42	2.44	2.40	1.00	down	7.10E-01	9.09E-01	-	-
1369252_a_at	Chrna4	cholinergic receptor, nicotinic, alpha 4	25590	Rn.9697	L31620	2.38	2.37	2.38	2.37	2.38	2.36	1.00	down	4.41E-01	8.95E-01	-	-
1397475_at	Papolg	poly(A) polymerase gamma	305586	Rn.27992	AW530171	2.36	2.37	2.37	2.36	2.36	2.36	1.00	down	1.74E-01	8.95E-01	-	-
1379505_at	Lix1	Lix1 homolog (chicken)	292381	Rn.162409	BG380642	2.32	2.31	2.33	2.31	2.32	2.31	1.00	down	4.05E-01	8.95E-01	-	-
1394955_at	---	---	---	Rn.170916	BF407191	2.39	2.38	2.40	2.39	2.40	2.38	1.00	down	4.51E-01	8.95E-01	-	-
1397309_at	RGD1308907	similar to FLJ20689	314325	Rn.198750	AI408217	2.33	2.32	2.33	2.32	2.33	2.35	1.00	up	4.82E-01	8.95E-01	-	-
1368699_at	Dscam	Down syndrome cell adhesion molecule	171119	Rn.24399	NM_133587	2.37	2.35	2.39	2.36	2.37	2.35	1.00	down	6.98E-01	9.07E-01	-	-
1371285_at	Hoxc4	homeo box C4	24459	Rn.12051	M37567	2.38	2.37	2.39	2.37	2.38	2.36	1.00	down	4.46E-01	8.95E-01	-	-
1395615_at	---	---	---	Rn.49842	BE099150	2.34	2.33	2.35	2.33	2.35	2.33	1.00	down	5.12E-01	8.95E-01	-	-
1395241_at	---	---	---	---	BF389886	2.36	2.35	2.37	2.35	2.36	2.34	1.00	down	5.33E-01	8.95E-01	-	-
1368912_at	Trh	thyrotropin releasing hormone	25569	Rn.22	M12138	2.35	2.34	2.37	2.34	2.35	2.33	1.00	down	5.73E-01	8.95E-01	-	-
1391918_at	---	---	---	Rn.47915	AW532287	2.41	2.43	2.41	2.39	2.49	2.38	1.00	up	8.65E-01	9.58E-01	-	-
1379045_at	---	---	---	Rn.206007	AI639215	2.34	2.32	2.33	2.32	2.33	2.31	1.00	down	4.78E-01	8.95E-01	-	-
1393386_at	Fam183b	family with sequence similarity 183, member B	287346	Rn.23162	BF284080	2.40	2.38	2.41	2.39	2.40	2.38	1.00	down	5.76E-01	8.95E-01	-	-
1369843_at	Chrna1	cholinergic receptor, nicotinic, alpha 1 (muscle)	79557	Rn.44633	NM_024485	2.32	2.32	2.34	2.32	2.33	2.31	1.00	down	4.41E-01	8.95E-01	-	-
1387191_at	Pbsn	probasin	54193	Rn.9862	NM_019125	2.34	2.33	2.35	2.33	2.34	2.32	1.00	down	5.17E-01	8.95E-01	-	-
1369210_at	Scn1a	sodium channel, voltage-gated, type I, alpha	81574	Rn.32079	NM_030875	2.40	2.39	2.41	2.40	2.41	2.38	1.00	down	6.45E-01	8.95E-01	-	-
1370777_at	Ear11	eosinophil-associated, ribonuclease A family, member 11	192264	Rn.10626	D88586	2.44	2.43	2.46	2.43	2.45	2.43	1.00	down	5.60E-01	8.95E-01	-	-
1381177_at	Afap1	actin filament associated protein 1	140935	Rn.208751	BF413483	2.31	2.29	2.31	2.30	2.30	2.29	1.00	down	3.86E-01	8.95E-01	-	-
1378959_at	---	---	---	Rn.141069	BE096415	2.37	2.35	2.39	2.36	2.37	2.36	1.00	down	5.90E-01	8.95E-01	-	-
1369180_at	Bcl2l1	Bcl2-like 1	24888	Rn.10323	NM_031535	2.37	2.40	2.37	2.41	2.37	2.34	1.00	down	8.03E-01	9.37E-01	-	-
1382501_at	RGD1306215	Similar to hypothetical protein MGC36831	296565	Rn.96042	BG375021	2.67	2.57	2.74	2.67	2.77	2.53	1.00	down	9.48E-01	9.85E-01	-	-
1382078_at	---	---	---	---	BF283802	2.38	2.37	2.39	2.37	2.39	2.36	1.00	down	5.83E-01	8.95E-01	-	-
1387088_at	Gal	galanin preproppeptide	29141	Rn.8929	NM_032337	2.37	2.36	2.38	2.36	2.37	2.35	1.00	down	5.53E-01	8.95E-01	-	-
1396482_at	---	---	---	---	BF405754	2.34	2.32	2.35	2.33	2.34	2.32	1.00	down	5.78E-01	8.95E-01	-	-
1389409_at	Tes	testis derived transcript	500040	Rn.44847	AI177869	2.50	2.49	2.53	2.50	2.52	2.49	1.00	down	6.91E-01	9.05E-01	-	-
1378187_at	Dnajc7	DnaJ (Hsp40) homolog, subfamily C, member 7	303536	Rn.92155	BF420102	2.43	2.41	2.44	2.42	2.43	2.40	1.00	down	6.41E-01	8.95E-01	-	-
1392015_at	---	---	---	Rn.200003	BF392359	2.46	2.45	2.46	2.45	2.46	2.44	1.00	down	3.98E-01	8.95E-01	-	-
1370046_at	Polg	polymerase (DNA directed), gamma	85472	Rn.19327	AW435444	2.36	2.35	2.37	2.35	2.36	2.34	1.00	down	5.48E-01	8.95E-01	-	-
1392371_at	---	---	---	Rn.147342	BF393540	2.33	2.33	2.34	2.33	2.34	2.32	1.00	down	4.01E-01	8.95E-01	-	-
1398470_at	LOC689619	similar to nuclear receptor interacting protein 2	689619	Rn.206830	BE104945	2.35	2.34	2.36	2.34	2.35	2.33	1.00	down	4.66E-01	8.95E-01	-	-
1379392_at	Adprhl1	ADP-ribosylhydrolase like 1	290880	Rn.144754	AI105087	2.30	2.29	2.32	2.30	2.30	2.29	1.00	down	4.81E-01	8.95E-01	-	-
1394882_at	Il20rb	interleukin 20 receptor beta	501043	Rn.43407	BF289542	2.31	2.30	2.32	2.30	2.31	2.30	1.00	down	4.00E-01	8.95E-01	-	-
1385489_at	03-Sep	Septin 3	56003	Rn.48803	BI291076	2.28	2.28	2.30	2.28	2.28	2.27	1.00	down	4.37E-01	8.95E-01	-	-
1385692_at	Slc10a4	solute carrier family 10 (sodium/bile acid cotransporter family), member 4	305309	Rn.79638	BI294864	2.36	2.35	2.37	2.36	2.37	2.34	1.00	down	4.96E-01	8.95E-01	-	-
1387380_at	Slc32a1	solute carrier family 32 (GABA vesicular transporter), member 1	83612	Rn.10846	NM_031782	2.33	2.32	2.35	2.33	2.34	2.33	1.00	down	5.60E-01	8.95E-01	-	-
1372341_at	Slc25a36	solute carrier family 25, member 36	501039	Rn.17305	AI233213	5.63	6.23	5.15	5.82	5.28	5.93	1.00	up	9.88E-01	9.96E-01	-	-
1368112_at	Sag	S-antigen; retina and pineal gland (arrestin)	25539	Rn.9856	NM_013023	2.81	2.74	2.79	2.77	2.79	2.77	1.00	down	8.12E-01	9.39E-01	-	-
1390991_at	Hbq1	hemoglobin, theta 1	303007	---	BE113606	2.26	2.25	2.28	2.26	2.26	2.25	1.00	down	4.47E-01	8.95E-01	-	-
1392824_at	Bnipl	BCL2/adenovirus E1B 19kD interacting protein like	361994	Rn.82427	BF417701	2.34	2.33	2.35	2.33	2.34	2.32	1.00	down	4.56E-01	8.95E-01	-	-
1397130_at	---	---	---	Rn.208798	BE102200	2.31	2.31	2.32	2.31	2.32	2.30	1.00	down	3.57E-01	8.95E-01	-	-
1380207_at	---	---	---	Rn.211609	BF289968	2.32	2.31	2.33	2.32	2.33	2.30	1.00	down	4.64E-01	8.95E-01	-	-
1397173_at	RGD1563131	similar to Serine/threonine-protein kinase WNK3 (Protein kinase, lysine-deficie	317420	Rn.31723	BE109095	2.35	2.35	2.38	2.35	2.37	2.34	1.00	down	6.44E-01	8.95E-01	-	-
1368263_a_at	Mobp	myelin-associated oligodendrocyte basic protein	25037	Rn.91185	X90402	2.34	2.34	2.35	2.34	2.35	2.33	1.00	down	5.17E-01	8.95E-01	-	-
1387563_at	Pgr	progesterone receptor	25154	Rn.10303	NM_022847	2.38	2.36	2.38	2.37	2.38	2.36	1.00	down	5.57E-01	8.95E-01	-	-
1369045_at	Rgs14	regulator of G-protein signaling 14	114705	Rn.9795	NM_053764	2.39	2.38	2.38	2.38	2.38	2.37	1.00	down	3.84E-01	8.95E-01	-	-
1375184_at	---	---	---	Rn.35278	BI281837	2.36	2.35	2.36	2.35	2.36	2.34	1.00	down	3.66E-01	8.95E-01	-	-
1390106_at	---	---	---	---	AI574843	2.30	2.29	2.31	2.29	2.30	2.29	1.00	down	4.59E-01	8.95E-01	-	-
1384532_at	---	---	---	Rn.15526	BF556192	2.90	2.89	2.91	2.89	2.90	2.89	1.00	down	4.10E-01	8.95E-01	-	-
1387955_at	Ugt2b5	UDP glucuronosyltransferase 2 family, polypeptide B5	266685	---	M31109	2.51	2.48	2.52	2.50	2.54	2.45	1.00	down	8.47E-01	9.52E-01	-	-
1368028_at	Prph	peripherin	24688	Rn.11086	NM_012633	2.38	2.38	2.39	2.38	2.43	2.36	1.00	up	8.10E-01	9.39E-01	-	-
1394999_at	Lce1d	late cornified envelope 1D	685981	---	BI286074	2.48	2.46	2.50	2.48	2.49	2.48	1.00	up	6.91E-01	9.05E-01	-	-
1384539_at	---	---	---	Rn.171597	BE118695	2.41	2.40	2.42	2.41	2.42	2.39	1.00	down	5.89E-01	8.95E-01	-	-
1375241_at	Mcat	Malonyl CoA-ACP acyltransferase (mitochondrial)	315173	Rn.23115	BF408498	2.37	2.36	2.37	2.36	2.37	2.35	1.00	down	3.63E-01	8.95E-01	-	-
1369136_at	Cyp2a3a	cytochrome P450, family 2, subfamily A, polypeptide 3a	24299	Rn.2063	NM_012542	2.32	2.31	2.32	2.31	2.32	2.30	1.00	down	3.98E-01	8.95E-01	-	-
1370671_at	Gucy2g	guanylate cyclase 2G	245708	Rn.10198	U33847	2.32	2.30	2.32	2.31	2.31	2.30	1.00	down	4.38E-01	8.95E-01	-	-
1368739_s_at	1 /// Cyp11b2 /// C	Cytochrome P450, subfamily 11B, polypeptide 1 /// cytochrome P450, subfamil	24304	Rn.144549	NM_012539	2.33	2.32	2.33	2.32	2.33	2.31	1.00	down	4.59E-01	8.95E-01	-	-
1381709_at	---	---	---	Rn.206901	AW531577	2.33	2.32	2.34	2.32	2.33	2.31	1.00	down	5.34E-01	8.95E-01	-	-
1396581_at	Scyl2	SCY1-like 2 (S. cerevisiae)	314717	Rn.103930	BE103137	2.39	2.74	2.40	2.39	2.78	2.38	1.00	up	9.74E-01	9.92E-01	-	-
1368475_at	Colq	collagen-like tail subunit (single strand of homotrimer) of asymmetric acetylch	29755	Rn.87303	NM_019274	2.26	2.25	2.30	2.26	2.28	2.25	1.00	down	7.43E-01	9.17E-01	-	-
1384656_at	---	---	---	---	AA943596	2.37	2.36	2.38	2.37	2.37	2.36	1.00	down	4.24E-01	8.95E-01	-	-
1380924_at	---	---	---	---	BF395816	2.33	2.32	2.33	2.32	2.33	2.31	1.00	down	4.50E-01	8.95E-01	-	-
1393830_at	Sh2d2a	SH2 domain protein 2A	310688	Rn.9034	AA956603	2.34	2.33	2.35	2.33	2.34	2.33	1.00	down	4.33E-01	8.95E-01	-	-
1384450_at	---	---	---	Rn.134645	AW697717	2.27	2.27	2.28	2.27	2.28	2.30	1.00	up	5.02E-01	8.95E-01	-	-
1372382_at	---	---	---	Rn.204766	AW527165	2.45	2.43	2.46	2.44	2.46	2.42	1.00	down	7.01E-01	9.07E-01	-	-
1380928_at	---	---	---	---	BF390223	2.38	2.38	2.39	2.38	2.39	2.36	1.00	down	5.40E-01	8.95E-01	-	-
1379135_at	Ttll3	tubulin tyrosine ligase-like family, member 3	362415	Rn.198684	BE112728	2.45	2.43	2.46	2.45	2.46	2.42	1.00	down	7.24E-01	9.13E-01	-	-
1371167_at	Mpp3	membrane protein, palmitoylated 3 (MAGUK p55 subfamily member 3)	114202	Rn.144626	AF087697	2.39	2.38	2.40	2.39	2.40	2.38	1.00	down	5.35E-01	8.95E-01	-	-
1370601_a_at	Grin3a	glutamate receptor, ionotropic, N-methyl-D-aspartate 3A	191573	Rn.202958	AF073379	2.37	2.35	2.38	2.36	2.37	2.35	1.00	down	5.62E-01	8.95E-01	-	-
1379586_at	Adamts19	ADAM metalloppeptidase with thrombospondin type 1 motif, 19	361332	Rn.218303	BF564116	2.42	2.40	2.43	2.41	2.43	2.39	1.00	down	7.00E-01	9.07E-01	-	-
1377191_at	Atp5i	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit E	140608	Rn.66347	BI291386	2.42	2.41	2.44	2.41	2.43	2.41	1.00	down	6.43E-01	8.95E-01	-	-
1397420_at	---	---	---	Rn.177865	BM390412	2.37	2.37	2.39	2.37	2.38	2.36	1.00	down	4.69E-01	8.95E-01	-	-
1379920_at	---	---	---	Rn.206697	BG671844	2.49	2.47	2.55	2.48	2.56	2.45	1.00	down	8.86E-01	9.65E-01	-	-
1387992_at	Lilrb3l	leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domai	361493	Rn.207198	AF169637	2.38	2.38	2.39	2.38	2.39	2.36	1.00	down	5.17E-01	8.95E-01	-	-
1389831_at	---	---	---	Rn.212189	BI296721	2.42	2.42	2.42	2.41	2.42	2.40	1.00	down	3.65E-01	8.95E-01	-	-
1394919_at	---	---	---	Rn.204817	BF284043	2.39	2.38	2.40	2.38	2.40	2.37	1.00	down	5.87E-01	8.95E-01	-	-
1368328_at	Gys2	glycogen synthase 2	25623	Rn.2906	NM_013089	2.38	2.38	2.39	2.38	2.39	2.36	1.00	down	5.00E-01	8.95E-01	-	-
1368673_at	Ddr2	discoidin domain receptor tyrosine kinase 2	685781	Rn.92730	NM_031764	2.43	2.42	2.46	2.43	2.44	2.42	1.00	down	6.64E-01	8.99E-01	-	-
1396540_at	---	---	---	Rn.147749	BF419647	2.37	2.36	2.38	2.36	2.41	2.36	1.00	up	7.67E-01	9.24E-01	-	-
1375218_at	---	---	---	Rn.212198	BI291250	2.30	2.29	2.30	2.33	2.30	2.28	1.00	up	6.55E-01	8.97E-01	-	-
1396165_at	Myh6	Myosin, heavy chain 6, cardiac muscle, alpha	29556	Rn.54399	AI601887	2.40	2.38	2.41	2.40	2.43	2.38	1.00	up	7.62E-01	9.22E-01	-	-
1397051_at	---	---	---	Rn.209998	BF392817	2.28	2.28	2.30	2.28	2.29	2.27	1.00	down	4.11E-01	8.95E-01	-	-
1392794_at	---	---	---	Rn.148291	AA893579	2.36	2.35	2.38	2.35	2.38	2.34	1.00	down	7.12E-01	9.10E-01	-	-
1368345_at	Map6	microtubule-associated protein 6	29457	Rn.37490	NM_017204	2.49	2.51	2.46	2.49	2.51	2.48	1.00	up	7.67E-01	9.24E-01	-	-
1387252_at	Sec14l2	SEC14-like 2 (S. cerevisiae)	116486	Rn.46850	NM_053801	2.40	2.39	2.41	2.40	2.41	2.38	1.00	down	5.33E-01	8.95E-01	-	-
1396413_at	---	---	---	Rn.53271	BE119473	2.37	2.36	2.38	2.36	2.37	2.35	1.00	down	5.17E-01	8.95E-01	-	-
1397050_at	Cpne8	copine VIII	362988	Rn.11746	BE102830	2.37	2.36	2.39	2.37	2.38	2.35	1.00	down	6.27E-01	8.95E-01	-	-
1393442_at	---	---	---	Rn.20648	AI071817	2.30	2.30	2.31	2.30	2.31	2.29	1.00	down	4.05E-01	8.95E-01	-	-
1370831_at	Reg3g	regenerating islet-derived 3 gamma	24620	Rn.9729	L20869	2.30	2.30	2.31	2.30	2.31	2.29	1.00	down	4.59E-01	8.95E-01	-	-
1374250_at	---	---	---	Rn.79816	BI291291	2.35	2.34	2.36	2.34	2.35	2.33	1.00	down	5.28E-01	8.95E-01	-	-
1392147_at	---	---	---	Rn.132094	BG374840	2.31	2.30	2.31	2.30	2.31	2.29	1.00	down	4.46E-01	8.95E-01	-	-
1383034_at	Rybp	RING1 and YY1 binding protein	312603	Rn.33148	AA998572	2.69	2.73	2.74	2.70	2.79	2.69	1.00	up	8.72E-01	9.60E-01	-	-
1370889_at	Cyp4v3	cytochrome P450, family 4, subfamily v, polypeptide 3	266761	Rn.201722	AI170346	2.33	2.32	2.35	2.32	2.34	2.31	1.00	down	6.44E-01	8.95E-01	-	-
1385421_at	RGD1563263	similar to RIKEN cDNA 1700029I15	499836	Rn.145601	BF393060	2.38	2.38	2.38	2.37	2.39	2.36	1.00	down	5.82E-01	8.95E-01	-	-
1397025_at	---	---	---	Rn.207966	BF400595	2.33	2.32	2.34	2.32	2.33	2.32	1.00	down	3.79E-01	8.95E-01	-	-
1381054_at	Nlp	ninein-like	311529	Rn.60010	BI275310	2.31	2.30	2.32	2.31	2.31	2.30	1.00	down	4.58E-01	8.95E-01	-	-
1384503_at	Klk8	kallikrein related-peptidase 8	308565	Rn.77746	BI282567	2.48	2.47	2.49	2.47	2.48	2.47	1.00	down	5.08E-01	8.95E-01	-	-
1375075_at	---	---	---	Rn.212203	BI300000	2.34	2.32	2.35	2.33	2.35	2.32	1.00	down	6.09E-01	8.95E-01	-	-
1387564_at	Slc8a2	solute carrier family 8 (sodium/calcium exchanger), member 2	140447	Rn.10305	NM_078619	2.34	2.33	2.34	2.33	2.34	2.32	1.00	down	4.28E-01	8.95E-01	-	-
1378910_at	---	---	---	Rn.206110	BG378480	2.37	2.36	2.37	2.37	2.37	2.35	1.00	down	4.41E-01	8.95E-01	-	-
1385731_at	---	---	---	Rn.152120	BE113552	2.37	2.35	2.38	2.37	2.37	2.35	1.00	down	6.35E-01	8.95E-01	-	-
1391698_at	MAST1	microtubule associated serine/threonine kinase 1	353118	Rn.161721	AI072348	2.35	2.34	2.36	2.35	2.36	2.33	1.00	down	5.59E-01	8.95E-01	-	-
1394657_at	Nr2c1	Nuclear receptor subfamily 2, group C, member 1	252924	Rn.79804	BM386387	2.31	2.31	2.33	2.31	2.32	2.31	1.00	down	5.32E-01	8.95E-01	-	-
1369753_at	Camk4	calcium/calmodulin-dependent protein kinase IV	25050	Rn.11046	M63334	2.30	2.29	2.31	2.29	2.30	2.29	1.00	down	3.88E-01	8.95E-01	-	-
1398159_at	Klf5	Kruppel-like factor 5	84410	Rn.8954	BM389817	2.39	2.42	2.41	2.40	2.41	2.40	1.00	down	5.31E-01	8.95E-01	-	-
1384709_at	---	---	---	---	AA800711	2.35	2.35	2.37	2.35	2.36	2.34	1.00	down	5.60E-01	8.95E-01	-	-
1380801_at	---	---	---	Rn.63341	BF417999	2.45	2.43	2.45	2.44	2.43	2.43	1.00	down	3.35E-01	8.95E-01	-	-
1396997_at	---	---	---	Rn.200097	BF399577	2.34	2.33	2.35	2.36	2.35	2.33	1.00	up	5.35E-01	8.95E-01	-	-
1391943_at	---	---	---	Rn.57975	BF393061	2.36	2.35	2.37	2.35	2.36	2.34	1.00	down	4.31E-01	8.95E-01	-	-
1395668_at	Znf593	Zinc finger protein 593	298546	Rn.147537	BF404249	2.34	2.33	2.35	2.34	2.35	2.33	1.00	down	5.18E-01	8.95E-01	-	-
1395096_at	---	---	---	Rn.26526	BE098725	2.34	2.34	2.35	2.34	2.35	2.33	1.00	down	4.94E-01	8.95E-01	-	-
1370667_at	Slc9a4	solute carrier family 9 (sodium/hydrogen exchanger), member 4	24785	Rn.9707	M85301	2.35	2.34	2.36	2.34	2.36	2.33	1.00	down	5.65E-01	8.95E-01	-	-
1389816_at	Endog	endonuclease G	362100	Rn.3807	AA926357	2.37	2.36	2.37	2.35	2.37	2.36	1.00	down	3.34E-01	8.95E-01	-	-
1368108_at	Atp2a1	ATPase, Ca++ transporting, cardiac muscle, fast twitch 1	116601	Rn.218029	NM_058213	2.25	2.25	2.27	2.25	2.25	2.25	1.00	down	3.46E-01	8.95E-01	-	-
1392053_at	Mmm1	multimerin 1	500152	Rn.43194	AI639113	2.34	2.34	2.35	2.34	2.35	2.33	1.00	down	5.18E-01	8.95E-01	-	-
1390004_at	---	---	---	Rn.212021	BI291316	2.37	2.36	2.38	2.36	2.37	2.35	1.00	down	5.32E-01	8.95E-01	-	-
1396851_at	---	---	---	Rn.147194	AI556089	2.34	2.33	2.35	2.33	2.34	2.32	1.00	down	5.16E-01	8.95E-01	-	-
1396857_at	---	---	---	Rn.155893	AW140998	2.34	2.33	2.35	2.33	2.35	2.35	1.00	up	4.32E-01	8.95E-01	-	-
1371079_at	Fcgr2b	Fc fragment of IgG, low affinity IIb, receptor (CD32)	289211	Rn.33323	X73371	2.46	2.44	2.48	2.45	2.47	2.44	1.00	down	7.12E-01	9.10E-01	-	-
1371829_at	Nrl	neural retina leucine zipper	290221	Rn.19691	BG371822	2.30	2.29	2.31	2.29	2.30	2.29	1.00	down	3.49E-01	8.95E-01	-	-
1389005_at	Ipl6k2	inositol hexakisphosphate kinase 2	59268	Rn.112574	BI282843	3.11	3.61	2.93	3.18	3.18	3.10	1.00	up	9.79E-01	9.94E-01	-	-
1398571_x_at	LOC685249	hypothetical protein LOC685249	685249	Rn.201713	AI101732	2.34	2.33	2.34	2.34	2.34	2.32	1.00	down	4.81E-01	8.95E-01	-	-
1381606_at	Strа6	stimulated by retinoic acid gene 6	363071	Rn.12735	AI044428	2.58	2.57	2.60	2.57	2.61	2.55	1.00	down	7.70E-01	9.25E-01	-	-
1376264_at	---	---	---	Rn.92582	AW526697	2.37	2.36	2.39	2.37	2.38	2.36	1.00	down	5.89E-01	8.95E-01	-	-
1397962_at	---	---	---	---	BF405788	2.56	2.50	2.59	2.52	2.65	2.47	1.00	down	9.27E-01	9.79E-01	-	-
1391420_at	---	---	---	Rn.203688	AA964818

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1395443_at	---	---	---	Rn.210215	BF396088	2.46	2.45	2.47	2.45	2.47	2.45	1.00	down	5.75E-01	8.95E-01	-	-
1379331_at	Tnn	tenascin N	304913	Rn.3715	AA965084	2.33	2.33	2.34	2.33	2.33	2.31	1.00	down	4.65E-01	8.95E-01	-	-
1380356_at	Slc39a2	solute carrier family 39 (zinc transporter), member 2	305846	Rn.51972	BE110209	2.30	2.29	2.31	2.30	2.34	2.29	1.00	up	7.48E-01	9.18E-01	-	-
1370028_at	Ace	angiotensin I converting enzyme (peptidyl-dipeptidase A) 1	24310	Rn.10149	AF201331	2.34	2.33	2.35	2.34	2.34	2.33	1.00	down	4.26E-01	8.95E-01	-	-
1392751_at	Fndc3c1	fibronectin type III domain containing 3C1	317224	Rn.18216	AI029410	2.38	2.37	2.42	2.37	2.42	2.36	1.00	down	8.29E-01	9.46E-01	-	-
1396667_at	---	---	---	Rn.51596	BE110325	2.42	2.41	2.43	2.41	2.44	2.40	1.00	down	6.68E-01	9.00E-01	-	-
1394245_at	---	---	---	Rn.130910	H31734	2.39	2.39	2.41	2.39	2.40	2.38	1.00	down	5.60E-01	8.95E-01	-	-
1379517_at	---	---	---	Rn.199537	AI716595	2.35	2.34	2.36	2.35	2.35	2.34	1.00	down	4.76E-01	8.95E-01	-	-
1390694_at	---	---	---	Rn.140405	BF391611	2.33	2.32	2.33	2.32	2.33	2.31	1.00	down	4.79E-01	8.95E-01	-	-
1367615_at	Sva5	seminal vesicle secretory protein 5	171027	Rn.9941	NM_133516	2.44	2.42	2.45	2.43	2.46	2.42	1.00	down	7.28E-01	9.13E-01	-	-
1391981_at	---	---	---	Rn.206005	AI639181	2.52	2.52	2.61	2.55	2.55	2.53	1.00	down	8.57E-01	9.55E-01	-	-
1378195_at	Des	Desmin	64362	Rn.39196	AI574951	2.31	2.30	2.32	2.30	2.31	2.30	1.00	down	3.69E-01	8.95E-01	-	-
1374246_at	---	---	---	Rn.146581	BF402392	2.34	2.32	2.34	2.33	2.34	2.32	1.00	down	5.01E-01	8.95E-01	-	-
1394892_at	Igfl3	IGF-like family member 3	361516	Rn.17980	AI779741	2.30	2.30	2.31	2.30	2.31	2.29	1.00	down	3.60E-01	8.95E-01	-	-
1390397_at	RGD1310753	similar to chromosome 20 open reading frame 39	362235	Rn.162709	BF413152	2.28	2.27	2.28	2.27	2.28	2.27	1.00	down	2.92E-01	8.95E-01	-	-
1380968_at	---	---	---	Rn.207481	BE101985	2.33	2.32	2.34	2.32	2.33	2.31	1.00	down	5.58E-01	8.95E-01	-	-
1376956_at	---	---	---	Rn.171004	BE106664	2.34	2.33	2.35	2.33	2.34	2.32	1.00	down	5.16E-01	8.95E-01	-	-
1377278_at	---	---	---	Rn.203598	AA957384	2.30	2.30	2.32	2.30	2.31	2.29	1.00	down	4.52E-01	8.95E-01	-	-
1397126_at	---	---	---	Rn.202037	BF403942	2.43	2.42	2.43	2.41	2.43	2.42	1.00	down	5.09E-01	8.95E-01	-	-
1392345_at	---	---	---	Rn.216029	BF387482	2.31	2.30	2.31	2.30	2.30	2.30	1.00	down	3.37E-01	8.95E-01	-	-
1370106_at	Fgf18	fibroblast growth factor 18	29369	Rn.44478	NM_019199	2.36	2.35	2.37	2.35	2.36	2.34	1.00	down	5.17E-01	8.95E-01	-	-
1370342_at	Kcnk2	potassium channel, subfamily K, member 2	170899	Rn.21984	AF385402	2.41	2.39	2.42	2.40	2.41	2.39	1.00	down	5.34E-01	8.95E-01	-	-
1369735_at	Gas6	growth arrest specific 6	58935	Rn.52228	NM_057100	2.40	2.39	2.40	2.40	2.40	2.38	1.00	down	5.20E-01	8.95E-01	-	-
1368489_at	Ins3	insulin receptor substrate 3	84021	Rn.9751	NM_032074	2.31	2.30	2.32	2.30	2.31	2.29	1.00	down	5.26E-01	8.95E-01	-	-
1395930_at	---	---	---	Rn.66260	BI299765	2.29	2.27	2.29	2.28	2.28	2.27	1.00	down	3.73E-01	8.95E-01	-	-
1388092_at	Olr1493	olfactory receptor gene Olr1493	363640	Rn.111156	M64387	2.27	2.26	2.28	2.26	2.28	2.26	1.00	down	4.86E-01	8.95E-01	-	-
1394858_at	---	---	---	Rn.166863	AI145089	2.30	2.29	2.32	2.30	2.31	2.29	1.00	down	5.06E-01	8.95E-01	-	-
1396816_at	---	---	---	Rn.169773	BE107655	2.34	2.34	2.35	2.34	2.35	2.33	1.00	down	4.67E-01	8.95E-01	-	-
1371110_at	LOC287004	Mg1 protein	287004	Rn.69588	AY035343	2.55	2.52	2.54	2.53	2.54	2.52	1.00	down	6.33E-01	8.95E-01	-	-
1397091_at	---	---	---	Rn.149089	BF411156	2.45	2.45	2.46	2.44	2.45	2.44	1.00	down	2.10E-01	8.95E-01	-	-
1390895_at	LOC302495	hypothetical LOC302495	302495	Rn.204468	AA957047	7.15	6.71	6.52	6.91	6.46	7.02	1.00	up	9.83E-01	9.95E-01	-	-
1382746_s_at	---	---	---	Rn.207980	BE108581	2.36	2.36	2.38	2.36	2.37	2.36	1.00	down	5.21E-01	8.95E-01	-	-
1374776_at	Vash2	vasohibin 2	498309	Rn.13814	BG380430	2.35	2.34	2.37	2.35	2.36	2.34	1.00	down	4.97E-01	8.95E-01	-	-
1398329_at	---	---	---	---	BI288821	2.29	2.29	2.30	2.29	2.32	2.29	1.00	up	5.55E-01	8.95E-01	-	-
1386403_at	---	---	---	---	AI639252	2.37	2.35	2.38	2.36	2.37	2.35	1.00	down	6.00E-01	8.95E-01	-	-
1386847_at	---	---	---	---	BF554661	2.37	2.36	2.37	2.36	2.37	2.35	1.00	down	5.54E-01	8.95E-01	-	-
1381218_at	---	---	---	Rn.203718	BF386446	2.28	2.28	2.29	2.28	2.29	2.27	1.00	down	4.41E-01	8.95E-01	-	-
1385738_at	---	---	---	Rn.168798	BE112479	2.48	2.47	2.50	2.49	2.48	2.46	1.00	down	6.63E-01	8.99E-01	-	-
1387251_at	Msmb	microseminoprotein, beta	29311	Rn.10615	NM_019188	2.38	2.37	2.39	2.37	2.43	2.36	1.00	up	7.89E-01	9.32E-01	-	-
1391515_at	---	---	---	Rn.23074	AW916135	2.34	2.33	2.34	2.33	2.34	2.33	1.00	down	3.20E-01	8.95E-01	-	-
1382583_at	---	---	---	Rn.14998	AA899919	2.37	2.36	2.38	2.36	2.38	2.35	1.00	down	6.21E-01	8.95E-01	-	-
1369238_at	Inhbe	inhibin beta E	83711	Rn.30020	NM_031815	2.45	2.43	2.45	2.45	2.46	2.44	1.00	up	6.33E-01	8.95E-01	-	-
1389707_at	---	---	---	Rn.156572	AW251681	2.42	2.41	2.43	2.42	2.44	2.39	1.00	down	6.85E-01	9.03E-01	-	-
1381388_at	Ccdc19	coiled-coil domain containing 19	304984	Rn.137285	BF419626	2.44	2.43	2.45	2.43	2.44	2.43	1.00	down	4.00E-01	8.95E-01	-	-
1384719_at	---	---	---	Rn.148818	AI112966	2.32	2.31	2.33	2.31	2.32	2.30	1.00	down	4.26E-01	8.95E-01	-	-
1379531_at	---	---	---	Rn.160916	BF283384	2.32	2.31	2.33	2.31	2.32	2.30	1.00	down	4.88E-01	8.95E-01	-	-
1380318_at	---	---	---	Rn.159858	BF401102	2.37	2.35	2.38	2.36	2.40	2.36	1.00	up	7.04E-01	9.07E-01	-	-
1387935_at	Il3ra	interleukin 3 receptor, alpha	246144	Rn.144673	AF030243	4.28	4.22	4.23	4.23	4.23	4.35	1.00	down	9.32E-01	9.81E-01	-	-
1394403_at	Spata20	spermatogenesis associated 20	360604	Rn.50006	BI289580	2.36	2.34	2.36	2.34	2.36	2.34	1.00	down	5.06E-01	8.95E-01	-	-
1375949_at	---	---	---	---	BF391673	2.34	2.32	2.34	2.33	2.33	2.32	1.00	down	4.49E-01	8.95E-01	-	-
1396962_at	---	---	---	Rn.212681	BI296196	2.34	2.34	2.35	2.34	2.35	2.33	1.00	down	4.26E-01	8.95E-01	-	-
1375038_at	---	---	---	Rn.216852	AI112199	2.47	2.46	2.49	2.47	2.48	2.46	1.00	down	6.03E-01	8.95E-01	-	-
1370110_at	Kcnk4	potassium channel, subfamily K, member 4	116489	Rn.46453	NM_053804	2.36	2.35	2.37	2.35	2.37	2.34	1.00	down	6.03E-01	8.95E-01	-	-
1396751_at	---	---	---	Rn.35941	AI501450	2.33	2.32	2.34	2.33	2.34	2.32	1.00	down	4.88E-01	8.95E-01	-	-
1370735_at	Olr1278	olfactory receptor 1278	286913	Rn.10792	AF010293	2.34	2.33	2.35	2.33	2.34	2.32	1.00	down	5.34E-01	8.95E-01	-	-
1399160_a_at	Ube2d3	ubiquitin-conjugating enzyme E2D 3 (UBC4/5 homolog, yeast)	81920	Rn.2778	U13177	10.44	10.41	10.76	10.50	10.47	10.62	1.00	down	9.65E-01	9.90E-01	-	-
1371117_at	Adam32	ADAM metallopeptidase domain 32	361170	Rn.170874	AJ131563	2.37	2.36	2.38	2.37	2.38	2.36	1.00	down	5.43E-01	8.95E-01	-	-
1392451_at	---	---	---	---	BI293843	2.26	2.26	2.27	2.26	2.26	2.25	1.00	down	3.72E-01	8.95E-01	-	-
1384291_at	---	---	---	Rn.166850	AI144851	2.40	2.39	2.42	2.40	2.41	2.39	1.00	down	5.87E-01	8.95E-01	-	-
1397166_at	---	---	---	Rn.165580	AI713223	2.33	2.33	2.34	2.33	2.33	2.32	1.00	down	4.20E-01	8.95E-01	-	-
1381787_at	Ngdn	Neuroguidin, Elf4E binding protein	305887	Rn.98692	AI535411	2.31	2.30	2.31	2.30	2.31	2.29	1.00	down	4.60E-01	8.95E-01	-	-
1379440_at	Fstl3	follistatin-like 3 (secreted glycoprotein)	114031	Rn.48835	AW1442239	2.31	2.30	2.31	2.30	2.31	2.30	1.00	down	3.44E-01	8.95E-01	-	-
1377073_at	---	---	---	Rn.160158	BE109756	2.41	2.41	2.42	2.40	2.42	2.41	1.00	down	4.10E-01	8.95E-01	-	-
1370863_at	Krt5	keratin 5	369017	Rn.129725	BF283692	2.43	2.41	2.45	2.42	2.44	2.44	1.00	up	6.48E-01	8.96E-01	-	-
1372818_at	Colec12	collectin sub-family member 12	361289	Rn.31273	BI284441	2.46	2.45	2.47	2.46	2.44	2.44	1.00	down	4.77E-01	8.95E-01	-	-
1380351_at	---	---	---	---	AI137310	2.45	2.44	2.48	2.45	2.47	2.44	1.00	down	7.23E-01	9.12E-01	-	-
1385850_at	---	---	---	---	BE096970	2.36	2.35	2.37	2.36	2.37	2.34	1.00	down	6.06E-01	8.95E-01	-	-
1396831_at	---	---	---	Rn.204533	AI501417	2.37	2.36	2.38	2.36	2.38	2.36	1.00	down	4.81E-01	8.95E-01	-	-
1394195_at	---	---	---	Rn.124931	AI639883	3.96	4.18	3.01	4.03	4.22	4.92	1.00	up	9.90E-01	9.97E-01	-	-
1396823_at	---	---	---	Rn.206957	BF409093	2.37	2.36	2.38	2.36	2.37	2.35	1.00	down	4.47E-01	8.95E-01	-	-
1369375_a_at	Capn3	calpain 3	29155	Rn.9726	AF052540	2.35	2.34	2.36	2.35	2.36	2.33	1.00	down	6.50E-01	8.96E-01	-	-
1392060_at	---	---	---	---	BF414374	2.37	2.35	2.38	2.36	2.38	2.35	1.00	down	6.29E-01	8.95E-01	-	-
1372598_at	RGD1309651	similar to 1190005I06Rik protein	361424	Rn.144207	BE112738	2.32	2.31	2.33	2.32	2.32	2.31	1.00	down	4.02E-01	8.95E-01	-	-
1389213_at	Vash1	vasohibin 1	503052	Rn.137541	AI408955	2.24	2.27	2.24	2.23	2.25	2.25	1.00	down	6.35E-01	8.95E-01	-	-
1373573_at	Pp3111	PP3111 protein	246185	H31907	7.74	8.34	7.58	7.26	8.61	7.82	1.00	up	9.90E-01	9.97E-01	-	-
1382425_at	---	---	---	Rn.149115	AI236482	2.33	2.32	2.34	2.33	2.33	2.32	1.00	down	4.96E-01	8.95E-01	-	-
1383210_at	---	---	---	Rn.165233	BF554576	2.38	2.37	2.39	2.37	2.39	2.36	1.00	down	5.76E-01	8.95E-01	-	-
1378348_at	RGD1561734	similar to KIAA1913	501201	Rn.121539	AI764000	2.45	2.44	2.47	2.45	2.48	2.42	1.00	down	7.80E-01	9.28E-01	-	-
1385189_at	Duoxa1	dual oxidase maturation factor 1	311374	Rn.66838	BG372602	2.30	2.29	2.30	2.29	2.31	2.27	1.00	down	6.06E-01	8.95E-01	-	-
1385628_at	---	---	---	---	BG057544	2.28	2.27	2.29	2.28	2.28	2.26	1.00	down	4.21E-01	8.95E-01	-	-
1378277_at	---	---	---	Rn.167451	BF412939	2.36	2.35	2.38	2.35	2.37	2.34	1.00	down	6.81E-01	9.03E-01	-	-
1377044_at	---	---	---	Rn.107122	AW143175	2.39	2.38	2.40	2.39	2.39	2.38	1.00	down	3.84E-01	8.95E-01	-	-
1397686_at	Psmd9	Proteasome (prosome, macropain) 26S subunit, non-ATPase, 9	161475	Rn.24127	BF566984	2.37	2.37	2.38	2.37	2.37	2.39	1.00	up	3.61E-01	8.95E-01	-	-
1395972_at	---	---	---	---	BI294455	2.40	2.39	2.40	2.39	2.40	2.39	1.00	down	2.91E-01	8.95E-01	-	-
1378657_at	---	---	---	Rn.154185	BF404012	2.37	2.36	2.37	2.36	2.37	2.34	1.00	down	5.67E-01	8.95E-01	-	-
1394600_at	Rgs17	regulator of G-protein signaling 17	308118	Rn.166916	AI146026	2.34	2.33	2.35	2.34	2.35	2.33	1.00	down	4.84E-01	8.95E-01	-	-
1369873_at	Avpr2	arginine vasopressin receptor 2	25108	Rn.209041	NM_019136	2.24	2.24	2.25	2.27	2.25	2.24	1.00	up	5.29E-01	8.95E-01	-	-
1380664_at	---	---	---	---	BF416244	2.32	2.32	2.33	2.32	2.32	2.30	1.00	down	3.94E-01	8.95E-01	-	-
1386955_at	Gp1bb /// Sept5	glycoprotein Ib (platelet), beta polypeptide /// septin 5	116727 /// 116728	Rn.96497	BM387903	2.34	2.33	2.35	2.34	2.35	2.33	1.00	down	5.47E-01	8.95E-01	-	-
1372974_at	---	---	---	Rn.44131	BM384605	2.33	2.31	2.33	2.32	2.33	2.31	1.00	down	4.84E-01	8.95E-01	-	-
1393210_at	---	---	---	---	AI070116	2.33	2.32	2.34	2.33	2.34	2.32	1.00	down	5.04E-01	8.95E-01	-	-
1397733_at	Ogfod2	2-oxoglutarate and iron-dependent oxygenase domain containing 2	288857	Rn.61120	AI578257	2.28	2.27	2.28	2.27	2.28	2.27	1.00	down	4.34E-01	8.95E-01	-	-
1382986_at	Gpam	glycerol-3-phosphate acyltransferase, mitochondrial	29653	Rn.44456	BI288209	2.59	2.58	2.65	2.56	2.67	2.57	1.00	down	8.99E-01	9.69E-01	-	-
1387973_at	Cyp4f4	cytochrome P450, family 4, subfamily f, polypeptide 4	286904	Rn.10170	U39206	2.38	2.36	2.38	2.37	2.38	2.36	1.00	down	5.24E-01	8.95E-01	-	-
1370727_at	Pdgfd	platelet-derived growth factor, D polypeptide	66018	Rn.64493	AB052170	2.40	2.39	2.42	2.40	2.41	2.38	1.00	down	6.50E-01	8.96E-01	-	-
1378622_at	---	---	---	Rn.155667	BE119435	2.35	2.36	2.35	2.39	2.32	2.34	1.00	down	7.86E-01	9.31E-01	-	-
1394685_at	Nudt5	Nudix (nucleoside diphosphate linked moiety X)-type motif 5	361274	Rn.55388	BF286880	2.42	2.40	2.43	2.41	2.45	2.41	1.00	up	7.17E-01	9.10E-01	-	-
1376456_at	Nmnat2	nicotinamide nucleotide adenylyltransferase 2	289095	Rn.145458	BE114264	2.32	2.31	2.33	2.32	2.33	2.31	1.00	down	4.72E-01	8.95E-01	-	-
1391909_at	Ubqln2	ubiquilin 2	317396	Rn.23446	AI072611	2.54	2.53	2.54	2.53	2.54	2.52	1.00	down	3.45E-01	8.95E-01	-	-
1377347_at	Foxj3	forkhead box J3	313556	Rn.202594	AW531892	6.55	7.86	6.41	7.81	7.12	7.88	1.00	down	9.93E-01	9.98E-01	-	-
1380834_at	Btnl8	butyrophilin-like 8	406160	Rn.198088	BM383031	2.32	2.31	2.33	2.32	2.33	2.31	1.00	down	4.98E-01	8.95E-01	-	-
1378059_at	---	---	---	Rn.169995	BF412644	2.27	2.26	2.28	2.26	2.27	2.26	1.00	down	4.95E-01	8.95E-01	-	-
1384672_at	RGD1561029	similar to RIKEN cDNA 4930434E21	304252	---	AI045518	2.33	2.32	2.33	2.32	2.32	2.31	1.00	down	3.50E-01	8.95E-01	-	-
1368104_at	Tspan2	tetraspanin 2	64521	Rn.5872	AI228231	2.36	2.35	2.37	2.36	2.37	2.34	1.00	down	6.02E-01	8.95E-01	-	-
1398118_at	---	---	---	---	AI555503	2.35	2.35	2.37	2.35	2.36	2.34	1.00	down	5.83E-01	8.95E-01	-	-
1387504_at	Il1rl2	interleukin 1 receptor-like 2	171106	Rn.10235	NM_133575	2.33	2.32	2.34	2.33	2.34	2.32	1.00	down	5.48E-01	8.95E-01	-	-
1392176_at	---	---	---	Rn.207224	BE095647	2.34	2.33	2.35	2.33	2.34	2.32	1.00	down	5.20E-01	8.95E-01	-	-
1379900_at	---	---	---	Rn.18691	AI043697	2.35	2.35	2.37	2.35	2.36	2.34	1.00	down	5.60E-01	8.95E-01	-	-
1368344_at	Gad1	glutamate decarboxylase 1	24379	Rn.91245	NM_017007	2.38	2.37	2.39	2.37	2.39	2.36	1.00	down	6.13E-01	8.95E-01	-	-
1380454_at	---	---	---	Rn.43044	AI549209	2.34	2.33	2.35	2.34	2.35	2.32	1.00	down	5.23E-01	8.95E-01	-	-
1389237_at	Zc3hc1	zinc finger, C3HC-type containing 1	296957	Rn.56620	BM383698	3.51	3.83	3.63	3.66	3.47	3.86	1.00	up	9.71E-01	9.91E-01	-	-
1380509_at	---	---	---	---	AW253985	2.31	2.30	2.31	2.30	2.31	2.29	1.00	down	3.89E-01	8.95E-01	-	-
1395531_at	Cep76	centrosomal protein 76kDa	291540	Rn.98568	AW251707	2.40	2.40	2.42	2.40	2.40	2.39	1.00	down	4.54E-01	8.95E-01	-	-
1379161_at	---	---	---	Rn.29310	AI556639	2.33	2.32	2.34	2.32	2.33	2.31	1.00	down	5.12E-01	8.95E-01	-	-
1377822_at	Ccdc64	coiled-coil domain containing 64	304537	Rn.166161	AI179605	2.51	2.52	2.52	2.52	2.52	2.53	1.00	up	2.87E-01	8.95E-01	-	-
1385127_at	Bmp5	bone morphogenetic protein 5	315824	Rn.135799	BE116364	2.47	2.45	2.50	2.47	2.49	2.44	1.00	down	7.94E-01	9.34E-01	-	-
1396502_at	---	---	---	Rn.173237	BF405162	2.37	2.37	2.38	2.37	2.38	2.36	1.00	down	4.22E-01	8.95E-01	-	-
1394603_at	---	---	---	Rn.206494	AW527711	2.34	2.33	2.35	2.33	2.34	2.32	1.00	down	5.13E-01	8.95E-01	-	-
1397665_at	---	---	---	Rn.199431	BF566506	2.35	2.34	2.35	2.34	2.35	2.33	1.00	down	5.21E-01	8.95E-01	-	-
1387435_at	St8sia3	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 3	25547	Rn.90977	NM_013029	2.35	2.35	2.36	2.35	2.36	2.33	1.00	down	5.52E-01	8.95E-01	-	-
1384457_at	Fbxw17	F-box and WD-40 domain protein 17	361219	Rn.100575	AI030755	2.75	2.81	3.59	3.04	2.72	3.37	1.00	down	9.87E-01	9.96E-01	-	-
1397739_at	Slc25a31	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator	689108	Rn.198589	BF395799	2.40	2.39	2.42	2.40	2.41	2.38	1.00	down	6.22E-01	8.95E-01	-	-
1398182_at	---	---	---	Rn.147926	BF411782	2.39	2.38	2.42	2.39	2.41	2.38	1.00	down	7.50E-01	9.19E-01	-	-
1370620_at	Ccl22	chemokine (C-C motif) ligand 22	117551	Rn.48727	AF163477	2.30	2.29	2.31	2.29	2.30	2.28	1.00	down	4.73E-01	8.95E-01	-	-
1389696_at	---	---	---	Rn.62928	BF409820	2.41	2.40	2.42	2.40	2.42	2.40	1.00	down	5.55E-01	8.95E-01	-	-
1394731_at	Csnk1g3	casein kinase 1, gamma 3	64823	Rn.10084	AI547718	3.41	4.17	3.43	3.40	4.18	3.41	1.00	down	9.88E-01	9.96E-01	-	-
1368701_at	Atp1a3	ATPase, Na+/K+ transporting, alpha 3 polypeptide	24213	Rn.87329	NM_012506	2.27	2.26	2.28	2.26	2.27	2.26	1.00	down	4.90E-01	8.95E-01	-	-
1386664_at	Rasgef1a	RasGEF domain family, member 1A	312664	Rn.29825	BF545895	2.41	2.40	2.41	2.40	2.41	2.38	1.00	down	5.89E-01	8.95E-01	-	-
1397621_at	---	---	---	Rn.199475	AI502942	2.43	2.42	2.43	2.42	2.43	2.42	1.00	down	2.35E-01	8.95E-01	-	-
1393676_at	---	---	---	Rn.207739	BE106495	2.33	2.33	2.35	2.33	2.34	2.32	1.00	down	4.76E-01	8.95E-01	-	-
1376570_at	Cct5	chaperonin containing Tcp1, subunit 5 (epsilon)	294864	Rn.92645	BF417274	10.10	9.93	10.24	9.95	9.98	10.35	1.00	up	9.73E-01	9.92E-01	-	-
1384793_at	Dab1	disabled homolog 1 (Drosophila)	266729	Rn.206534	BF406318	2.94	2.95	3.01	2.96	2.99	2.94	1.00	down	8.34E-01	9.48E-01	-	-
1394220_at	---	---	---	Rn.135714	H31648	2.34	2.34	2.36	2.34	2.35	2.34	1.00	down	4.98E-01	8.95E-01	-	-
1389202_at	Rpe	ribulose-5-phosphate-3-epimerase	501157	Rn.222022	AA944520	3.03	3.01	3.53	2.93	3.58	3.03	1.00	down	9.84E-01	9.95E-01	-	-
1387460_at	Sftpa1	surfactant protein A1	24773	Rn.11343	BI295853	2.35	2.34	2.36	2.34	2.36	2.33	1.00	down	5.56E-01	8.95E-01	-	-
1382562_at	---	---	---	---	AI051209	2.41	2.39	2.42	2.40	2.42	2.39	1.00	down	6.51E-01	8.96E-01	-	-
1391707_at	---	---	---	Rn.154089	AI408920	2.38	2.37	2.39	2.37	2.39	2.36	1.00	down	5.74E-01	8.95E-01	-	-
1380897_at	---	---	---	Rn.94179	BE105590	2.35	2.33	2.36	2.34	2.39	2.33	1.00	up	7.87E-01	9.31E-01	-	-
1381727_at	---	---	---	---	BF405596	2.33	2.32	2.33	2.32	2.33	2.31	1.00	down	5.00E-01	8.95E-01	-	-
1371009_at	Muc5ac	mucin 5AC, oligomeric mucus/gel-forming	682837	Rn.10789	U83139	2.34	2.33	2.35	2.34	2.35	2.32	1.00	down	5.24E-01	8.95E-01	-	-
1382883_at	---	---	---	Rn.166453	AI071492	2.33	2.32	2.35	2.33	2.34	2.32	1.00	down	5.38E-01	8.95E-01	-	-
1393163_at	---	---	---	---	AI112184	2.27	2.25	2.27	2.26	2.26	2.25	1.00	down	3.55E-01	8.95E-01	-	-
1374338_at	RGD1562059	similar to RIKEN cDNA 1110038F21	361993	Rn.136919	BI290720	2.41	2.38	2.40	2.39	2.45	2.36	1.00	up	8.43E-01	9.51E-01	-	-
1386732_at	Bbs1	Bardet-Biedl syndrome 1 homolog (human)	309156	Rn.12497	BF558083	2.39	2.38	2.39	2.38	2.40	2.36	1.00	down	5.78E-01	8.95E-01	-	-
1375287_at	---	---	---	Rn.212020	BI299020	2.32	2.31	2.33	2.32	2.33	2.31	1.00	down	5.30E-01	8.95E-01	-	-
1377028_at	---	---	---	Rn.27597	BG373675	2.30	2.30	2.32	2.30	2.30	2.30	1.00	down	5.19E-01	8.95E-01	-	-
1370584_a_at	Adora1	adenosine A1 receptor	29290	Rn.32078	M69046	2.33	2.32	2.33	2.32	2.33	2.30	1.00	down	5.97E-01	8.95E-01	-	-
1381172_at

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1368592_at	Il1a	interleukin 1 alpha	24493	Rn.12300	NM_017019	2.30	2.30	2.31	2.30	2.30	2.29	1.00	down	4.39E-01	8.95E-01	-	-
1378105_at	---	---	---	Rn.25296	BF289201	2.40	2.38	2.41	2.39	2.40	2.38	1.00	down	5.27E-01	8.95E-01	-	-
1378593_at	---	---	---	Rn.156344	BF405943	2.41	2.40	2.42	2.40	2.41	2.40	1.00	down	4.21E-01	8.95E-01	-	-
1396074_at	---	---	---	Rn.207810	BF525157	2.38	2.38	2.38	2.38	2.38	2.37	1.00	down	2.46E-01	8.95E-01	-	-
1369766_at	Ptger2	prostaglandin E receptor 2, subtype EP2	81752	Rn.10264	U48858	2.28	2.27	2.28	2.27	2.28	2.26	1.00	down	4.23E-01	8.95E-01	-	-
1378655_at	---	---	---	Rn.156255	BF399516	2.31	2.30	2.32	2.31	2.31	2.30	1.00	down	4.58E-01	8.95E-01	-	-
1376345_at	Caly	calcyon neuron-specific vesicular protein	192349	Rn.27756	BG381734	2.39	2.37	2.39	2.37	2.40	2.36	1.00	down	7.22E-01	9.11E-01	-	-
1381034_at	Wnt10a	wingless-type MMTV integration site family, member 10A	316527	Rn.18155	AI029140	2.36	2.35	2.37	2.36	2.36	2.35	1.00	down	2.92E-01	8.95E-01	-	-
1388949_at	---	---	---	Rn.57310	BI297693	2.38	2.37	2.39	2.37	2.41	2.36	1.00	up	7.55E-01	9.20E-01	-	-
1384317_at	---	---	---	Rn.203751	BF413978	2.28	2.28	2.29	2.30	2.28	2.27	1.00	up	5.65E-01	8.95E-01	-	-
1370844_at	Trpv5	transient receptor potential cation channel, subfamily V, member 5	116469	Rn.137513	AB032019	2.34	2.33	2.34	2.33	2.34	2.32	1.00	down	4.79E-01	8.95E-01	-	-
1381094_at	---	---	---	Rn.207726	BG376156	2.38	2.37	2.40	2.38	2.39	2.36	1.00	down	6.37E-01	8.95E-01	-	-
1398816_at	Lamp1	lysosomal-associated membrane protein 1	25328	Rn.40177	BE105853	2.34	2.34	2.35	2.34	2.34	2.33	1.00	down	3.59E-01	8.95E-01	-	-
1368167_at	Ctse	cathepsin E	25424	Rn.92738	NM_012938	2.34	2.33	2.35	2.33	2.34	2.32	1.00	down	5.38E-01	8.95E-01	-	-
1385049_at	---	---	---	Rn.131384	BE116124	2.34	2.33	2.35	2.33	2.34	2.33	1.00	down	5.13E-01	8.95E-01	-	-
1375408_at	---	---	---	---	BF401660	2.42	2.26	2.27	2.27	2.41	2.26	1.00	down	9.39E-01	9.83E-01	-	-
1394218_s_at	Zfpm2	zinc finger protein, multitype 2	314930	Rn.135463	AI175842	3.98	2.51	2.58	2.53	4.06	2.47	1.00	down	9.94E-01	9.98E-01	-	-
1370595_a_at	Kcnip4	Kv channel interacting protein 4	259243	Rn.205864	AF345444	2.33	2.32	2.34	2.33	2.34	2.32	1.00	down	5.32E-01	8.95E-01	-	-
1370559_at	Kcnc2	potassium voltage gated channel, Shaw-related subfamily, member 2	246153	Rn.9733	BF400847	2.34	2.33	2.35	2.33	2.34	2.32	1.00	down	4.94E-01	8.95E-01	-	-
1384409_at	---	---	---	Rn.11479	AA863930	2.45	2.42	2.46	2.44	2.46	2.45	1.00	up	6.81E-01	9.03E-01	-	-
1398018_at	---	---	---	Rn.73072	BF466265	2.36	2.34	2.36	2.35	2.34	2.35	1.00	down	4.90E-01	8.95E-01	-	-
1375078_at	---	---	---	Rn.156476	BF404061	2.57	2.55	2.58	2.56	2.60	2.52	1.00	down	8.35E-01	9.48E-01	-	-
1397659_at	Znf76	zinc finger protein 76 (expressed in testis)	361809	Rn.13446	BF548753	2.29	2.28	2.29	2.29	2.29	2.27	1.00	down	4.48E-01	8.95E-01	-	-
1379034_at	---	---	---	Rn.45299	AI029552	2.50	2.49	2.53	2.49	2.55	2.49	1.00	up	8.31E-01	9.47E-01	-	-
1380782_at	---	---	---	Rn.206624	AW528654	2.44	2.42	2.45	2.44	2.44	2.41	1.00	down	7.37E-01	9.16E-01	-	-
1371048_at	Foxe1	forkhead box E1 (thyroid transcription factor 2)	192274	Rn.26546	Y11321	2.32	2.32	2.33	2.32	2.33	2.31	1.00	down	4.64E-01	8.95E-01	-	-
1380736_at	---	---	---	Rn.209360	BF388553	2.39	2.38	2.41	2.39	2.41	2.37	1.00	down	7.12E-01	9.10E-01	-	-
1397117_at	---	---	---	Rn.146904	BF400245	2.27	2.26	2.28	2.26	2.27	2.26	1.00	down	4.48E-01	8.95E-01	-	-
1370291_at	Pdlim3	PDZ and LIM domain 3	114108	Rn.13361	AF002281	2.41	2.40	2.43	2.41	2.42	2.40	1.00	down	6.66E-01	8.99E-01	-	-
1379129_at	LOC502371	similar to 40S ribosomal protein S21	502371	Rn.206378	AW528596	2.35	2.34	2.35	2.34	2.34	2.34	1.00	down	2.84E-01	8.95E-01	-	-
1388025_at	Opn1sw	opsin 1 (cone pigments), short-wave-sensitive	81444	Rn.10549	U63972	2.31	2.31	2.32	2.31	2.32	2.30	1.00	down	3.29E-01	8.95E-01	-	-
1398011_at	---	---	---	Rn.146133	AI555486	2.32	2.31	2.33	2.32	2.32	2.30	1.00	down	4.46E-01	8.95E-01	-	-
1376836_at	---	---	---	Rn.63595	BF419655	2.39	2.37	2.39	2.38	2.40	2.36	1.00	down	7.20E-01	9.11E-01	-	-
1389861_at	---	---	---	---	BE111612	2.56	2.55	2.58	2.56	2.58	2.54	1.00	down	6.88E-01	9.04E-01	-	-
1370022_at	Tnp2	transition protein 2	24840	Rn.10430	NM_017057	2.47	2.45	2.47	2.46	2.49	2.44	1.00	down	7.34E-01	9.15E-01	-	-
1382640_at	---	---	---	Rn.7742	AA944498	2.42	2.40	2.41	2.41	2.42	2.39	1.00	down	5.67E-01	8.95E-01	-	-
1379653_s_at	Nova2	neuro-oncological ventral antigen 2	292681	---	AI058678	2.30	2.30	2.31	2.30	2.31	2.29	1.00	down	4.59E-01	8.95E-01	-	-
1378042_at	RGD1563109	RGD1563109	499586	Rn.203239	AA801132	2.44	2.42	2.46	2.43	2.46	2.41	1.00	down	7.96E-01	9.34E-01	-	-
1385610_at	Sephs1	selenophosphate synthetase 1	291314	Rn.100803	BF412640	2.42	2.41	2.43	2.41	2.42	2.41	1.00	down	4.77E-01	8.95E-01	-	-
1367975_at	Anxa3	annexin A3	25291	Rn.6589	NM_012823	2.35	2.35	2.37	2.35	2.36	2.34	1.00	down	5.79E-01	8.95E-01	-	-
1374262_at	---	---	---	Rn.32615	BF396371	2.41	2.39	2.42	2.41	2.44	2.39	1.00	up	7.58E-01	9.21E-01	-	-
1391732_at	---	---	---	Rn.148385	BI278779	2.34	2.34	2.35	2.34	2.35	2.32	1.00	down	5.15E-01	8.95E-01	-	-
1387516_at	Pnliprp2	pancreatic lipase-related protein 2	117554	Rn.87688	NM_057206	2.38	2.38	2.41	2.38	2.40	2.37	1.00	down	6.69E-01	9.00E-01	-	-
1393826_at	Chid1	Chitinase domain containing 1	293628	Rn.162505	AI145205	2.40	2.38	2.48	2.39	2.50	2.35	1.00	down	9.24E-01	9.78E-01	-	-
1389272_at	---	---	---	Rn.62685	BF406302	2.36	2.34	2.35	2.33	2.35	2.34	1.00	down	4.41E-01	8.95E-01	-	-
1369924_at	Sncb	synuclein, beta	113893	Rn.20352	NM_080777	2.58	2.57	2.60	2.58	2.59	2.57	1.00	down	5.92E-01	8.95E-01	-	-
1368367_at	Cuzd1	CUB and zona pellucida-like domains 1	117179	Rn.10825	NM_054005	2.37	2.36	2.39	2.36	2.39	2.35	1.00	down	6.87E-01	9.04E-01	-	-
1370961_at	Dci	dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoyl-Coenzyme A isome	29740	Rn.80835	BI282349	2.32	2.31	2.33	2.31	2.33	2.30	1.00	down	5.47E-01	8.95E-01	-	-
1377906_at	Dhx36	DEAH (Asp-Glu-Ala-His) box polypeptide 36	310461	Rn.2744	BF404389	2.49	2.48	2.53	2.49	2.54	2.48	1.00	up	8.32E-01	9.47E-01	-	-
1381392_at	---	---	---	Rn.209300	BF387435	2.50	2.49	2.49	2.49	2.49	2.49	1.00	down	2.71E-01	8.95E-01	-	-
1395995_at	---	---	---	---	BF390557	2.37	2.36	2.38	2.36	2.38	2.35	1.00	down	6.33E-01	8.95E-01	-	-
1396888_at	---	---	---	---	AW527274	2.47	2.52	2.54	2.54	2.53	2.47	1.00	up	8.55E-01	9.55E-01	-	-
1379171_at	---	---	---	---	BF388150	2.96	2.83	3.02	2.99	3.14	2.70	1.00	up	9.70E-01	9.91E-01	-	-
1391229_at	Camk1g	calcium/calmodulin-dependent protein kinase IG	171358	Rn.91453	BG381458	2.31	2.30	2.32	2.30	2.32	2.29	1.00	down	5.83E-01	8.95E-01	-	-
1396756_at	---	---	---	---	BF410531	2.31	2.31	2.34	2.31	2.32	2.31	1.00	down	5.64E-01	8.95E-01	-	-
1389812_at	LOC494538	ABP beta	494538	Rn.78317	BI279486	2.42	2.40	2.44	2.41	2.44	2.39	1.00	down	7.85E-01	9.30E-01	-	-
1374242_at	---	---	---	Rn.154188	BI296522	2.47	2.46	2.55	2.59	2.42	2.45	1.00	down	9.31E-01	9.81E-01	-	-
1385308_at	Mogat1	monoacylglycerol O-acyltransferase 1	363261	Rn.79245	BI291282	2.47	2.46	2.48	2.46	2.48	2.46	1.00	down	6.07E-01	8.95E-01	-	-
1394520_at	---	---	---	Rn.173688	AW143476	2.32	2.32	2.33	2.32	2.32	2.31	1.00	down	3.99E-01	8.95E-01	-	-
1377736_at	---	---	---	Rn.8982	BF284308	2.41	2.39	2.41	2.40	2.41	2.38	1.00	down	6.93E-01	9.05E-01	-	-
1392883_at	RGD1305269	similar to hypothetical protein	305332	Rn.114006	AI013730	6.28	5.22	3.39	4.92	4.99	4.96	1.00	down	9.95E-01	9.98E-01	-	-
1387481_at	Npbr	neuronal pentraxin receptor	81095	Rn.34907	NM_030841	2.40	2.40	2.42	2.40	2.40	2.40	1.00	down	4.79E-01	8.95E-01	-	-
1381753_at	---	---	---	Rn.208843	BF416214	2.60	2.60	2.61	2.60	2.61	2.59	1.00	down	4.30E-01	8.95E-01	-	-
1377495_at	---	---	---	Rn.15032	AA900220	2.37	2.36	2.38	2.36	2.37	2.36	1.00	down	4.87E-01	8.95E-01	-	-
1394770_at	Pik3c2b	phosphoinositide-3-kinase, class 2, beta polypeptide	289021	Rn.72591	AI556187	2.40	2.39	2.42	2.40	2.41	2.39	1.00	down	6.55E-01	8.98E-01	-	-
1398104_at	---	---	---	Rn.48337	AW535543	2.32	2.31	2.33	2.31	2.32	2.30	1.00	down	5.11E-01	8.95E-01	-	-
1372308_at	---	---	---	Rn.8110	BM386869	2.37	2.36	2.38	2.36	2.38	2.35	1.00	down	5.80E-01	8.95E-01	-	-
1368731_at	Orm1	orosomucoid 1	24614	Rn.10295	NM_053288	2.35	2.34	2.36	2.35	2.36	2.33	1.00	down	5.46E-01	8.95E-01	-	-
1396986_at	---	---	---	Rn.148935	BF405878	2.34	2.34	2.35	2.34	2.32	2.32	1.00	down	5.35E-01	8.95E-01	-	-
1383532_at	---	---	---	---	AA956411	2.34	2.33	2.35	2.33	2.34	2.32	1.00	down	5.74E-01	8.95E-01	-	-
1396484_at	---	---	---	Rn.205239	AI511211	2.38	2.36	2.42	2.37	2.42	2.36	1.00	down	8.41E-01	9.50E-01	-	-
1388834_at	---	---	---	Rn.26912	BI291422	2.32	2.31	2.32	2.31	2.32	2.30	1.00	down	5.07E-01	8.95E-01	-	-
1396689_at	---	---	---	Rn.208295	BE114452	2.49	2.48	2.51	2.53	2.49	2.47	1.00	up	7.93E-01	9.34E-01	-	-
1375477_at	---	---	---	---	AA999104	2.41	2.41	2.42	2.41	2.41	2.40	1.00	down	2.56E-01	8.95E-01	-	-
1373596_at	RGD1310423	similar to hypothetical protein FLJ31737	361112	Rn.23137	AI230766	2.37	2.38	2.41	2.38	2.39	2.37	1.00	down	7.10E-01	9.09E-01	-	-
1387963_a_at	Uox	urate oxidase	114768	Rn.11330	M24396	2.43	2.37	2.37	2.45	2.38	2.36	1.00	up	8.75E-01	9.61E-01	-	-
1369637_at	Kif3c	kinesin family member 3C	85248	Rn.10894	AF083330	2.30	2.30	2.31	2.30	2.30	2.29	1.00	down	3.83E-01	8.95E-01	-	-
1380714_at	---	---	---	Rn.132092	AI600230	2.43	2.42	2.44	2.43	2.43	2.42	1.00	down	4.80E-01	8.95E-01	-	-
1397841_at	---	---	---	Rn.208160	BG379062	2.45	2.44	2.46	2.45	2.46	2.43	1.00	down	6.09E-01	8.95E-01	-	-
1382444_at	---	---	---	Rn.8243	AA925250	2.34	2.33	2.35	2.33	2.34	2.32	1.00	down	4.46E-01	8.95E-01	-	-
1384911_at	Alox12e	arachidonate lipoxygenase, epidermal	303252	Rn.41827	AI547806	2.38	2.36	2.39	2.37	2.38	2.36	1.00	down	5.95E-01	8.95E-01	-	-
1377555_at	---	---	---	Rn.47180	BF387432	2.33	2.32	2.34	2.32	2.33	2.31	1.00	down	5.36E-01	8.95E-01	-	-
1390456_at	---	---	---	Rn.169454	AW524471	2.64	2.99	2.63	2.62	2.63	3.03	1.00	up	9.77E-01	9.93E-01	-	-
1381736_at	---	---	---	Rn.107723	BF405604	2.35	2.35	2.37	2.35	2.36	2.35	1.00	down	4.88E-01	8.95E-01	-	-
1370632_at	Obp2b	odorant binding protein 2B	286933	Rn.11371	M76734	2.35	2.34	2.36	2.35	2.36	2.34	1.00	down	5.51E-01	8.95E-01	-	-
1386250_at	Snx12	Sorting nexin 12	363478	Rn.2280	BG153370	2.43	2.41	2.44	2.42	2.44	2.40	1.00	down	7.28E-01	9.13E-01	-	-
1396617_at	---	---	---	---	BE115265	2.45	2.43	2.45	2.44	2.48	2.43	1.00	up	7.60E-01	9.22E-01	-	-
1389541_at	---	---	---	Rn.219219	AI410836	2.49	2.65	2.49	2.48	2.51	2.65	1.00	up	9.45E-01	9.84E-01	-	-
1396843_at	---	---	---	Rn.28613	AI145781	2.26	2.25	2.26	2.25	2.26	2.24	1.00	down	3.71E-01	8.95E-01	-	-
1369576_at	Tas2r105	taste receptor, type 2, member 105	78985	Rn.48788	NM_023999	2.34	2.33	2.36	2.34	2.35	2.33	1.00	down	5.68E-01	8.95E-01	-	-
1387221_at	Gch1	GTP cyclohydrolase 1	29244	Rn.28195	NM_024356	2.35	2.34	2.36	2.34	2.35	2.34	1.00	down	4.89E-01	8.95E-01	-	-
1379828_at	---	---	---	Rn.24192	AI113302	2.41	2.39	2.41	2.40	2.41	2.38	1.00	down	6.62E-01	8.98E-01	-	-
1378798_at	Stox2	storkhead box 2	306459	Rn.61788	BF406062	2.42	2.41	2.43	2.42	2.47	2.40	1.00	up	8.18E-01	9.42E-01	-	-
1378091_at	---	---	---	Rn.169745	AW528824	2.36	2.35	2.37	2.36	2.37	2.34	1.00	down	5.31E-01	8.95E-01	-	-
1385630_at	---	---	---	---	AA925114	2.48	2.47	2.48	2.47	2.50	2.45	1.00	down	7.41E-01	9.17E-01	-	-
1368162_at	Cst8	cystatin E/M	171096	Rn.9609	NM_133566	2.65	2.64	2.66	2.64	2.70	2.62	1.00	up	8.41E-01	9.50E-01	-	-
1369171_at	Mst1	Macrophage stimulating 1 (hepatocyte growth factor-like)	24566	Rn.10613	NM_024352	2.31	2.30	2.32	2.31	2.32	2.30	1.00	down	4.66E-01	8.95E-01	-	-
1369869_at	Capza3	capping protein (actin filament) muscle Z-line, alpha 3	29324	Rn.42865	NM_017164	2.46	2.45	2.47	2.45	2.46	2.44	1.00	down	5.43E-01	8.95E-01	-	-
1369748_at	Serpini2	serine (or cysteine) peptidase inhibitor, clade I, member 2	171149	Rn.54500	NM_133612	2.43	2.40	2.43	2.41	2.45	2.40	1.00	down	7.83E-01	9.30E-01	-	-
1375983_at	Mamdc2	MAM domain containing 2	309410	Rn.23730	AI234287	2.41	2.40	2.44	2.41	2.43	2.39	1.00	down	7.22E-01	9.11E-01	-	-
1383801_at	---	---	---	Rn.24331	BF550887	2.38	2.37	2.39	2.37	2.39	2.36	1.00	down	5.78E-01	8.95E-01	-	-
1393299_at	Dpp10	dipeptidylpeptidase 10	363972	Rn.217077	BF567794	2.32	2.31	2.33	2.31	2.32	2.30	1.00	down	4.69E-01	8.95E-01	-	-
1384613_at	---	---	---	Rn.16232	AI060035	2.30	2.30	2.30	2.30	2.31	2.28	1.00	down	5.00E-01	8.95E-01	-	-
1379607_at	---	---	---	Rn.148105	AW527767	2.39	2.41	2.40	2.38	2.43	2.37	1.00	down	7.92E-01	9.33E-01	-	-
1393779_x_at	Sc65	synaptonemal complex protein SC65	59101	Rn.90100	BI303187	2.36	2.35	2.37	2.36	2.36	2.34	1.00	down	4.65E-01	8.95E-01	-	-
1395872_at	---	---	---	---	BF419422	2.48	2.47	2.49	2.47	2.49	2.46	1.00	down	6.34E-01	8.95E-01	-	-
1382626_at	---	---	---	Rn.46849	AW528353	2.37	2.36	2.38	2.36	2.38	2.36	1.00	down	5.86E-01	8.95E-01	-	-
1392305_at	---	---	---	Rn.51078	BE106921	2.33	2.32	2.34	2.33	2.34	2.32	1.00	down	5.19E-01	8.95E-01	-	-
1393988_at	---	---	---	---	AA860014	2.33	2.33	2.34	2.33	2.34	2.32	1.00	down	4.54E-01	8.95E-01	-	-
1380092_at	Bnip1	BCL2/adenovirus E1B 19kDa-interacting protein 1	140932	Rn.16757	AI146096	2.47	2.43	2.45	2.44	2.45	2.44	1.00	down	6.26E-01	8.95E-01	-	-
1395938_at	---	---	---	---	AW529739	2.33	2.33	2.34	2.33	2.34	2.32	1.00	down	4.97E-01	8.95E-01	-	-
1396893_at	---	---	---	Rn.204407	AI576209	2.36	2.36	2.38	2.36	2.37	2.35	1.00	down	5.42E-01	8.95E-01	-	-
1384308_at	Meis1	Meis homeobox 1	686117	Rn.32289	AW550997	2.49	2.48	2.50	2.49	2.49	2.48	1.00	down	4.51E-01	8.95E-01	-	-
1387308_at	Epo	erythropoietin	24335	Rn.11365	NM_017001	2.34	2.33	2.35	2.33	2.34	2.32	1.00	down	5.42E-01	8.95E-01	-	-
1368411_a_at	Map2	microtubule-associated protein 2	25595	Rn.10484	X74211	2.34	2.33	2.35	2.34	2.35	2.33	1.00	down	5.65E-01	8.95E-01	-	-
1380896_at	---	---	---	Rn.153941	BF399974	2.35	2.34	2.36	2.34	2.35	2.33	1.00	down	5.66E-01	8.95E-01	-	-
1391164_at	Tanaxip1	translin-associated factor X interacting protein 1	498944	Rn.21094	BF394231	2.39	2.37	2.40	2.38	2.39	2.37	1.00	down	5.47E-01	8.95E-01	-	-
1384654_at	---	---	---	Rn.204477	AI113214	2.38	2.36	2.39	2.37	2.39	2.35	1.00	down	6.79E-01	9.03E-01	-	-
1390393_at	---	---	---	Rn.38809	BF388422	2.32	2.32	2.33	2.32	2.33	2.31	1.00	down	5.05E-01	8.95E-01	-	-
1378388_at	---	---	---	Rn.176893	BI290092	2.35	2.35	2.36	2.35	2.35	2.34	1.00	down	2.56E-01	8.95E-01	-	-
1372711_at	LOC498750	similar to cDNA sequence BC005537	498750	Rn.23910	AI409292	9.37	8.95	9.49	9.25	9.15	9.41	1.00	down	9.77E-01	9.93E-01	-	-
1392050_at	---	---	---	Rn.206874	BE119691	2.23	2.23	2.24	2.23	2.24	2.22	1.00	down	5.31E-01	8.95E-01	-	-
1381178_at	Ncoa3	nuclear receptor coactivator 3	84584	Rn.20691	AF322224	2.34	2.33	2.36	2.34	2.35	2.33	1.00	down	5.63E-01	8.95E-01	-	-
1398734_at	---	---	---	Rn.208886	BE120772	2.36	2.35	2.37	2.36	2.36	2.35	1.00	down	4.34E-01	8.95E-01	-	-
1381536_at	---	---	---	---	AI501200	2.31	2.30	2.31	2.30	2.31	2.30	1.00	down	3.45E-01	8.95E-01	-	-
1368999_a_at	Begain	brain-enriched guanylate kinase-associated	79146	Rn.30036	AF064869	2.32	2.32	2.33	2.32	2.32	2.31	1.00	down	4.83E-01	8.95E-01	-	-
1387215_at	Agxt	alanine-glyoxylate aminotransferase	24792	Rn.9931	NM_030656	2.32	2.33	2.32	2.36	2.32	2.30	1.00	up	7.64E-01	9.23E-01	-	-
1396477_at	Csde1	cold shock domain containing E1, RNA binding	117180	Rn.3562	AI010663	2.26	2.25	2.26	2.25	2.26	2.25	1.00	down	3.89E-01	8.95E-01	-	-
1384785_at	---	---	---	Rn.208708	BE120224	2.48	2.47	2.48	2.55	2.49	2.42	1.00	up	8.85E-01	9.64E-01	-	-
1396490_at	---	---	---	---	BI296616	2.33	2.34	2.35	2.33	2.34	2.32	1.00	down	5.69E-01	8.95E-01	-	-
1391176_at	RGD1563278	similar to Ubiquitin ligase protein DZIP3 (DAZ-interacting protein 3 homolog)	303963	Rn.162050	BF419661	2.36	2.36	2.37	2.36	2.37	2.35	1.00	down	3.26E-01	8.95E-01	-	-
1379432_at	---	---	---	Rn.58915	AW918404	2.31	2.30	2.32	2.30	2.31	2.29	1.00	down	4.72E-01	8.95E-01	-	-
1381501_at	---	---	---	Rn.66760	BG380668	2.30	2.30	2.31	2.30	2.31	2.29	1.00	down	4.00E-01	8.95E-01	-	-
1368394_at	Sfrp4	secreted frizzled-related protein 4	89803	Rn.10788	AF140346	2.32	2.31	2.33	2.32	2.33	2.31	1.00	down	5.06E-01	8.95E-01	-	-
1369246_a_at	Npy5r	neuropeptide Y receptor Y5	25340	Rn.10532	NM_012869	2.31	2.30	2.32	2.30	2.31	2.30	1.00	down	4.92E-01	8.95E-01	-	-
1379340_at	Lamc2	laminin, gamma 2	192362	Rn.9278	BM385282	2.34	2.32	2.35	2.33	2.34	2.32	1.00	down	6.11E-01	8.95E-01	-	-
1389720_at	---	---	---	Rn.34454	BI274428	2.37	2.36	2.37	2.36	2.37	2.35	1.00	down	5.40E-01	8.95E-01	-	-
1398924_at	Manbal	mannosidase, beta A, lysosomal-like	499934	Rn.6510	AA894774	2.84	3.53	3.03	3.06	3.09	3.27	1.00	up	9.81E-01	9.94E-01	-	-
1378485_at	---	---	---	Rn.149111	BF405179	2.30	2.29	2.31	2.30	2.30	2.29	1.00	down	4.34E-01	8.95E-01	-	-
1389112_at	Nkd1	naked cuticle homolog 1 (Drosophila)	364952	Rn.8826	AI017280	2.63	2.56	2.55	2.56	2.63	2.54	1.00	down	8.91E-01	9.66E-01	-	-
1391651_at	Atad2	ATPase family, AAA domain containing 2	314993	Rn.6690	BF408842	2.24	2.24	2.26	2.24	2.25	2.24	1.00	down	4.30E-01	8.95E-01	-	-
1373345_at	Amigo2	adhesion molecule with Ig like domain 2	300186	Rn.98123	AW523747	2.35	2.35	2.37	2.35	2.36	2.34	1.00	down	4.83E-01	8.95E-01	-	-
1397523_at	Lrp11	low density lipoprotein receptor-related protein 11	292462	Rn.40930	BF554118	3.36	3.23	2.93	3.04	3.13	3.33	1.00	down	9.73E-01	9.92E-01	-	-
1383704_at	Actr3b	ARP3 actin-related protein 3 homolog B (yeast)	362298	Rn.108042	BF410844	2.34	2.34	2.35	2.34	2.35	2.33	1.00	down	5.38E-01	8.95E-01	-	-
1387729_at	Ggt5	gamma-glutamyltransferase 5	29566	Rn.44367	NM_019235	2.29	2.28	2.30	2.28	2.29	2.28	1.00	down	4.22E-01	8.95E-01	-	-
1397662_at	---	---	---	Rn.207952	BF395791	2.54	2.51	2.56	2.53	2.62	2.48	1.00	up	9.03E-01	9.70E-01	-	-
1370958_at	Kcnc3	potassium voltage-gated channel, Shaw-related subfamily, member 3	117101	Rn.9885	AI547447	2.35	2.35	2.36	2.34	2.35	2.34	1.00	down	3.40E-01	8.95E-01	-	-
1384351_at	Taf7l

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1385899_at	Trim16	tripartite motif-containing 16	303214	Rn.171348	BE113381	2.37	2.36	2.37	2.36	2.37	2.36	1.00	down	2.49E-01	8.95E-01	-	-
1371426_at	---	---	---	Rn.161236	BI298508	2.35	2.34	2.36	2.35	2.36	2.33	1.00	down	5.70E-01	8.95E-01	-	-
1373685_at	Ankrd37	ankyrin repeat domain 37	361149	Rn.21120	BI291430	4.86	5.12	5.01	5.17	4.81	5.00	1.00	down	9.69E-01	9.91E-01	-	-
1391126_at	Ndufa12	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 12	299739	Rn.86466	BG379351	2.44	2.42	2.46	2.43	2.45	2.45	1.00	up	6.97E-01	9.07E-01	-	-
1381180_at	---	---	---	Rn.155307	BG376806	2.37	2.36	2.38	2.36	2.38	2.35	1.00	down	5.75E-01	8.95E-01	-	-
1387742_at	Ccr2	chemokine (C-C motif) receptor 2	60463	Rn.211983	NM_021866	2.41	2.40	2.42	2.40	2.42	2.39	1.00	down	6.41E-01	8.95E-01	-	-
1392079_at	Akap7	A kinase (PRKA) anchor protein 7	361458	Rn.204773	AW526284	2.54	2.53	2.53	2.54	2.55	2.52	1.00	up	5.38E-01	8.95E-01	-	-
1383835_at	---	---	---	Rn.32756	BI303704	3.23	5.10	3.69	3.76	4.18	4.10	1.00	up	9.93E-01	9.98E-01	-	-
1368677_at	Bdnf	brain derived neurotrophic factor	24225	Rn.11266	X67108	2.37	2.36	2.38	2.37	2.37	2.35	1.00	down	5.60E-01	8.95E-01	-	-
1368155_at	Cyp2c12	cytochrome P450, family 2, subfamily c, polypeptide 12	25011	Rn.2566	NM_031572	2.34	2.33	2.36	2.34	2.35	2.33	1.00	down	5.72E-01	8.95E-01	-	-
1385548_at	Ube2d1	ubiquitin-conjugating enzyme E2D 1, UBC4/5 homolog (yeast)	361831	Rn.24937	AW140348	2.40	2.39	2.40	2.39	2.43	2.39	1.00	up	6.91E-01	9.05E-01	-	-
1394623_at	---	---	---	---	AA851041	2.34	2.33	2.35	2.33	2.34	2.32	1.00	down	4.53E-01	8.95E-01	-	-
1397728_at	---	---	---	---	AI113065	2.36	2.35	2.36	2.35	2.36	2.34	1.00	down	4.07E-01	8.95E-01	-	-
1396610_at	---	---	---	Rn.210714	BF400869	2.36	2.35	2.36	2.36	2.36	2.34	1.00	down	4.75E-01	8.95E-01	-	-
1397230_at	LOC684158	similar to chromosome 1 open reading frame 36	684158	---	BE096562	2.32	2.31	2.33	2.32	2.32	2.31	1.00	down	4.47E-01	8.95E-01	-	-
1396528_at	---	---	---	Rn.209086	BF404786	2.35	2.34	2.37	2.38	2.36	2.33	1.00	up	7.62E-01	9.22E-01	-	-
1375744_at	Foxd1	Forkhead box D1	171299	Rn.50822	BE105894	2.41	2.40	2.42	2.40	2.41	2.39	1.00	down	5.50E-01	8.95E-01	-	-
1391284_at	Srgap2	SLIT-ROBO Rho GTPase activating protein 2	360840	Rn.220450	BE099274	2.37	2.36	2.37	2.36	2.38	2.35	1.00	down	5.89E-01	8.95E-01	-	-
1369385_at	Afap1	actin filament associated protein 1	140935	Rn.208751	NM_080900	2.28	2.28	2.28	2.28	2.28	2.27	1.00	down	3.05E-01	8.95E-01	-	-
1396158_at	Rem1	RAS (RAD and GEM)-like GTP-binding 1	366232	Rn.88325	BE099900	2.40	2.37	2.40	2.38	2.39	2.38	1.00	down	6.30E-01	8.95E-01	-	-
1380034_at	---	---	---	Rn.176459	BF286957	2.35	2.34	2.36	2.35	2.35	2.34	1.00	down	2.83E-01	8.95E-01	-	-
1383583_at	---	---	---	Rn.209044	AW144730	2.37	2.36	2.38	2.36	2.38	2.35	1.00	down	6.50E-01	8.96E-01	-	-
1368210_at	Il24	interleukin 24	170819	Rn.48710	NM_133311	2.25	2.25	2.26	2.25	2.25	2.24	1.00	down	4.47E-01	8.95E-01	-	-
1388046_at	Itgam	integrin alpha M	25021	Rn.54465	AF268593	2.40	2.39	2.42	2.39	2.41	2.39	1.00	down	6.23E-01	8.95E-01	-	-
1397023_at	---	---	---	Rn.211482	BF414016	2.27	2.31	2.25	2.30	2.28	2.27	1.00	up	7.88E-01	9.31E-01	-	-
1372326_at	Slc2a3	Solute carrier family 2 (facilitated glucose transporter), member 3	25551	Rn.95055	AA901341	2.34	2.33	2.35	2.33	2.34	2.33	1.00	down	5.24E-01	8.95E-01	-	-
1392512_at	Hist3h2ba	histone cluster 3, H2ba	303175	Rn.39174	AW553007	2.39	2.38	2.41	2.39	2.40	2.37	1.00	down	6.73E-01	9.01E-01	-	-
1383823_at	---	---	---	Rn.204089	AI045143	2.36	2.35	2.37	2.36	2.36	2.36	1.00	up	4.46E-01	8.95E-01	-	-
1369914_at	Hrh2	histamine receptor H 2	25461	Rn.138113	NM_012965	2.28	2.28	2.29	2.28	2.29	2.27	1.00	down	4.40E-01	8.95E-01	-	-
1391734_at	---	---	---	Rn.146168	AA956267	2.33	2.32	2.34	2.33	2.34	2.32	1.00	down	5.55E-01	8.95E-01	-	-
1381890_at	---	---	---	---	BF390097	2.38	2.37	2.40	2.38	2.39	2.36	1.00	down	6.40E-01	8.95E-01	-	-
1380007_at	---	---	---	Rn.208071	BE109875	2.43	2.42	2.45	2.48	2.43	2.40	1.00	up	8.38E-01	9.49E-01	-	-
1393026_at	Rnase1	ribonuclease, RNase A family, 1 (pancreatic)	364304	Rn.9397	BI289531	2.31	2.30	2.31	2.30	2.31	2.29	1.00	down	4.14E-01	8.95E-01	-	-
1368439_at	Sox10	SRY (sex determining region Y)-box 10	29361	Rn.10883	NM_019193	2.33	2.32	2.34	2.33	2.34	2.32	1.00	down	5.40E-01	8.95E-01	-	-
1368900_at	Thbd	thrombomodulin	83580	Rn.88295	BG666306	2.33	2.32	2.34	2.32	2.33	2.31	1.00	down	5.18E-01	8.95E-01	-	-
1397524_at	---	---	---	Rn.146479	AA942689	2.38	2.37	2.38	2.37	2.38	2.36	1.00	down	4.49E-01	8.95E-01	-	-
1378094_at	---	---	---	Rn.205029	BM389654	9.20	9.19	9.15	9.17	9.20	9.16	1.00	down	7.91E-01	9.33E-01	-	-
1371233_at	Vcan	versican	114122	Rn.35686	AF084544	2.32	2.31	2.33	2.32	2.33	2.31	1.00	down	5.10E-01	8.95E-01	-	-
1390180_at	Prdm8	PR domain containing 8	305198	Rn.162242	AI575012	2.26	2.27	2.27	2.26	2.27	2.26	1.00	down	2.10E-01	8.95E-01	-	-
1395249_at	RGD1563912	RGD1563912	362256	Rn.9944	BF400750	2.58	2.56	2.62	2.57	2.65	2.56	1.00	up	8.82E-01	9.64E-01	-	-
1373596_at	RGD1310262	hypothetical LOC304650	304650	Rn.40355	AI411304	2.34	2.34	2.35	2.34	2.34	2.33	1.00	down	2.95E-01	8.95E-01	-	-
1367598_at	Ttr	transthyretin	24856	Rn.1404	NM_012681	2.39	2.38	2.40	2.39	2.40	2.37	1.00	down	6.68E-01	9.00E-01	-	-
1379234_a_at	Cdc45l	CDC45 cell division cycle 45-like (S. cerevisiae)	287961	Rn.98535	AI179539	2.33	2.32	2.34	2.32	2.34	2.31	1.00	down	6.50E-01	8.96E-01	-	-
1385156_at	---	---	---	Rn.150904	BE120415	2.32	2.31	2.33	2.31	2.32	2.30	1.00	down	4.90E-01	8.95E-01	-	-
1369812_at	Itgb4	integrin beta 4	25724	Rn.198908	NM_013180	2.41	2.40	2.42	2.41	2.41	2.40	1.00	down	4.64E-01	8.95E-01	-	-
1397577_at	---	---	---	---	BF397749	2.34	2.33	2.34	2.33	2.34	2.32	1.00	down	5.35E-01	8.95E-01	-	-
1369513_at	Ccl28	chemokine (C-C motif) ligand 28	114492	Rn.195764	NM_053700	2.37	2.36	2.39	2.36	2.41	2.33	1.00	down	8.46E-01	9.52E-01	-	-
1381638_at	---	---	---	Rn.173568	BM386607	2.33	2.32	2.34	2.32	2.33	2.32	1.00	down	4.85E-01	8.95E-01	-	-
1384121_at	---	---	---	Rn.198260	AI058309	2.30	2.29	2.30	2.29	2.30	2.28	1.00	down	4.29E-01	8.95E-01	-	-
1393891_at	Col8a1	collagen, type VIII, alpha 1	304021	Rn.53843	BE128699	2.41	2.40	2.42	2.40	2.41	2.40	1.00	down	6.22E-01	8.95E-01	-	-
1377233_at	---	---	---	Rn.129750	BF400740	2.31	2.30	2.32	2.30	2.31	2.29	1.00	down	4.35E-01	8.95E-01	-	-
1391722_at	Hsf2bp	heat shock transcription factor 2 binding protein	499413	Rn.24054	BI289088	4.64	2.85	4.07	4.07	3.74	3.73	1.00	down	9.93E-01	9.98E-01	-	-
1377332_at	---	---	---	Rn.61756	BF403350	2.42	2.41	2.44	2.42	2.44	2.44	1.00	up	5.97E-01	8.95E-01	-	-
1385748_at	Spata21	spermatogenesis associated 21	366491	Rn.57304	BF390864	2.27	2.27	2.28	2.27	2.27	2.26	1.00	down	4.00E-01	8.95E-01	-	-
1380056_at	---	---	---	---	BF407351	2.31	2.30	2.31	2.30	2.31	2.29	1.00	down	4.85E-01	8.95E-01	-	-
1387337_at	Cort	cortistatin	25305	Rn.10490	NM_012835	2.57	2.56	2.57	2.57	2.59	2.57	1.00	up	5.51E-01	8.95E-01	-	-
1369481_at	Tnfsf4	tumor necrosis factor (ligand) superfamily, member 4	89814	Rn.30043	NM_053552	2.31	2.30	2.32	2.31	2.32	2.30	1.00	down	5.20E-01	8.95E-01	-	-
1385278_at	---	---	---	Rn.204330	AI072041	2.43	2.42	2.45	2.45	2.42	2.42	1.00	down	7.18E-01	9.11E-01	-	-
1391540_at	---	---	---	---	BE107120	2.35	2.35	2.37	2.35	2.36	2.34	1.00	down	5.84E-01	8.95E-01	-	-
1397129_at	---	---	---	Rn.147931	BE109908	2.38	2.36	2.38	2.37	2.39	2.35	1.00	down	7.04E-01	9.07E-01	-	-
1380585_at	---	---	---	Rn.154626	BF396335	2.31	2.30	2.31	2.30	2.31	2.29	1.00	down	3.66E-01	8.95E-01	-	-
1397036_at	---	---	---	Rn.147464	BF400685	2.34	2.33	2.35	2.34	2.36	2.31	1.00	down	6.98E-01	9.07E-01	-	-
1396122_at	---	---	---	Rn.170612	BE097234	2.34	2.34	2.35	2.34	2.35	2.33	1.00	down	4.98E-01	8.95E-01	-	-
1369478_at	Nr0b1	nuclear receptor subfamily 0, group B, member 1	58850	Rn.10596	NM_053317	2.29	2.29	2.30	2.29	2.30	2.28	1.00	down	3.40E-01	8.95E-01	-	-
1393960_at	---	---	---	Rn.133784	AI072197	2.33	2.33	2.34	2.33	2.34	2.32	1.00	down	5.01E-01	8.95E-01	-	-
1369466_at	Chrna9	cholinergic receptor, nicotinic, alpha 9	65024	Rn.54463	NM_022930	2.35	2.34	2.36	2.34	2.36	2.33	1.00	down	5.74E-01	8.95E-01	-	-
1380249_at	---	---	---	---	AA848842	2.40	2.37	2.45	2.40	2.42	2.38	1.00	down	8.51E-01	9.54E-01	-	-
1391993_at	---	---	---	Rn.209897	BF395823	2.36	2.35	2.38	2.36	2.38	2.35	1.00	down	6.79E-01	9.02E-01	-	-
1398675_at	---	---	---	---	AI639084	2.58	2.57	2.59	2.57	2.59	2.57	1.00	down	5.68E-01	8.95E-01	-	-
1369452_a_at	Picalm	phosphatidylinositol binding clathrin assembly protein	89816	Rn.24871	NM_053554	7.21	7.36	7.50	7.48	7.03	7.57	1.00	up	9.79E-01	9.93E-01	-	-
1396739_at	---	---	---	---	BE120455	2.35	2.34	2.37	2.35	2.36	2.34	1.00	down	6.18E-01	8.95E-01	-	-
1379333_at	Armcx6	armadillo repeat containing, X-linked 6	363496	Rn.121931	BI296377	2.34	2.33	2.38	2.34	2.37	2.33	1.00	down	8.03E-01	9.37E-01	-	-
1377499_a_at	Hrc	histidine rich calcium binding protein	292905	Rn.41521	BF420810	2.35	2.34	2.36	2.34	2.36	2.34	1.00	down	5.79E-01	8.95E-01	-	-
1392282_at	---	---	---	Rn.208308	BE114642	2.38	2.37	2.39	2.37	2.38	2.37	1.00	down	3.71E-01	8.95E-01	-	-
1395397_at	Hectd2	HECT domain containing 2	309514	Rn.219294	AI010952	2.35	2.34	2.36	2.35	2.35	2.33	1.00	down	5.36E-01	8.95E-01	-	-
1374889_at	Birc7	baculoviral IAP repeat-containing 7	296468	Rn.17989	BI294745	2.26	2.25	2.26	2.25	2.26	2.25	1.00	down	3.00E-01	8.95E-01	-	-
1393635_x_at	Tubb4	tubulin, beta 4	29213	Rn.195342	AI230430	2.33	2.32	2.34	2.32	2.34	2.31	1.00	down	6.25E-01	8.95E-01	-	-
1369913_at	Opn1mw	opsin 1 (cone pigments), medium-wave-sensitive	89810	Rn.81056	NM_053548	2.36	2.35	2.37	2.35	2.36	2.35	1.00	down	4.75E-01	8.95E-01	-	-
1370504_a_at	Prnp22	peripheral myelin protein 22	24680	Rn.1476	AW252810	2.20	2.19	2.19	2.19	2.19	2.19	1.00	down	3.38E-01	8.95E-01	-	-
1369185_a_at	Syt7	synaptotagmin VII	59267	Rn.91884	AI713274	2.45	2.44	2.46	2.44	2.45	2.44	1.00	down	4.58E-01	8.95E-01	-	-
1377229_at	---	---	---	Rn.208324	BF394058	2.33	2.32	2.34	2.33	2.34	2.32	1.00	down	5.63E-01	8.95E-01	-	-
1382507_at	Cd96	CD96 molecule	498079	Rn.55482	AW919878	2.38	2.38	2.40	2.38	2.40	2.37	1.00	down	7.04E-01	9.07E-01	-	-
1376310_at	---	---	---	Rn.46109	BI285686	2.34	2.33	2.36	2.33	2.35	2.33	1.00	down	6.27E-01	8.95E-01	-	-
1386804_at	---	---	---	Rn.81000	BF553434	2.42	2.40	2.44	2.41	2.45	2.39	1.00	down	7.99E-01	9.35E-01	-	-
1382512_at	---	---	---	Rn.164504	AA850695	5.34	4.85	4.50	5.07	4.51	5.10	1.00	down	9.87E-01	9.96E-01	-	-
1391746_at	---	---	---	---	BI286076	2.32	2.30	2.32	2.31	2.31	2.30	1.00	down	4.15E-01	8.95E-01	-	-
1382170_at	LOC498685	similar to UPF0308 protein C9orf21	498685	Rn.24906	AA799427	2.32	2.31	2.32	2.31	2.32	2.30	1.00	down	4.53E-01	8.95E-01	-	-
1377269_at	---	---	---	---	BI288720	2.43	2.41	2.44	2.42	2.43	2.41	1.00	down	5.68E-01	8.95E-01	-	-
1368635_at	Tnfsf8	tumor necrosis factor receptor superfamily, member 8	25069	Rn.11322	NM_019135	2.40	2.38	2.41	2.39	2.41	2.38	1.00	down	6.92E-01	9.05E-01	-	-
1370700_at	Pcyt1b	phosphate cytidylyltransferase 1, choline, beta	286936	Rn.48742	AF190256	2.27	2.27	2.28	2.27	2.27	2.26	1.00	down	4.31E-01	8.95E-01	-	-
1387473_at	Tnp1	transition protein 1	24839	Rn.9959	NM_017056	2.44	2.44	2.46	2.44	2.46	2.43	1.00	down	6.23E-01	8.95E-01	-	-
1370774_at	Dcm5	Dcm5 protein	257653	Rn.81019	AF412817	2.34	2.33	2.35	2.34	2.35	2.33	1.00	down	5.94E-01	8.95E-01	-	-
1368551_at	Prps2	phosphoribosyl pyrophosphate synthetase 2	24689	Rn.11320	NM_012634	2.34	2.35	2.34	2.34	2.35	2.33	1.00	down	4.87E-01	8.95E-01	-	-
1392703_at	Tbx4	T-box 4	303399	Rn.183708	AA945957	2.43	2.42	2.44	2.43	2.44	2.41	1.00	down	6.73E-01	9.01E-01	-	-
1397109_at	---	---	---	---	BF390889	2.41	2.41	2.42	2.41	2.42	2.40	1.00	down	4.32E-01	8.95E-01	-	-
1396652_at	---	---	---	Rn.210004	BF392621	2.43	2.42	2.44	2.42	2.44	2.42	1.00	down	4.87E-01	8.95E-01	-	-
1394604_at	---	---	---	Rn.206117	BF562920	2.36	2.35	2.36	2.35	2.36	2.37	1.00	up	3.96E-01	8.95E-01	-	-
1392866_at	---	---	---	Rn.20780	AI044609	2.39	2.38	2.40	2.38	2.39	2.38	1.00	down	4.87E-01	8.95E-01	-	-
1387173_at	Cma1	chymase 1, mast cell	25627	Rn.10182	NM_013092	2.35	2.33	2.36	2.34	2.35	2.33	1.00	down	5.96E-01	8.95E-01	-	-
1392963_at	Scrn1	secernin 1	502776	Rn.154317	BI276033	2.32	2.32	2.33	2.32	2.32	2.31	1.00	down	3.78E-01	8.95E-01	-	-
1393023_at	---	---	---	Rn.177410	AA997035	2.33	2.28	2.30	2.29	2.36	2.28	1.00	up	8.62E-01	9.57E-01	-	-
1387362_at	Scn4a	sodium channel, voltage-gated, type 4, alpha subunit	25722	Rn.9700	NM_013178	2.33	2.32	2.34	2.32	2.33	2.31	1.00	down	5.34E-01	8.95E-01	-	-
1376922_at	---	---	---	Rn.18692	AW523772	2.33	2.32	2.33	2.32	2.33	2.31	1.00	down	4.55E-01	8.95E-01	-	-
1384630_at	---	---	---	Rn.7499	AI229071	2.36	2.35	2.36	2.35	2.36	2.34	1.00	down	5.32E-01	8.95E-01	-	-
1379798_at	---	---	---	Rn.166771	AW144116	2.42	2.40	2.42	2.41	2.41	2.42	1.00	up	4.84E-01	8.95E-01	-	-
1386041_a_at	Klf2	Kruppel-like factor 2 (lung)	306330	Rn.92653	BF288243	2.36	2.35	2.37	2.35	2.37	2.34	1.00	down	6.67E-01	8.96E-01	-	-
1378076_at	---	---	---	Rn.11429	AA963273	2.30	2.29	2.30	2.29	2.30	2.28	1.00	down	4.81E-01	8.95E-01	-	-
1395222_at	---	---	---	Rn.204794	BF287049	2.40	2.39	2.41	2.39	2.44	2.35	1.00	down	8.54E-01	9.55E-01	-	-
1369724_at	F13a1	coagulation factor XIII, A1 polypeptide	60327	Rn.42925	NM_021698	2.32	2.32	2.34	2.32	2.33	2.31	1.00	down	5.96E-01	8.95E-01	-	-
1397213_at	---	---	---	Rn.170259	AI169412	2.33	2.33	2.35	2.33	2.34	2.32	1.00	down	4.86E-01	8.95E-01	-	-
1369377_at	Hcrtr2	hypocretin (orexin) receptor 2	25605	Rn.9893	NM_013074	2.35	2.34	2.36	2.34	2.35	2.34	1.00	down	5.18E-01	8.95E-01	-	-
1381723_at	---	---	---	---	BF389527	2.30	2.30	2.32	2.30	2.31	2.30	1.00	down	4.27E-01	8.95E-01	-	-
1377559_at	---	---	---	---	BF405014	2.34	2.34	2.35	2.34	2.35	2.33	1.00	down	3.81E-01	8.95E-01	-	-
1370423_at	Gna15	guanine nucleotide binding protein, alpha 15	89788	Rn.3574	AB015308	2.40	2.39	2.42	2.40	2.40	2.39	1.00	down	4.86E-01	8.95E-01	-	-
1389597_at	Pgbd5	piggyBac transposable element derived 5	292098	Rn.23325	BI293445	2.34	2.33	2.36	2.34	2.35	2.33	1.00	down	6.44E-01	8.95E-01	-	-
1369761_at	Pou1f1	POU class 1 homeobox 1	25517	Rn.10445	NM_013008	2.33	2.33	2.34	2.33	2.34	2.32	1.00	down	5.09E-01	8.95E-01	-	-
1394001_at	Optc	Opticin	304802	Rn.154120	BM384538	2.64	2.88	2.65	2.89	2.66	2.64	1.00	up	9.65E-01	9.90E-01	-	-
1394359_at	Bclaf1	BCL2-associated transcription factor 1	293017	Rn.202401	BF553498	2.36	2.35	2.36	2.36	2.36	2.34	1.00	down	3.94E-01	8.95E-01	-	-
1372785_at	Ash1l	ash1 (absent, small, or homeotic)-like (Drosophila)	310638	Rn.206058	BG671790	7.15	7.03	7.04	6.66	7.29	7.27	1.00	up	9.81E-01	9.94E-01	-	-
1380315_at	---	---	---	Rn.39492	BF409953	2.31	2.30	2.31	2.30	2.31	2.29	1.00	down	4.32E-01	8.95E-01	-	-
1381841_at	---	---	---	Rn.211020	BF411958	2.31	2.30	2.31	2.30	2.31	2.29	1.00	down	4.39E-01	8.95E-01	-	-
1396988_at	---	---	---	Rn.172810	BF396476	2.31	2.30	2.32	2.30	2.31	2.30	1.00	down	4.78E-01	8.95E-01	-	-
1374313_at	Map1s	microtubule-associated protein 1S	290640	Rn.38446	BI294383	2.68	2.67	2.68	2.67	2.68	2.66	1.00	down	3.90E-01	8.95E-01	-	-
1373637_at	---	---	---	---	BG372823	2.29	2.28	2.30	2.28	2.29	2.28	1.00	down	4.60E-01	8.95E-01	-	-
1381521_at	---	---	---	Rn.167800	AI454580	2.80	2.80	2.82	2.79	2.81	2.80	1.00	down	5.46E-01	8.95E-01	-	-
1378144_at	Kank4	KN motif and ankyrin repeat domains 4	313385	Rn.21560	BI296384	2.42	2.41	2.43	2.41	2.43	2.40	1.00	down	6.95E-01	9.06E-01	-	-
1384710_at	Tdrd12	tudor domain containing 12	292813	Rn.161838	BF403316	2.36	2.34	2.36	2.34	2.35	2.33	1.00	down	5.93E-01	8.95E-01	-	-
1390970_at	---	---	---	Rn.210971	BF413658	2.35	2.34	2.36	2.34	2.35	2.34	1.00	down	4.42E-01	8.95E-01	-	-
1369203_at	Wif1	Wnt inhibitory factor 1	114557	Rn.74256	NM_053738	2.43	2.41	2.45	2.43	2.44	2.40	1.00	down	7.52E-01	9.20E-01	-	-
1368503_at	Gch1	GTP cyclohydrolase 1	29244	Rn.28195	NM_024358	2.53	2.51	2.52	2.51	2.52	2.51	1.00	down	5.60E-01	8.95E-01	-	-
1378039_at	---	---	---	Rn.169613	BG381187	2.42	2.40	2.45	2.46	2.43	2.40	1.00	up	8.36E-01	9.48E-01	-	-
1381693_at	---	---	---	Rn.148005	AW526413	2.31	2.31	2.32	2.31	2.32	2.30	1.00	down	4.77E-01	8.95E-01	-	-
1375738_at	Sprn	Shadow of prion protein homolog (zebrafish)	541462	Rn.23342	BF404416	2.32	2.31	2.33	2.31	2.32	2.30	1.00	down	4.86E-01	8.95E-01	-	-
1369093_at	Reln	reelin	24718	Rn.98353	NM_080394	2.33	2.32	2.33	2.32	2.33	2.30	1.00	down	5.59E-01	8.95E-01	-	-
1387396_at	Hamp	hepcidin antimicrobial peptide	84604	Rn.7865	NM_053469	2.39	2.40	2.40	2.40	2.37	2.40	1.00	down	6.22E-01	8.95E-01	-	-
1382706_at	---	---	---	Rn.35579	AI501895	2.37	2.34	2.39	2.36	2.38	2.35	1.00	down	7.63E-01	9.23E-01	-	-
1394769_at	---	---	---	Rn.205298	AI554998	2.40	2.38	2.42	2.39	2.42	2.38	1.00	down	7.48E-01	9.19E-01	-	-
1386012_at	---	---	---	Rn.151445	BG672820	2.32	2.31	2.32	2.31	2.32	2.30	1.00	down	3.92E-01	8.95E-01	-	-
1379836_at	---	---	---	Rn.55340	BF400850	2.35	2.34	2.36	2.34	2.35	2.34	1.00	down	5.89E-01	8.95E-01	-	-
1370593_at	Cyp3a2	cytochrome P450, family 3, subfamily a, polypeptide 2	266882	---	U09742	2.34	2.33	2.35	2.34	2.35	2.33	1.00	down	5.36E-01	8.95E-01	-	-
1392582_at	Lrrc4c	leucine rich repeat containing 4C	311236	Rn.219303	AA819053	2.34	2.33	2.36	2.34	2.35	2.33	1.00	down	6.32E-01	8.95E-01	-	-
1398307_at	Cyp3a18	cytochrome P450, 3a18	252931	Rn.32085	D38381	2.34	2.34	2.36	2.34	2.35	2.33	1.00	down	4.81E-01	8.95E-01	-	-
1387282_at	Hspb8	heat shock protein 8	113906	Rn.102906	NM_053612	2.36	2.35	2.38	2.38	2.38	2.35	1.00	up	7.02E-01	9.07E-01	-	-
1396890_at	Dclk2	Doublecortin-like kinase 2	310998	Rn.23327	BE096662	2.24	2.23	2.25	2.23	2.24	2.23	1.00	down	4.07E-01	8.95E-01	-	-
1398028_at	---	---	---	Rn.153841	BF399371	2.25	2.24	2.25	2.25	2.25	2.23	1.00	down	4.05E-01	8.95E-01	-	-
1390413_at	RGD1310371	similar to RIKEN cDNA 1700026D08	308794	Rn.23589	AI112629	2.42	2.41	2.43	2.41	2.43	2.39	1.00	down	6.42E-01	8.95E-01	-	-
1391364_at	---	---	---	---

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1369581_at	Pemt	phosphatidylethanolamine N-methyltransferase	25511	Rn.9875	NM_013003	2.35	2.34	2.35	2.34	2.35	2.34	1.00	down	3.94E-01	8.95E-01	-	-
1388277_at	RGD1564318	similar to immunoglobulin light chain variable region	363828	---	AI029631	2.28	2.28	2.29	2.28	2.29	2.27	1.00	down	4.83E-01	8.95E-01	-	-
1377381_at	---	---	---	Rn.40969	AW252431	2.35	2.34	2.36	2.34	2.35	2.33	1.00	down	5.32E-01	8.95E-01	-	-
1381562_at	RGD1565197	Similar to hypothetical protein BC018697	308587	Rn.78502	BI284650	2.46	2.45	2.47	2.45	2.52	2.42	1.00	up	8.66E-01	9.58E-01	-	-
1392213_at	---	---	---	Rn.207945	BM389936	2.38	2.37	2.38	2.37	2.38	2.37	1.00	down	3.62E-01	8.95E-01	-	-
1398025_at	---	---	---	---	BF403174	2.33	2.32	2.35	2.32	2.34	2.32	1.00	down	5.53E-01	8.95E-01	-	-
1378005_at	---	---	---	Rn.24818	AW527486	2.53	2.52	2.52	2.50	2.54	2.51	1.00	down	7.21E-01	9.11E-01	-	-
1396626_at	---	---	---	---	BF410555	2.28	2.27	2.29	2.27	2.28	2.26	1.00	down	4.71E-01	8.95E-01	-	-
1396531_at	---	---	---	Rn.208666	BF416287	2.37	2.36	2.39	2.37	2.38	2.36	1.00	down	6.18E-01	8.95E-01	-	-
1396491_at	---	---	---	---	BF401671	2.33	2.32	2.33	2.33	2.33	2.31	1.00	down	4.85E-01	8.95E-01	-	-
1384929_at	Apob48r	apolipoprotein B48 receptor	499264	Rn.107719	AI072252	2.37	2.36	2.37	2.36	2.37	2.34	1.00	down	5.88E-01	8.95E-01	-	-
1369874_at	Gpr1	G protein-coupled receptor 1	25457	Rn.81208	NM_012961	2.29	2.29	2.30	2.29	2.30	2.28	1.00	down	3.45E-01	8.95E-01	-	-
1369417_a_at	Opcml	opioid binding protein/cell adhesion molecule-like	116597	Rn.11366	NM_053848	2.33	2.32	2.34	2.33	2.34	2.32	1.00	down	4.65E-01	8.95E-01	-	-
1376939_at	---	---	---	Rn.18481	BI284907	2.54	2.53	2.54	2.53	2.54	2.52	1.00	down	5.55E-01	8.95E-01	-	-
1392355_at	---	---	---	Rn.154063	AW527665	2.36	2.33	2.38	2.36	2.37	2.36	1.00	up	7.17E-01	9.10E-01	-	-
1370718_at	Syt10	synaptotagmin X	60567	Rn.212261	AF375463	2.38	2.37	2.39	2.37	2.38	2.37	1.00	down	3.80E-01	8.95E-01	-	-
1372983_at	---	---	---	Rn.210541	BF398986	2.37	2.36	2.37	2.36	2.37	2.35	1.00	down	4.34E-01	8.95E-01	-	-
1373187_at	---	---	---	Rn.63144	AT005533	2.45	2.43	2.45	2.43	2.48	2.41	1.00	down	8.22E-01	9.43E-01	-	-
1369394_at	Unc5a	unc-5 homolog A (C. elegans)	60629	Rn.44433	NM_022206	2.39	2.38	2.40	2.39	2.40	2.38	1.00	down	5.56E-01	8.95E-01	-	-
1369424_at	Cyp2a2	cytochrome P450, subfamily 2A, polypeptide 1	24895	Rn.9867	NM_012893	2.46	2.45	2.47	2.46	2.48	2.43	1.00	down	7.61E-01	9.22E-01	-	-
1377252_at	RGD1306862	similar to RIKEN cDNA 1200011M11	287596	Rn.45630	BF411321	2.85	2.84	2.77	2.78	2.86	2.83	1.00	up	8.84E-01	9.64E-01	-	-
1397131_at	---	---	---	Rn.61698	BG376825	2.37	2.36	2.39	2.37	2.38	2.36	1.00	down	6.17E-01	8.95E-01	-	-
1381851_at	Cpeb3	Cytoplasmic polyadenylation element binding protein 3	309510	Rn.106130	AW521903	2.24	2.24	2.25	2.24	2.24	2.23	1.00	down	4.60E-01	8.95E-01	-	-
1398128_at	Rev3l	REV3-like, catalytic subunit of DNA polymerase zeta (yeast)	309812	Rn.8189	AI548626	2.48	2.47	2.49	2.47	2.49	2.46	1.00	down	6.27E-01	8.95E-01	-	-
1369330_at	Unc13a	unc-13 homolog A (C. elegans)	64829	Rn.10126	NM_022861	2.52	2.52	2.53	2.50	2.55	2.51	1.00	down	7.51E-01	9.19E-01	-	-
1367992_at	Scg5	secretogranin V	25719	Rn.6173	NM_013175	2.32	2.31	2.33	2.31	2.32	2.30	1.00	down	5.73E-01	8.95E-01	-	-
1381608_at	---	---	---	Rn.202803	BF394383	2.35	2.34	2.36	2.34	2.35	2.33	1.00	down	5.57E-01	8.95E-01	-	-
1395225_at	---	---	---	---	AI409427	3.14	3.23	2.72	2.79	2.69	3.60	1.00	down	9.88E-01	9.96E-01	-	-
1388124_at	Ctsj	cathepsin J	29174	---	BI277835	2.35	2.34	2.36	2.35	2.36	2.34	1.00	down	5.74E-01	8.95E-01	-	-
1379624_at	---	---	---	Rn.22683	AA964442	2.55	2.53	2.55	2.54	2.56	2.52	1.00	down	6.43E-01	8.95E-01	-	-
1398284_at	Rax	retina and anterior neural fold homeobox	114213	Rn.87955	NM_053678	2.35	2.34	2.36	2.35	2.36	2.34	1.00	down	5.88E-01	8.95E-01	-	-
1369041_at	Nlgn1	neuroligin 1	116647	Rn.10173	NM_053868	2.37	2.37	2.39	2.37	2.38	2.36	1.00	down	5.24E-01	8.95E-01	-	-
1391251_at	---	---	---	Rn.20351	BI290666	2.44	2.43	2.47	2.44	2.46	2.43	1.00	down	7.01E-01	9.07E-01	-	-
1395629_at	---	---	---	Rn.30788	BE105336	2.33	2.32	2.34	2.33	2.34	2.32	1.00	down	5.41E-01	8.95E-01	-	-
1376320_at	---	---	---	Rn.8449	BF393051	2.51	2.57	2.50	2.50	2.53	2.56	1.00	up	8.68E-01	9.59E-01	-	-
1398483_at	Rgs17	regulator of G-protein signaling 17	308118	Rn.166916	AI229118	2.30	2.30	2.31	2.30	2.31	2.29	1.00	down	4.37E-01	8.95E-01	-	-
1385590_at	---	---	---	---	BI296811	2.32	2.31	2.32	2.31	2.32	2.30	1.00	down	5.41E-01	8.95E-01	-	-
1375575_at	Camk2b	calcium/calmodulin-dependent protein kinase II beta	24245	Rn.9743	BF403410	2.28	2.28	2.30	2.28	2.29	2.27	1.00	down	4.87E-01	8.95E-01	-	-
1370138_at	Lef1	lymphoid enhancer binding factor 1	161452	Rn.21926	NM_130429	2.34	2.33	2.35	2.33	2.34	2.32	1.00	down	5.11E-01	8.95E-01	-	-
1391960_at	LOC503361 /// LO	similar to nidogen 2 protein /// similar to nidogen 2 /// similar to nidogen 2 /// sl27 /// 499004 /// 50		Rn.13869	AW253967	2.33	2.32	2.33	2.32	2.33	2.31	1.00	down	4.66E-01	8.95E-01	-	-
1369818_at	Gabrb2	gamma-aminobutyric acid (GABA) A receptor, beta 2	25451	Rn.207158	NM_012957	2.34	2.34	2.36	2.34	2.35	2.33	1.00	down	5.30E-01	8.95E-01	-	-
1395936_at	---	---	---	---	BF392796	2.40	2.39	2.40	2.39	2.40	2.38	1.00	down	5.41E-01	8.95E-01	-	-
1369151_at	Dlk1	delta-like 1 homolog (Drosophila)	114587	Rn.14547	NM_053744	2.34	2.33	2.35	2.33	2.34	2.33	1.00	down	4.96E-01	8.95E-01	-	-
1383846_at	RGD1562846	similar to Docking protein 5 (Downstream of tyrosine kinase 5) (Protein dok-5	502694	Rn.74088	AI576094	2.36	2.36	2.37	2.36	2.37	2.35	1.00	down	5.89E-01	8.95E-01	-	-
1392344_at	---	---	---	Rn.14797	AI709455	2.37	2.36	2.38	2.37	2.38	2.36	1.00	down	5.53E-01	8.95E-01	-	-
1390349_at	---	---	---	Rn.210904	BF404126	2.32	2.32	2.33	2.32	2.33	2.30	1.00	down	5.32E-01	8.95E-01	-	-
1378756_at	Papolb	poly (A) polymerase beta (testis specific)	304300	Rn.210888	BF409203	2.29	2.29	2.30	2.29	2.30	2.28	1.00	down	2.99E-01	8.95E-01	-	-
1369600_at	Fgf11	fibroblast growth factor 11	170832	Rn.73083	NM_130816	2.33	2.32	2.34	2.33	2.34	2.32	1.00	down	5.66E-01	8.95E-01	-	-
1377054_at	---	---	---	Rn.41884	BF418563	2.42	2.41	2.44	2.41	2.42	2.41	1.00	down	6.26E-01	8.95E-01	-	-
1388207_at	PRP-2	proline-rich protein	287750	Rn.81196	BM384711	2.32	2.31	2.33	2.31	2.32	2.30	1.00	down	5.26E-01	8.95E-01	-	-
1382871_at	---	---	---	Rn.199443	AW920165	2.24	2.23	2.24	2.24	2.23	2.25	1.00	up	6.08E-01	8.95E-01	-	-
1369664_at	Avpr1a	arginine vasopressin receptor 1A	25107	Rn.32282	NM_053019	2.46	2.44	2.49	2.46	2.47	2.45	1.00	down	7.44E-01	9.17E-01	-	-
1392392_at	---	---	---	---	AI012510	2.41	2.41	2.41	2.40	2.41	2.40	1.00	down	3.81E-01	8.95E-01	-	-
1391975_at	---	---	---	Rn.147227	BF400601	2.35	2.34	2.36	2.34	2.35	2.33	1.00	down	5.99E-01	8.95E-01	-	-
1372163_at	---	---	---	Rn.164028	BG670246	2.35	2.33	2.36	2.34	2.35	2.33	1.00	down	6.22E-01	8.95E-01	-	-
1376918_at	---	---	---	Rn.11698	AI029930	2.80	2.79	2.80	2.80	2.83	2.76	1.00	up	7.95E-01	9.34E-01	-	-
1388061_a_at	Epha7	Eph receptor A7	171287	Rn.10181	U21955	2.35	2.35	2.37	2.35	2.36	2.34	1.00	down	5.91E-01	8.95E-01	-	-
1391461_at	RGD1306576	similar to hypothetical protein	298002	Rn.21605	BF285149	4.11	4.31	3.99	3.98	4.12	4.33	1.00	up	9.72E-01	9.92E-01	-	-
1384717_at	---	---	---	---	AA894199	2.41	2.40	2.42	2.40	2.41	2.39	1.00	down	5.59E-01	8.95E-01	-	-
1371270_at	Olr442	olfactory receptor 442	295713	Rn.142988	U50948	2.32	2.31	2.33	2.31	2.32	2.31	1.00	down	5.21E-01	8.95E-01	-	-
1396883_at	---	---	---	Rn.43679	AI548898	2.37	2.36	2.38	2.36	2.38	2.36	1.00	down	5.76E-01	8.95E-01	-	-
1376995_at	Palb2	partner and localizer of BRCA2	293452	Rn.43638	BE108967	2.50	2.49	2.50	2.49	2.55	2.44	1.00	down	8.82E-01	9.64E-01	-	-
1396792_at	---	---	---	---	BF392277	2.47	2.45	2.47	2.46	2.48	2.45	1.00	up	6.32E-01	8.95E-01	-	-
1383145_at	Lamp3	lysosomal-associated membrane protein 3	303801	Rn.19784	BF283924	2.36	2.35	2.37	2.35	2.36	2.35	1.00	down	6.13E-01	8.95E-01	-	-
1369030_at	Prss1	protease, serine, 1 (trypsin 1)	24691	Rn.34435	NM_012935	2.31	2.31	2.33	2.31	2.32	2.30	1.00	down	5.38E-01	8.95E-01	-	-
1368688_at	Ntsr2	neurotensin receptor 2	64636	Rn.127792	NM_022695	2.34	2.33	2.35	2.33	2.34	2.32	1.00	down	4.96E-01	8.95E-01	-	-
1393821_at	Nkain3	Na+/K+ transporting ATPase interacting 3	689576	Rn.211572	BF416086	2.47	2.47	2.50	2.46	2.49	2.48	1.00	down	7.43E-01	9.17E-01	-	-
1396584_at	Pvrl4	poliovirus receptor-related 4	498281	Rn.20370	AI764405	2.35	2.35	2.36	2.35	2.35	2.34	1.00	down	4.42E-01	8.95E-01	-	-
1380936_at	RGD1561665	similar to spatial-delta	499429	Rn.163425	AI229699	2.44	2.43	2.45	2.44	2.46	2.43	1.00	up	6.36E-01	8.95E-01	-	-
1393549_at	---	---	---	Rn.156368	BF390163	2.47	2.46	2.51	2.46	2.55	2.44	1.00	up	8.97E-01	9.68E-01	-	-
1389378_at	Cdc42ep5	CDC42 effector protein (Rho GTPase binding) 5	361505	Rn.198486	AI599324	2.43	2.43	2.44	2.43	2.44	2.42	1.00	down	4.81E-01	8.95E-01	-	-
1384927_at	Tubb4	tubulin, beta 4	29213	Rn.19534	AI230430	2.33	2.32	2.33	2.32	2.33	2.32	1.00	down	3.53E-01	8.95E-01	-	-
1379777_at	---	---	---	Rn.155659	AI070855	2.32	2.31	2.33	2.32	2.34	2.32	1.00	up	5.79E-01	8.95E-01	-	-
1394734_at	Acbd3	acyl-Coenzyme A binding domain containing 3	289312	Rn.57036	BE120590	2.82	2.82	2.83	2.82	2.83	2.81	1.00	down	4.50E-01	8.95E-01	-	-
1397504_at	Wsb2	WD repeat and SOCS box-containing 2	288692	Rn.4063	BE119297	2.33	2.32	2.34	2.33	2.33	2.32	1.00	down	4.22E-01	8.95E-01	-	-
1384828_at	Kif7	Kinesin family member 7	293047	Rn.145008	AI058952	2.36	2.35	2.37	2.36	2.36	2.35	1.00	down	4.65E-01	8.95E-01	-	-
1381517_at	---	---	---	Rn.209351	BF413506	2.61	2.57	2.70	2.59	2.69	2.58	1.00	down	9.26E-01	9.79E-01	-	-
1393967_at	---	---	---	---	AI764726	2.30	2.29	2.29	2.29	2.29	2.28	1.00	down	3.32E-01	8.95E-01	-	-
1398198_at	---	---	---	Rn.173111	BF400669	2.32	2.31	2.33	2.31	2.32	2.30	1.00	down	4.87E-01	8.95E-01	-	-
1375123_at	Sox4	SRY (sex determining region Y)-box 4	364712	Rn.163667	BE115519	2.26	2.25	2.27	2.25	2.26	2.25	1.00	down	3.87E-01	8.95E-01	-	-
1389356_at	---	---	---	Rn.203553	AW915885	2.39	2.38	2.40	2.38	2.39	2.37	1.00	down	5.20E-01	8.95E-01	-	-
1390828_at	Npy1r	neuropeptide Y receptor Y1	29358	Rn.11642	BI395810	2.38	2.38	2.40	2.38	2.39	2.37	1.00	down	5.90E-01	8.95E-01	-	-
1369025_at	Cd5	Cd5 molecule	54236	Rn.11337	NM_019295	2.35	2.35	2.36	2.35	2.36	2.34	1.00	down	5.06E-01	8.95E-01	-	-
1384044_at	Sgcb	sarcoglycan, beta (dystrophin-associated glycoprotein)	680229	Rn.98258	AA964882	2.37	2.44	2.39	2.47	2.35	2.37	1.00	down	9.11E-01	9.73E-01	-	-
1393614_at	Necab3	N-terminal EF-hand calcium binding protein 3	311562	Rn.19404	AI060247	2.37	2.37	2.38	2.37	2.37	2.36	1.00	down	3.96E-01	8.95E-01	-	-
1384625_at	RGD1306224	similar to RIKEN cDNA 2410116G06	366244	Rn.46316	BF408700	2.34	2.33	2.36	2.34	2.35	2.33	1.00	down	6.10E-01	8.95E-01	-	-
1375787_at	RGD1304878	Similar to 2410024A21Rik protein	314415	Rn.20310	BF387587	2.61	2.60	2.63	2.61	2.62	2.60	1.00	down	6.60E-01	8.98E-01	-	-
1390073_at	Ankrd43	ankyrin repeat domain 43	497903	---	AI715122	2.39	2.37	2.40	2.39	2.39	2.37	1.00	down	6.83E-01	9.03E-01	-	-
1394791_at	---	---	---	Rn.204610	AI138038	2.35	2.34	2.37	2.35	2.36	2.34	1.00	down	6.33E-01	8.95E-01	-	-
1377279_at	LOC689791	Hypothetical protein LOC689791	689791	Rn.134767	BF394097	2.42	2.41	2.44	2.42	2.43	2.41	1.00	down	6.07E-01	8.95E-01	-	-
1380797_at	---	---	---	Rn.207767	BE106817	2.36	2.35	2.37	2.36	2.36	2.35	1.00	down	4.70E-01	8.95E-01	-	-
1384159_at	---	---	---	Rn.9039	AA956611	2.33	2.32	2.33	2.32	2.33	2.31	1.00	down	5.21E-01	8.95E-01	-	-
1394631_at	Prdm8	PR domain containing 8	305198	Rn.162242	BM392159	2.33	2.32	2.33	2.33	2.33	2.31	1.00	down	4.10E-01	8.95E-01	-	-
1392108_at	---	---	---	Rn.166608	BF390648	2.30	2.29	2.30	2.29	2.30	2.28	1.00	down	4.61E-01	8.95E-01	-	-
1397329_at	---	---	---	Rn.160396	AI576277	2.41	2.39	2.41	2.40	2.40	2.39	1.00	down	4.78E-01	8.95E-01	-	-
1378613_at	---	---	---	Rn.210837	BF404986	2.31	2.30	2.32	2.30	2.31	2.30	1.00	down	4.34E-01	8.95E-01	-	-
1372455_at	Tspan12	tetraspanin 12	362326	Rn.2146	AI410264	3.65	2.77	2.72	2.60	2.61	3.96	1.00	up	9.93E-01	9.98E-01	-	-
1378723_at	---	---	---	Rn.23575	BF419153	2.33	2.32	2.34	2.33	2.33	2.32	1.00	down	5.13E-01	8.95E-01	-	-
1394124_at	LOC684996	Similar to chromosome 7 open reading frame 11	684996	Rn.30	AA891753	2.54	2.51	2.58	2.53	2.56	2.52	1.00	down	8.47E-01	9.52E-01	-	-
1397842_at	---	---	---	Rn.205581	AI712398	2.28	2.27	2.28	2.27	2.28	2.26	1.00	down	3.85E-01	8.95E-01	-	-
1397669_at	LOC683722	similar to Fgfr1 oncogene partner	683722	Rn.166829	BG666098	2.52	2.49	2.55	2.51	2.52	2.51	1.00	down	7.70E-01	9.25E-01	-	-
1380783_at	Slco5a1	solute carrier organic anion transporter family, member 5A1	312907	Rn.49225	BE113959	2.32	2.31	2.34	2.32	2.33	2.31	1.00	down	5.72E-01	8.95E-01	-	-
1375999_at	RGD1312005	similar to DD1	291580	Rn.7600	AW143197	2.36	2.35	2.37	2.36	2.37	2.35	1.00	down	5.52E-01	8.95E-01	-	-
1389542_at	Cenpe	centromere protein E	362044	Rn.44998	BE108837	2.33	2.32	2.34	2.32	2.34	2.31	1.00	down	5.50E-01	8.95E-01	-	-
1389513_at	---	---	---	Rn.166411	AI501128	2.37	2.36	2.37	2.36	2.37	2.35	1.00	down	5.13E-01	8.95E-01	-	-
1369175_a_at	Ambn	ameloblastin	25376	Rn.11370	NM_012900	2.38	2.37	2.40	2.38	2.39	2.37	1.00	down	5.67E-01	8.95E-01	-	-
1376283_at	---	---	---	Rn.161392	BG378070	2.33	2.32	2.34	2.33	2.34	2.32	1.00	down	5.53E-01	8.95E-01	-	-
1396732_at	---	---	---	Rn.146266	BF405262	2.88	2.83	2.85	2.90	2.84	2.80	1.00	down	8.84E-01	9.64E-01	-	-
1396163_at	---	---	---	Rn.209085	BF406167	2.38	2.37	2.39	2.37	2.38	2.36	1.00	down	5.59E-01	8.95E-01	-	-
1367913_at	Fez1	fasciculation and elongation protein zeta 1 (zygin I)	81730	Rn.5468	NM_031066	2.31	2.31	2.32	2.31	2.32	2.30	1.00	down	5.33E-01	8.95E-01	-	-
1386933_at	Gp2	glycoprotein 2 (zymogen granule membrane)	171459	Rn.11223	NM_134418	2.33	2.32	2.32	2.32	2.33	2.31	1.00	down	4.29E-01	8.95E-01	-	-
1380325_at	---	---	---	Rn.45648	BE115778	2.36	2.36	2.39	2.36	2.38	2.35	1.00	down	7.44E-01	9.17E-01	-	-
1391806_at	LOC498793	similar to inter-alpha-inhibitor H2 chain	498793	Rn.23167	AA957557	2.35	2.35	2.37	2.35	2.36	2.34	1.00	down	6.29E-01	8.95E-01	-	-
1392436_at	Prex1	Phosphatidylinositol-3,4,5-trisphosphate-dependent Rac exchange factor 1	311647	Rn.14163	AI180303	2.31	2.31	2.32	2.30	2.35	2.30	1.00	up	8.01E-01	9.36E-01	-	-
1390302_at	---	---	---	Rn.62273	BF413182	2.45	2.44	2.46	2.44	2.45	2.44	1.00	down	5.24E-01	8.95E-01	-	-
1377592_at	Zfpm2	Zinc finger protein, multitype 2	314930	Rn.135463	BF408982	2.30	2.30	2.31	2.30	2.31	2.29	1.00	down	4.66E-01	8.95E-01	-	-
1396947_at	---	---	---	Rn.210990	BF404382	2.36	2.36	2.37	2.35	2.37	2.35	1.00	down	4.54E-01	8.95E-01	-	-
1394987_at	---	---	---	Rn.203361	BE120450	2.32	2.31	2.33	2.31	2.32	2.30	1.00	down	4.85E-01	8.95E-01	-	-
1371225_at	Drp2	dystrophin related protein 2	66027	Rn.162341	AF195789	2.32	2.32	2.34	2.32	2.33	2.31	1.00	down	4.99E-01	8.95E-01	-	-
1368836_a_at	Acan	aggrecan	58963	Rn.54529	BM385639	2.35	2.34	2.36	2.35	2.36	2.34	1.00	down	5.46E-01	8.95E-01	-	-
1382406_at	Map3k9	mitogen-activated protein kinase kinase kinase 9	500690	Rn.18840	AA892737	2.30	2.29	2.30	2.29	2.30	2.28	1.00	down	3.57E-01	8.95E-01	-	-
1389137_at	Cit	Citron (rho-interacting, serine/threonine kinase 21)	83620	Rn.89069	AA957183	2.40	2.32	2.33	2.32	2.40	2.31	1.00	down	8.96E-01	9.67E-01	-	-
1394470_at	Fam49a	family with sequence similarity 49, member A	298890	Rn.36104	AI502258	2.33	2.32	2.33	2.32	2.35	2.32	1.00	up	6.64E-01	8.99E-01	-	-
1389931_at	---	---	---	Rn.208784	BF415984	2.36	2.36	2.36	2.35	2.36	2.34	1.00	down	5.96E-01	8.95E-01	-	-
1392267_at	Dennd2a	DENN/MADD domain containing 2A	312257	Rn.50302	BE102449	2.42	2.42	2.44	2.46	2.43	2.40	1.00	up	8.15E-01	9.40E-01	-	-
1382360_at	Fzd5	frizzled homolog 5 (Drosophila)	317674	Rn.24792	AA998744	2.38	2.37	2.39	2.38	2.39	2.36	1.00	down	5.81E-01	8.95E-01	-	-
1390061_at	Tnnt2	Troponin T type 2 (cardiac)	24837	Rn.9965	BI289643	2.30	2.31	2.30	2.31	2.29	2.31	1.00	down	5.58E-01	8.95E-01	-	-
1383800_at	Fam155a	family with sequence similarity 155, member A	498667	Rn.45013	AW523537	2.33	2.32	2.34	2.32	2.33	2.31	1.00	down	5.16E-01	8.95E-01	-	-
1378196_at	Slc43a1	solute carrier family 43, member 1	311168	Rn.35465	BI290895	2.35	2.34	2.37	2.34	2.36	2.33	1.00	down	6.92E-01	9.05E-01	-	-
1387945_at	---	---	---	Rn.43233	S75437	2.34	2.34	2.36	2.34	2.35	2.33	1.00	down	5.24E-01	8.95E-01	-	-
1369127_a_at	Ptgfr	prostaglandin F receptor	25652	Rn.97602	X83856	2.29	2.29	2.31	2.30	2.30	2.31	1.00	up	6.06E-01	8.95E-01	-	-
1378496_at	---	---	---	Rn.78549	BM384963	2.44	2.47	2.46	2.46	2.50	2.39	1.00	down	8.89E-01	9.65E-01	-	-
1391405_at	Thsd7a	thrombospondin, type I, domain containing 7A	500032	Rn.206326	BE116739	2.36	2.36	2.37	2.36	2.36	2.35	1.00	down	4.03E-01	8.95E-01	-	-
1394383_at	RGD1303066	Similar to RIKEN cDNA 2610110G12	361789	Rn.136935	BF543872	2.28	2.27	2.28	2.27	2.28	2.26	1.00	down	4.74E-01	8.95E-01	-	-
1371757_s_at	LOC683295	similar to keratin complex 2, basic, gene 6a	683295	---	BI286411	2.34	2.33	2.34	2.32	2.34	2.32	1.00	down	4.78E-01	8.95E-01	-	-
1368618_at	Grb14	growth factor receptor bound protein 14	58844	Rn.30028	NM_031623	2.32	2.31	2.32	2.31	2.32	2.31	1.00	down	4.39E-01	8.95E-01	-	-
1391717_at	---	---	---	---	AW530220	2.39	2.38	2.40	2.39	2.40	2.38	1.00	down	5.56E-01	8.95E-01	-	-
1371303_at	Tdh	L-threonine dehydrogenase	290315	Rn.18003	AI013458	2.47	2.46	2.48	2.47	2.47	2.46	1.00	down	4.64E-01	8.95E-01	-	-
1392900_at	Capza1	capping protein (actin filament) muscle Z-line, alpha 1	691149	Rn.13838	AW888327	7.77	8.44	8.64	8.25	7.62	8.99	1.00	up	9.92E-01	9.97E-01	-	-
1393463_at	Tmem63c	transmembrane protein 63c	314332	Rn.47482	BM390801	2.38	2.37	2.39	2.37	2.38	2.37	1.00	down	3.97E-01	8.95E-01	-	-
1370612_at	Kcna2	potassium voltage-gated channel, shaker-related subfamily, member 2	25468	Rn.10298	M74449	2.37	2.36	2.37	2.36	2.37	2.36	1.00	down	4.58E-01	8.95E-01	-	-
1369332_a_at	Rims1	regulating synaptic membrane exocytosis 1	84556	Rn.10799	NM_052829	2.33	2.33	2.35	2.33	2.34	2.32	1.00	down	5.66E-01	8.95E-01	-	-
1390884_a_at	B3gnt7	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 7	316583	Rn.39638	BE098162	2.41	2.40	2.42	2.41	2.42	2.39	1.00	down	6.31E-01	8.95E-01	-	-
1371112_at	Ret	ret proto-oncogene	24716	Rn.93200	AJ299017

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1376928_at	---	---	---	Rn.206421	BE106737	2.39	2.38	2.40	2.38	2.39	2.37	1.00	down	6.15E-01	8.95E-01	-	-
1397116_at	---	---	---	Rn.210018	BF392810	2.43	2.40	2.43	2.45	2.43	2.40	1.00	up	7.85E-01	9.30E-01	-	-
1369235_at	Unc5b	unc-5 homolog B (C. elegans)	60630	Rn.34617	NM_022207	2.33	2.32	2.34	2.32	2.33	2.32	1.00	down	4.45E-01	8.95E-01	-	-
1369166_at	Mmp9	matrix metallopeptidase 9	81687	Rn.10209	NM_031055	2.36	2.35	2.37	2.35	2.36	2.35	1.00	down	5.58E-01	8.95E-01	-	-
1369490_at	Glp2r	glucagon-like peptide 2 receptor	60432	Rn.163105	NM_021848	2.30	2.29	2.31	2.29	2.30	2.29	1.00	down	4.87E-01	8.95E-01	-	-
1395599_at	---	---	---	Rn.210585	BF399239	2.38	2.37	2.39	2.37	2.38	2.37	1.00	down	5.39E-01	8.95E-01	-	-
1368815_at	Mpz	myelin protein zero	24564	Rn.8997	BG699098	2.33	2.32	2.34	2.33	2.33	2.32	1.00	down	4.59E-01	8.95E-01	-	-
1391366_at	Dnajc11	DnaJ (Hsp40) homolog, subfamily C, member 11	362666	Rn.66161	BF419435	2.51	2.49	2.53	2.50	2.52	2.49	1.00	down	7.00E-01	9.07E-01	-	-
1376913_at	---	---	---	Rn.203488	AA925375	2.62	2.62	2.62	2.61	2.62	2.61	1.00	down	2.34E-01	8.95E-01	-	-
1387476_at	Kcnd2	potassium voltage gated channel, Shal-related family, member 2	65180	Rn.87841	NM_031730	2.36	2.35	2.37	2.36	2.37	2.35	1.00	down	5.34E-01	8.95E-01	-	-
1380580_at	---	---	---	Rn.21652	AI137791	2.33	2.32	2.34	2.33	2.33	2.32	1.00	down	5.22E-01	8.95E-01	-	-
1388841_at	---	---	---	Rn.38106	BI300909	2.29	2.28	2.30	2.29	2.29	2.28	1.00	down	4.30E-01	8.95E-01	-	-
1371154_a_at	Pou2f3	POU class 2 homeobox 3	116544	Rn.81060	U23862	2.42	2.41	2.43	2.41	2.42	2.41	1.00	down	6.17E-01	8.95E-01	-	-
1381792_at	Mrps15	mitochondrial ribosomal protein S15	298517	Rn.12127	BF411995	2.38	2.38	2.39	2.38	2.39	2.37	1.00	down	4.19E-01	8.95E-01	-	-
1380675_s_at	Car11	carbonic anhydrase 11	308588	Rn.44281	BM385197	2.32	2.32	2.31	2.32	2.32	2.32	1.00	up	3.12E-01	8.95E-01	-	-
1374674_at	---	---	---	Rn.164207	AW528792	6.35	6.41	7.92	6.34	6.83	7.52	1.00	up	9.94E-01	9.98E-01	-	-
1392853_at	---	---	---	---	BF417654	2.42	2.42	2.42	2.44	2.42	2.42	1.00	up	5.47E-01	8.95E-01	-	-
1394662_at	---	---	---	---	BI295646	2.70	2.66	2.77	2.69	2.78	2.64	1.00	down	9.29E-01	9.80E-01	-	-
1379962_at	---	---	---	Rn.167857	AI013378	2.28	2.27	2.29	2.27	2.28	2.27	1.00	down	4.15E-01	8.95E-01	-	-
1397062_at	---	---	---	Rn.200107	BF404845	2.34	2.33	2.35	2.33	2.34	2.33	1.00	down	5.10E-01	8.95E-01	-	-
1380930_at	RGD1564142	similar to chromosome 10 open reading frame 64	498582	---	BM389240	2.49	2.49	2.50	2.49	2.50	2.48	1.00	down	5.48E-01	8.95E-01	-	-
1395607_at	---	---	---	Rn.162474	BE109775	2.34	2.33	2.35	2.34	2.35	2.32	1.00	down	5.71E-01	8.95E-01	-	-
1374284_at	Rassf4	Ras association (RalGDS/AF-6) domain family member 4	362423	Rn.195253	AI227769	2.36	2.36	2.37	2.36	2.37	2.35	1.00	down	5.17E-01	8.95E-01	-	-
1378107_at	---	---	---	Rn.24020	AI146051	2.35	2.34	2.36	2.34	2.36	2.34	1.00	down	5.89E-01	8.95E-01	-	-
1387275_at	Sox11	SRY (sex determining region Y)-box 11	84046	Rn.162854	NM_053349	2.44	2.42	2.45	2.43	2.44	2.43	1.00	down	5.58E-01	8.95E-01	-	-
1379174_at	---	---	---	---	BE121123	2.46	2.46	2.53	2.46	2.52	2.45	1.00	down	8.85E-01	9.64E-01	-	-
1395926_at	---	---	---	---	AW919941	2.34	2.33	2.35	2.33	2.34	2.33	1.00	down	5.01E-01	8.95E-01	-	-
1369646_at	Oprl1	opiate receptor-like 1	29256	Rn.9762	U05239	2.33	2.32	2.34	2.33	2.34	2.32	1.00	down	5.45E-01	8.95E-01	-	-
1390084_at	---	---	---	Rn.176539	BI300563	2.43	2.43	2.46	2.44	2.45	2.42	1.00	down	6.39E-01	8.95E-01	-	-
1388026_at	Cd247	Cd247 molecule	25300	Rn.9997	L08447	2.32	2.32	2.33	2.32	2.32	2.31	1.00	down	3.89E-01	8.95E-01	-	-
1392075_at	---	---	---	Rn.49023	BE098246	2.31	2.30	2.32	2.31	2.32	2.30	1.00	down	5.11E-01	8.95E-01	-	-
1369885_at	---	---	---	---	NM_022688	2.30	2.29	2.30	2.29	2.30	2.28	1.00	down	5.16E-01	8.95E-01	-	-
1375472_at	---	---	---	---	BF394923	2.33	2.32	2.34	2.33	2.33	2.32	1.00	down	5.54E-01	8.95E-01	-	-
1390581_at	---	---	---	Rn.2077	AA819481	2.44	2.41	2.44	2.43	2.44	2.43	1.00	up	6.95E-01	9.08E-01	-	-
1377305_at	---	---	---	Rn.207347	BE097699	2.31	2.30	2.33	2.31	2.32	2.33	1.00	up	6.52E-01	8.97E-01	-	-
1384631_at	---	---	---	Rn.147162	AI029762	2.32	2.31	2.32	2.31	2.32	2.30	1.00	down	5.03E-01	8.95E-01	-	-
1369300_at	Ncr1	natural cytotoxicity triggering receptor 1	117547	Rn.30049	NM_057199	2.39	2.37	2.40	2.38	2.39	2.37	1.00	down	6.33E-01	8.95E-01	-	-
1394428_at	---	---	---	Rn.208778	BF403190	2.38	2.37	2.39	2.39	2.39	2.36	1.00	down	6.77E-01	9.02E-01	-	-
1392501_at	---	---	---	Rn.153837	BE120710	2.28	2.27	2.29	2.28	2.29	2.27	1.00	down	5.80E-01	8.95E-01	-	-
1390608_at	---	---	---	Rn.63397	BF404618	2.43	2.42	2.45	2.43	2.45	2.42	1.00	down	7.32E-01	9.14E-01	-	-
1390902_at	---	---	---	Rn.35394	BI276056	2.34	2.33	2.35	2.33	2.34	2.32	1.00	down	5.78E-01	8.95E-01	-	-
1396519_at	---	---	---	---	BF399103	2.34	2.33	2.34	2.33	2.34	2.32	1.00	down	6.33E-01	8.95E-01	-	-
1369880_at	Msx2	msh homeobox 2	25483	Rn.10414	NM_012982	2.36	2.35	2.38	2.36	2.37	2.34	1.00	down	7.01E-01	9.07E-01	-	-
1387804_at	Trim63	tripartite motif-containing 63	140939	Rn.40636	NM_080903	2.37	2.36	2.37	2.37	2.37	2.36	1.00	down	4.66E-01	8.95E-01	-	-
1381630_at	RGD1563222	similar to RIKEN cDNA A930018P22	362175	Rn.57377	BE102619	2.39	2.39	2.41	2.39	2.41	2.38	1.00	down	6.78E-01	9.02E-01	-	-
1368380_at	Vtn	vitronectin	29169	Rn.87493	NM_019156	2.32	2.32	2.33	2.32	2.32	2.31	1.00	down	3.49E-01	8.95E-01	-	-
1385175_at	Hoxb13	homeo box B13	303480	Rn.83970	BI292168	2.41	2.39	2.42	2.40	2.42	2.40	1.00	down	6.56E-01	8.98E-01	-	-
1369627_at	Sv2b	synaptic vesicle glycoprotein 2b	117556	Rn.58137	BG672437	2.28	2.28	2.30	2.28	2.29	2.27	1.00	down	5.87E-01	8.95E-01	-	-
1371168_at	Mpp2	membrane protein, palmitoylated 2 (MAGUK p55 subfamily member 2)	85275	Rn.44271	AF087696	2.70	2.68	2.71	2.69	2.71	2.68	1.00	down	6.76E-01	9.02E-01	-	-
1390232_at	RGD1311946	similar to RIKEN cDNA 1810055G02	309145	Rn.16921	BM388441	2.34	2.33	2.34	2.34	2.36	2.34	1.00	up	6.25E-01	8.95E-01	-	-
1389512_at	---	---	---	Rn.199834	BF410571	2.49	2.48	2.49	2.50	2.49	2.48	1.00	up	5.31E-01	8.95E-01	-	-
1378636_at	Chmp4b	chromatin modifying protein 4B	312254	---	BE116139	2.34	2.33	2.35	2.33	2.34	2.32	1.00	down	5.01E-01	8.95E-01	-	-
1381852_at	---	---	---	Rn.19484	AI059908	2.39	2.38	2.40	2.38	2.40	2.37	1.00	down	7.04E-01	9.07E-01	-	-
1370944_at	Col10a1	collagen, type X, alpha 1	25681	Rn.217522	AI230238	2.29	2.28	2.30	2.29	2.29	2.28	1.00	down	5.82E-01	8.95E-01	-	-
1384570_at	Plekha4	pleckstrin homology domain containing, family A (phosphoinositide binding sp	308584	Rn.99114	BI296108	2.31	2.30	2.32	2.31	2.31	2.30	1.00	down	4.86E-01	8.95E-01	-	-
1377712_at	---	---	---	Rn.204484	AI556865	2.30	2.29	2.31	2.30	2.31	2.29	1.00	down	5.40E-01	8.95E-01	-	-
1391382_at	---	---	---	Rn.172387	BF402496	2.33	2.33	2.34	2.33	2.34	2.32	1.00	down	4.90E-01	8.95E-01	-	-
1379065_at	Serpina12	serine (or cysteine) peptidase inhibitor, clade A (alpha-1 antiproteinase, antitr	191570	Rn.79035	BI295014	2.43	2.43	2.44	2.43	2.47	2.42	1.00	up	7.73E-01	9.28E-01	-	-
1371227_at	Csf2	colony stimulating factor 2 (granulocyte-macrophage)	116630	Rn.44285	U00620	2.28	2.27	2.28	2.27	2.28	2.26	1.00	down	4.96E-01	8.95E-01	-	-
1368940_at	P2ry2	purinergic receptor P2Y, G-protein coupled 2	29597	Rn.11102	NM_017255	2.40	2.39	2.41	2.39	2.41	2.39	1.00	down	5.82E-01	8.95E-01	-	-
1368506_at	Rgs4	regulator of G-protein signaling 4	29480	Rn.11065	U27767	2.35	2.34	2.36	2.35	2.36	2.33	1.00	down	6.04E-01	8.95E-01	-	-
1378430_at	Moxd1	monooxygenase, DBH-like 1	294119	Rn.26552	AI555053	2.32	2.31	2.33	2.32	2.32	2.31	1.00	down	4.45E-01	8.95E-01	-	-
1386275_at	---	---	---	Rn.130654	AI170541	2.37	2.36	2.38	2.36	2.38	2.35	1.00	down	7.01E-01	9.07E-01	-	-
1378306_at	---	---	---	Rn.204454	AW529689	2.34	2.33	2.35	2.34	2.35	2.33	1.00	down	5.70E-01	8.95E-01	-	-
1390339_at	Usp13	Ubiquitin specific protease 13 (isopeptidase T-3)	310306	Rn.16802	BE099435	2.35	2.34	2.36	2.34	2.35	2.33	1.00	down	5.23E-01	8.95E-01	-	-
1368795_at	Nmur1	neuromedin U receptor 1	65276	Rn.54457	NM_023100	2.34	2.32	2.34	2.33	2.34	2.32	1.00	down	4.64E-01	8.95E-01	-	-
1397021_at	---	---	---	Rn.199956	BF404503	2.37	2.36	2.38	2.36	2.37	2.35	1.00	down	5.53E-01	8.95E-01	-	-
1378970_at	Mybphl	Myosin binding protein H-like	310782	Rn.139442	AW252385	2.39	2.36	2.41	2.39	2.41	2.38	1.00	up	7.86E-01	9.31E-01	-	-
1377557_at	---	---	---	---	BE097459	2.32	2.31	2.33	2.31	2.32	2.31	1.00	down	4.88E-01	8.95E-01	-	-
1380436_at	RT1-A2	RT1 class Ia, locus A2	24974	---	AW252814	2.36	2.36	2.38	2.36	2.37	2.36	1.00	down	4.45E-01	8.95E-01	-	-
1398019_at	---	---	---	Rn.146761	BG376789	2.35	2.34	2.35	2.34	2.35	2.34	1.00	down	3.50E-01	8.95E-01	-	-
1368979_at	Kalrn	kalirin, RhoGEF kinase	84009	Rn.87882	NM_032062	2.32	2.31	2.33	2.31	2.32	2.30	1.00	down	5.19E-01	8.95E-01	-	-
1393962_at	---	---	---	---	BI288778	2.20	2.20	2.21	2.20	2.20	2.19	1.00	down	4.24E-01	8.95E-01	-	-
1390929_at	---	---	---	Rn.205015	BI275447	2.35	2.34	2.36	2.35	2.36	2.34	1.00	down	5.46E-01	8.95E-01	-	-
1376893_at	Nrsn1	neurensin 1	291129	Rn.146842	AI408821	2.30	2.30	2.31	2.30	2.31	2.32	1.00	up	5.05E-01	8.95E-01	-	-
1387488_a_at	Calcr	calcitonin receptor	116506	Rn.10062	L13041	2.37	2.36	2.38	2.37	2.38	2.34	1.00	down	7.01E-01	9.07E-01	-	-
1382980_at	---	---	---	Rn.147566	AA964943	2.40	2.40	2.41	2.40	2.41	2.38	1.00	down	6.07E-01	8.95E-01	-	-
1375328_at	Prss21	protease, serine, 21	353251	Rn.60786	BF405109	2.32	2.30	2.31	2.30	2.32	2.29	1.00	down	6.15E-01	8.95E-01	-	-
1381598_at	Ddx50	DEAD (Asp-Glu-Ala-Asp) box polypeptide 50	361848	Rn.98470	AA818165	2.22	2.23	2.23	2.22	2.23	2.22	1.00	down	1.78E-01	8.95E-01	-	-
1381682_at	---	---	---	---	BE106750	2.42	2.42	2.43	2.42	2.43	2.41	1.00	down	5.55E-01	8.95E-01	-	-
1384580_at	C6	complement component 6	24237	Rn.16145	AI045191	2.33	2.33	2.34	2.33	2.34	2.32	1.00	down	5.15E-01	8.95E-01	-	-
1386257_at	---	---	---	Rn.16559	AA858641	2.33	2.33	2.34	2.33	2.34	2.32	1.00	down	4.47E-01	8.95E-01	-	-
1378799_at	---	---	---	Rn.205489	BF394913	2.37	2.36	2.38	2.36	2.37	2.36	1.00	down	4.92E-01	8.95E-01	-	-
1369516_at	Pdx1	pancreatic and duodenal homeobox 1	29535	Rn.54603	NM_022852	2.40	2.38	2.41	2.41	2.40	2.37	1.00	down	7.25E-01	9.13E-01	-	-
1381995_at	Brunol4	bruno-like 4, RNA binding protein (Drosophila)	307540	Rn.23878	AW530502	2.29	2.28	2.29	2.28	2.29	2.27	1.00	down	4.34E-01	8.95E-01	-	-
1374025_at	Nmnat3	nicotinamide nucleotide adenylyltransferase 3	363118	Rn.101356	AA863282	4.08	2.71	2.80	2.82	3.49	3.29	1.00	up	9.82E-01	9.98E-01	-	-
1381387_at	---	---	---	Rn.52153	BI288963	2.43	2.43	2.43	2.41	2.44	2.42	1.00	down	5.78E-01	8.95E-01	-	-
1382432_at	---	---	---	Rn.203939	AI030021	2.33	2.32	2.34	2.32	2.33	2.31	1.00	down	5.63E-01	8.95E-01	-	-
1369700_at	Clcn7	chloride channel 7	29233	Rn.10338	NM_031568	2.37	2.35	2.36	2.35	2.36	2.35	1.00	down	4.17E-01	8.95E-01	-	-
1378635_at	---	---	---	Rn.208738	BI275013	2.29	2.29	2.30	2.29	2.30	2.28	1.00	down	3.80E-01	8.95E-01	-	-
1379591_at	---	---	---	---	AI228518	2.33	2.33	2.34	2.34	2.33	2.31	1.00	down	5.64E-01	8.95E-01	-	-
1385053_at	---	---	---	Rn.150119	BE108648	2.34	2.34	2.35	2.34	2.35	2.33	1.00	down	5.33E-01	8.95E-01	-	-
1393206_at	---	---	---	Rn.35121	BM383684	2.42	2.41	2.44	2.42	2.43	2.41	1.00	down	7.05E-01	9.08E-01	-	-
1383392_at	C2	complement component 2	24231	Rn.98333	AI716125	2.22	2.20	2.22	2.22	2.23	2.22	1.00	up	4.77E-01	8.95E-01	-	-
1392634_at	---	---	---	Rn.45378	AW522386	2.34	2.32	2.34	2.33	2.34	2.31	1.00	down	6.83E-01	9.03E-01	-	-
1395851_at	Kbtbd5	kelch repeat and BTB (POZ) domain containing 5	316088	Rn.48046	BG371944	2.32	2.32	2.33	2.32	2.31	1.00	down	3.97E-01	8.95E-01	-	-
1383435_at	Scn3b	sodium channel, voltage-gated, type III, beta	245956	Rn.3402	BF542912	2.33	2.32	2.34	2.33	2.34	2.31	1.00	down	6.04E-01	8.95E-01	-	-
1394828_at	---	---	---	Rn.173406	BF406986	2.36	2.36	2.37	2.36	2.37	2.35	1.00	down	4.38E-01	8.95E-01	-	-
1379732_at	Stx11	syntaxin 11	292483	Rn.52178	AW920037	2.35	2.34	2.36	2.34	2.36	2.33	1.00	down	6.23E-01	8.95E-01	-	-
1381032_at	---	---	---	Rn.165824	AI600243	2.43	2.42	2.44	2.42	2.44	2.41	1.00	down	6.77E-01	9.02E-01	-	-
1372584_at	Cnrip1	cannabinoid receptor interacting protein 1	364208	Rn.8173	BG672517	2.36	2.36	2.37	2.36	2.37	2.35	1.00	down	5.45E-01	8.95E-01	-	-
1393682_at	LOC689618	similar to Protein C20orf85 homolog	689618	Rn.153866	AI144849	2.33	2.32	2.34	2.32	2.33	2.32	1.00	down	5.25E-01	8.95E-01	-	-
1379551_at	Dus4l	dihydrouridine synthase 4-like (S. cerevisiae)	366593	Rn.41975	AI170351	2.39	2.37	2.38	2.37	2.40	2.36	1.00	down	6.97E-01	9.07E-01	-	-
1394515_at	---	---	---	Rn.178608	BF287046	2.37	2.36	2.38	2.36	2.39	2.35	1.00	down	7.44E-01	9.17E-01	-	-
1382872_at	---	---	---	---	AA851616	2.33	2.33	2.34	2.33	2.34	2.32	1.00	down	5.27E-01	8.95E-01	-	-
1379779_at	---	---	---	Rn.18479	BF285405	2.40	2.38	2.41	2.39	2.40	2.38	1.00	down	6.66E-01	8.99E-01	-	-
1374651_at	Dopey2	dopey family member 2	304077	Rn.52409	BM386987	2.31	2.30	2.31	2.30	2.31	2.29	1.00	down	3.57E-01	8.95E-01	-	-
1380260_at	Barx1	BARX homeobox 1	364680	Rn.12744	BM387765	2.34	2.33	2.36	2.34	2.35	2.33	1.00	down	6.78E-01	9.02E-01	-	-
1383084_at	---	---	---	Rn.139571	BG671922	2.34	2.32	2.34	2.33	2.34	2.32	1.00	down	6.07E-01	8.95E-01	-	-
1397232_at	Lrrn1	leucine rich repeat neuronal 1	500280	Rn.96330	AW529295	2.33	2.32	2.34	2.32	2.33	2.31	1.00	down	5.55E-01	8.95E-01	-	-
1390840_at	---	---	---	---	BF398182	2.43	2.42	2.43	2.42	2.45	2.39	1.00	down	8.13E-01	9.40E-01	-	-
1370444_at	Cacna1b	calcium channel, voltage-dependent, N type, alpha 1B subunit	257648	Rn.85880	AF055477	2.38	2.38	2.39	2.38	2.39	2.36	1.00	down	6.30E-01	8.95E-01	-	-
1381241_at	---	---	---	Rn.176462	BE102033	2.31	2.30	2.32	2.31	2.32	2.30	1.00	down	5.38E-01	8.95E-01	-	-
1393659_at	Tram1l1	translocation associated membrane protein 1-like 1	310846	Rn.103881	BE109193	2.34	2.33	2.35	2.34	2.35	2.33	1.00	down	5.39E-01	8.95E-01	-	-
1369193_at	Cdkn2b	cyclin-dependent kinase inhibitor 2B (p15, inhibits CDK4)	25164	Rn.105626	AF474979	2.41	2.40	2.42	2.40	2.42	2.40	1.00	down	6.11E-01	8.95E-01	-	-
1391751_at	Fam154a	Family with sequence similarity 154, member A	679802	Rn.198261	BE107919	2.34	2.33	2.35	2.33	2.34	2.33	1.00	down	3.43E-01	8.95E-01	-	-
1391579_at	P2rx7	purinergic receptor P2X, ligand-gated ion channel, 7	29665	Rn.10510	AI385229	2.34	2.34	2.35	2.34	2.35	2.33	1.00	down	4.12E-01	8.95E-01	-	-
1384664_at	Sftpb	surfactant protein B	192155	Rn.1952	AI233855	2.38	2.38	2.40	2.38	2.39	2.37	1.00	down	6.36E-01	8.95E-01	-	-
1395237_at	Eif5b	eukaryotic translation initiation factor 5B	308306	Rn.107482	BE117773	10.45	9.84	9.72	10.15	10.09	9.80	1.00	up	9.85E-01	9.96E-01	-	-
1375782_at	---	---	---	Rn.203959	BF412915	2.35	2.34	2.36	2.35	2.35	2.33	1.00	down	5.06E-01	8.95E-01	-	-
1385782_at	---	---	---	Rn.152260	AW524067	2.37	2.36	2.38	2.36	2.38	2.35	1.00	down	6.61E-01	8.98E-01	-	-
1368393_at	Cd93	CD93 molecule	84398	Rn.162695	AF136537	2.34	2.33	2.35	2.33	2.35	2.33	1.00	down	5.20E-01	8.95E-01	-	-
1382092_at	Kcnj3	potassium inwardly-rectifying channel, subfamily J, member 3	50599	Rn.9859	U91449	2.36	2.37	2.38	2.39	2.38	2.36	1.00	up	6.93E-01	9.05E-01	-	-
1393149_at	ha3 /// Pcdha4 ///	protocadherin alpha 1 /// protocadherin alpha 10 /// protocadherin alpha 11 /// 5 /// 393086 /// 39		Rn.217578	BG663483	2.40	2.39	2.41	2.39	2.39	2.40	1.00	down	4.74E-01	8.95E-01	-	-
1368564_at	Slc17a6	solute carrier family 17 (sodium-dependent inorganic phosphate cotransporte	84487	Rn.19372	NM_053427	2.33	2.32	2.33	2.33	2.33	2.31	1.00	down	4.05E-01	8.95E-01	-	-
1377146_at	Vip	vasoactive intestinal peptide	117064	Rn.18675	AI412212	2.30	2.30	2.31	2.30	2.31	2.29	1.00	down	5.20E-01	8.95E-01	-	-
1390643_at	---	---	---	Rn.60736	BF403311	2.32	2.31	2.33	2.31	2.32	2.31	1.00	down	4.90E-01	8.95E-01	-	-
1392948_at	---	---	---	Rn.7412	BI290737	2.31	2.30	2.32	2.30	2.31	2.29	1.00	down	4.99E-01	8.95E-01	-	-
1396644_at	---	---	---	Rn.62429	BF413700	2.34	2.34	2.34	2.34	2.35	2.33	1.00	down	4.83E-01	8.95E-01	-	-
1368786_a_at	Gpcr12	G-protein coupled receptor 12	80840	Rn.88417	NM_030831	2.31	2.31	2.32	2.31	2.32	2.30	1.00	down	4.95E-01	8.95E-01	-	-
1395705_at	---	---	---	Rn.27810	BF412848	2.36	2.35	2.36	2.35	2.36	2.34	1.00	down	4.94E-01	8.95E-01	-	-
1397989_at	---	---	---	Rn.207862	BF401779	2.36	2.35	2.36	2.35	2.37	2.33	1.00	down	7.12E-01	9.10E-01	-	-
1381232_at	---	---	---	---	BF410410	2.34	2.33	2.35	2.33	2.35	2.32	1.00	down	6.06E-01	8.95E-01	-	-
1395238_at	---	---	---	---	AI237240	2.34	2.33	2.35	2.33	2.34	2.32	1.00	down	5.75E-01	8.95E-01	-	-
1396314_at	---	---	---	Rn.148769	AI137838	2.30	2.30	2.31	2.30	2.31	2.29	1.00	down	5.02E-01	8.95E-01	-	-
1369755_at	B3galt2	beta-1,3-glucuronyltransferase 2 (glucuronosyltransferase S)	64544	Rn.42869	AF106624	2.34	2.33	2.36	2.34	2.35	2.33	1.00	down	6.25E-01	8.95E-01	-	-
1387163_at	Hort	hypocretin	25723	Rn.7628	NM_013179	2.31	2.30	2.31	2.30	2.31	2.29	1.00	down	4.28E-01	8.95E-01	-	-
1368483_a_at	Slit1	slit homolog 1 (Drosophila)	65047	Rn.30002	NM_022953	2.77	2.76	2.79	2.77	2.78	2.76	1.00	down	6.26E-01	8.95E-01	-	-
1377245_a_at	RGD1311723	similar to KIAA1731 protein	363018	Rn.160168	AI146147	2.83	3.08	3.20	2.92	2.99	3.18	1.00	down	9.72E-01	9.92E-01	-	-
1386552_at	---	---	---	Rn.171981	BF284027	2.37	2.36	2.39	2.37	2.38	2.36	1.00	down	6.21E-01	8.95E-01	-	-
1375273_at	Trim47	tripartite motif-containing 47	690374	Rn.198921	AW251625	2.40	2.41	2.40	2.40	2.40	2.40	1.00	down	3.15E-01	8.95E-01	-	-
1397970_at	---	---	---	Rn.44661	AW252251	2.39	2.39	2.40	2.39	2.40	2.38	1.00	down	5.43E-01	8.95E-01	-	-
1385555_at	Fam101a	family with sequence similarity 101, member A	689711	Rn.15321	AA924444	2.33	2.32	2.34	2.32	2.33	2.31	1.00	down	5.74E-01	8.95E-01	-	-
1381314_at	---	---	---	Rn.161879	BE119779	2.29	2.28	2.30	2.28	2.29	2.28	1.00	down	5.41E-01	8.95E-01	-	-
1396034_at	Ces7	carboxylesterase 7	307660	Rn.61848	BF402373	2.27	2.26	2.27	2.26	2.30	2.26	1.00	up	7.34E-01	9.15E-01	-	-
1374646_at	Csnk1a1	casein kinase 1, alpha 1	113927	Rn.23810	BM387173	8.23	7.74	7.16	7.62	7.53	7.99

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1396874_at	---	---	---	Rn.26913	AI500976	2.32	2.31	2.32	2.31	2.32	2.30	1.00	down	4.78E-01	8.95E-01	-	-
1393839_x_at	---	---	---	Rn.203806	AA998494	2.36	2.35	2.37	2.35	2.37	2.34	1.00	down	6.59E-01	8.98E-01	-	-
1369873_at	P2rx5	purinergic receptor P2X, ligand-gated ion channel, 5	113995	Rn.10257	X92069	2.37	2.36	2.38	2.37	2.37	2.35	1.00	down	6.63E-01	8.98E-01	-	-
1376606_a_at	Eny2	enhancer of yellow 2 homolog (Drosophila)	685258	---	BM387118	10.17	10.56	10.72	10.33	10.39	10.72	1.00	down	9.82E-01	9.95E-01	-	-
1391991_at	---	---	---	---	BI296617	2.70	2.59	2.78	2.83	2.70	2.52	1.00	down	9.66E-01	9.90E-01	-	-
1392291_at	---	---	---	Rn.153681	BF415328	2.22	2.21	2.23	2.22	2.22	2.21	1.00	down	4.16E-01	8.95E-01	-	-
1385426_at	Ccdc109b	coiled-coil domain containing 109B	295462	Rn.35486	AI502796	2.42	2.40	2.42	2.40	2.43	2.39	1.00	down	7.34E-01	9.15E-01	-	-
1375688_at	Foxo1	Forkhead box O1	84482	Rn.116108	BE106518	2.38	2.38	2.38	2.37	2.38	2.38	1.00	down	4.46E-01	8.95E-01	-	-
1380780_at	---	---	---	---	BI300306	2.62	2.56	2.69	2.58	2.68	2.59	1.00	down	9.26E-01	9.79E-01	-	-
1388589_at	Dot1l	DOT1-like, histone H3 methyltransferase (S. cerevisiae)	362831	Rn.18027	BG381046	2.45	2.44	2.45	2.47	2.45	2.43	1.00	up	6.65E-01	8.99E-01	-	-
1394061_at	---	---	---	Rn.14703	AA891650	2.30	2.30	2.31	2.30	2.31	2.29	1.00	down	5.08E-01	8.95E-01	-	-
1375133_at	Scarf2	Scavenger receptor class F, member 2	287949	Rn.22134	AW253950	2.32	2.31	2.33	2.32	2.32	2.31	1.00	down	5.12E-01	8.95E-01	-	-
1381613_at	---	---	---	Rn.132156	BI290213	2.52	2.49	2.54	2.50	2.52	2.51	1.00	down	7.83E-01	9.30E-01	-	-
1374635_at	LOC689663	Hypothetical protein LOC689663	689663	Rn.167316	AW527151	2.31	2.30	2.31	2.30	2.31	2.29	1.00	down	4.83E-01	8.95E-01	-	-
1373354_at	---	---	---	Rn.48532	BF418347	2.37	2.37	2.39	2.37	2.38	2.37	1.00	down	6.19E-01	8.95E-01	-	-
1368753_at	Camkk2	calcium/calmodulin-dependent protein kinase kinase 2, beta	83506	Rn.88589	NM_031338	2.52	2.51	2.53	2.51	2.52	2.51	1.00	down	4.12E-01	8.95E-01	-	-
1383009_at	---	---	---	Rn.201333	BE117039	2.46	2.45	2.47	2.45	2.46	2.45	1.00	down	4.79E-01	8.95E-01	-	-
1370692_at	Il1rl1	interleukin 1 receptor-like 1	25556	Rn.10072	U04317	2.44	2.43	2.44	2.44	2.44	2.43	1.00	down	3.91E-01	8.95E-01	-	-
1396443_at	---	---	---	Rn.55472	BF287908	2.25	2.24	2.25	2.24	2.25	2.24	1.00	down	4.18E-01	8.95E-01	-	-
1370793_at	---	---	---	---	D89965	2.30	2.30	2.31	2.30	2.31	2.29	1.00	down	5.28E-01	8.95E-01	-	-
1390912_at	Pcp4l1	Purkinje cell protein 4-like 1	685448	Rn.155340	BE101168	2.34	2.34	2.35	2.33	2.34	2.33	1.00	down	3.94E-01	8.95E-01	-	-
1370596_a_at	Wipf3	WAS/WASL interacting protein family, member 3	259242	Rn.11272	U31159	2.41	2.41	2.43	2.41	2.42	2.41	1.00	down	5.97E-01	8.95E-01	-	-
1376517_at	LOC680117	similar to T-cell leukemia homeobox protein 2 (Homeobox protein Hox-11L1) (	680117	Rn.159786	AW530281	2.31	2.30	2.31	2.30	2.32	2.31	1.00	up	5.57E-01	8.95E-01	-	-
1395911_at	---	---	---	Rn.27255	AI511220	2.30	2.30	2.31	2.30	2.31	2.29	1.00	down	4.88E-01	8.95E-01	-	-
1377877_at	Nlp	ninein-like	311529	Rn.60010	BF397870	2.39	2.39	2.40	2.39	2.40	2.38	1.00	down	4.52E-01	8.95E-01	-	-
1390002_at	---	---	---	Rn.212190	BI296438	2.22	2.21	2.22	2.21	2.22	2.21	1.00	down	3.64E-01	8.95E-01	-	-
1394484_at	---	---	---	Rn.155768	AI170114	2.37	2.36	2.37	2.35	2.36	2.35	1.00	down	3.39E-01	8.95E-01	-	-
1369574_at	Tas2r13	taste receptor, type 2, member 13	78984	Rn.48787	NM_023998	2.41	2.40	2.42	2.40	2.41	2.40	1.00	down	4.53E-01	8.95E-01	-	-
1368930_at	Kcnn4	potassium intermediate/small conductance calcium-activated channel, subfan	65206	Rn.44212	NM_023021	2.43	2.42	2.44	2.42	2.44	2.41	1.00	down	5.89E-01	8.95E-01	-	-
1373674_at	Mfap5	microfibrillar associated protein 5	362429	Rn.25217	BI283094	2.33	2.31	2.34	2.32	2.34	2.31	1.00	down	7.07E-01	9.08E-01	-	-
1370206_at	Accn4	amiloride-sensitive cation channel 4, pituitary	63882	Rn.44831	BM386997	2.31	2.30	2.32	2.31	2.32	2.30	1.00	down	5.36E-01	8.95E-01	-	-
1376485_at	Traip	TRAF-interacting protein	367167	Rn.8891	BG377082	2.39	2.38	2.40	2.38	2.40	2.37	1.00	down	6.33E-01	8.95E-01	-	-
1380871_at	---	---	---	Rn.206588	AW528400	2.28	2.28	2.29	2.28	2.29	2.27	1.00	down	4.55E-01	8.95E-01	-	-
1397006_at	---	---	---	Rn.210770	BF401586	2.38	2.37	2.38	2.37	2.38	2.36	1.00	down	6.28E-01	8.95E-01	-	-
1398661_at	Egflam	EGF-like, fibronectin type III and laminin G domains	365691	Rn.27713	BG372341	2.46	2.45	2.48	2.46	2.48	2.45	1.00	down	7.29E-01	9.14E-01	-	-
1368065_at	Gipc1	GIPC PDZ domain containing family, member 1	83823	Rn.30044	NM_053341	2.81	2.77	2.78	2.72	2.80	2.86	1.00	up	9.14E-01	9.75E-01	-	-
1374269_at	---	---	---	Rn.6402	BF398756	2.36	2.35	2.37	2.36	2.37	2.35	1.00	down	5.83E-01	8.95E-01	-	-
1369477_at	Pnma1	paraneoplastic antigen MA1	170636	Rn.81186	NM_130820	2.38	2.37	2.40	2.38	2.39	2.37	1.00	down	6.75E-01	9.01E-01	-	-
1369397_at	Tas1r3	taste receptor, type 1, member 3	170634	Rn.81025	NM_130818	2.34	2.34	2.36	2.34	2.35	2.33	1.00	down	5.84E-01	8.95E-01	-	-
1387739_at	Cd8b	CD8b molecule	24931	Rn.10330	NM_031539	2.33	2.32	2.34	2.32	2.34	2.31	1.00	down	6.17E-01	8.95E-01	-	-
1369447_at	Slc28a3	solute carrier family 28 (sodium-coupled nucleoside transporter), member 3	140944	Rn.81200	NM_080908	2.30	2.29	2.31	2.30	2.30	2.29	1.00	down	4.26E-01	8.95E-01	-	-
1370430_at	86277 /// RGD15	similar to LIM-only protein 3 (Neuronal-specific transcription factor DAT1) /// s	497798 /// 686277	Rn.127746	AF353304	2.31	2.30	2.32	2.31	2.32	2.30	1.00	down	5.17E-01	8.95E-01	-	-
1368514_at	Maob	monoamine oxidase B	25750	Rn.6656	NM_013198	2.35	2.34	2.35	2.34	2.35	2.34	1.00	down	4.62E-01	8.95E-01	-	-
1370679_at	Pld1	phospholipase D1	25096	Rn.11130	AF017251	2.37	2.37	2.38	2.36	2.38	2.36	1.00	down	4.72E-01	8.95E-01	-	-
1398403_at	---	---	---	---	BG381546	2.38	2.38	2.39	2.38	2.38	2.37	1.00	down	4.20E-01	8.95E-01	-	-
1380153_at	---	---	---	Rn.206450	AW527209	2.42	2.41	2.43	2.42	2.42	2.41	1.00	down	4.76E-01	8.95E-01	-	-
1392314_at	---	---	---	Rn.169645	BG380439	2.34	2.33	2.35	2.33	2.34	2.33	1.00	down	5.76E-01	8.95E-01	-	-
1386009_at	Csf3r	colony stimulating factor 3 receptor (granulocyte)	298518	Rn.134664	AA946110	2.35	2.34	2.36	2.35	2.36	2.34	1.00	down	6.09E-01	8.95E-01	-	-
1395174_at	---	---	---	Rn.70307	BI289214	2.40	2.38	2.40	2.39	2.40	2.38	1.00	down	6.29E-01	8.95E-01	-	-
1370668_a_at	Cnksr2	connector enhancer of kinase suppressor of Ras 2	59322	Rn.42893	AF102853	2.84	2.51	2.53	2.86	2.52	2.48	1.00	down	9.78E-01	9.93E-01	-	-
1396107_at	Syf2	SYF2 homolog, RNA splicing factor (S. cerevisiae)	170933	Rn.162117	BF549155	2.34	2.33	2.35	2.33	2.34	2.33	1.00	down	5.22E-01	8.95E-01	-	-
1369096_at	Epha7	Eph receptor A7	171287	Rn.10181	NM_134331	2.36	2.35	2.36	2.35	2.36	2.34	1.00	down	5.35E-01	8.95E-01	-	-
1396475_at	---	---	---	Rn.177620	BM385312	2.35	2.31	2.33	2.31	2.35	2.31	1.00	down	8.02E-01	9.36E-01	-	-
1398459_at	Cacna1a	calcium channel, voltage-dependent, P/Q type, alpha 1A subunit	25398	Rn.87769	BF405130	2.37	2.36	2.37	2.36	2.39	2.36	1.00	up	6.33E-01	8.95E-01	-	-
1395123_at	Wtkkn1	WAP, FS_Ig_KU, and NTR-containing protein 1	363555	Rn.221886	BM389871	2.29	2.28	2.30	2.29	2.30	2.28	1.00	down	4.96E-01	8.95E-01	-	-
1370083_at	Ccr1	chemokine (C-C motif) receptor 1	57301	Rn.34673	NM_020542	2.34	2.34	2.35	2.34	2.35	2.33	1.00	down	5.36E-01	8.95E-01	-	-
1385126_at	---	---	---	---	AI060037	2.48	2.46	2.51	2.46	2.49	2.48	1.00	down	8.09E-01	9.38E-01	-	-
1383211_at	---	---	---	Rn.148381	BE109736	2.30	2.30	2.31	2.30	2.31	2.29	1.00	down	5.34E-01	8.95E-01	-	-
1381479_at	---	---	---	Rn.153910	BF419055	2.27	2.26	2.27	2.26	2.26	2.25	1.00	down	4.13E-01	8.95E-01	-	-
1390679_at	---	---	---	Rn.176540	BI300412	2.31	2.30	2.32	2.30	2.31	2.29	1.00	down	4.93E-01	8.95E-01	-	-
1393986_at	Hmgb4	high-mobility group box 4	685271	Rn.172241	BF386455	2.53	2.49	2.57	2.54	2.58	2.49	1.00	up	8.95E-01	9.67E-01	-	-
1383732_at	RGD1307603	similar to hypothetical protein MGC37914	293556	Rn.16868	AA819810	2.32	2.31	2.33	2.31	2.32	2.31	1.00	down	4.85E-01	8.95E-01	-	-
1397863_at	---	---	---	Rn.34551	BI288592	2.35	2.33	2.36	2.34	2.35	2.33	1.00	down	6.02E-01	8.95E-01	-	-
1375808_at	Prss27	protease, serine 27	287108	Rn.21284	AI070303	2.36	2.35	2.37	2.35	2.36	2.35	1.00	down	4.04E-01	8.95E-01	-	-
1384737_at	---	---	---	Rn.203452	BF555973	2.38	2.37	2.39	2.37	2.39	2.36	1.00	down	7.22E-01	9.11E-01	-	-
1391687_at	---	---	---	Rn.199594	AI228002	2.42	2.40	2.43	2.40	2.44	2.39	1.00	down	7.96E-01	9.34E-01	-	-
1390550_at	Efr3a	EFR3 homolog A (S. cerevisiae)	362923	Rn.21009	BF403636	2.34	2.33	2.35	2.34	2.34	2.32	1.00	down	5.79E-01	8.95E-01	-	-
1369691_at	Scn3a	sodium channel, voltage-gated, type III, alpha	497770	Rn.87394	NM_013119	2.32	2.31	2.33	2.32	2.33	2.31	1.00	down	5.45E-01	8.95E-01	-	-
1376716_at	---	---	---	Rn.17634	AI044539	2.48	2.46	2.47	2.47	2.47	2.46	1.00	down	5.61E-01	8.95E-01	-	-
1383763_at	---	---	---	Rn.16753	BF396631	2.44	2.44	2.44	2.44	2.44	2.43	1.00	down	1.86E-01	8.95E-01	-	-
1391721_at	---	---	---	Rn.19506	AI009102	2.31	2.30	2.32	2.30	2.32	2.29	1.00	down	6.63E-01	8.99E-01	-	-
1384669_at	---	---	---	Rn.204325	BF553125	2.55	2.50	2.58	2.55	2.57	2.49	1.00	down	8.91E-01	9.66E-01	-	-
1394114_at	---	---	---	Rn.136112	AA799434	2.33	2.32	2.34	2.32	2.33	2.32	1.00	down	6.18E-01	8.95E-01	-	-
1370532_at	Pld1	phospholipase D1	25096	Rn.11130	U69550	2.43	2.42	2.44	2.42	2.45	2.40	1.00	down	7.84E-01	9.30E-01	-	-
1395740_at	---	---	---	Rn.199829	BE118705	2.37	2.36	2.39	2.36	2.38	2.36	1.00	down	6.38E-01	8.95E-01	-	-
1375968_at	Ctnna2	catenin (cadherin associated protein), alpha 2	297357	Rn.34514	AI556268	2.32	2.31	2.33	2.32	2.32	2.31	1.00	down	5.54E-01	8.95E-01	-	-
1378198_at	Ophn1	oligophrenin 1	312108	Rn.51010	BG372528	2.25	2.24	2.25	2.26	2.25	2.24	1.00	up	5.44E-01	8.95E-01	-	-
1387291_at	Itih3	inter-alpha trypsin inhibitor, heavy chain 3	50693	Rn.89576	NM_017351	2.34	2.33	2.34	2.34	2.32	2.32	1.00	down	5.46E-01	8.95E-01	-	-
1381639_at	---	---	---	Rn.29183	BF388894	2.48	2.48	2.50	2.47	2.49	2.48	1.00	down	5.55E-01	8.95E-01	-	-
1380601_at	---	---	---	Rn.27174	AI136567	2.42	2.41	2.43	2.41	2.42	2.41	1.00	down	5.47E-01	8.95E-01	-	-
1396153_at	---	---	---	Rn.168131	AI555740	2.30	2.29	2.32	2.30	2.34	2.29	1.00	up	8.06E-01	9.38E-01	-	-
1378145_at	---	---	---	Rn.156066	BE113971	2.34	2.34	2.35	2.34	2.35	2.34	1.00	down	3.28E-01	8.95E-01	-	-
1376104_at	RGD1308319	similar to KIAA0802 protein	316764	Rn.24141	BG381010	2.45	2.45	2.70	2.45	2.46	2.68	1.00	down	9.68E-01	9.91E-01	-	-
1385985_at	---	---	---	Rn.217073	BG663205	2.30	2.29	2.31	2.29	2.30	2.29	1.00	down	5.50E-01	8.95E-01	-	-
1390334_at	RGD1308215	similar to hypothetical protein DKFZp434I2117	293493	Rn.128103	BG381537	2.35	2.32	2.33	2.33	2.37	2.31	1.00	up	8.19E-01	9.42E-01	-	-
1394334_at	Chst8	carbohydrate (N-acetylgalactosamine 4-0) sulfotransferase 8	308511	Rn.55646	BF545197	2.34	2.34	2.35	2.34	2.35	2.33	1.00	down	5.18E-01	8.95E-01	-	-
1384286_at	---	---	---	Rn.146558	BI285501	2.37	2.36	2.38	2.36	2.38	2.36	1.00	down	6.55E-01	8.98E-01	-	-
1368708_a_at	Drd2	dopamine receptor D2	24318	Rn.87299	NM_012547	2.25	2.25	2.26	2.25	2.25	2.24	1.00	down	4.75E-01	8.95E-01	-	-
1390282_a_at	Agap3	ArfGAP with GTPase domain, ankyrin repeat and PH domain 3	362300	Rn.98623	AI705744	2.51	2.50	2.52	2.51	2.52	2.49	1.00	down	6.84E-01	9.03E-01	-	-
1397975_at	---	---	---	Rn.208949	BF393089	2.38	2.36	2.39	2.37	2.39	2.36	1.00	down	6.90E-01	9.05E-01	-	-
1387025_at	Dync1i1	dynein cytoplasmic 1 intermediate chain 1	29564	Rn.11273	NM_019234	2.35	2.35	2.36	2.35	2.36	2.34	1.00	down	5.73E-01	8.95E-01	-	-
1374046_at	Hs3st2	heparan sulfate (glucosamine) 3-O-sulfotransferase 2	293451	Rn.49010	BG376092	2.35	2.34	2.36	2.35	2.36	2.34	1.00	down	6.15E-01	8.95E-01	-	-
1379875_at	Cd300a	CD300A molecule	501736	Rn.11988	BI284779	2.61	2.60	2.62	2.60	2.61	2.59	1.00	down	5.94E-01	8.95E-01	-	-
1384471_at	---	---	---	Rn.205649	AI716461	2.41	2.42	2.51	2.49	2.42	2.42	1.00	down	9.11E-01	9.73E-01	-	-
1377929_at	---	---	---	Rn.15929	BF550844	2.35	2.34	2.37	2.35	2.36	2.34	1.00	down	6.58E-01	8.98E-01	-	-
1396622_at	---	---	---	Rn.201998	BF387611	2.34	2.33	2.37	2.34	2.36	2.32	1.00	down	7.66E-01	9.24E-01	-	-
1380647_at	---	---	---	---	BF413183	2.41	2.40	2.42	2.40	2.41	2.40	1.00	down	5.56E-01	8.95E-01	-	-
1391892_at	---	---	---	---	BE098817	2.31	2.30	2.31	2.30	2.31	2.29	1.00	down	3.71E-01	8.95E-01	-	-
1397208_at	---	---	---	Rn.172195	AI409411	2.30	2.29	2.31	2.30	2.30	2.29	1.00	down	5.17E-01	8.95E-01	-	-
1369309_a_at	Tac1	tachykinin 1	24806	Rn.1920	BG671061	2.35	2.34	2.35	2.34	2.35	2.33	1.00	down	4.76E-01	8.95E-01	-	-
1385229_at	Pcdh20	protocadherin 20	306081	Rn.99314	AW524146	2.34	2.33	2.36	2.34	2.35	2.33	1.00	down	5.92E-01	8.95E-01	-	-
1382576_at	Tect2	tectonic 2	689779	Rn.208304	BE349645	2.94	2.94	2.95	2.97	2.91	2.94	1.00	down	8.08E-01	9.38E-01	-	-
1396164_at	Zrf668	zinc finger protein 668	309002	Rn.218034	BE105096	2.37	2.36	2.38	2.36	2.37	2.36	1.00	down	5.60E-01	8.95E-01	-	-
1388209_at	Tsga10	testis specific 10	252923	Rn.30052	AF092091	2.35	2.35	2.37	2.35	2.36	2.34	1.00	down	6.38E-01	8.95E-01	-	-
1374409_at	Taf6l	TAF6-like RNA polymerase II, p300/CBP-associated factor (PCAF)-associate	309194	Rn.137034	AW253760	2.30	2.30	2.31	2.30	2.31	2.29	1.00	down	5.23E-01	8.95E-01	-	-
1383729_at	LOC303566	ESI1-inducible gene	303566	Rn.46012	BE114522	2.44	2.43	2.45	2.43	2.46	2.43	1.00	down	7.07E-01	9.08E-01	-	-
1389268_at	Poli	polymerase (DNA directed), lambda	361767	Rn.11799	BI285816	3.32	3.29	3.25	3.43	3.48	2.97	1.00	up	9.78E-01	9.93E-01	-	-
1380054_at	Phactr3	phosphatase and actin regulator 3	362284	Rn.27183	BF405705	2.37	2.35	2.38	2.36	2.38	2.35	1.00	down	7.32E-01	9.14E-01	-	-
1390772_at	---	---	---	Rn.220060	AI711085	2.31	2.30	2.32	2.31	2.32	2.30	1.00	down	5.23E-01	8.95E-01	-	-
1393200_at	---	---	---	Rn.23430	AI500827	2.33	2.32	2.34	2.33	2.33	2.32	1.00	down	4.86E-01	8.95E-01	-	-
1396050_at	---	---	---	Rn.147732	BI298666	2.32	2.31	2.33	2.31	2.32	2.30	1.00	down	5.28E-01	8.95E-01	-	-
1390626_at	---	---	---	Rn.167061	BF398788	2.34	2.33	2.35	2.33	2.34	2.32	1.00	down	5.89E-01	8.95E-01	-	-
1379095_at	---	---	---	Rn.56809	BF388738	2.32	2.31	2.32	2.31	2.32	2.31	1.00	down	4.34E-01	8.95E-01	-	-
1369564_at	Rem2	RAS (RAD and GEM) like GTP binding 2	64626	Rn.48804	NM_022685	2.33	2.32	2.33	2.32	2.33	2.31	1.00	down	4.88E-01	8.95E-01	-	-
1367656_at	Psmb7	proteasome (prosome, macropain) subunit, beta type 7	85492	Rn.3846	NM_053532	10.08	10.24	10.22	10.07	10.18	10.30	1.00	up	9.57E-01	9.88E-01	-	-
1381322_at	---	---	---	Rn.173202	BF402728	2.38	2.37	2.39	2.38	2.38	2.37	1.00	down	5.16E-01	8.95E-01	-	-
1396676_at	---	---	---	Rn.58039	BF394718	2.34	2.32	2.34	2.33	2.34	2.32	1.00	down	5.59E-01	8.95E-01	-	-
1387838_at	Lalba	lactalbumin, alpha	24528	Rn.10479	NM_012594	2.32	2.31	2.34	2.31	2.33	2.31	1.00	down	7.06E-01	9.08E-01	-	-
1382848_at	---	---	---	Rn.212788	BM383972	2.36	2.35	2.36	2.35	2.37	2.34	1.00	down	6.57E-01	8.98E-01	-	-
1393266_at	---	---	---	Rn.140998	AI029813	2.39	2.31	2.31	2.38	2.32	2.29	1.00	down	9.07E-01	9.71E-01	-	-
1388081_at	Olr1867	olfactory receptor 1867	100036582	Rn.217925	D12820	2.28	2.27	2.29	2.28	2.28	2.27	1.00	down	4.78E-01	8.95E-01	-	-
1387610_at	Cd46	CD46 molecule, complement regulatory protein	29333	Rn.163242	NM_019190	2.31	2.30	2.32	2.30	2.31	2.30	1.00	down	5.20E-01	8.95E-01	-	-
1377931_at	---	---	---	Rn.149200	BF523850	2.37	2.36	2.38	2.37	2.37	2.36	1.00	down	3.61E-01	8.95E-01	-	-
1381155_at	---	---	---	Rn.146159	BF406620	2.35	2.34	2.35	2.34	2.35	2.33	1.00	down	5.17E-01	8.95E-01	-	-
1397332_at	---	---	---	---	BI297281	2.43	2.42	2.44	2.42	2.43	2.41	1.00	down	6.04E-01	8.95E-01	-	-
1386807_at	Wnt2	wingless-type MMTV integration site family member 2	114487	Rn.203764	BF556985	2.31	2.30	2.31	2.30	2.31	2.32	1.00	up	5.48E-01	8.95E-01	-	-
1391894_at	---	---	---	Rn.208574	BE118274	2.31	2.30	2.31	2.30	2.31	2.30	1.00	down	4.47E-01	8.95E-01	-	-
1397643_at	---	---	---	Rn.176343	BG373964	2.26	2.25	2.26	2.25	2.26	2.25	1.00	down	3.86E-01	8.95E-01	-	-
1381802_at	RGD1560412	Similar to Leukosialin precursor (Leucocyte sialoglycoprotein)	501808	Rn.61952	BE121396	2.33	2.32	2.33	2.32	2.35	2.31	1.00	up	6.76E-01	9.02E-01	-	-
1378422_at	---	---	---	Rn.45384	BE117312	2.44	2.44	2.44	2.44	2.44	2.43	1.00	down	3.18E-01	8.95E-01	-	-
1383185_at	---	---	---	Rn.199283	BE105131	2.40	2.39	2.41	2.39	2.41	2.38	1.00	down	6.95E-01	9.06E-01	-	-
1378838_at	---	---	---	Rn.52554	BF410174	2.30	2.29	2.30	2.29	2.30	2.28	1.00	down	4.11E-01	8.95E-01	-	-
1394701_at	---	---	---	---	BF290084	2.34	2.34	2.35	2.34	2.34	2.33	1.00	down	3.91E-01	8.95E-01	-	-
1395441_at	Pdcp4	poly(rC) binding protein 4	363133	Rn.40405	BF562397	3.40	3.75	3.68	3.92	3.02	3.90	1.00	up	9.86E-01	9.96E-01	-	-
1393548_at	---	---	---	Rn.203663	AI137584	2.32	2.31	2.33	2.31	2.32	2.31	1.00	down	5.39E-01	8.95E-01	-	-
1396070_at	---	---	---	---	BI295775	2.37	2.37	2.38	2.37	2.38	2.36	1.00	down	4.90E-01	8.95E-01	-	-
1397076_at	tm1 /// RGD15597	chimerin (chimaerin) 1 /// similar to n-chimaerin	498895 /// 84030	Rn.11166	BF409722	2.41	2.40	2.41	2.41	2.41	2.40	1.00	down	4.41E-01	8.95E-01	-	-
1396837_at	---	---	---	Rn.205484	AI579389	2.32	2.31	2.33	2.31	2.32	2.31	1.00	down	5.43E-01	8.95E-01	-	-
1383480_at	560060 /// RGD15	similar to Gene model 784 /// similar to Gene model 784	501597 /// 501598	---	BI294850	2.38	2.37	2.39	2.38	2.42	2.36	1.00	up	8.33E-01	9.47E-01	-	-
1374182_at	Smarcc1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin,	301020	Rn.94211	AA965063	2.55	2.85	2.74	2.71	2.72	2.70	1.00	down	9.66E-01	9.89E-01	-	-
1391008_at	---	---	---	Rn.205447	AI578428	2.35	2.34	2.35	2.34	2.35	2.33	1.00	down	4.82E-01	8.95E-01	-	-
1387620_a_at	Tmprss11d	transmembrane protease, serine 11d	64565	Rn.48747	NM_022630	2.40	2.38	2.41	2.39	2.40	2.38	1.00	down	6.74E-01	9.01E-01	-	-
1384454_at	Cpa6	carboxypeptidase A6	312913	Rn.16761	AA819425	2.48	2.46	2.52	2.49	2.49	2.46	1.00	down	8.28E-01	9.45E-01	-	-
1377382_at	---	---	---	Rn.153806	BG373618	2.26	2.26	2.27	2.26	2.27	2.25	1.00	down	4.95E-01	8.95E-01	-	-
1378164_at	---	---	---	Rn.169371	AI227601	2.30	2.33	2.31	2.33	2.31	2.30	1.00	down	7

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1382589_at	Ankrd55	ankyrin repeat domain 55	361898	Rn.21785	AI072262	2.41	2.40	2.41	2.40	2.41	2.40	1.00	down	4.03E-01	8.95E-01	-	-
1380626_at	---	---	---	---	BF404596	2.32	2.31	2.33	2.31	2.32	2.30	1.00	down	5.49E-01	8.95E-01	-	-
1368891_at	Gria3	glutamate receptor, ionotrophic, AMPA 3	29628	Rn.74049	M85036	2.43	2.41	2.44	2.42	2.43	2.41	1.00	down	6.06E-01	8.95E-01	-	-
1395215_at	---	---	---	Rn.209534	BF404567	2.49	2.48	2.50	2.47	2.51	2.52	1.00	up	7.80E-01	9.29E-01	-	-
1387469_at	Galr3	galanin receptor 3	29235	Rn.30069	NM_019173	2.49	2.49	2.49	2.49	2.50	2.47	1.00	down	6.84E-01	9.03E-01	-	-
1376495_at	---	---	---	Rn.12470	AI172054	2.40	2.37	2.41	2.40	2.40	2.39	1.00	up	7.14E-01	9.10E-01	-	-
1390150_at	---	---	---	Rn.211734	AI599135	2.34	2.33	2.35	2.34	2.34	2.33	1.00	down	4.38E-01	8.95E-01	-	-
1394469_at	---	---	---	---	AI232647	2.34	2.33	2.35	2.34	2.35	2.33	1.00	down	6.16E-01	8.95E-01	-	-
1396367_at	---	---	---	Rn.160838	BF409474	2.41	2.40	2.42	2.40	2.41	2.40	1.00	down	5.33E-01	8.95E-01	-	-
1379523_at	---	---	---	Rn.14975	AA818187	2.30	2.29	2.30	2.29	2.30	2.29	1.00	down	2.62E-01	8.95E-01	-	-
1370165_at	Smpx	small muscle protein, X-linked	84416	Rn.4123	AI406565	2.37	2.35	2.36	2.36	2.37	2.34	1.00	down	6.67E-01	8.99E-01	-	-
1387829_at	Slc24a1	solute carrier family 24 (sodium/potassium/calcium exchanger), member 1	56814	Rn.205732	NM_020090	2.33	2.33	2.34	2.33	2.34	2.32	1.00	down	4.53E-01	8.95E-01	-	-
1385416_at	---	---	---	---	BI285540	2.42	2.41	2.45	2.42	2.44	2.41	1.00	down	7.63E-01	9.23E-01	-	-
1373945_at	Brunol5	bruno-like 5, RNA binding protein (Drosophila)	314647	Rn.12319	AI012571	2.30	2.29	2.31	2.29	2.30	2.29	1.00	down	4.57E-01	8.95E-01	-	-
1380536_at	RGD1305928	hypothetical LOC300207	300207	Rn.48052	BE096750	2.41	2.40	2.43	2.41	2.42	2.40	1.00	down	6.79E-01	9.02E-01	-	-
1396474_at	---	---	---	Rn.155689	AW254078	2.34	2.33	2.35	2.34	2.35	2.32	1.00	down	6.30E-01	8.95E-01	-	-
1391293_at	Bbox1	butyrobetaine (gamma), 2-oxoglutarate dioxygenase (gamma-butyrobetaine h	64564	Rn.16333	AI170038	2.23	2.22	2.24	2.22	2.23	2.22	1.00	down	4.84E-01	8.95E-01	-	-
1398291_at	Slc26a5	solute carrier family 26, member 5 (prestin)	83819	Rn.64631	NM_030840	2.35	2.34	2.36	2.34	2.36	2.34	1.00	down	5.48E-01	8.95E-01	-	-
1369794_a_at	Pfkfb3	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3	117276	Rn.10791	D87247	2.48	2.48	2.48	2.48	2.47	2.47	1.00	down	3.54E-01	8.95E-01	-	-
1394649_at	Ankrd6	ankyrin repeat domain 6	500430	Rn.45844	BF391635	2.36	2.35	2.38	2.36	2.37	2.35	1.00	down	6.58E-01	8.98E-01	-	-
1381458_at	---	---	---	Rn.147406	AA893697	2.31	2.30	2.32	2.31	2.31	2.30	1.00	down	4.16E-01	8.95E-01	-	-
1396856_at	---	---	---	---	AW528716	2.33	2.32	2.34	2.32	2.33	2.32	1.00	down	5.14E-01	8.95E-01	-	-
1369334_at	Kcnma1	potassium large conductance calcium-activated channel, subfamily M, alpha	83731	Rn.30616	NM_031828	2.30	2.29	2.31	2.29	2.30	2.28	1.00	down	4.90E-01	8.95E-01	-	-
1378219_at	Sgtb	small glutamine-rich tetratricopeptide repeat (TPR)-containing, beta	294708	Rn.23400	BF420086	2.33	2.32	2.34	2.33	2.33	2.32	1.00	down	5.10E-01	8.95E-01	-	-
1377378_at	Scn5a	sodium channel, voltage-gated, type V, alpha subunit	25665	Rn.32074	BF396369	2.42	2.40	2.44	2.42	2.45	2.41	1.00	up	8.12E-01	9.39E-01	-	-
1391024_at	Cpa4	carboxypeptidase A4	502736	Rn.148841	AA944450	2.29	2.28	2.29	2.28	2.29	2.27	1.00	down	4.66E-01	8.95E-01	-	-
1378128_at	---	---	---	Rn.211881	BM383749	2.34	2.32	2.35	2.33	2.34	2.32	1.00	down	6.58E-01	8.98E-01	-	-
1369199_at	Tacr1	tachykinin receptor 1	24807	Rn.89609	J05097	2.37	2.36	2.38	2.36	2.37	2.36	1.00	down	4.34E-01	8.95E-01	-	-
1378805_at	---	---	---	Rn.50616	BE104220	2.34	2.34	2.35	2.34	2.34	2.33	1.00	down	5.04E-01	8.95E-01	-	-
1395676_at	---	---	---	Rn.147248	BF416069	2.38	2.37	2.40	2.38	2.40	2.37	1.00	down	7.52E-01	9.20E-01	-	-
1396134_at	---	---	---	Rn.64266	BF418847	2.31	2.31	2.32	2.31	2.32	2.30	1.00	down	5.52E-01	8.95E-01	-	-
1394453_at	---	---	---	Rn.203830	BF389053	2.70	2.69	2.71	2.70	2.70	2.69	1.00	down	3.99E-01	8.95E-01	-	-
1370562_at	Calcb	calcitonin-related polypeptide, beta	171519	Rn.88080	M11596	2.34	2.33	2.35	2.34	2.35	2.33	1.00	down	6.06E-01	8.95E-01	-	-
1384593_at	---	---	---	Rn.9396	AA957799	2.37	2.35	2.37	2.36	2.37	2.35	1.00	down	5.50E-01	8.95E-01	-	-
1375778_at	---	---	---	Rn.66296	BI296704	2.36	2.35	2.37	2.36	2.37	2.35	1.00	down	6.55E-01	8.98E-01	-	-
1374168_at	Sphkap	SPHK1 interactor, AKAP domain containing	316561	Rn.15453	BE099608	2.36	2.35	2.37	2.35	2.37	2.34	1.00	down	6.46E-01	8.95E-01	-	-
1376471_at	---	---	---	Rn.210030	BF405630	2.28	2.28	2.29	2.28	2.29	2.27	1.00	down	4.50E-01	8.95E-01	-	-
1395400_at	RGD1305508	similar to hypothetical protein MGC23280	303275	Rn.25006	AI178515	2.36	2.35	2.37	2.36	2.36	2.35	1.00	down	4.52E-01	8.95E-01	-	-
1394860_at	---	---	---	---	AI234929	2.30	2.30	2.31	2.30	2.31	2.29	1.00	down	4.95E-01	8.95E-01	-	-
1370140_a_at	Pax4	paired box 4	83630	Rn.14531	AF053102	2.24	2.24	2.25	2.24	2.25	2.23	1.00	down	4.46E-01	8.95E-01	-	-
1378557_at	Fam19a4	family with sequence similarity 19 (chemokine (C-C motif)-like), member A4	689043	Rn.158675	AI408645	2.38	2.36	2.39	2.37	2.39	2.36	1.00	down	6.81E-01	9.03E-01	-	-
1397867_at	Akap6	A kinase (PRKA) anchor protein 6	64553	Rn.147642	BG379733	2.31	2.30	2.31	2.30	2.31	2.29	1.00	down	4.12E-01	8.95E-01	-	-
1388614_at	Sf3b2	splicing factor 3b, subunit 2	293671	Rn.103341	BM386768	6.38	7.35	7.16	6.96	6.44	7.48	1.00	down	9.92E-01	9.97E-01	-	-
1370484_at	38 /// Olr1469 /// O	olfactory receptor 1466 /// olfactory receptor 1467 /// olfactory receptor 1468 ///	84 /// 363639 /// 40	Rn.113464	M64392	2.37	2.36	2.38	2.36	2.37	2.35	1.00	down	6.02E-01	8.95E-01	-	-
1380564_at	---	---	---	Rn.32510	AW522823	2.29	2.29	2.30	2.29	2.30	2.28	1.00	down	4.81E-01	8.95E-01	-	-
1391020_at	Btbd17	BTB (POZ) domain containing 17	303660	Rn.101489	BE104465	2.34	2.33	2.35	2.34	2.34	2.32	1.00	down	6.25E-01	8.95E-01	-	-
1375225_at	RGD1308049	Similar to RIKEN cDNA 2410004C24	293690	Rn.12740	BE102330	2.39	2.37	2.39	2.38	2.40	2.36	1.00	down	7.66E-01	9.23E-01	-	-
1381067_at	Snx1	sulfredoxin 1 homolog (S. cerevisiae)	296271	Rn.2835	AF403167	2.49	2.47	2.49	2.48	2.48	2.46	1.00	down	5.49E-01	8.95E-01	-	-
1373321_at	---	---	---	Rn.96	BE111682	2.36	2.35	2.43	2.44	2.34	2.34	1.00	down	9.16E-01	9.75E-01	-	-
1377095_at	RGD1560070	similar to ataxin 2-binding protein 1 isoform 2	287847	Rn.143966	BG380409	2.44	2.43	2.46	2.44	2.45	2.46	1.00	up	6.88E-01	9.00E-01	-	-
1374884_at	Ppm1d	protein phosphatase 1D magnesium-dependent, delta isoform	287585	Rn.15540	AI233712	2.38	2.37	2.39	2.40	2.40	2.36	1.00	up	7.78E-01	9.28E-01	-	-
1394362_at	42077 /// RGD130	hypothetical LOC292199 /// similar to intracellular protein transport like (XM_	292199 /// 308053	Rn.38655	BF546803	2.51	2.49	2.54	2.50	2.60	2.46	1.00	up	9.23E-01	9.77E-01	-	-
1374728_at	---	---	---	Rn.9183	BG671786	2.32	2.31	2.33	2.32	2.32	2.31	1.00	down	5.35E-01	8.95E-01	-	-
1389793_at	---	---	---	Rn.157670	AW434402	3.05	3.33	3.77	3.46	3.38	3.32	1.00	up	9.84E-01	9.95E-01	-	-
1375244_at	---	---	---	Rn.212266	BI291447	2.49	2.48	2.50	2.49	2.50	2.48	1.00	down	5.15E-01	8.95E-01	-	-
1377370_at	---	---	---	Rn.168028	BF406860	2.40	2.40	2.41	2.40	2.41	2.39	1.00	down	4.92E-01	8.95E-01	-	-
1387433_a_at	Slc25a27	solute carrier family 25, member 27	85262	Rn.163043	NM_053500	2.30	2.29	2.30	2.29	2.30	2.28	1.00	down	4.96E-01	8.95E-01	-	-
1381462_at	RGD1566130	similar to mKIAA1940 protein	312504	Rn.147439	BI294541	2.35	2.34	2.36	2.34	2.37	2.34	1.00	up	7.26E-01	9.13E-01	-	-
1369582_at	Vax2	ventral anterior homeobox 2	64572	Rn.48765	NM_022637	2.41	2.40	2.41	2.41	2.42	2.40	1.00	up	4.12E-01	8.95E-01	-	-
1395262_at	---	---	---	Rn.210819	BF402135	2.42	2.40	2.42	2.44	2.43	2.39	1.00	up	8.03E-01	9.37E-01	-	-
1378584_at	---	---	---	Rn.146610	BF419393	2.35	2.34	2.35	2.34	2.36	2.33	1.00	down	6.47E-01	8.95E-01	-	-
1392092_at	Rab33a	RAB33A, member of RAS oncogene family	317580	Rn.28066	AI101329	2.36	2.35	2.37	2.36	2.36	2.35	1.00	down	5.21E-01	8.95E-01	-	-
1368451_at	Hrh3	histamine receptor H3	85268	Rn.7617	NM_053506	2.28	2.26	2.28	2.27	2.27	2.26	1.00	down	4.16E-01	8.95E-01	-	-
1396778_at	---	---	---	---	BF401043	2.28	2.27	2.29	2.28	2.28	2.27	1.00	down	5.23E-01	8.95E-01	-	-
1370815_at	Nefh	neurofilament, heavy polypeptide	24587	Rn.108194	AF031879	2.32	2.32	2.33	2.32	2.33	2.32	1.00	down	3.58E-01	8.95E-01	-	-
1392247_at	---	---	---	---	AA956305	2.35	2.34	2.36	2.35	2.36	2.34	1.00	down	6.14E-01	8.95E-01	-	-
1396948_at	---	---	---	---	BF399584	2.43	2.42	2.45	2.43	2.44	2.42	1.00	down	6.14E-01	8.95E-01	-	-
1398971_at	RGD1307929	similar to CG14967-PA	303280	Rn.3552	BI283725	8.44	8.77	8.38	8.66	8.27	8.67	1.00	up	9.81E-01	9.94E-01	-	-
1392412_at	---	---	---	Rn.199805	BE120096	2.47	2.45	2.48	2.48	2.46	2.46	1.00	up	6.85E-01	9.03E-01	-	-
1397412_at	---	---	---	Rn.207792	BE107094	2.33	2.32	2.33	2.32	2.33	2.31	1.00	down	5.87E-01	8.95E-01	-	-
1392711_at	---	---	---	Rn.28561	AA996440	2.43	2.41	2.45	2.42	2.46	2.40	1.00	down	8.24E-01	9.44E-01	-	-
1394806_at	Nccrp1	non-specific cytotoxic cell receptor protein 1 homolog (zebrafish)	292755	Rn.63376	BF418149	2.23	2.23	2.25	2.23	2.23	2.23	1.00	down	5.21E-01	8.95E-01	-	-
1396357_at	LOC304725	similar to contactin associated protein-like 5 isoform 1	304725	---	BF410752	2.41	2.40	2.42	2.41	2.41	2.39	1.00	down	6.40E-01	8.95E-01	-	-
1392791_at	---	---	---	Rn.203676	AA964492	2.40	2.38	2.42	2.39	2.42	2.38	1.00	down	7.89E-01	9.32E-01	-	-
1390166_at	---	---	---	Rn.147360	BE107612	2.32	2.32	2.33	2.32	2.33	2.31	1.00	down	5.43E-01	8.95E-01	-	-
1390760_at	---	---	---	---	BF411923	2.38	2.38	2.38	2.38	2.38	2.37	1.00	down	3.31E-01	8.95E-01	-	-
1371965_at	Mmadhc	methylmalonic aciduria (cobalamin deficiency) cblD type, with homocystinuria	362134	Rn.3269	BF283269	9.68	9.71	9.99	9.79	9.92	9.69	1.00	up	9.71E-01	9.92E-01	-	-
1370666_at	Dnm3	dynamin 3	171574	Rn.11191	AF201839	2.33	2.33	2.34	2.33	2.33	2.32	1.00	down	4.84E-01	8.95E-01	-	-
1377620_at	Znf655	Zinc finger protein 655	362764	Rn.6640	BI292731	2.42	2.57	2.46	2.52	2.45	2.46	1.00	down	9.32E-01	9.81E-01	-	-
1387523_at	Ptgdr /// Ptgdrl	prostaglandin D receptor /// prostaglandin D receptor-like	498475 /// 63889	Rn.220703	NM_022241	2.34	2.33	2.34	2.33	2.35	2.32	1.00	down	6.17E-01	8.95E-01	-	-
1394648_at	---	---	---	Rn.28810	BF284608	2.36	2.35	2.38	2.38	2.39	2.34	1.00	up	8.14E-01	9.40E-01	-	-
1383026_at	Arid1b	AT rich interactive domain 1B (Swi1 like)	282546	Rn.22598	BF420195	2.24	2.24	2.25	2.24	2.27	2.23	1.00	up	7.46E-01	9.18E-01	-	-
1374626_at	Lrg1	leucine-rich alpha-2-glycoprotein 1	367455	Rn.17847	BG371585	2.37	2.36	2.38	2.37	2.38	2.35	1.00	down	6.35E-01	8.95E-01	-	-
1369522_a_at	Cd244	Cd244 molecule, natural killer cell receptor 2B4	64025	Rn.53994	NM_022259	2.39	2.38	2.39	2.38	2.39	2.37	1.00	down	6.40E-01	8.95E-01	-	-
1396659_at	LOC688864	similar to transmembrane protein 61	688864	Rn.33698	AI715999	2.46	2.44	2.45	2.45	2.47	2.42	1.00	down	7.58E-01	9.21E-01	-	-
1388023_a_at	Cacnb2	calcium channel, voltage-dependent, beta 2 subunit	116600	Rn.10739	AF394941	2.36	2.37	2.37	2.36	2.36	2.36	1.00	down	3.34E-01	8.95E-01	-	-
1375732_at	---	---	---	Rn.2378	BE109509	2.41	2.41	2.42	2.41	2.42	2.40	1.00	down	5.46E-01	8.95E-01	-	-
1395084_at	---	---	---	Rn.204918	AI179556	2.29	2.27	2.28	2.28	2.28	2.27	1.00	down	4.11E-01	8.95E-01	-	-
1395111_at	---	---	---	Rn.132320	AI454738	2.29	2.28	2.28	2.27	2.28	2.27	1.00	down	2.73E-01	8.95E-01	-	-
1381373_at	Zpbp2	zona pellucida binding protein 2	363676	Rn.51329	BF403624	2.33	2.32	2.34	2.33	2.33	2.32	1.00	down	5.22E-01	8.95E-01	-	-
1368128_at	Pla2g2a	phospholipase A2, group IIA (platelets, synovial fluid)	29692	Rn.11346	NM_031598	2.33	2.32	2.34	2.33	2.34	2.32	1.00	down	5.52E-01	8.95E-01	-	-
1385935_at	---	---	---	Rn.176383	AI577552	2.40	2.39	2.41	2.39	2.43	2.40	1.00	up	7.31E-01	9.14E-01	-	-
1375586_at	---	---	---	---	BF413240	2.39	2.38	2.40	2.39	2.40	2.37	1.00	down	6.60E-01	8.98E-01	-	-
1391973_at	---	---	---	Rn.50629	BF404506	2.30	2.29	2.30	2.29	2.30	2.28	1.00	down	5.05E-01	8.95E-01	-	-
1368561_at	Abcd2	ATP-binding cassette, sub-family D (ALD), member 2	84356	Rn.19678	NM_033352	2.29	2.29	2.30	2.28	2.30	2.28	1.00	down	4.26E-01	8.95E-01	-	-
1390236_at	Hmcn2	hemicentin 2	686132	---	AI406334	2.34	2.33	2.34	2.34	2.34	2.32	1.00	down	6.00E-01	8.95E-01	-	-
1380296_at	---	---	---	---	AI406334	2.34	2.33	2.34	2.34	2.34	2.32	1.00	down	4.96E-01	8.95E-01	-	-
1395827_at	---	---	---	Rn.169146	BF411608	2.36	2.35	2.37	2.35	2.37	2.34	1.00	down	6.87E-01	9.04E-01	-	-
1386811_at	Ptpla2	protein tyrosine phosphatase-like A domain containing 2	362540	Rn.35165	BF542615	2.35	2.34	2.36	2.34	2.35	2.34	1.00	down	5.83E-01	8.95E-01	-	-
1391263_at	Htr4	5-hydroxytryptamine (serotonin) receptor 4	25324	Rn.10094	BF401317	2.36	2.34	2.37	2.35	2.37	2.34	1.00	down	6.99E-01	9.07E-01	-	-
1392632_at	Ttc9	tetratricopeptide repeat domain 9	500689	Rn.8149	AI044816	2.32	2.31	2.33	2.31	2.33	2.30	1.00	down	6.33E-01	8.95E-01	-	-
1393860_at	---	---	---	Rn.24515	AI059216	2.54	2.51	2.56	2.55	2.55	2.51	1.00	down	8.23E-01	9.43E-01	-	-
1388098_at	LOC246267	dissection-induced TPI (rs11)	246267	Rn.127819	AF007890	2.29	2.28	2.30	2.29	2.29	2.28	1.00	down	4.67E-01	8.95E-01	-	-
1379474_at	---	---	---	Rn.203295	AW526574	2.33	2.32	2.34	2.33	2.34	2.32	1.00	down	5.82E-01	8.95E-01	-	-
1390248_at	---	---	---	Rn.165891	AW142935	2.33	2.32	2.34	2.33	2.34	2.32	1.00	down	6.12E-01	8.95E-01	-	-
1385092_at	Epha6	Eph receptor A6	29202	Rn.102933	AW523694	2.27	2.26	2.28	2.27	2.27	2.26	1.00	down	4.13E-01	8.95E-01	-	-
1392531_at	Tlpal	tocopherol (alpha) transfer protein-like	296349	Rn.156438	AI178693	2.35	2.33	2.38	2.34	2.37	2.34	1.00	down	8.00E-01	9.35E-01	-	-
1368761_at	Ppp3r2	protein phosphatase 3, regulatory subunit B, alpha isoform (calcineurin B, typ	29749	Rn.42928	NM_021701	2.31	2.30	2.32	2.30	2.31	2.29	1.00	down	6.08E-01	8.95E-01	-	-
1368743_a_at	Dspp	dentin sialophosphoprotein	25254	Rn.21392	U02074	2.28	2.27	2.29	2.28	2.28	2.27	1.00	down	4.98E-01	8.95E-01	-	-
1382096_at	Cmtm5	CKLF-like MARVEL transmembrane domain containing 5	299214	Rn.100853	AI705040	2.43	2.41	2.43	2.42	2.45	2.41	1.00	up	7.36E-01	9.15E-01	-	-
1376424_at	---	---	---	Rn.199388	BF412664	2.30	2.30	2.31	2.30	2.31	2.29	1.00	down	4.59E-01	8.95E-01	-	-
1387318_at	Kcnmb4	potassium large conductance calcium-activated channel, subfamily M, beta m	66016	Rn.162953	AY028605	2.36	2.35	2.38	2.35	2.38	2.34	1.00	down	7.61E-01	9.22E-01	-	-
1385382_at	Adam19	a disintegrin and metalloprotease domain 19 (meltrin beta)	303068	Rn.163114	BI294158	2.34	2.33	2.35	2.34	2.35	2.32	1.00	down	6.30E-01	8.95E-01	-	-
1370707_at	Fev	FEV (ETS oncogene family)	246271	Rn.83616	U91679	2.19	2.19	2.20	2.19	2.19	2.18	1.00	down	4.53E-01	8.95E-01	-	-
1368721_at	Ascl2	achaete-scute complex homolog 2 (Drosophila)	24209	Rn.10486	NM_031503	2.34	2.33	2.34	2.33	2.34	2.33	1.00	down	4.09E-01	8.95E-01	-	-
1390051_at	RGD1562533	similar to mKIAA0774 protein	498136	Rn.38985	BI299098	2.35	2.34	2.36	2.35	2.36	2.34	1.00	down	6.22E-01	8.95E-01	-	-
1369411_at	Gfi1	growth factor independent 1 transcription repressor	24388	Rn.10935	NM_012566	2.43	2.42	2.43	2.42	2.45	2.42	1.00	up	6.55E-01	8.98E-01	-	-
1375290_at	LOC690139	Similar to RNA binding motif protein 24	690139	Rn.199020	AW525160	2.30	2.29	2.30	2.29	2.30	2.28	1.00	down	5.23E-01	8.95E-01	-	-
1383974_at	Eif5	E74-like factor 5	366142	Rn.27061	BG373166	2.43	2.42	2.43	2.42	2.46	2.41	1.00	up	7.96E-01	9.34E-01	-	-
1382410_at	Cd209b	CD209b antigen	288378	Rn.138846	AI549450	2.30	2.28	2.30	2.29	2.30	2.28	1.00	down	5.09E-01	8.95E-01	-	-
1374084_at	---	---	---	Rn.46408	BE119993	2.32	2.31	2.33	2.32	2.32	2.31	1.00	down	6.01E-01	8.95E-01	-	-
1380535_at	---	---	---	Rn.49052	BE097394	2.33	2.32	2.34	2.33	2.34	2.32	1.00	down	6.27E-01	8.95E-01	-	-
1374474_at	Cpne8	copine VIII	362988	Rn.11746	BE099085	2.28	2.27	2.28	2.27	2.28	2.27	1.00	down	4.06E-01	8.95E-01	-	-
1398542_at	Ankrd34a	ankyrin repeat domain 34A	295283	Rn.42835	BG381000	2.30	2.29	2.31	2.29	2.30	2.29	1.00	down	5.08E-01	8.95E-01	-	-
1392030_at	---	---	---	Rn.43054	AI639112	2.47	2.45	2.49	2.46	2.48	2.46	1.00	down	7.77E-01	9.28E-01	-	-
1373005_at	Krtdap	keratinocyte differentiation associated protein	65186	Rn.202626	BI282568	2.42	2.41	2.43	2.41	2.42	2.41	1.00	down	6.07E-01	8.95E-01	-	-
1378161_at	---	---	---	---	BF386703	2.28	2.28	2.30	2.29	2.30	2.28	1.00	down	5.67E-01	8.95E-01	-	-
1378607_at	---	---	---	Rn.171415	BE098816	2.80	2.82	2.21	2.24	2.62	2.95	1.00	down	9.88E-01	9.96E-01	-	-
1397354_at	RGD1305457	similar to RIKEN cDNA 1700023M03	314730	Rn.13471	AI412926	2.45	2.45	2.46	2.45	2.50	2.43	1.00	up	8.38E-01	9.49E-01	-	-
1388072_at	Sbk1	SH3-binding domain kinase 1	113907	Rn.35152	AB010154	2.28	2.28	2.30	2.28	2.29	2.28	1.00	down	5.88E-01	8.95E-01	-	-
1375121_at	Smad6	SMAD family member 6	367100	Rn.42472	BI301428	2.22	2.21	2.22	2.21	2.22	2.21	1.00	down	3.78E-01	8.95E-01	-	-
1368579_at	Prl2a1	Prolactin family 2, subfamily a, member 1	116474	Rn.17940	NM_053791	2.32	2.31	2.33	2.31	2.32	2.31	1.00	down	5.54E-01	8.95E-01	-	-
1395138_at	---	---	---	---	AW534201	2.37	2.36	2.38	2.36	2.38	2.35	1.00	down	7.24E-01	9.12E-01	-	-
1398394_at	---	---	---	Rn.205462	BE108058	2.39	2.38	2.41	2.38	2.40	2.38	1.00	down	6.76E-01	9.02E-01	-	-
1386964_at	Smgb	neonatal submandibular gland protein B	54303	Rn.9925	NM_080775	2.32	2.31	2.32	2.31	2.32	2.30	1.00	down	5.63E-01	8.95E-01	-	-
1385712_at	---	---	---	Rn.172842	BF396364	2.45	2.44	2.46	2.44	2.46	2.44	1.00	down	5.99E-01	8.95E-01	-	-
1378830_at	---	---	---	Rn.58765	BF386892	2.40	2.39	2.41	2.39	2.40	2.39	1.00	down	5.47E-01	8.95E-01	-	-
1388513_at	---	---	---	Rn.8512	BI281612	2.39	2.38	2.39	2.38	2.39	2.38	1.00	down	4.75E-01	8.95E-01	-	-
1375292_at	---	---	---	---	BF405916	2.35	2.34	2.36	2.34	2.35	2.34	1.00	down	5.95E-01	8.95E-01	-	-
1396744_at	Ndp	Norrie disease (pseudoglioma) (human)	363443	Rn.45519	BF394149	2.29	2.28	2.29	2.28	2.29	2.27	1.00	down	5.69E-01	8.95E-01	-	-
1373108_at	Ppp1r3c	protein phosphatase 1, regulatory (inhibitor) subunit 3C	309513	Rn.162528	BM390827	2.37	2.39	2.37	2.37	2.38	2.37	1.00	down	4.86E-01	8.95E-01	-	-
1368447_x_at	Spink3	serine peptidase inhibitor, Kazal type 3	24833	Rn.9767	M27882	2.44	2.42	2.45	2.43	2.45	2.42	1.00	down	7.69E-01	9.25E-01	-	-
1373646_at	Rab15	RAB15, member RAS oncogene family	299156	Rn.24234	BM384841

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1376030_at	Acap1	ArfGAP with coiled-coil, ankyrin repeat and PH domains 1	287443	Rn.2165	BI275873	2.29	2.28	2.29	2.28	2.29	2.27	1.00	down	4.63E-01	8.95E-01	-	-
1382678_at	Cfh /// Cfhl1	complement factor H /// complement component factor h-like 1	155012 /// 289057	Rn.101777	AA859019	2.72	2.63	2.79	2.70	2.76	2.67	1.00	down	9.37E-01	9.82E-01	-	-
1393820_at	---	---	---	Rn.161766	AW533433	2.22	2.21	2.23	2.21	2.22	2.21	1.00	down	4.61E-01	8.95E-01	-	-
1377212_at	---	---	---	Rn.210602	BF416289	2.42	2.41	2.43	2.42	2.43	2.41	1.00	down	5.55E-01	8.95E-01	-	-
1371220_at	Sqstm1	sequestosome 1	113894	Rn.107103	AF053095	2.34	2.34	2.35	2.34	2.35	2.34	1.00	down	3.57E-01	8.95E-01	-	-
1396850_at	Abi1	abl-interactor 1	79249	Rn.43675	AI501434	2.46	2.44	2.48	2.46	2.46	2.44	1.00	down	7.31E-01	9.14E-01	-	-
1374717_at	---	---	---	Rn.205693	BI295624	2.38	2.43	2.39	2.37	2.38	2.42	1.00	down	8.52E-01	9.54E-01	-	-
1376980_at	Htr2c	5-hydroxytryptamine (serotonin) receptor 2C	25187	Rn.9935	BF285539	2.45	2.43	2.48	2.45	2.48	2.42	1.00	down	8.41E-01	9.50E-01	-	-
1397810_at	---	---	---	Rn.216839	BG664708	2.33	2.33	2.34	2.33	2.36	2.33	1.00	up	6.94E-01	9.05E-01	-	-
1369484_at	Wisp2	WNT1 inducible signaling pathway protein 2	25676	Rn.53991	NM_031590	2.34	2.34	2.35	2.34	2.35	2.33	1.00	down	6.21E-01	8.95E-01	-	-
1381258_at	---	---	---	Rn.154088	BF410432	2.37	2.37	2.38	2.37	2.39	2.35	1.00	down	7.15E-01	9.10E-01	-	-
1371047_at	Slc6a5	solute carrier family 6 (neurotransmitter transporter, glycine), member 5	171148	Rn.34566	L21672	2.36	2.35	2.37	2.36	2.36	2.35	1.00	down	5.59E-01	8.95E-01	-	-
1380115_at	---	---	---	---	AA850751	2.37	2.36	2.37	2.36	2.37	2.35	1.00	down	5.54E-01	8.95E-01	-	-
1386181_at	---	---	---	Rn.156139	AI639056	2.38	2.38	2.39	2.38	2.39	2.37	1.00	down	6.06E-01	8.95E-01	-	-
1387556_at	Cntn6	contactin 6	27256	Rn.10644	NM_013225	2.33	2.32	2.34	2.32	2.33	2.31	1.00	down	6.00E-01	8.95E-01	-	-
1378837_at	---	---	---	Rn.207604	BE103216	2.30	2.30	2.31	2.30	2.33	2.30	1.00	up	7.30E-01	9.14E-01	-	-
1373837_at	Fls	fused toes	291906	Rn.220001	BI296633	7.91	8.51	8.42	8.44	7.84	8.54	1.00	down	9.88E-01	9.98E-01	-	-
1377771_at	---	---	---	Rn.23962	BF400896	2.31	2.31	2.32	2.31	2.32	2.30	1.00	down	5.71E-01	8.95E-01	-	-
1380657_at	---	---	---	Rn.204928	AI180398	2.35	2.34	2.35	2.37	2.35	2.34	1.00	up	6.61E-01	8.98E-01	-	-
1380854_at	Samd4b	sterile alpha motif domain containing 4B	308473	Rn.40291	AW535877	2.24	2.24	2.25	2.24	2.24	2.24	1.00	down	3.86E-01	8.95E-01	-	-
1380987_at	Aamp	angio-associated, migratory cell protein	301512	Rn.13592	AW525937	2.39	2.37	2.40	2.38	2.39	2.37	1.00	down	6.79E-01	9.02E-01	-	-
1398312_s_at	Slc14a2	Solute carrier family 14 (urea transporter), member 2	54302	Rn.10157	AF042167	2.27	2.26	2.28	2.27	2.27	2.26	1.00	down	4.58E-01	8.95E-01	-	-
1385312_at	---	---	---	Rn.203083	AA875209	2.46	2.44	2.48	2.44	2.51	2.43	1.00	up	8.84E-01	9.64E-01	-	-
1375547_at	Thap11	THAP domain containing 11	307806	Rn.2823	AI113190	2.28	2.27	2.28	2.28	2.28	2.27	1.00	down	3.47E-01	8.95E-01	-	-
1384294_at	---	---	---	Rn.204086	BF414285	2.40	2.39	2.41	2.39	2.41	2.39	1.00	down	5.64E-01	8.95E-01	-	-
1376426_at	---	---	---	Rn.156418	BG372438	2.33	2.31	2.33	2.33	2.33	2.31	1.00	up	6.52E-01	8.97E-01	-	-
1395306_at	Pbrm1	polybromo 1	306254	Rn.19314	AI502736	5.32	6.58	6.58	5.27	6.59	6.64	1.00	up	9.95E-01	9.98E-01	-	-
1378066_at	---	---	---	Rn.199621	BI274450	2.29	2.29	2.30	2.29	2.29	2.28	1.00	down	5.33E-01	8.95E-01	-	-
1398556_at	Zfyve28	zinc finger, FYVE domain containing 28	305454	Rn.91545	BE119321	2.25	2.23	2.25	2.24	2.24	2.23	1.00	down	4.57E-01	8.95E-01	-	-
1381635_at	---	---	---	Rn.210986	BF404357	2.27	2.26	2.28	2.27	2.27	2.26	1.00	down	5.43E-01	8.95E-01	-	-
1378298_at	/// LOC68477	immunoglobin superfamily, member 21 /// similar to immunoglobin superfamily 298591 /// 684776		Rn.38448	BG381331	2.26	2.24	2.26	2.25	2.25	2.24	1.00	down	4.59E-01	8.95E-01	-	-
1368033_at	Nolc1	nucleolar and coiled-body phosphoprotein 1	64896	Rn.9517	BI290791	7.86	7.04	6.88	7.46	7.44	6.86	1.00	down	9.91E-01	9.97E-01	-	-
1369580_at	Tas2r118	taste receptor, type 2, member 118	78980	Rn.48783	NM_023994	2.30	2.29	2.30	2.29	2.30	2.28	1.00	down	5.29E-01	8.95E-01	-	-
1368961_at	Mmp23	matrix metallopeptidase 23	94339	Rn.22562	NM_053808	2.49	2.48	2.49	2.48	2.49	2.47	1.00	down	4.26E-01	8.95E-01	-	-
1386325_at	---	---	---	---	BG153354	2.27	2.27	2.28	2.27	2.27	2.26	1.00	down	4.48E-01	8.95E-01	-	-
1373728_at	RGD1359634	similar to RIKEN cDNA 1700088E04	315126	Rn.24486	BE111811	2.56	2.54	2.59	2.55	2.58	2.55	1.00	down	8.18E-01	9.42E-01	-	-
1397786_at	---	---	---	Rn.209807	BF391927	2.28	2.27	2.29	2.28	2.28	2.27	1.00	down	5.12E-01	8.95E-01	-	-
1393853_at	---	---	---	Rn.33474	AI071003	2.37	2.36	2.38	2.37	2.38	2.35	1.00	down	7.19E-01	9.11E-01	-	-
1370624_at	F2rl2	coagulation factor II (thrombin) receptor-like 2	29636	Rn.206020	AF310076	2.41	2.40	2.43	2.41	2.43	2.41	1.00	up	6.96E-01	9.06E-01	-	-
1380953_at	---	---	---	Rn.207342	BE097660	2.39	2.38	2.40	2.39	2.40	2.37	1.00	down	7.57E-01	9.21E-01	-	-
1395569_at	---	---	---	---	BF282778	2.43	2.42	2.44	2.42	2.44	2.41	1.00	down	7.53E-01	9.20E-01	-	-
1396249_at	---	---	---	Rn.168212	AI574783	2.40	2.38	2.40	2.39	2.40	2.38	1.00	down	6.37E-01	8.95E-01	-	-
1368952_at	Gabbr2	gamma-aminobutyric acid (GABA) B receptor 2	83633	Rn.162814	NM_031802	2.47	2.42	2.44	2.41	2.41	2.50	1.00	down	8.98E-01	9.68E-01	-	-
1396379_at	Phldb3	pleckstrin homology-like domain, family B, member 3	308431	Rn.64424	BE096478	2.29	2.29	2.30	2.29	2.29	2.28	1.00	down	4.16E-01	8.95E-01	-	-
1387439_at	Megf8	multiple EGF-like-domains 8	65049	Rn.195598	NM_022955	2.30	2.29	2.30	2.29	2.30	2.28	1.00	down	4.58E-01	8.95E-01	-	-
1396566_at	---	---	---	---	BF394827	2.26	2.25	2.26	2.25	2.26	2.24	1.00	down	4.59E-01	8.95E-01	-	-
1373239_at	Snx33	sorting nexin 33	315696	Rn.220326	BM390617	2.36	2.35	2.36	2.37	2.36	2.35	1.00	up	5.70E-01	8.95E-01	-	-
1385000_at	RGD1565611	RGD1565611	497957	Rn.125045	BF399335	2.37	2.36	2.38	2.34	2.37	2.41	1.00	up	8.33E-01	9.47E-01	-	-
1380922_at	Zmym3	Zinc finger, MYM-type 3	317260	Rn.92967	AI412415	2.38	2.37	2.39	2.38	2.39	2.36	1.00	down	6.76E-01	9.01E-01	-	-
1369983_at	Ccl5	chemokine (C-C motif) ligand 5	81780	Rn.8019	NM_031116	2.35	2.33	2.34	2.34	2.34	2.33	1.00	down	4.21E-01	8.95E-01	-	-
1393781_at	---	---	---	Rn.156023	BM386897	2.43	2.42	2.45	2.42	2.49	2.40	1.00	up	8.88E-01	9.65E-01	-	-
1380347_at	---	---	---	Rn.18599	AI030806	2.29	2.28	2.30	2.28	2.30	2.28	1.00	down	6.31E-01	8.95E-01	-	-
1397615_at	---	---	---	Rn.66323	BG375528	2.39	2.38	2.41	2.39	2.41	2.37	1.00	down	7.81E-01	9.29E-01	-	-
1388261_at	Drp2	dystrophin related protein 2	66027	Rn.162341	AF195789	2.38	2.37	2.39	2.38	2.38	2.36	1.00	down	5.20E-01	8.95E-01	-	-
1383739_at	---	---	---	Rn.15335	BI288787	2.33	2.33	2.34	2.33	2.34	2.32	1.00	down	4.75E-01	8.95E-01	-	-
1386841_at	Ng35	Ng35 pseudogene	309613	Rn.55082	BF562309	2.26	2.25	2.26	2.25	2.25	2.25	1.00	down	4.61E-01	8.95E-01	-	-
1392186_at	---	---	---	Rn.209179	BF386624	2.32	2.31	2.33	2.32	2.33	2.31	1.00	down	5.70E-01	8.95E-01	-	-
1380305_at	nod3l	NOD3-like protein	501101	Rn.51041	BE106776	2.32	2.31	2.33	2.32	2.32	2.31	1.00	down	4.76E-01	8.95E-01	-	-
1387210_at	Dlg4	discs, large homolog 4 (Drosophila)	29495	Rn.9765	NM_019621	2.34	2.33	2.35	2.34	2.35	2.33	1.00	down	6.02E-01	8.95E-01	-	-
1381883_at	---	---	---	Rn.172334	BF406676	2.32	2.32	2.33	2.32	2.33	2.31	1.00	down	5.39E-01	8.95E-01	-	-
1378662_at	---	---	---	Rn.209973	BF415816	2.34	2.33	2.35	2.34	2.37	2.33	1.00	up	7.54E-01	9.20E-01	-	-
1382473_at	LOC682543	similar to histone 2a	682543	---	AI070981	2.34	2.33	2.34	2.33	2.34	2.32	1.00	down	5.67E-01	8.95E-01	-	-
1391605_at	---	---	---	Rn.162724	BG666431	2.38	2.37	2.39	2.38	2.38	2.36	1.00	down	6.05E-01	8.95E-01	-	-
1386138_at	Rerg	RAS-like, estrogen-regulated, growth-inhibitor	502916	Rn.19093	AI172174	2.30	2.29	2.31	2.30	2.31	2.29	1.00	down	5.81E-01	8.95E-01	-	-
1369469_s_at	Spdya	speedy homolog A (Xenopus laevis)	192209	Rn.19576	NM_138855	2.43	2.42	2.43	2.42	2.45	2.40	1.00	down	7.82E-01	9.30E-01	-	-
1394018_at	---	---	---	Rn.43836	BF417907	2.46	2.45	2.46	2.45	2.46	2.44	1.00	down	5.31E-01	8.95E-01	-	-
1385617_at	---	---	---	Rn.207263	BE096654	2.40	2.40	2.42	2.40	2.41	2.40	1.00	down	5.63E-01	8.95E-01	-	-
1398033_at	---	---	---	Rn.14479	BE121312	2.36	2.36	2.37	2.36	2.37	2.35	1.00	down	4.81E-01	8.95E-01	-	-
1370441_at	Prl3a1	Prolactin family 3, subfamily a, member 1	266782	Rn.22898	AB019791	2.34	2.33	2.35	2.33	2.35	2.32	1.00	down	6.62E-01	8.98E-01	-	-
1370410_at	Igsf1	immunoglobulin superfamily, member 1	302822	Rn.23738	AF322216	2.29	2.28	2.29	2.28	2.29	2.28	1.00	down	4.09E-01	8.95E-01	-	-
1367626_at	Ckm	creatine kinase, muscle	24265	Rn.10756	NM_012530	2.42	2.44	2.43	2.42	2.46	2.41	1.00	down	7.94E-01	9.34E-01	-	-
1377767_at	---	---	---	Rn.146580	AW526033	2.29	2.28	2.30	2.29	2.29	2.28	1.00	down	4.58E-01	8.95E-01	-	-
1376958_at	RGD1562844	similar to serine (or cysteine) proteinase inhibitor, clade B, member 9	306892	Rn.35280	BI274644	2.28	2.27	2.29	2.28	2.29	2.27	1.00	down	5.51E-01	8.95E-01	-	-
1374810_at	---	---	---	Rn.124281	BI293282	2.30	2.29	2.32	2.30	2.30	2.30	1.00	down	6.27E-01	8.95E-01	-	-
1371013_at	Gria1	glutamate receptor, ionotropic, AMPA 1	50592	Rn.29971	BG376217	2.55	2.53	2.56	2.54	2.57	2.51	1.00	down	8.32E-01	9.47E-01	-	-
1383995_at	---	---	---	---	BG670749	2.32	2.31	2.32	2.31	2.32	2.30	1.00	down	5.82E-01	8.95E-01	-	-
1373085_at	Cbr3	carbonyl reductase 3	304078	Rn.8624	BI282197	2.34	2.33	2.35	2.33	2.34	2.32	1.00	down	6.23E-01	8.95E-01	-	-
1384411_at	LOC296684	Hypothetical LOC296884	296884	Rn.45039	AA962968	2.76	2.74	2.98	2.75	2.80	2.94	1.00	up	9.65E-01	9.90E-01	-	-
1370221_at	Wisp1	WNT1 inducible signaling pathway protein 1	65154	Rn.63486	BF419320	2.33	2.32	2.33	2.32	2.33	2.31	1.00	down	5.54E-01	8.95E-01	-	-
1396177_at	---	---	---	Rn.41634	BF565900	2.37	2.35	2.38	2.36	2.37	2.36	1.00	down	6.99E-01	9.07E-01	-	-
1390081_at	lix4	iroquois homeobox 4	306655	Rn.44726	AW252608	2.31	2.30	2.31	2.30	2.31	2.29	1.00	down	5.52E-01	8.95E-01	-	-
1389459_at	RGD1309613	similar to RIKEN cDNA 1600012F09	306994	Rn.8045	BE116947	6.35	6.29	6.30	6.08	6.69	6.19	1.00	up	9.83E-01	9.95E-01	-	-
1395724_at	Nrm	nurim (nuclear envelope membrane protein)	361791	Rn.38521	AW144414	2.39	2.38	2.40	2.39	2.39	2.37	1.00	down	5.90E-01	8.95E-01	-	-
1395161_at	Myt1	myelin transcription factor 1	362291	Rn.102945	AW531604	2.41	2.40	2.43	2.41	2.44	2.39	1.00	down	8.17E-01	9.42E-01	-	-
1393410_at	---	---	---	Rn.19100	BG666397	2.44	2.41	2.45	2.43	2.49	2.40	1.00	up	8.86E-01	9.65E-01	-	-
1393617_at	---	---	---	Rn.132795	AW530317	2.40	2.39	2.41	2.40	2.41	2.38	1.00	down	6.69E-01	9.00E-01	-	-
1392285_at	Shisa4	shisa homolog 4 (Xenopus laevis)	360848	Rn.40771	AI044729	2.29	2.29	2.30	2.29	2.30	2.28	1.00	down	5.01E-01	8.95E-01	-	-
1376417_at	---	---	---	Rn.56562	BI300887	2.35	2.34	2.36	2.36	2.36	2.35	1.00	up	5.31E-01	8.95E-01	-	-
1398091_at	---	---	---	Rn.205418	AI576636	2.38	2.37	2.40	2.38	2.39	2.37	1.00	down	6.77E-01	9.02E-01	-	-
1392750_at	---	---	---	---	BF288406	2.31	2.30	2.33	2.31	2.35	2.30	1.00	up	7.99E-01	9.35E-01	-	-
1380816_at	RGD1563235	similar to 1700054N08Rik protein	307926	Rn.163417	BF400676	2.33	2.33	2.35	2.33	2.34	2.33	1.00	down	4.44E-01	8.95E-01	-	-
1369856_at	Drd5	dopamine receptor D5	25195	Rn.138110	NM_012768	2.33	2.33	2.34	2.33	2.34	2.32	1.00	down	5.23E-01	8.95E-01	-	-
1382994_at	---	---	---	Rn.25481	AI236143	2.41	2.40	2.41	2.40	2.43	2.40	1.00	up	6.44E-01	8.95E-01	-	-
1374417_at	Nrbp2	nuclear receptor binding protein 2	680451	Rn.198238	BE113111	2.30	2.29	2.31	2.30	2.31	2.29	1.00	down	5.18E-01	8.95E-01	-	-
1393948_at	Atpbd3	ATP binding domain 3	292847	Rn.104880	BG380678	2.33	2.32	2.34	2.32	2.33	2.31	1.00	down	6.29E-01	8.95E-01	-	-
1396587_at	---	---	---	Rn.205425	AI576181	2.33	2.32	2.34	2.32	2.33	2.32	1.00	down	5.80E-01	8.95E-01	-	-
1393158_at	Cenpq	centromere protein Q	363198	Rn.155071	BI298434	2.42	2.40	2.45	2.41	2.48	2.39	1.00	up	8.95E-01	9.67E-01	-	-
1370963_at	Gas7	growth arrest specific 7	85246	Rn.17160	AJ131902	2.35	2.34	2.36	2.34	2.35	2.34	1.00	down	4.71E-01	8.95E-01	-	-
1381477_at	Ank1	ankyrin 1, erythrocytic	306570	Rn.20868	AI102148	2.31	2.30	2.32	2.30	2.31	2.30	1.00	down	5.18E-01	8.95E-01	-	-
1396976_at	---	---	---	Rn.59416	BF395599	2.31	2.31	2.32	2.31	2.31	2.31	1.00	down	5.16E-01	8.95E-01	-	-
1386183_at	---	---	---	---	AI172334	2.39	2.39	2.40	2.39	2.40	2.38	1.00	down	5.38E-01	8.95E-01	-	-
1373558_at	---	---	---	Rn.154118	BF396446	2.32	2.31	2.33	2.32	2.32	2.31	1.00	down	5.21E-01	8.95E-01	-	-
1373928_at	---	---	---	Rn.22494	BF282810	2.37	2.37	2.38	2.37	2.38	2.36	1.00	down	4.55E-01	8.95E-01	-	-
1398152_at	---	---	---	Rn.156302	BF393832	2.35	2.34	2.36	2.35	2.36	2.34	1.00	down	6.23E-01	8.95E-01	-	-
1375137_at	Arpc2	actin related protein 2/3 complex, subunit 2	301511	Rn.93317	AI070323	8.20	8.12	5.26	6.34	7.43	7.83	1.00	up	9.97E-01	9.99E-01	-	-
1396854_at	---	---	---	Rn.206652	BE102681	2.49	2.46	2.48	2.47	2.51	2.43	1.00	down	8.78E-01	9.62E-01	-	-
1375055_at	Jsrp1	junctional sarcoplasmic reticulum protein 1	690423	Rn.72542	AI112084	2.32	2.30	2.32	2.31	2.31	2.30	1.00	down	5.47E-01	8.95E-01	-	-
1396146_at	---	---	---	Rn.101417	BF522113	2.36	2.35	2.36	2.35	2.36	2.35	1.00	down	4.81E-01	8.95E-01	-	-
1394959_at	---	---	---	Rn.148616	AI502099	2.46	2.46	2.48	2.48	2.48	2.45	1.00	up	6.85E-01	9.03E-01	-	-
1395030_at	---	---	---	Rn.205069	BM390366	2.37	2.37	2.39	2.37	2.38	2.35	1.00	down	4.84E-01	8.95E-01	-	-
1388009_at	Trhr2	thyrotropin releasing hormone receptor 2	252859	Rn.216691	AB015645	2.33	2.32	2.34	2.33	2.33	2.32	1.00	down	4.95E-01	8.95E-01	-	-
1378856_at	0C679974 /// 7cea	similar to transcription elongation factor A (SII)-like 3 /// transcription elongatio	501628 /// 679974	Rn.28648	BE097672	2.29	2.29	2.30	2.29	2.30	2.28	1.00	down	5.43E-01	8.95E-01	-	-
1371147_at	Serpina3m	serine (or cysteine) proteinase inhibitor, clade A, member 3M	299270	Rn.107050	X69834	2.37	2.35	2.37	2.36	2.38	2.35	1.00	down	7.40E-01	9.16E-01	-	-
1387705_at	Sstr4	somatostatin receptor 4	25555	Rn.9936	U04738	2.32	2.31	2.32	2.32	2.32	2.30	1.00	down	4.86E-01	8.95E-01	-	-
1386917_at	Pc	pyruvate carboxylase	25104	Rn.11094	NM_012744	7.62	7.24	7.29	7.78	6.96	7.44	1.00	up	9.88E-01	9.96E-01	-	-
1395471_at	---	---	---	Rn.34102	AW524834	2.54	2.53	2.55	2.53	2.58	2.53	1.00	up	8.27E-01	9.45E-01	-	-
1369591_at	Csn3	casein kappa	29188	Rn.10746	NM_031562	2.31	2.30	2.32	2.31	2.31	2.30	1.00	down	5.68E-01	8.95E-01	-	-
1375592_at	---	---	---	---	BF406429	2.37	2.37	2.39	2.37	2.38	2.36	1.00	down	6.70E-01	9.00E-01	-	-
1387937_at	Tpbpa	trophoblast specific protein alpha	64509	Rn.8816	AB009890	2.29	2.29	2.30	2.29	2.30	2.28	1.00	down	5.09E-01	8.95E-01	-	-
1385484_s_at	RGD1561571	similar to Riken cDNA C230021P08	315297	Rn.198253	BE110831	2.48	2.47	2.50	2.49	2.49	2.48	1.00	up	5.40E-01	8.95E-01	-	-
1384881_at	Zdhhc19	zinc finger, DHHC-type containing 19	288045	Rn.48042	AW532959	2.37	2.36	2.38	2.36	2.37	2.36	1.00	down	5.23E-01	8.95E-01	-	-
1391328_at	---	---	---	---	AI575783	2.30	2.28	2.31	2.29	2.30	2.28	1.00	down	6.23E-01	8.95E-01	-	-
1374378_at	Arl9	ADP-ribosylation factor-like 9	289565	Rn.144736	BF413271	2.42	2.43	2.44	2.42	2.46	2.41	1.00	up	7.84E-01	9.30E-01	-	-
1384348_at	LOC688800	similar to transcription factor 23	688800	---	AI548285	2.29	2.30	2.29	2.29	2.30	2.28	1.00	down	5.39E-01	8.95E-01	-	-
1387760_a_at	Onecut1	one cut homeobox 1	25231	Rn.48812	NM_022671	2.32	2.31	2.32	2.31	2.32	2.30	1.00	down	5.64E-01	8.95E-01	-	-
1377203_at	---	---	---	Rn.172284	BF393845	2.35	2.34	2.35	2.34	2.35	2.33	1.00	down	5.79E-01	8.95E-01	-	-
1385267_at	---	---	---	---	AW433616	2.43	2.41	2.44	2.42	2.43	2.41	1.00	down	6.90E-01	9.05E-01	-	-
1381306_at	---	---	---	Rn.30695	AI013365	2.43	2.42	2.44	2.42	2.43	2.42	1.00	down	6.23E-01	8.95E-01	-	-
1378432_at	---	---	---	Rn.210153	BF404641	2.38	2.37	2.39	2.38	2.38	2.36	1.00	down	5.74E-01	8.95E-01	-	-
1390158_at	LOC304903	similar to Pappalysin-2 precursor (Pregnancy-associated plasma protein-A2) (	304903	---	BI290752	2.32	2.32	2.33	2.33	2.31	2.31	1.00	up	7.43E-01	9.17E-01	-	-
1397777_at	RGD1565416	similar to talin 2	315776	Rn.147817	AI710453	2.38	2.37	2.39	2.38	2.39	2.37	1.00	down	6.50E-01	8.96E-01	-	-
1397104_at	---	---	---	Rn.199646	AW527590	2.32	2.32	2.33	2.32	2.33	2.31	1.00	down	5.31E-01	8.95E-01	-	-
1367768_at	Lxn	latexin	59073	Rn.11404	NM_031655	2.67	2.69	2.72	2.64	2.70	2.72	1.00	down	8.92E-01	9.66E-01	-	-
1378233_at	---	---	---	Rn.199268	BF284235	2.49	2.48	2.51	2.50	2.50	2.47	1.00	down	7.87E-01	9.31E-01	-	-
1395673_at	---	---	---	Rn.147105	BF412214	2.33	2.32	2.34	2.33	2.34	2.32	1.00	down	6.50E-01	8.96E-01	-	-
1395189_at	---	---	---	---	BE111371	2.37	2.36	2.40	2.37	2.38	2.37	1.00	down	7.34E-01	9.15E-01	-	-
1375598_at	---	---	---	---	BE119628	2.33	2.32	2.35	2.33	2.34	2.32	1.00	down	7.27E-01	9.13E-01	-	-
1375216_at	Pvrl2	poliovirus receptor-related 2	308417	Rn.203297	AA850909	2.38	2.38	2.42	2.39	2.45	2.36	1.00	up	8.78E-01	9.63E-01	-	-
1388293_at	Myl2	myosin, light polypeptide 2, regulatory, cardiac, slow	363925	Rn.37176	BI288091	2.31	2.30	2.31	2.30	2.31	2.29	1.00	down	4.35E-01	8.95E-01	-	-
1389240_at	---	---	---	Rn.18153	AW527026	2.35	2.34	2.35	2.35	2.36	2.33	1.00	down	6.74E-01	9.01E-01	-	-
1389920_at	Znf787	Zinc finger protein 787	365176	Rn.23427	BF414325	2.30	2.30	2.31	2.30	2.30	2.29	1.00	down	4.56E-01	8.95E-01	-	-
1372966_at	Mfsd2	major facilitator superfamily domain containing 2	298504	Rn.20566	AI178784	2.35	2.34	2.36	2.35	2.35	2.34	1.00	down	4.71E-01	8.95E-01	-	-
1380029_at	Atmin	ATM interactor	315037	Rn.19593	BI278674	2.39	2.38	2.39	2.38	2.39	2.37	1.00	down	4.54E-01	8.95E-01	-	-
1381991_at	Ccdc91	Colled-coil domain containing 91	312863	Rn.42180	AI177144	2.42	2.42	2.42	2.42	2.44	2.42	1.00	up	5.57E-01	8.95E-01	-	-
1383828_at	---	---	---	Rn.204932	AI228058	2.40	2.38	2.40	2.39	2.40	2.39	1.00	down	5.59E-01	8.95E-01	-	-
1388278_at	Hspa1l	Heat shock 70kD protein 1-like (mapped)	24963	Rn.187184	X77209	2.40	2.38	2.40	2

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1390609_at	---	---	---	Rn.27672	BI296683	2.31	2.30	2.31	2.30	2.31	2.30	1.00	down	5.07E-01	8.95E-01	-	-
1388188_at	Cyp7b1	cytochrome P450, family 7, subfamily b, polypeptide 1	25429	Rn.53969	BF283070	2.51	2.44	2.49	2.50	2.50	2.46	1.00	up	8.71E-01	9.60E-01	-	-
1382979_at	---	---	---	Rn.196166	AI229202	2.41	2.40	2.42	2.40	2.43	2.40	1.00	down	7.07E-01	9.08E-01	-	-
1388069_at	Klrb1b	killer cell lectin-like receptor subfamily B member 1B	25192	Rn.101826	U56936	2.31	2.29	2.30	2.29	2.30	2.29	1.00	down	5.49E-01	8.95E-01	-	-
1383032_at	---	---	---	Rn.121052	BG666286	2.33	2.32	2.34	2.32	2.34	2.31	1.00	down	6.98E-01	9.07E-01	-	-
1391699_at	Polr2f	polymerase (RNA) II (DNA directed) polypeptide F	83503	Rn.28212	AI556892	2.85	2.91	2.85	2.85	2.85	2.93	1.00	up	9.06E-01	9.71E-01	-	-
1369883_at	Pth	parathyroid hormone	24694	Rn.9768	NM_017044	2.33	2.32	2.33	2.32	2.33	2.31	1.00	down	5.31E-01	8.95E-01	-	-
1393254_at	Stk36	serine/threonine kinase 36 (fused homolog, Drosophila)	301516	Rn.198846	BF402382	2.34	2.34	2.37	2.34	2.37	2.33	1.00	down	8.05E-01	9.37E-01	-	-
1382798_at	---	---	---	Rn.166111	AI045251	2.28	2.27	2.29	2.28	2.28	2.27	1.00	down	5.41E-01	8.95E-01	-	-
1398236_at	---	---	---	Rn.177687	BM386693	2.45	2.43	2.46	2.44	2.47	2.44	1.00	up	7.47E-01	9.18E-01	-	-
1391783_at	---	---	---	Rn.171605	BE120803	2.30	2.29	2.30	2.29	2.30	2.28	1.00	down	5.26E-01	8.95E-01	-	-
1378240_at	Fancd2	Fanconi anemia, complementation group D2	312641	Rn.203979	AI031007	2.85	3.30	2.81	2.80	3.66	2.51	1.00	up	9.92E-01	9.97E-01	-	-
1386237_at	---	---	---	Rn.206019	AI639466	2.41	2.40	2.44	2.41	2.44	2.40	1.00	down	8.02E-01	9.36E-01	-	-
1390617_at	---	---	---	Rn.200024	BF405095	2.30	2.29	2.31	2.29	2.30	2.29	1.00	down	5.63E-01	8.95E-01	-	-
1382027_at	---	---	---	Rn.17129	BI296880	2.24	2.23	2.25	2.23	2.24	2.23	1.00	down	5.28E-01	8.95E-01	-	-
1382666_at	---	---	---	Rn.129721	AI011667	2.29	2.29	2.30	2.28	2.30	2.28	1.00	down	5.77E-01	8.95E-01	-	-
1398241_at	---	---	---	Rn.161297	AW252411	2.35	2.33	2.35	2.35	2.36	2.34	1.00	up	7.34E-01	9.15E-01	-	-
1387708_at	Adra2a	adrenergic, alpha-2A-, receptor	25083	Rn.170171	U79031	2.33	2.32	2.34	2.33	2.34	2.32	1.00	down	5.93E-01	8.95E-01	-	-
1370982_at	Pygm	phosphorylase, glycogen, muscle	24701	Rn.11238	BI275633	2.26	2.25	2.27	2.25	2.26	2.25	1.00	down	5.10E-01	8.95E-01	-	-
1378495_at	---	---	---	Rn.210077	BF414427	2.40	2.39	2.41	2.39	2.41	2.38	1.00	down	6.73E-01	9.01E-01	-	-
1369324_at	Sval2	seminal vesicle antigen-like 2	84605	Rn.74250	NM_133291	2.34	2.33	2.35	2.33	2.34	2.33	1.00	down	6.84E-01	8.95E-01	-	-
1369608_at	Fgf16	fibroblast growth factor 16	60464	Rn.44348	NM_021867	2.29	2.28	2.29	2.28	2.29	2.27	1.00	down	5.76E-01	8.95E-01	-	-
1380247_at	---	---	---	Rn.200224	BM385840	2.31	2.31	2.33	2.31	2.32	2.30	1.00	down	6.53E-01	8.97E-01	-	-
1384487_at	Dmrt2	doublesex and mab-3 related transcription factor 2	309430	Rn.11448	BF557192	2.47	2.45	2.48	2.46	2.47	2.45	1.00	down	6.87E-01	9.04E-01	-	-
1382347_at	---	---	---	Rn.7022	AA850576	2.32	2.32	2.34	2.32	2.33	2.32	1.00	down	5.99E-01	8.95E-01	-	-
1386448_at	---	---	---	Rn.134917	AI639182	2.33	2.32	2.34	2.33	2.34	2.31	1.00	down	6.71E-01	9.00E-01	-	-
1387529_a_at	Tagln3	transgelin 3	63837	Rn.10998	NM_031676	2.38	2.36	2.40	2.37	2.40	2.36	1.00	down	8.02E-01	9.36E-01	-	-
1370683_at	Kcnk15	potassium channel, subfamily K, member 15	156873	Rn.161865	AF467250	2.29	2.28	2.29	2.28	2.29	2.27	1.00	down	4.72E-01	8.95E-01	-	-
1380396_at	---	---	---	Rn.34850	BE115208	2.35	2.34	2.36	2.34	2.35	2.33	1.00	down	6.32E-01	8.95E-01	-	-
1382081_at	Scara3	scavenger receptor class A, member 3	364405	Rn.9379	AA957749	2.35	2.34	2.35	2.34	2.35	2.34	1.00	down	5.55E-01	8.95E-01	-	-
1367794_at	A2m	alpha-2-macroglobulin	24153	Rn.109457	NM_012488	2.40	2.38	2.42	2.39	2.41	2.39	1.00	down	7.02E-01	9.07E-01	-	-
1385321_at	LOC688502	similar to Protein arginine N-methyltransferase 4 (Heterogeneous nuclear ribo	688502	Rn.152082	AW532713	2.37	2.37	2.38	2.37	2.38	2.36	1.00	down	6.27E-01	8.95E-01	-	-
1377584_at	LOC688990	Hypothetical protein LOC688990	688990	Rn.37063	BI297375	2.45	2.44	2.46	2.45	2.46	2.44	1.00	down	6.21E-01	8.95E-01	-	-
1368285_at	Shbg	sex hormone binding globulin	24775	Rn.37473	NM_012650	2.26	2.26	2.28	2.26	2.27	2.26	1.00	down	5.60E-01	8.95E-01	-	-
1397172_at	Eif2c3	eukaryotic translation initiation factor 2C, 3	313593	Rn.92025	AW917094	2.35	2.34	2.36	2.35	2.35	2.34	1.00	down	6.17E-01	8.95E-01	-	-
1368751_at	Kcns3	potassium voltage-gated channel, delayed-rectifier, subfamily S, member 3	83588	Rn.10878	NM_031778	2.37	2.36	2.38	2.36	2.37	2.36	1.00	down	5.60E-01	8.95E-01	-	-
1377780_at	Tspan9	tetraspanin 9	312728	Rn.16430	AI179881	2.31	2.30	2.32	2.31	2.31	2.30	1.00	down	5.38E-01	8.95E-01	-	-
1369829_at	Gjb4	gap junction protein, beta 4	117055	Rn.10344	NM_053984	2.27	2.27	2.28	2.27	2.27	2.26	1.00	down	5.41E-01	8.95E-01	-	-
1375539_at	Tbr1	T-box, brain, 1	680427	Rn.8247	BF411127	2.34	2.33	2.34	2.33	2.34	2.32	1.00	down	6.17E-01	8.95E-01	-	-
1390596_at	Mlana	melan-A	293890	Rn.12340	BG378791	2.32	2.31	2.33	2.32	2.32	2.31	1.00	down	5.76E-01	8.95E-01	-	-
1382759_at	---	---	---	Rn.132931	AI454681	2.52	2.50	2.55	2.50	2.60	2.45	1.00	down	9.32E-01	9.81E-01	-	-
1387356_at	Wfs1	Wolfram syndrome 1 homolog (human)	83725	Rn.16015	NM_031823	2.32	2.31	2.33	2.32	2.33	2.31	1.00	down	5.88E-01	8.95E-01	-	-
1370233_at	Fgf12	fibroblast growth factor 12	170630	Rn.45965	AW252096	2.41	2.40	2.42	2.45	2.41	2.39	1.00	up	8.38E-01	9.49E-01	-	-
1398100_at	Ncoa2	nuclear receptor coactivator 2	83724	Rn.49136	AW528677	2.30	2.29	2.31	2.30	2.30	2.29	1.00	down	4.88E-01	8.95E-01	-	-
1380048_at	Nlgn3	Neuroligin 3	171297	Rn.10283	AF401725	2.45	2.44	2.46	2.44	2.46	2.44	1.00	down	5.89E-01	8.95E-01	-	-
1368767_at	Cst8	cystatin 8 (cystatin-related epididymal specific)	29679	Rn.18514	NM_019258	2.32	2.31	2.33	2.32	2.33	2.31	1.00	down	6.37E-01	8.95E-01	-	-
1376654_at	RGD1308448	similar to RIKEN cDNA B130016O10 gene	310358	Rn.102997	AW521378	2.45	2.44	2.47	2.45	2.47	2.43	1.00	down	8.13E-01	9.39E-01	-	-
1375468_at	Abcc5	ATP-binding cassette, sub-family C (CFTR/MRP), member 5	116721	Rn.9491	AW252983	2.38	2.38	2.39	2.37	2.39	2.38	1.00	down	4.22E-01	8.95E-01	-	-
1380352_at	---	---	---	Rn.203551	AA956439	2.35	2.34	2.36	2.35	2.35	2.34	1.00	down	5.60E-01	8.95E-01	-	-
1378033_at	---	---	---	Rn.18164	AI029178	2.27	2.26	2.29	2.26	2.27	2.30	1.00	up	7.85E-01	9.30E-01	-	-
1387576_at	Trim17	tripartite motif-containing 17	64702	Rn.48706	AW022798	2.33	2.32	2.34	2.32	2.34	2.32	1.00	down	5.58E-01	8.95E-01	-	-
1391648_at	Dscr6	Down syndrome critical region homolog 6 (human)	288239	Rn.13025	BF545697	2.56	2.56	2.58	2.55	2.62	2.52	1.00	down	8.99E-01	9.68E-01	-	-
1384063_at	Cthrc1	collagen triple helix repeat containing 1	282836	Rn.9468	AA958001	2.33	2.33	2.34	2.33	2.34	2.33	1.00	down	4.85E-01	8.95E-01	-	-
1396534_at	---	---	---	Rn.207986	BF401551	2.32	2.31	2.34	2.31	2.34	2.30	1.00	down	7.79E-01	9.28E-01	-	-
1394522_at	---	---	---	Rn.155976	AW527950	2.33	2.32	2.34	2.36	2.33	2.31	1.00	up	7.83E-01	9.30E-01	-	-
1373979_at	---	---	---	Rn.203871	BF281977	2.49	2.49	2.48	2.47	2.53	2.48	1.00	up	8.50E-01	9.53E-01	-	-
1386352_at	---	---	---	Rn.132398	AA892204	2.52	2.49	2.54	2.52	2.55	2.49	1.00	up	8.54E-01	9.55E-01	-	-
1377397_at	RGD1563440	similar to hypothetical protein	298301	Rn.61954	BF393128	2.29	2.29	2.30	2.29	2.30	2.28	1.00	down	5.33E-01	8.95E-01	-	-
1369745_at	Grin2b	glutamate receptor, ionotropic, N-methyl D-aspartate 2B	24410	Rn.9711	M91562	2.36	2.36	2.37	2.36	2.37	2.35	1.00	down	6.24E-01	8.95E-01	-	-
1381341_at	rCG_43687	hypothetical protein LOC688459	688459	Rn.161109	BE111796	2.47	2.45	2.48	2.46	2.47	2.45	1.00	down	6.43E-01	8.95E-01	-	-
1391259_at	---	---	---	Rn.206815	BE104618	2.27	2.27	2.28	2.28	2.27	2.26	1.00	down	5.54E-01	8.95E-01	-	-
1382229_at	---	---	---	Rn.203793	AA998299	2.29	2.27	2.29	2.30	2.29	2.28	1.00	up	5.91E-01	8.95E-01	-	-
1396016_at	---	---	---	Rn.172695	BF415547	2.34	2.33	2.35	2.33	2.35	2.33	1.00	down	6.02E-01	8.95E-01	-	-
1387970_at	Slc38a5	solute carrier family 38, member 5	192208	Rn.81033	AF276870	2.27	2.26	2.28	2.26	2.27	2.26	1.00	down	4.66E-01	8.95E-01	-	-
1393675_at	Btnl1	butyrophilin-like 1	407781	Rn.81283	BM383075	2.27	2.27	2.28	2.27	2.28	2.26	1.00	down	5.83E-01	8.95E-01	-	-
1380791_at	---	---	---	Rn.172734	BF405304	2.41	2.40	2.42	2.41	2.42	2.40	1.00	down	6.24E-01	8.95E-01	-	-
1368441_at	Msln	mesothelin	60333	Rn.18607	NM_031658	2.47	2.47	2.48	2.47	2.47	2.46	1.00	down	3.44E-01	8.95E-01	-	-
1376777_at	Rbp3	retinol binding protein 3, interstitial	24711	Rn.41214	AI575415	2.32	2.31	2.33	2.32	2.33	2.31	1.00	down	6.31E-01	8.95E-01	-	-
1370392_at	Trpm4	transient receptor potential cation channel, subfamily M, member 4	171143	Rn.205039	AB040857	2.39	2.38	2.40	2.39	2.40	2.38	1.00	down	6.12E-01	8.95E-01	-	-
1385997_at	---	---	---	Rn.14821	AA893688	2.41	2.40	2.43	2.41	2.43	2.39	1.00	down	7.86E-01	9.30E-01	-	-
1371092_at	LOC286960	preprotrypsinogen IV	286960	Rn.10387	X15679	2.39	2.39	2.40	2.39	2.40	2.38	1.00	down	6.00E-01	8.95E-01	-	-
1376148_at	---	---	---	Rn.148007	AW535240	2.30	2.29	2.30	2.29	2.30	2.28	1.00	down	5.31E-01	8.95E-01	-	-
1380860_at	---	---	---	Rn.147798	BI295181	2.26	2.25	2.26	2.25	2.26	2.25	1.00	down	4.69E-01	8.95E-01	-	-
1376815_at	Stox2	Storkhead box 2	306459	Rn.61768	BF401000	2.33	2.32	2.34	2.32	2.33	2.32	1.00	down	5.81E-01	8.95E-01	-	-
1384806_at	---	---	---	---	AI502875	2.43	2.40	2.44	2.41	2.45	2.39	1.00	down	8.48E-01	9.53E-01	-	-
1370439_a_at	Kcnc2	potassium voltage gated channel, Shaw-related subfamily, member 2	246153	Rn.9733	M34052	2.34	2.33	2.35	2.33	2.35	2.32	1.00	down	7.09E-01	9.09E-01	-	-
1374510_at	---	---	---	Rn.199295	BI296300	2.53	2.47	2.55	2.51	2.52	2.50	1.00	down	8.65E-01	9.58E-01	-	-
1387702_at	Galr1	galanin receptor 1	50577	Rn.10213	U30290	2.36	2.36	2.38	2.36	2.37	2.35	1.00	down	6.53E-01	8.97E-01	-	-
1397479_at	Smyd1	SET and MYND domain containing 1	297333	Rn.203854	BE113370	2.30	2.29	2.30	2.29	2.30	2.29	1.00	down	4.70E-01	8.95E-01	-	-
1393398_at	---	---	---	---	BF412064	2.30	2.29	2.30	2.29	2.30	2.28	1.00	down	4.46E-01	8.95E-01	-	-
1395181_at	---	---	---	Rn.168979	AI407570	2.43	2.42	2.41	2.43	2.44	2.41	1.00	up	6.77E-01	9.02E-01	-	-
1396509_at	Tmem132e	transmembrane protein 132E	287564	Rn.46621	BE096132	2.24	2.24	2.25	2.24	2.24	2.23	1.00	down	4.22E-01	8.95E-01	-	-
1385280_at	---	---	---	Rn.206180	AW523198	2.37	2.36	2.38	2.37	2.38	2.36	1.00	down	6.30E-01	8.95E-01	-	-
1398547_at	---	---	---	Rn.153909	BE107624	2.46	2.46	2.47	2.46	2.47	2.46	1.00	up	5.17E-01	8.95E-01	-	-
1376844_at	Ap3b2	adaptor-related protein complex 3, beta 2 subunit	308777	Rn.217954	BI298352	2.46	2.42	2.46	2.45	2.46	2.44	1.00	up	7.78E-01	9.28E-01	-	-
1392150_at	---	---	---	Rn.171000	BE106587	2.31	2.31	2.32	2.31	2.32	2.30	1.00	down	4.83E-01	8.95E-01	-	-
1382246_at	---	---	---	Rn.214355	AI172596	2.37	2.36	2.37	2.36	2.37	2.35	1.00	down	6.46E-01	8.95E-01	-	-
1370641_s_at	Cacna1i	calcium channel, voltage-dependent, T type, alpha 1I subunit	56827	Rn.48680	AF290214	2.37	2.37	2.38	2.37	2.37	2.36	1.00	down	5.01E-01	8.95E-01	-	-
1391103_at	---	---	---	Rn.209908	BF400883	2.35	2.34	2.36	2.34	2.35	2.33	1.00	down	5.91E-01	8.95E-01	-	-
1382133_at	---	---	---	Rn.41801	AW526024	2.34	2.34	2.35	2.34	2.35	2.33	1.00	down	4.71E-01	8.95E-01	-	-
1389239_at	---	---	---	---	BM384377	2.36	2.35	2.37	2.36	2.37	2.35	1.00	down	6.13E-01	8.95E-01	-	-
1385104_at	Efs	embryonal Fyn-associated substrate	290212	Rn.219271	BE118590	2.29	2.28	2.30	2.28	2.29	2.28	1.00	down	3.71E-01	8.95E-01	-	-
1387570_at	Manea	mannosidase, endo-alpha	140808	Rn.10855	NM_080785	2.40	2.41	2.42	2.40	2.41	2.40	1.00	down	5.42E-01	8.95E-01	-	-
1390537_at	Slc25a18	solute carrier family 25 (mitochondrial carrier), member 18	681896	Rn.42043	BG380364	2.31	2.31	2.32	2.31	2.31	2.30	1.00	down	4.12E-01	8.95E-01	-	-
1398123_at	---	---	---	Rn.46970	AW529164	2.40	2.39	2.42	2.39	2.41	2.40	1.00	down	6.44E-01	8.95E-01	-	-
1380208_at	---	---	---	Rn.210614	BF402618	2.50	2.49	2.50	2.50	2.50	2.48	1.00	down	5.79E-01	8.95E-01	-	-
1393755_at	Plk3cd	phosphatidylinositol 3-kinase catalytic delta polypeptide	366508	Rn.11530	BE109926	2.31	2.30	2.32	2.31	2.32	2.30	1.00	down	6.02E-01	8.95E-01	-	-
1370586_a_at	Cacna1e	calcium channel, voltage-dependent, R type, alpha 1E subunit	54234	Rn.10742	AY029412	2.35	2.34	2.36	2.35	2.36	2.34	1.00	down	6.54E-01	8.97E-01	-	-
1397344_at	---	---	---	---	AI178200	2.32	2.30	2.33	2.31	2.32	2.30	1.00	down	7.14E-01	9.10E-01	-	-
1382819_at	Tyrp1	tyrosinase-related protein 1	298182	Rn.40774	AI717472	2.29	2.28	2.30	2.29	2.29	2.28	1.00	down	4.94E-01	8.95E-01	-	-
1391407_at	---	---	---	Rn.206040	BF392634	2.27	2.26	2.27	2.26	2.27	2.26	1.00	down	4.73E-01	8.95E-01	-	-
1398649_at	Slitrk3	SLIT and NTRK-like family, member 3	310519	Rn.68333	AA819827	2.37	2.36	2.38	2.37	2.38	2.36	1.00	down	5.96E-01	8.95E-01	-	-
1375743_at	RGD1565416	similar to talin 2	315776	Rn.147817	BE110400	2.39	2.37	2.39	2.38	2.39	2.36	1.00	down	7.03E-01	9.07E-01	-	-
1395276_at	Rnf7	Ring finger protein 7	300948	Rn.2768	AA899483	2.56	2.56	2.58	2.51	2.57	2.62	1.00	up	9.03E-01	9.70E-01	-	-
1396517_at	RGD1563533	Similar to novel protein	313713	Rn.91524	AW533284	2.26	2.25	2.27	2.26	2.26	2.25	1.00	down	4.39E-01	8.95E-01	-	-
1398101_at	---	---	---	---	AI236382	2.31	2.30	2.32	2.30	2.31	2.30	1.00	down	5.04E-01	8.95E-01	-	-
1397068_at	---	---	---	Rn.210784	BF402399	2.31	2.27	2.28	2.31	2.28	2.26	1.00	down	8.33E-01	9.47E-01	-	-
1380661_at	Pld3	phospholipase D family, member 3	361527	Rn.128036	BF405873	2.38	2.37	2.38	2.38	2.38	2.36	1.00	down	5.92E-01	8.95E-01	-	-
1395156_at	---	---	---	Rn.156679	BF567237	2.27	2.26	2.28	2.27	2.27	2.26	1.00	down	5.01E-01	8.95E-01	-	-
1396579_at	---	---	---	Rn.210805	BF415619	2.34	2.33	2.35	2.34	2.35	2.32	1.00	down	6.41E-01	8.95E-01	-	-
1395069_at	---	---	---	Rn.210691	BF406622	2.33	2.31	2.36	2.33	2.34	2.32	1.00	down	7.78E-01	9.28E-01	-	-
1392235_at	---	---	---	Rn.170956	BE105570	2.40	2.38	2.40	2.38	2.42	2.36	1.00	down	8.31E-01	9.47E-01	-	-
1393920_at	---	---	---	Rn.132781	BM391842	2.35	2.34	2.36	2.34	2.36	2.34	1.00	down	6.33E-01	8.95E-01	-	-
1380656_at	---	---	---	Rn.204250	BM390299	2.33	2.33	2.33	2.32	2.33	2.32	1.00	down	3.78E-01	8.95E-01	-	-
1383506_at	Bcl11a	B-cell CLL/lymphoma 11A (zinc finger protein)	305589	Rn.16729	AW254062	2.37	2.36	2.38	2.36	2.37	2.35	1.00	down	6.61E-01	8.98E-01	-	-
1394503_at	---	---	---	Rn.55282	AI171987	2.31	2.30	2.31	2.30	2.31	2.30	1.00	down	4.71E-01	8.95E-01	-	-
1387180_at	Il1r2	interleukin 1 receptor, type II	117022	Rn.10758	NM_053953	2.32	2.31	2.33	2.31	2.31	2.31	1.00	down	5.88E-01	8.95E-01	-	-
1380175_at	Ptplad2	protein tyrosine phosphatase-like A domain containing 2	362540	Rn.35165	AI501853	2.30	2.29	2.31	2.30	2.30	2.29	1.00	down	5.40E-01	8.95E-01	-	-
1377892_at	Sema3f	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (se	315996	Rn.205616	BM390000	2.30	2.29	2.30	2.29	2.30	2.28	1.00	down	4.91E-01	8.95E-01	-	-
1378040_at	Chst14	carbohydrate (N-acetylgalactosamine 4-0) sulfotransferase 14	691394	Rn.106173	BE111867	2.28	2.28	2.29	2.28	2.28	2.27	1.00	down	3.25E-01	8.95E-01	-	-
1391144_at	---	---	---	Rn.24820	AI227988	2.32	2.31	2.32	2.31	2.32	2.30	1.00	down	5.83E-01	8.95E-01	-	-
1387509_at	Dio3	deiodinase, iodothyronine, type III	29475	Rn.11237	NM_017210	2.33	2.32	2.33	2.32	2.33	2.32	1.00	down	5.33E-01	8.95E-01	-	-
1397825_at	Ankib1	ankyrin repeat and IBR domain containing 1	368062	Rn.2999	BE109247	3.96	3.64	2.52	4.03	2.58	3.53	1.00	up	9.95E-01	9.98E-01	-	-
1375109_at	---	---	---	Rn.212087	BI296722	2.37	2.36	2.37	2.36	2.37	2.36	1.00	down	4.22E-01	8.95E-01	-	-
1391227_at	---	---	---	Rn.20252	AW530423	2.34	2.33	2.35	2.33	2.34	2.33	1.00	down	5.02E-01	8.95E-01	-	-
1378000_at	---	---	---	Rn.34520	AA801075	2.39	2.38	2.41	2.39	2.41	2.37	1.00	down	7.28E-01	9.13E-01	-	-
1391934_at	---	---	---	Rn.156328	AI059392	2.51	2.50	2.52	2.51	2.51	2.50	1.00	down	4.81E-01	8.95E-01	-	-
1396425_at	---	---	---	Rn.161305	BF402681	2.29	2.28	2.29	2.28	2.29	2.27	1.00	down	4.92E-01	8.95E-01	-	-
1394990_at	---	---	---	Rn.52524	BI301740	2.36	2.36	2.37	2.36	2.37	2.35	1.00	down	5.88E-01	8.95E-01	-	-
1369372_at	Gabbr1	gamma-aminobutyric acid (GABA) B receptor 1	81657	Rn.30059	NM_031028	2.44	2.43	2.44	2.43	2.43	2.43	1.00	down	3.22E-01	8.95E-01	-	-
1371815_at	Mfap2	microfibrillar-associated protein 2	313662	Rn.17012	BM386326	2.35	2.34	2.35	2.35	2.35	2.34	1.00	down	4.30E-01	8.95E-01	-	-
1380081_at	---	---	---	Rn.34177	AA819551	2.30	2.29	2.31	2.30	2.31	2.29	1.00	down	5.67E-01	8.95E-01	-	-
1393955_at	Wdr44	WD repeat domain 44	246152	Rn.79380	BI293101	5.13	3.88	5.07	4.69	5.04	4.37	1.00	up	9.93E-01	9.98E-01	-	-
1379716_at	---	---	---	Rn.203204	AA956555	2.28	2.27	2.28	2.27	2.28	2.27	1.00	down	3.78E-01	8.95E-01	-	-
1368586_at	Zg16	zymogen granule protein 16	171449	Rn.10439	NM_134409	2.29	2.28	2.30	2.29	2.29	2.28	1.00	down	5.33E-01	8.95E-01	-	-
1378725_at	---	---	---	Rn.206358	BE105927	2.36	2.35	2.36	2.35	2.36	2.35	1.00	down	5.82E-01	8.95E-01	-	-
1375694_at	Rasip1	Ras interacting protein 1	292912	Rn.23451	BF406888	2.28	2.27	2.28	2.28	2.28	2.27	1.00	down	5.07E-01	8.95E-01	-	-
1390570_at	Crtc3	CREB regulated transcription coactivator 3	365297	Rn.153601	BI299811	2.33	2.32	2.34	2.33	2.34	2.32	1.00	down	5.70E-01	8.95E-01	-	-
1393286_at	Nr5a1	nuclear receptor subfamily 5, group A, member 1	83826	Rn.6586	AI453929	2.28	2.28	2.29	2.28	2.29	2.27	1.00	down	5.33E-01	8.95E-01	-	-
1376344_at	---	---	---	Rn.13660	AI010267	2.46	2.44	2.49	2.46	2.48	2.44	1.00	down	8.13E-01	9.40E-01	-	-
1378071_at	---	---	---	Rn.155717	AA942941	2.34	2.33	2.35	2.34	2.35	2.32	1.00	down	7.16E-01	9.10E-01	-	-
1385057_at	---	---	---	Rn.97315	AA819868	2.28	2.28	2.29	2.28	2.28	2.27	1.00	down	4.92E-01	8.95E-01	-	-
1378102_at	Pcnxl2	pecanex-like 2 (Drosophila)	307949	Rn.142549	AI502785	2.25	2.25	2.27	2.25	2.26	2.24	1.00	down	6.00E-01	8.95E-01	-	-
1384099_at	Slc39a6	solute carrier family 39 (metal ion transporter), member 6	291733	Rn.99415	AA997670	2.96	3.04	2.97	3.02	2.97	2.96	1.00	down	8.95E-01	9.67E-01	-	-
1387638_a_at	Ctla4	cytotoxic T-lymphocyte-associated protein 4	63835	Rn.10259	U90271	2.31	2.30	2.32

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1398744_at	---	---	---	Rn.206025	AW253984	2.36	2.35	2.37	2.36	2.37	2.35	1.00	down	6.66E-01	8.99E-01	-	-
1382830_at	Suv39h2	suppressor of variegation 3-9 homolog 2 (Drosophila)	364785	Rn.154750	AI071877	2.34	2.33	2.35	2.34	2.35	2.33	1.00	down	6.27E-01	8.95E-01	-	-
1388811_at	---	---	---	Rn.203113	BF401593	2.32	2.31	2.33	2.31	2.32	2.31	1.00	down	5.67E-01	8.95E-01	-	-
1393007_at	---	---	---	Rn.164628	BF554509	2.31	2.30	2.31	2.30	2.31	2.30	1.00	down	5.14E-01	8.95E-01	-	-
1397236_at	---	---	---	Rn.200036	AI453924	2.31	2.30	2.31	2.30	2.31	2.30	1.00	down	4.46E-01	8.95E-01	-	-
1377801_at	Bttd12	BTB (POZ) domain containing 12	302953	Rn.25408	AI237031	2.70	2.76	3.05	2.81	2.97	2.76	1.00	up	9.75E-01	9.93E-01	-	-
1370598_a_at	Kcnj6	potassium inwardly-rectifying channel, subfamily J, member 6	25743	Rn.10185	AB073755	2.30	2.30	2.31	2.30	2.31	2.29	1.00	down	5.38E-01	8.95E-01	-	-
1384693_at	---	---	---	Rn.17484	AI009768	2.29	2.28	2.29	2.28	2.29	2.28	1.00	down	4.33E-01	8.95E-01	-	-
1395594_at	Wnt11	wingless-type MMTV integration site family, member 11	140584	Rn.55941	AW526032	2.30	2.29	2.31	2.29	2.30	2.29	1.00	down	5.47E-01	8.95E-01	-	-
1368312_at	Oxt	oxytocin, preropeptide	25504	Rn.48915	M25649	2.24	2.24	2.25	2.24	2.24	2.23	1.00	down	4.16E-01	8.95E-01	-	-
1392012_at	---	---	---	Rn.199760	BE100353	2.36	2.34	2.36	2.34	2.35	2.35	1.00	down	5.55E-01	8.95E-01	-	-
1370560_at	Znf689	zinc finger protein 689	286996	Rn.205819	AF277902	2.34	2.33	2.35	2.33	2.34	2.33	1.00	down	5.90E-01	8.95E-01	-	-
1381908_at	Tspyl5	TSPY-like 5	314555	Rn.16194	BE114525	2.31	2.30	2.31	2.30	2.31	2.31	1.00	up	3.84E-01	8.95E-01	-	-
1389506_x_at	Cdc20	Cell division cycle 20 homolog (S. cerevisiae)	64515	Rn.9282	BI288458	2.37	2.36	2.38	2.36	2.37	2.36	1.00	down	5.03E-01	8.95E-01	-	-
1390286_at	RGD1562406	similar to FLJ00248 protein	288559	Rn.59091	BM387144	2.32	2.31	2.33	2.32	2.32	2.31	1.00	down	5.02E-01	8.95E-01	-	-
1393646_at	Dppa3	developmental pluripotency-associated 3	297576	Rn.79056	BI289609	2.40	2.39	2.40	2.39	2.40	2.38	1.00	down	6.34E-01	8.95E-01	-	-
1368951_at	Grin2d	glutamate receptor, ionotropic, N-methyl D-aspartate 2D	24412	Rn.91209	NM_022797	2.37	2.35	2.36	2.35	2.36	2.35	1.00	down	5.25E-01	8.95E-01	-	-
1381427_at	rCG_44068	forkhead box C1	364706	Rn.11816	AI111819	2.55	2.54	2.64	2.56	2.67	2.51	1.00	up	9.45E-01	9.84E-01	-	-
1381959_at	---	---	---	---	BF386978	2.34	2.34	2.35	2.34	2.34	2.35	1.00	up	4.75E-01	8.95E-01	-	-
1380286_at	Tbl1l	tubulin tyrosine ligase-like family, member 11	689746	Rn.56580	BG376326	2.32	2.31	2.32	2.32	2.32	2.31	1.00	down	4.34E-01	8.95E-01	-	-
1368384_at	Klk6	kallikrein related-peptidase 6	29245	Rn.10732	NM_019175	2.33	2.32	2.37	2.33	2.34	2.37	1.00	up	8.40E-01	9.50E-01	-	-
1379707_at	---	---	---	Rn.170591	BF284363	2.35	2.34	2.36	2.34	2.35	2.34	1.00	down	6.38E-01	8.95E-01	-	-
1377307_at	Fam89a	family with sequence similarity 89, member A	361441	Rn.66325	BM385387	2.32	2.32	2.33	2.32	2.32	2.31	1.00	down	4.04E-01	8.95E-01	-	-
1382407_at	---	---	---	Rn.24753	BF283320	2.44	2.43	2.45	2.46	2.44	2.42	1.00	up	7.44E-01	9.17E-01	-	-
1379723_at	RGD1565584	similar to tyrosine kinase-associated leucine zipper protein LAZIpII	293112	Rn.35776	BG673264	4.02	4.17	3.97	4.02	3.96	4.19	1.00	up	9.67E-01	9.90E-01	-	-
1398203_at	---	---	---	Rn.177738	BM387488	2.33	2.32	2.34	2.32	2.33	2.32	1.00	down	5.71E-01	8.95E-01	-	-
1379922_at	---	---	---	Rn.205125	BM389053	2.29	2.28	2.30	2.29	2.29	2.28	1.00	down	5.17E-01	8.95E-01	-	-
1388812_at	Tp53i13	tumor protein p53 inducible protein 13	287550	Rn.17771	AI230362	2.40	2.39	2.40	2.39	2.39	2.39	1.00	down	3.07E-01	8.95E-01	-	-
1369283_at	Tub	tubby homolog (mouse)	25609	Rn.30017	NM_013077	2.33	2.32	2.33	2.32	2.33	2.31	1.00	down	5.40E-01	8.95E-01	-	-
1389243_at	---	---	---	---	AI599794	6.41	5.18	5.03	5.60	5.01	5.99	1.00	down	9.94E-01	9.98E-01	-	-
1371538_at	Brsk1	BR serine/threonine kinase 1	499073	Rn.112844	BF407786	2.28	2.28	2.30	2.28	2.30	2.27	1.00	down	7.03E-01	9.07E-01	-	-
1376513_a_at	---	---	---	Rn.125774	BE098803	2.40	2.40	2.42	2.40	2.41	2.39	1.00	down	6.55E-01	8.98E-01	-	-
1385307_at	---	---	---	---	BI289808	2.35	2.35	2.35	2.35	2.36	2.36	1.00	up	2.71E-01	8.95E-01	-	-
1387304_at	Uhrf2	ubiquitin-like, containing PHD and RING finger domains 2	57305	Rn.44230	NM_020537	2.29	2.28	2.29	2.28	2.29	2.28	1.00	down	4.78E-01	8.95E-01	-	-
1390505_a_at	LOC688721	similar to leucine rich repeat and fibronectin type III domain containing 4	688721	Rn.219382	BF419854	2.25	2.25	2.26	2.25	2.26	2.24	1.00	down	4.95E-01	8.95E-01	-	-
1379127_at	---	---	---	---	AW532225	2.29	2.28	2.29	2.28	2.28	2.28	1.00	down	5.06E-01	8.95E-01	-	-
1392630_at	---	---	---	Rn.19395	AI060221	2.26	2.26	2.28	2.26	2.27	2.25	1.00	down	7.08E-01	9.09E-01	-	-
1369699_at	Glp1r	glucagon-like peptide 1 receptor	25051	Rn.11408	NM_012728	2.30	2.30	2.31	2.30	2.31	2.29	1.00	down	5.47E-01	8.95E-01	-	-
1388232_a_at	Lepr	leptin receptor	24536	Rn.9891	AF007819	2.31	2.31	2.32	2.31	2.31	2.31	1.00	down	2.86E-01	8.95E-01	-	-
1369823_at	Adam7	ADAM metallopeptidase domain 7	29641	Rn.10357	NM_020301	2.29	2.28	2.30	2.29	2.29	2.28	1.00	down	5.57E-01	8.95E-01	-	-
1372424_at	---	---	---	Rn.161440	BF393937	2.40	2.38	2.40	2.39	2.41	2.37	1.00	down	7.83E-01	9.30E-01	-	-
1392185_at	Tnxa	tenascin XA	25602	Rn.36545	BE096485	2.31	2.30	2.31	2.31	2.30	2.30	1.00	down	5.01E-01	8.95E-01	-	-
1396898_at	---	---	---	Rn.38908	AI575429	2.35	2.34	2.35	2.34	2.35	2.33	1.00	down	6.28E-01	8.95E-01	-	-
1378363_at	---	---	---	---	BF404637	2.30	2.29	2.30	2.30	2.30	2.29	1.00	down	2.42E-01	8.95E-01	-	-
1369861_at	Gabra6	gamma-aminobutyric acid (GABA) A receptor, alpha 6	29708	Rn.211981	NM_021841	2.30	2.30	2.30	2.30	2.30	2.29	1.00	down	4.74E-01	8.95E-01	-	-
1376291_at	Wdr4	WD repeat domain 4	690032	Rn.116634	BI282331	2.36	2.36	2.37	2.36	2.37	2.35	1.00	down	6.34E-01	8.95E-01	-	-
1391249_at	RGD1312005	similar to DD1	291580	Rn.7600	BF392349	2.35	2.35	2.36	2.35	2.35	2.34	1.00	down	3.92E-01	8.95E-01	-	-
1391351_at	LOC680133	Similar to TBC1 domain family, member 8	680133	Rn.205305	AI556000	2.26	2.25	2.26	2.25	2.26	2.25	1.00	down	3.82E-01	8.95E-01	-	-
1390190_at	Plac1	placenta-specific 1	317316	Rn.24205	BI293691	2.34	2.33	2.35	2.33	2.35	2.32	1.00	down	7.26E-01	9.13E-01	-	-
1387483_at	Plcg2	phospholipase C, gamma 2	29337	Rn.9751	NM_017168	2.40	2.40	2.41	2.40	2.41	2.39	1.00	down	5.84E-01	8.95E-01	-	-
1387465_a_at	Gnrhr	gonadotropin releasing hormone receptor	81668	Rn.112595	NM_031038	2.31	2.30	2.32	2.30	2.31	2.30	1.00	down	5.38E-01	8.95E-01	-	-
1396666_at	---	---	---	Rn.147782	BF401640	2.32	2.31	2.33	2.32	2.33	2.31	1.00	down	6.03E-01	8.95E-01	-	-
1379791_at	Cd3e	CD3 molecule, epsilon polypeptide	315609	Rn.96221	AW915948	2.24	2.24	2.24	2.24	2.24	2.23	1.00	down	3.91E-01	8.95E-01	-	-
1375768_at	Jund	Jun D proto-oncogene	24518	Rn.46225	BE096021	2.35	2.35	2.36	2.35	2.36	2.34	1.00	down	4.03E-01	8.95E-01	-	-
1374650_at	---	---	---	Rn.172618	BF400611	2.38	2.38	2.40	2.38	2.39	2.37	1.00	down	6.50E-01	8.96E-01	-	-
1384470_at	---	---	---	Rn.39323	BE114218	2.32	2.31	2.33	2.32	2.32	2.31	1.00	down	5.53E-01	8.95E-01	-	-
1370013_at	Cnga1	cyclic nucleotide gated channel alpha 1	85259	Rn.54534	NM_053497	2.29	2.29	2.30	2.29	2.30	2.28	1.00	down	5.24E-01	8.95E-01	-	-
1383741_at	---	---	---	Rn.9410	BE100721	2.42	2.42	2.44	2.41	2.47	2.41	1.00	up	8.68E-01	9.59E-01	-	-
1375937_a_at	Cenpt	centromere protein T	307805	Rn.194991	BE104344	2.41	2.41	2.42	2.41	2.41	2.40	1.00	down	4.23E-01	8.95E-01	-	-
1387475_at	Adarb2	adenosine deaminase, RNA-specific, B2	117088	Rn.10683	NM_133302	2.32	2.31	2.33	2.32	2.32	2.31	1.00	down	5.23E-01	8.95E-01	-	-
1393826_at	Apon	apolipoprotein N	304603	Rn.18716	AI043761	2.31	2.30	2.32	2.31	2.32	2.30	1.00	down	6.47E-01	8.95E-01	-	-
1369006_at	Hk2	hexokinase 2	25059	Rn.91375	NM_012735	2.31	2.30	2.32	2.30	2.31	2.30	1.00	down	5.63E-01	8.95E-01	-	-
1381854_at	---	---	---	Rn.199699	BF418164	2.34	2.33	2.35	2.33	2.34	2.33	1.00	down	5.43E-01	8.95E-01	-	-
1396181_at	F8	coagulation factor VIII, procoagulant component	302470	Rn.95452	BF420450	2.34	2.34	2.35	2.34	2.35	2.33	1.00	down	6.31E-01	8.95E-01	-	-
1379483_at	Prl7b1	prolactin family 7, subfamily b, member 1	266804	Rn.79989	BI274659	2.33	2.32	2.34	2.32	2.34	2.32	1.00	down	6.45E-01	8.95E-01	-	-
1379586_at	Rbm11	RNA binding motif protein 11	288321	Rn.154372	AW527929	2.31	2.30	2.32	2.30	2.32	2.30	1.00	down	5.64E-01	8.95E-01	-	-
1398055_at	Ifnar1	interferon (alpha, beta and omega) receptor 1	288264	Rn.105738	BF412899	2.44	2.44	2.44	2.44	2.43	2.43	1.00	down	4.25E-01	8.95E-01	-	-
1377249_at	Gspt2	G1 to S phase transition 2	501582	Rn.45722	AW526060	2.29	2.28	2.29	2.28	2.29	2.28	1.00	down	4.45E-01	8.95E-01	-	-
1381011_at	---	---	---	Rn.153063	BF402331	2.39	2.38	2.41	2.39	2.41	2.38	1.00	down	7.35E-01	9.15E-01	-	-
1392137_at	---	---	---	Rn.58583	BF404497	2.32	2.31	2.32	2.31	2.32	2.30	1.00	down	6.00E-01	8.95E-01	-	-
1372669_at	---	---	---	Rn.63325	BF404426	2.27	2.26	2.27	2.27	2.27	2.26	1.00	down	4.30E-01	8.95E-01	-	-
1368449_at	Adap1	ArfGAP with dual PH domains 1	171097	Rn.10539	U51013	2.37	2.35	2.38	2.36	2.39	2.36	1.00	up	7.39E-01	9.16E-01	-	-
1392962_at	---	---	---	Rn.22780	AW525482	2.35	2.34	2.36	2.35	2.35	2.34	1.00	down	5.45E-01	8.95E-01	-	-
1397001_at	---	---	---	Rn.60739	BF406166	2.38	2.37	2.39	2.37	2.38	2.36	1.00	down	6.58E-01	8.98E-01	-	-
1388115_at	Svs3	seminal vesicle secretion 3	192239	Rn.205057	D00920	2.37	2.36	2.37	2.36	2.37	2.35	1.00	down	6.08E-01	8.95E-01	-	-
1375155_at	---	---	---	Rn.216617	BF409816	2.23	2.23	2.23	2.23	2.23	2.22	1.00	down	3.44E-01	8.95E-01	-	-
1390062_at	---	---	---	---	BF413176	2.36	2.35	2.37	2.36	2.37	2.34	1.00	down	7.20E-01	9.11E-01	-	-
1369947_at	Ctsk	cathepsin K	29175	Rn.5598	NM_031560	2.46	2.45	2.48	2.46	2.47	2.45	1.00	down	6.70E-01	9.00E-01	-	-
1380016_at	---	---	---	Rn.209609	BF388694	2.34	2.34	2.35	2.33	2.35	2.33	1.00	down	5.87E-01	8.95E-01	-	-
1388228_at	Mthfr	5,10-methylenetetrahydrofolate reductase (NADPH)	362657	Rn.10494	U57049	2.38	2.37	2.39	2.40	2.38	2.37	1.00	up	6.43E-01	8.95E-01	-	-
1388189_at	Grm3	glutamate receptor, metabotropic 3	24416	Rn.214604	AW522430	2.36	2.35	2.37	2.35	2.37	2.34	1.00	down	7.16E-01	9.10E-01	-	-
1391958_at	---	---	---	Rn.168110	BE119699	2.34	2.33	2.37	2.34	2.36	2.33	1.00	down	8.05E-01	9.37E-01	-	-
1395713_at	---	---	---	Rn.204526	AI136510	2.29	2.28	2.30	2.29	2.29	2.28	1.00	down	4.98E-01	8.95E-01	-	-
1376567_at	Mad1l1	MAD1 mitotic arrest deficient-like 1 (yeast)	680006	Rn.95132	AI044868	2.24	2.24	2.25	2.24	2.24	2.23	1.00	down	3.97E-01	8.95E-01	-	-
1370077_at	Ins2	insulin 2	24506	Rn.989	NM_019130	2.25	2.24	2.26	2.25	2.25	2.24	1.00	down	5.43E-01	8.95E-01	-	-
1378073_at	Cacnb1	calcium channel, voltage-dependent, beta 1 subunit	50688	Rn.9413	BF400810	2.33	2.33	2.34	2.33	2.33	2.33	1.00	down	3.79E-01	8.95E-01	-	-
1376895_at	Il16	interleukin 16	116996	Rn.104665	AI137163	2.29	2.28	2.29	2.28	2.31	2.28	1.00	up	7.26E-01	9.13E-01	-	-
1385300_at	Klhl10	kelch-like 10 (Drosophila)	303533	Rn.207863	BE107758	2.34	2.34	2.35	2.34	2.35	2.33	1.00	down	6.88E-01	9.04E-01	-	-
1381407_at	---	---	---	---	AA900580	2.33	2.32	2.33	2.33	2.33	2.32	1.00	down	4.65E-01	8.95E-01	-	-
1396209_at	Mcart1l	mitochondrial carrier triple repeat 1-like	679135	Rn.217078	BE117343	2.25	2.25	2.26	2.25	2.26	2.25	1.00	down	4.86E-01	8.95E-01	-	-
1390220_at	---	---	---	---	AW144082	2.32	2.31	2.32	2.31	2.32	2.31	1.00	down	3.42E-01	8.95E-01	-	-
1368093_at	Myh6	myosin, heavy chain 6, cardiac muscle, alpha	29556	Rn.54399	BI296041	2.48	2.46	2.51	2.47	2.53	2.44	1.00	down	9.02E-01	9.70E-01	-	-
1396237_at	---	---	---	---	AA923873	2.32	2.31	2.34	2.32	2.36	2.31	1.00	up	8.25E-01	9.45E-01	-	-
1394748_at	---	---	---	---	BF288156	2.38	2.38	2.39	2.38	2.38	2.38	1.00	down	5.02E-01	8.95E-01	-	-
1387520_at	Drd4	dopamine receptor D4	25432	Rn.10159	NM_012944	2.35	2.34	2.36	2.34	2.35	2.34	1.00	down	5.90E-01	8.95E-01	-	-
1375204_at	---	---	---	Rn.212187	BI298526	2.59	2.54	2.60	2.58	2.59	2.55	1.00	down	8.64E-01	9.58E-01	-	-
1368786_at	Mmp7	matrix metallopeptidase 7	25335	Rn.10282	NM_012864	2.34	2.32	2.34	2.32	2.34	2.31	1.00	down	7.29E-01	9.13E-01	-	-
1378992_at	Fbxl7	F-box and leucine-rich repeat protein 7	361907	Rn.45065	AW520855	2.44	2.44	2.45	2.44	2.45	2.43	1.00	down	6.82E-01	9.03E-01	-	-
1376459_at	Aak1	AP2 associated kinase 1	500244	Rn.203307	AW533060	2.25	2.24	2.25	2.24	2.25	2.24	1.00	down	4.44E-01	8.95E-01	-	-
1369613_at	Stag3	stromal antigen 3	114522	Rn.18997	NM_053730	2.28	2.28	2.29	2.28	2.29	2.27	1.00	down	4.74E-01	8.95E-01	-	-
1387734_at	Bmp15	bone morphogenetic protein 15	59302	Rn.42867	NM_021670	2.33	2.32	2.33	2.32	2.33	2.31	1.00	down	5.60E-01	8.95E-01	-	-
1397790_at	---	---	---	---	BF394731	2.50	2.49	2.51	2.50	2.50	2.49	1.00	down	4.99E-01	8.95E-01	-	-
1377732_at	Bttd16	BTB (POZ) domain containing 16	361658	Rn.13700	AA956543	2.45	2.43	2.45	2.43	2.45	2.43	1.00	down	6.67E-01	8.96E-01	-	-
1383340_at	Atcay	ataxia, cerebellar, Cayman type	362826	Rn.198771	BG671011	2.25	2.25	2.25	2.25	2.25	2.24	1.00	down	4.34E-01	8.95E-01	-	-
1397428_at	---	---	---	Rn.148356	BE119034	2.26	2.26	2.27	2.26	2.26	2.25	1.00	down	4.71E-01	8.95E-01	-	-
1380286_x_at	RGD1311723	similar to KIAA1731 protein	363018	Rn.160168	BM386844	2.64	2.64	2.65	2.64	2.64	2.63	1.00	down	5.46E-01	8.95E-01	-	-
1396084_at	---	---	---	Rn.211240	R47116	2.34	2.33	2.35	2.33	2.34	2.33	1.00	down	5.91E-01	8.95E-01	-	-
1369551_at	Gpr173	G-protein coupled receptor 173	64021	Rn.53986	NM_022255	2.32	2.31	2.32	2.31	2.32	2.30	1.00	down	5.78E-01	8.95E-01	-	-
1389842_at	RGD1564664	Similar to LOC387763 protein	499839	Rn.22639	AW253423	2.26	2.25	2.27	2.26	2.26	2.25	1.00	down	5.87E-01	8.95E-01	-	-
1369360_at	Gucy2e	guanylate cyclase 2E	79222	Rn.10060	NM_024380	2.28	2.28	2.29	2.28	2.29	2.27	1.00	down	5.60E-01	8.95E-01	-	-
1376114_at	Kcng2	potassium voltage-gated channel, subfamily G, member 2	307234	Rn.163389	AI234817	2.34	2.33	2.35	2.33	2.34	2.32	1.00	down	6.35E-01	8.95E-01	-	-
1397677_at	Mgat5	mannosyl (alpha-1,6-)-glycoprotein beta-1,6-N-acetyl-glucosaminyltransferase	65271	Rn.53998	AI501069	2.41	2.41	2.42	2.41	2.41	2.40	1.00	down	4.75E-01	8.95E-01	-	-
1392156_at	---	---	---	Rn.209411	BF388086	2.30	2.30	2.31	2.30	2.30	2.29	1.00	down	4.64E-01	8.95E-01	-	-
1384660_at	---	---	---	---	AI045790	2.26	2.25	2.27	2.26	2.26	2.25	1.00	down	4.83E-01	8.95E-01	-	-
1392714_at	Serpinb11	serine (or cysteine) peptidase inhibitor, clade B (ovalbumin), member 11	304689	Rn.77422	BM389831	2.35	2.34	2.36	2.34	2.36	2.33	1.00	down	6.72E-01	9.01E-01	-	-
1370762_at	Olr287	olfactory receptor 287	287001	Rn.44382	M64378	2.31	2.30	2.31	2.30	2.31	2.30	1.00	down	5.27E-01	8.95E-01	-	-
1395562_at	---	---	---	Rn.206195	---	2.43	2.41	2.45	2.42	2.44	2.41	1.00	down	7.88E-01	9.32E-01	-	-
1398132_at	---	---	---	Rn.46203	AW527144	2.31	2.30	2.32	2.30	2.31	2.30	1.00	down	5.88E-01	8.95E-01	-	-
1391620_at	---	---	---	---	AI231422	2.29	2.27	2.29	2.28	2.29	2.27	1.00	down	5.45E-01	8.95E-01	-	-
1371750_at	---	---	---	Rn.169505	BF418087	2.48	2.46	2.50	2.47	2.49	2.48	1.00	down	7.21E-01	9.11E-01	-	-
1384298_at	Myo1f	myosin IF	314654	Rn.198774	AI764088	2.35	2.34	2.35	2.35	2.33	2.33	1.00	down	6.58E-01	8.98E-01	-	-
1374784_at	Prfdc1	phosphoribosyl transferase domain containing 1	291355	Rn.33792	AI407006	2.26	2.25	2.26	2.26	2.26	2.25	1.00	down	4.40E-01	8.95E-01	-	-
1390485_at	05-Mar	membrane-associated ring finger (C3HC4) 5	294079	Rn.218003	BI290680	7.98	8.89	8.88	8.55	8.33	8.86	1.00	down	9.91E-01	9.97E-01	-	-
1377253_at	---	---	---	Rn.212001	BG374305	2.46	2.45	2.48	2.46	2.47	2.45	1.00	down	7.04E-01	9.07E-01	-	-
1394394_at	---	---	---	Rn.54184	BF407181	2.33	2.32	2.34	2.32	2.33	2.32	1.00	down	6.04E-01	8.95E-01	-	-
1394670_at	Obfc1	oligonucleotide/oligosaccharide-binding fold containing 1	294025	Rn.15899	AA859595	2.36	2.35	2.37	2.36	2.36	2.37	1.00	up	6.07E-01	8.95E-01	-	-
1372125_at	Gpx7	glutathione peroxidase 7	298376	Rn.4130	BF408445	2.42	2.41	2.47	2.42	2.46	2.41	1.00	down	8.78E-01	9.62E-01	-	-
1369894_at	Htr2a	5-hydroxytryptamine (serotonin) receptor 2A	29595	Rn.214221	NM_021862	2.31	2.30	2.32	2.31	2.32	2.30	1.00	down	5.95E-01	8.95E-01	-	-
1369208_at	Il7	interleukin 7	25647	Rn.10793	AF367210	2.30	2.29	2.31	2.30	2.30	2.29	1.00	down	5.25E-01	8.95E-01	-	-
1396308_at	LOC688126	hypothetical protein LOC688126	688126	---	AI763614	2.29	2.28	2.29	2.28	2.29	2.28	1.00	down	4.55E-01	8.95E-01	-	-
1368805_at	Uts2	urotensin 2	29180	Rn.48886	NM_019160	2.28	2.28	2.29	2.28	2.29	2.27	1.00	down	5.52E-01	8.95E-01	-	-
1373985_at	Pnma2	PNMA-like 2	308393	Rn.98225	BI282311	2.50	2.77	2.51	2.50	2.49	2.79	1.00	up	9.78E-01	9.93E-01	-	-
1388257_at	Lrrc7	leucine rich repeat containing 7	117284	Rn.89629	AF266164	2.32	2.31	2.33	2.32	2.32	2.31	1.00	down	5.17E-01	8.95E-01	-	-
1399147_at	---	---	---	Rn.204427	AI119975	2.44	2.43	2.46	2.43	2.46	2.42	1.00	down	7.66E-01	9.23E-01	-	-
1382645_at	---	---	---	Rn.203859	AW920335	2.28	2.28	2.29	2.28	2.29	2.27	1.00	down	4.80E-01	8.95E-01	-	-
1394672_at	---	---	---	Rn.211491	BF414556	2.29	2.29	2.30	2.29	2.30	2.28	1.00	down	5.34E-01	8.95E-01	-	-
1396213_at	---	---	---	Rn.153619	BF547413	2.31	2.30	2.31	2.30	2.31	2.30	1.00	down	5.28E-01	8.95E-01	-	-
1388600_at	---	---	---	Rn.17067	AI011713	2.42	2.41	2.42	2.40	2.42	2.41	1.00	down	6.01E-01	8.95E-01	-	-
1397070_at	---	---	---	Rn.127454	BF402703	2.27	2.26	2.27	2.26	2.27	2.25	1.00	down	4.69E-01	8.95E-01	-	-
1369838_at	Hif3a	hypoxia inducible factor 3, alpha subunit	64345	Rn.16184	NM_022528	2.37	2.37	2.38	2.36	2.37	2.36	1.00	down	5.21E-01	8.95E-01	-	-
1393418_at	Tmod2	tropomodulin 2	58814	Rn.74047	BF567833	2.30	2.29	2.31	2.30	2.30	2.29	1.00	down	4.69E-01	8.95E-01	-	-
1373320_at	---	---	---	Rn.160173	BG373883	2.33	2.32	2.33	2.32	2.33	2.31	1.00	down	6.63E-01	8.99E-01	-	-
1376806_at	---	---	---	Rn.42977	BF403853	2.31	2.30	2.32	2.30	2.31	2.30	1.00	down	5.71E-01	8.95E-01	-	-
1376959_at	Spir3	small proline-rich protein 3	310575	Rn.19820	BI285461	2.31	2.30	2.32	2.31	2.31	2.30	1.00	down	5.93E-01	8.95E-01	-	-
1380911_at	RGD1311564	LOC360590	360590	Rn.200147	BF419206

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1377631_at	Col9a3	procollagen, type IX, alpha 3	362285	Rn.218031	BM389001	2.33	2.32	2.34	2.32	2.36	2.32	1.00	up	7.94E-01	9.34E-01	-	-
1395090_at	---	---	---	---	BE102987	2.40	2.39	2.40	2.39	2.40	2.38	1.00	down	6.12E-01	8.95E-01	-	-
1369128_at	Grik5	glutamate receptor, ionotropic, kainate 5	24407	Rn.74042	NM_017262	2.41	2.39	2.42	2.40	2.42	2.39	1.00	down	7.01E-01	9.07E-01	-	-
1377689_at	Kntc1	kinetochore associated 1	304477	Rn.47918	BF564273	2.33	2.32	2.34	2.32	2.34	2.32	1.00	down	5.92E-01	8.95E-01	-	-
1375098_at	Svs7	seminal vesicle secretory protein 7	363041	Rn.78071	BI280571	2.70	2.64	2.74	2.69	2.72	2.66	1.00	down	9.18E-01	9.76E-01	-	-
1377552_at	LOC691504	Similar to Zinc finger protein ZFPM1 (Zinc finger protein multitype 1) (Friend c	691504	Rn.160024	BE098467	2.24	2.24	2.25	2.24	2.24	2.26	1.00	up	5.87E-01	8.95E-01	-	-
1397120_at	---	---	---	Rn.209443	BF409530	2.33	2.33	2.34	2.33	2.34	2.32	1.00	down	5.12E-01	8.95E-01	-	-
1370998_at	Grm2	glutamate receptor, metabotropic 2	24415	Rn.9681	M92075	2.40	2.40	2.40	2.40	2.40	2.39	1.00	down	4.54E-01	8.95E-01	-	-
1397055_at	---	---	---	Rn.160372	BF418021	2.29	2.28	2.30	2.29	2.29	2.28	1.00	down	5.04E-01	8.95E-01	-	-
1381049_at	Zfyve9	zinc finger, FYVE domain containing 9	313477	Rn.23612	BG375951	4.08	4.30	4.11	4.13	3.65	4.69	1.00	down	9.91E-01	9.97E-01	-	-
1389909_at	Ncoa1	Nuclear receptor coactivator 1	313929	Rn.165307	AI137280	2.28	2.27	2.29	2.28	2.28	2.27	1.00	down	5.07E-01	8.95E-01	-	-
1394940_at	Fam46a	family with sequence similarity 46, member A	300870	Rn.788	BI294811	2.35	2.34	2.35	2.34	2.35	2.33	1.00	down	5.51E-01	8.95E-01	-	-
1398111_at	Ndrg2	NDRG family member 2	171114	Rn.3407	AI501635	2.29	2.29	2.30	2.29	2.29	2.28	1.00	down	4.86E-01	8.95E-01	-	-
1381055_at	---	---	---	Rn.62736	BF415544	2.37	2.35	2.37	2.36	2.37	2.35	1.00	down	6.46E-01	8.95E-01	-	-
1376188_at	LOC691153	Hypothetical protein LOC691153	691153	Rn.33084	AA997156	2.28	2.27	2.29	2.28	2.28	2.27	1.00	down	6.28E-01	8.95E-01	-	-
1379792_at	---	---	---	Rn.46595	BF408715	2.31	2.29	2.31	2.30	2.31	2.29	1.00	down	6.06E-01	8.95E-01	-	-
1383490_at	RGD1563996	similar to Protein UNQ9166/PRO28631 precursor	315163	Rn.141004	AA943025	2.58	2.57	2.59	2.58	2.59	2.56	1.00	down	7.21E-01	9.11E-01	-	-
1388008_at	Trhr2	thyrotropin releasing hormone receptor 2	252859	Rn.216691	AB015645	2.32	2.31	2.32	2.31	2.31	2.31	1.00	down	4.11E-01	8.95E-01	-	-
1391491_a_at	Rad23b	RAD23 homolog B (S. cerevisiae)	298012	Rn.67042	BG377084	5.43	5.53	5.96	5.71	5.65	5.56	1.00	up	9.83E-01	9.95E-01	-	-
1375106_at	Amn	amnionless homolog (mouse)	314459	Rn.7787	AI103368	2.27	2.27	2.28	2.27	2.27	2.26	1.00	down	3.25E-01	8.95E-01	-	-
1381280_at	Mthfd2l	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 2-like	305248	Rn.206715	BG375951	4.08	4.30	4.11	4.13	3.65	4.69	1.00	down	9.91E-01	9.97E-01	-	-
1370756_at	Olr1082	olfactory receptor 1082	287002	Rn.44383	M64381	2.25	2.24	2.26	2.25	2.25	2.24	1.00	down	5.01E-01	8.95E-01	-	-
1375391_at	---	---	---	Rn.209991	BF403352	2.34	2.33	2.35	2.34	2.35	2.33	1.00	down	6.72E-01	9.01E-01	-	-
1369144_a_at	Kcnd3	potassium voltage gated channel, Shal-related family, member 3	65195	Rn.10540	U75448	2.40	2.39	2.42	2.41	2.42	2.40	1.00	up	6.45E-01	8.95E-01	-	-
1380510_at	---	---	---	---	BF553029	2.29	2.28	2.29	2.28	2.29	2.27	1.00	down	5.36E-01	8.95E-01	-	-
1369867_at	St8sia1	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 1	25280	Rn.96242	U53883	2.32	2.32	2.34	2.32	2.33	2.32	1.00	down	6.87E-01	9.04E-01	-	-
1389843_at	Brd2	Bromodomain containing 2	294276	Rn.98146	AI556436	2.28	2.27	2.28	2.27	2.28	2.27	1.00	down	4.95E-01	8.95E-01	-	-
1398071_at	---	---	---	Rn.210583	BF405181	2.42	2.41	2.45	2.42	2.44	2.41	1.00	down	7.77E-01	9.28E-01	-	-
1369293_at	Rtn4r	reticulon 4 receptor	113912	Rn.45686	NM_053613	2.45	2.44	2.45	2.45	2.45	2.44	1.00	down	5.27E-01	8.95E-01	-	-
1398139_at	RGD1311993	hypothetical LOC315072	315072	Rn.46772	AW528104	2.30	2.29	2.30	2.29	2.30	2.29	1.00	down	5.10E-01	8.95E-01	-	-
1380084_at	---	---	---	Rn.210605	BF396367	2.35	2.34	2.36	2.35	2.35	2.34	1.00	down	5.61E-01	8.95E-01	-	-
1386414_at	Bri3	brain protein I3	304284	Rn.7700	AW523909	2.29	2.29	2.29	2.29	2.29	2.28	1.00	down	4.85E-01	8.95E-01	-	-
1394763_at	Hadha	Hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/er	170670	Rn.3340	AI234944	2.29	2.28	2.30	2.29	2.29	2.28	1.00	down	4.65E-01	8.95E-01	-	-
1377488_at	Mapk8ip2	Mitogen-activated protein kinase 8 interacting protein 2	315220	Rn.91464	AI576972	2.47	2.46	2.48	2.47	2.47	2.45	1.00	down	6.46E-01	8.95E-01	-	-
1370016_at	Nell2	NEL-like 2 (chicken)	81734	Rn.11567	NM_031070	2.28	2.27	2.29	2.27	2.28	2.27	1.00	down	5.79E-01	8.95E-01	-	-
1394624_at	---	---	---	Rn.206538	AW528017	2.39	2.38	2.40	2.39	2.39	2.38	1.00	down	5.08E-01	8.95E-01	-	-
1395466_at	Anxa9	annexin A9	689830	Rn.73434	AW527441	2.37	2.36	2.39	2.37	2.38	2.36	1.00	down	6.95E-01	9.06E-01	-	-
1395996_at	---	---	---	Rn.216959	BF393838	2.58	2.57	2.60	2.57	2.62	2.56	1.00	up	8.63E-01	9.57E-01	-	-
1370833_at	Pex5i	peroxisomal biogenesis factor 5-like	286937	Rn.207886	AF324454	2.38	2.37	2.39	2.38	2.39	2.37	1.00	down	7.19E-01	9.11E-01	-	-
1373188_at	Scn4b	sodium channel, type IV, beta	315611	Rn.22230	AI137995	2.29	2.28	2.30	2.28	2.29	2.28	1.00	down	5.64E-01	8.95E-01	-	-
1391079_at	---	---	---	Rn.203929	BI295875	2.72	2.61	2.68	2.66	2.65	2.68	1.00	down	9.11E-01	9.73E-01	-	-
1384837_at	Cd69	Cd69 molecule	29187	Rn.23779	AI137672	2.32	2.30	2.32	2.31	2.34	2.31	1.00	up	7.40E-01	9.16E-01	-	-
1377629_at	---	---	---	Rn.168884	AA874846	2.38	2.37	2.39	2.37	2.39	2.36	1.00	down	6.61E-01	8.98E-01	-	-
1389775_at	---	---	---	---	AI412304	2.80	2.90	2.69	2.80	2.81	2.80	1.00	up	9.52E-01	9.86E-01	-	-
1383390_at	Fam123a	family with sequence similarity 123A	498529	---	AI111642	2.42	2.41	2.43	2.41	2.43	2.40	1.00	down	6.73E-01	9.01E-01	-	-
1391903_at	RGD1562446	similar to 60S ribosomal protein L7a	499344	---	BF408516	2.32	2.31	2.33	2.31	2.32	2.31	1.00	down	5.81E-01	8.95E-01	-	-
1384014_at	---	---	---	Rn.166585	BE109675	2.35	2.34	2.36	2.37	2.36	2.33	1.00	up	7.67E-01	9.24E-01	-	-
1389637_at	---	---	---	Rn.24257	AI227731	2.35	2.34	2.36	2.35	2.36	2.34	1.00	down	5.98E-01	8.95E-01	-	-
1380992_at	---	---	---	Rn.204411	AI111694	2.38	2.37	2.39	2.38	2.39	2.37	1.00	down	6.02E-01	8.95E-01	-	-
1379837_at	---	---	---	Rn.205985	AI548995	2.60	2.52	2.66	2.58	2.66	2.55	1.00	up	9.44E-01	9.84E-01	-	-
1368534_at	Adra1d	adrenergic, alpha-1D-, receptor	29413	Rn.11314	NM_024483	2.34	2.33	2.35	2.34	2.35	2.33	1.00	down	6.25E-01	8.95E-01	-	-
1383460_at	---	---	---	---	AI058976	2.30	2.29	2.30	2.29	2.30	2.29	1.00	down	5.35E-01	8.95E-01	-	-
1389954_at	---	---	---	Rn.212022	BI300513	2.30	2.29	2.30	2.30	2.30	2.29	1.00	down	4.36E-01	8.95E-01	-	-
1394757_at	---	---	---	---	BF288751	2.33	2.33	2.35	2.33	2.34	2.32	1.00	down	6.98E-01	9.07E-01	-	-
1397391_at	---	---	---	Rn.129992	AI454739	2.38	2.38	2.39	2.38	2.39	2.37	1.00	down	5.60E-01	8.95E-01	-	-
1385792_at	Fam132a	family with sequence similarity 132, member A	313774	Rn.16254	BF550897	2.34	2.33	2.35	2.33	2.34	2.33	1.00	down	5.61E-01	8.95E-01	-	-
1372887_at	Scarf2	scavenger receptor class F, member 2	287949	Rn.22134	BM391741	2.33	2.32	2.33	2.32	2.33	2.31	1.00	down	6.15E-01	8.95E-01	-	-
1394057_at	Ndp	Norrie disease (pseudoglioma) (human)	363443	Rn.45519	AW552944	2.40	2.40	2.42	2.40	2.41	2.40	1.00	down	6.19E-01	8.95E-01	-	-
1377543_at	---	---	---	---	BF415477	2.60	2.59	2.61	2.60	2.64	2.58	1.00	up	8.25E-01	9.45E-01	-	-
1394405_at	---	---	---	---	AI232356	2.27	2.27	2.28	2.27	2.28	2.26	1.00	down	5.30E-01	8.95E-01	-	-
1393112_at	Tcp11	t-complex protein 11	309641	Rn.33200	BF410059	2.43	2.42	2.44	2.42	2.44	2.41	1.00	down	7.44E-01	9.17E-01	-	-
1387758_at	Alg3	alkaline phosphatase 3, intestine, not Mn requiring	64021	Rn.138122	NM_022680	2.33	2.32	2.34	2.32	2.33	2.32	1.00	down	5.31E-01	8.95E-01	-	-
1389458_at	---	---	---	Rn.27753	AW435191	2.37	2.36	2.38	2.36	2.38	2.35	1.00	down	6.37E-01	8.95E-01	-	-
1393475_at	Me2	malic enzyme 2, NAD(+)-dependent, mitochondrial	307270	Rn.16233	AI045487	2.54	2.51	2.57	2.53	2.58	2.49	1.00	down	9.05E-01	9.71E-01	-	-
1369374_at	Selp	selectin, platelet	25651	Rn.10012	NM_013114	2.36	2.30	2.41	2.36	2.37	2.34	1.00	down	9.13E-01	9.74E-01	-	-
1369781_at	Grm7	glutamate receptor, metabotropic 7	81672	Rn.10409	U06832	2.32	2.32	2.33	2.32	2.33	2.31	1.00	down	5.51E-01	8.95E-01	-	-
1392253_at	---	---	---	---	AI071513	2.32	2.32	2.33	2.32	2.33	2.31	1.00	down	4.83E-01	8.95E-01	-	-
1391160_at	---	---	---	Rn.209174	BF399457	2.35	2.34	2.35	2.34	2.35	2.34	1.00	down	5.35E-01	8.95E-01	-	-
1370495_s_at	Cyp2c13	cytochrome P450 2c13	171521	Rn.82715	J02861	2.30	2.29	2.31	2.30	2.31	2.29	1.00	down	5.53E-01	8.95E-01	-	-
1374813_at	---	---	---	Rn.156176	BF409617	2.29	2.28	2.30	2.29	2.29	2.28	1.00	down	4.68E-01	8.95E-01	-	-
1387031_at	Erp29	endoplasmic reticulum protein 29	117030	Rn.32904	U36482	10.43	10.68	10.73	10.72	10.55	10.58	1.00	up	9.72E-01	9.92E-01	-	-
1369280_at	Kcnk9	potassium channel, subfamily K, member 9	84429	Rn.48796	NM_053405	2.28	2.28	2.29	2.28	2.28	2.27	1.00	down	5.35E-01	8.95E-01	-	-
1398593_at	LOC298139	similar to RIKEN cDNA 2310003M01	298139	Rn.37554	AI172305	2.32	2.32	2.33	2.32	2.33	2.32	1.00	down	4.51E-01	8.95E-01	-	-
1397136_at	---	---	---	Rn.208206	BE113047	2.35	2.34	2.36	2.34	2.36	2.34	1.00	down	6.39E-01	8.95E-01	-	-
1378950_at	---	---	---	Rn.204580	AI178991	2.32	2.31	2.33	2.32	2.33	2.31	1.00	down	5.97E-01	8.95E-01	-	-
1397866_at	Serpinb6b	serine (or cysteine) peptidase inhibitor, clade B, member 6b	364705	Rn.115081	BG380122	2.44	2.42	2.44	2.43	2.45	2.41	1.00	down	7.59E-01	9.21E-01	-	-
1393672_at	Hmcn1	hemicentin 1	289094	Rn.52931	BE117954	2.39	2.38	2.41	2.39	2.40	2.38	1.00	down	7.17E-01	9.10E-01	-	-
1393970_at	LOC689582	similar to jumonji domain containing 2D	689582	Rn.202733	AW528808	2.22	2.20	2.21	2.21	2.21	2.20	1.00	down	5.18E-01	8.95E-01	-	-
1375596_at	Trpm1	transient receptor potential cation channel, subfamily M, member 1	361586	Rn.211311	BI291219	2.28	2.28	2.29	2.28	2.29	2.27	1.00	down	5.59E-01	8.95E-01	-	-
1395024_at	---	---	---	Rn.166825	BE119978	2.28	2.28	2.29	2.28	2.29	2.28	1.00	down	5.08E-01	8.95E-01	-	-
1375690_at	---	---	---	---	AI138004	2.32	2.31	2.33	2.32	2.32	2.32	1.00	up	4.89E-01	8.95E-01	-	-
1394302_at	Gpr115	G protein-coupled receptor 115	501108	---	BF556622	2.49	2.44	2.48	2.48	2.51	2.41	1.00	down	9.08E-01	9.72E-01	-	-
1387141_at	Dpysl5	dihydropyrimidinase-like 5	65208	Rn.44871	NM_023023	2.39	2.38	2.41	2.39	2.42	2.39	1.00	up	7.85E-01	9.30E-01	-	-
1392225_at	---	---	---	Rn.43312	BE120990	2.47	2.43	2.54	2.46	2.53	2.43	1.00	down	9.32E-01	9.81E-01	-	-
1387487_a_at	Calcr	calcitonin receptor	116506	Rn.10062	NM_053816	2.29	2.28	2.30	2.29	2.29	2.28	1.00	down	5.19E-01	8.95E-01	-	-
1397561_at	---	---	---	Rn.28108	BG667110	2.38	2.37	2.40	2.38	2.40	2.37	1.00	down	7.84E-01	9.30E-01	-	-
1396721_at	---	---	---	Rn.199948	AF404888	2.34	2.34	2.35	2.34	2.35	2.33	1.00	down	5.41E-01	8.95E-01	-	-
1385472_at	Zbtb8a	zinc finger and BTB domain containing 8a	313049	Rn.82564	AA963583	2.41	2.40	2.43	2.41	2.43	2.39	1.00	down	8.09E-01	9.38E-01	-	-
1395381_at	---	---	---	---	BF542239	7.51	8.26	7.12	8.13	6.96	7.82	1.00	up	9.94E-01	9.98E-01	-	-
1370380_s_at	OC688367 /// Nr2	similar to Orphan nuclear receptor EAR-2 (V-erbA-related protein EAR-2) /// rp245980 /// 688367	---	Rn.25840	AA997437	2.36	2.35	2.38	2.35	2.37	2.35	1.00	down	7.86E-01	9.31E-01	-	-
1390362_at	---	---	---	Rn.51336	BF394081	2.31	2.31	2.32	2.31	2.32	2.30	1.00	down	6.05E-01	8.95E-01	-	-
1379004_at	Mtdh	metadherin	170910	Rn.6864	BE113115	2.36	2.34	2.37	2.35	2.37	2.34	1.00	down	7.64E-01	9.23E-01	-	-
1368495_at	Rln1	relaxin 1	25616	Rn.9830	NM_013413	2.32	2.32	2.33	2.32	2.33	2.30	1.00	down	6.99E-01	9.07E-01	-	-
1376803_at	Rgs3	regulator of G-protein signaling 3	54293	Rn.53900	AW144044	2.32	2.32	2.33	2.32	2.33	2.31	1.00	down	5.71E-01	8.95E-01	-	-
1390001_at	Rhobtb2	Rho-related BTB domain containing 2	306004	Rn.163307	BF402407	2.26	2.25	2.26	2.25	2.26	2.25	1.00	down	5.58E-01	8.95E-01	-	-
1368544_at	Noi3	nucleolar protein 3 (apoptosis repressor with CARD domain)	85383	Rn.86956	NM_053516	2.37	2.36	2.38	2.37	2.38	2.36	1.00	down	6.92E-01	9.05E-01	-	-
1391504_at	---	---	---	Rn.24960	AI103714	2.38	2.36	2.38	2.37	2.38	2.36	1.00	down	6.81E-01	9.03E-01	-	-
1381139_at	---	---	---	Rn.207750	BM387383	2.78	2.54	2.57	2.82	2.56	2.54	1.00	up	9.75E-01	9.92E-01	-	-
1387689_at	Kcnab2	potassium voltage-gated channel, shaker-related subfamily, beta member 2	29738	Rn.10757	NM_017304	2.36	2.35	2.37	2.35	2.37	2.34	1.00	down	6.75E-01	9.01E-01	-	-
1396753_at	---	---	---	Rn.209828	BF406142	2.42	2.40	2.42	2.41	2.42	2.40	1.00	down	7.25E-01	9.15E-01	-	-
1381433_at	---	---	---	---	AW251893	2.21	2.21	2.22	2.21	2.23	2.18	1.00	down	7.96E-01	9.34E-01	-	-
1376375_at	---	---	---	Rn.200252	BG374350	2.28	2.27	2.29	2.27	2.28	2.27	1.00	down	5.86E-01	8.95E-01	-	-
1397214_at	---	---	---	Rn.6731	BF288533	2.35	2.34	2.35	2.34	2.35	2.33	1.00	down	6.75E-01	9.01E-01	-	-
1371116_at	Masp1	mannan-binding lectin serine peptidase 1	64023	Rn.203236	AJ277423	2.48	2.47	2.50	2.51	2.48	2.46	1.00	up	8.49E-01	9.53E-01	-	-
1376352_at	---	---	---	Rn.153741	BF394095	2.31	2.30	2.32	2.31	2.31	2.30	1.00	down	4.94E-01	8.95E-01	-	-
1369233_at	Kcnk10	potassium channel, subfamily K, member 10	65272	Rn.53999	AF196995	2.39	2.38	2.40	2.39	2.40	2.38	1.00	down	6.89E-01	9.04E-01	-	-
1370042_at	Stmn2	stathmin-like 2	84510	Rn.34335	BG668493	2.41	2.40	2.41	2.40	2.41	2.39	1.00	down	5.21E-01	8.95E-01	-	-
1377430_at	---	---	---	Rn.19694	BF413556	2.44	2.43	2.46	2.44	2.45	2.43	1.00	down	7.09E-01	9.09E-01	-	-
1398046_at	Fam20b	family with sequence similarity 20, member B	304885	Rn.34667	BF416612	2.47	2.45	2.47	2.45	2.49	2.45	1.00	up	8.12E-01	9.39E-01	-	-
1375192_at	---	---	---	Rn.51394	BF393977	2.28	2.28	2.29	2.28	2.28	2.27	1.00	down	5.04E-01	8.95E-01	-	-
1391188_at	RGD1560720	RGD1560720	313311	Rn.47750	BF389480	2.35	2.34	2.36	2.35	2.36	2.34	1.00	down	6.57E-01	8.98E-01	-	-
1377989_at	Vamp5	Vesicle-associated membrane protein 5	89818	Rn.22616	AI229496	2.42	2.41	2.43	2.42	2.45	2.40	1.00	down	8.18E-01	9.42E-01	-	-
1373209_at	RGD1305572	similar to hypothetical protein MGC30618	289315	Rn.16374	AI599284	3.48	3.46	2.96	3.28	3.29	3.34	1.00	up	9.83E-01	9.95E-01	-	-
1384914_at	---	---	---	Rn.15486	BF556255	2.27	2.26	2.27	2.26	2.27	2.26	1.00	down	5.18E-01	8.95E-01	-	-
1393069_at	Sfrp5	secreted frizzled-related protein 5	309377	Rn.40184	AA899309	2.39	2.38	2.40	2.38	2.40	2.38	1.00	down	6.23E-01	8.95E-01	-	-
1379884_at	Asph	aspartate-beta-hydroxylase	312981	Rn.22695	AA799621	2.42	2.42	2.42	2.42	2.44	2.42	1.00	up	6.47E-01	8.95E-01	-	-
1378777_at	---	---	---	Rn.172770	BF402045	2.39	2.37	2.40	2.38	2.40	2.36	1.00	down	8.00E-01	9.35E-01	-	-
1384917_at	Ccno	cyclin O	499528	Rn.219975	BF547287	2.31	2.31	2.32	2.31	2.31	2.30	1.00	down	4.97E-01	8.95E-01	-	-
1370222_at	Pitx3	paired-like homeodomain 3	29609	Rn.22092	AI145840	2.33	2.33	2.34	2.33	2.34	2.32	1.00	down	3.46E-01	8.95E-01	-	-
1386977_at	Car3	carbonic anhydrase 3	54232	Rn.1647	NM_019292	2.26	2.25	2.26	2.25	2.25	2.25	1.00	down	3.91E-01	8.95E-01	-	-
1391695_at	---	---	---	Rn.155885	BE118403	2.27	2.26	2.27	2.26	2.27	2.26	1.00	down	4.17E-01	8.95E-01	-	-
1377066_at	---	---	---	Rn.63900	BF387267	2.39	2.39	2.40	2.39	2.40	2.38	1.00	down	5.38E-01	8.95E-01	-	-
1386801_at	LOC685707	similar to neuron navigator 1	685707	Rn.154566	BF547251	2.32	2.31	2.32	2.31	2.32	2.30	1.00	down	6.07E-01	8.95E-01	-	-
1390371_at	---	---	---	---	BI296619	2.44	2.43	2.45	2.44	2.43	2.43	1.00	down	6.45E-01	8.95E-01	-	-
1391582_at	---	---	---	Rn.31458	AI180053	2.36	2.35	2.36	2.35	2.36	2.34	1.00	down	4.98E-01	8.95E-01	-	-
1377008_at	RGD1566401	similar to GTL2, imprinted maternally expressed untranslated	500717	Rn.202990	BI296868	2.30	2.30	2.31	2.30	2.31	2.29	1.00	down	5.37E-01	8.95E-01	-	-
1396147_at	---	---	---	Rn.209268	BF394600	2.36	2.35	2.37	2.36	2.37	2.35	1.00	down	7.13E-01	9.10E-01	-	-
1396969_at	---	---	---	Rn.208962	BF402366	2.35	2.35	2.36	2.35	2.36	2.35	1.00	down	4.57E-01	8.95E-01	-	-
1369257_at	Grk1	G protein-coupled receptor kinase 1	81760	Rn.10548	NM_031096	2.29	2.29	2.30	2.29	2.30	2.29	1.00	down	4.70E-01	8.95E-01	-	-
1379166_at	---	---	---	Rn.200020	BF394273	2.39	2.38	2.40	2.38	2.39	2.38	1.00	down	5.75E-01	8.95E-01	-	-
1369418_at	Kcnj9	potassium inwardly-rectifying channel, subfamily J, member 9	116560	---	NM_053834	2.32	2.31	2.32	2.31	2.32	2.31	1.00	down	5.57E-01	8.95E-01	-	-
1376165_at	Slc24a3	solute carrier family 24 (sodium/potassium/calcium exchanger), member 3	85267	Rn.206123	BE098153	2.27	2.27	2.28	2.27	2.28	2.26	1.00	down	5.48E-01	8.95E-01	-	-
1368972_at	Ntrk2	neurotrophic tyrosine kinase, receptor, type 2	25054	Rn.11246	NM_012731	2.36	2.35	2.37	2.36	2.37	2.35	1.00	down	6.98E-01	9.07E-01	-	-
1380292_at	---	---	---	Rn.6466	AI556943	2.35	2.34	2.36	2.34	2.36	2.34	1.00	down	6.28E-01	8.95E-01	-	-
1369437_at	Slco4a1	solute carrier organic anion transporter family, member 4a1	171144	Rn.67081	NM_133608	2.29	2.28	2.30	2.28	2.30	2.28	1.00	down	6.47E-01	8.95E-01	-	-
1378901_at	---	---	---	---	AI070883	2.34	2.33	2.35	2.34	2.34	2.33	1.00	down	5.60E-01	8.95E-01	-	-
1397279_at	Itgb5	integrin, beta 5	257645	Rn.16988	AW920727	2.33	2.32	2.34	2.33	2.33	2.31	1.00	down	8.62E-01	9.88E-01	-	-
1392626_at	Pkmyt1	protein kinase, membrane associated tyrosine/threonine 1	287101	Rn.204349	BE110801	2.39	2.38	2.40	2.38	2.41	2.37	1.00	down	7.80E-01	9.28E-01	-	-
1379543_at	---	---	---	---	AA924568	2.50	2.47	2.50	2.50	2.53	2.45	1.00	up	8.87E-01	9.65E-01	-	-
1375332_at	P4ha2	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), al	360526	Rn.79891	BI296576	2.30	2.30	2.31	2.30	2.31	2.29	1.00	down	5.92E-01	8.95E-01	-	-
1396799_at	---	---	---	Rn.210372	AI716266	2.39	2.39	2.40	2.38	2.40	2.39	1.00	down	6.00E-01	8.95E-01	-	-
1378153_at	---	---	---	Rn.147180	AI715156	2.29	2.28	2.29	2.29	2.29	2.28	1.00	down	5.10E-01	8.95E-01	-	-
1394443_at	---	---	---	Rn.170073	AW534370	2.34	2.33	2.34	2.33	2.34	2.32	1.00	down	5.97E-01	8.95E-01	-	-
1385909_at	---	---	---	Rn.87819	BE118035	2.30	2.29	2.31	2.30	2.31	2.29	1.00	down	5.79E-01	8.95E-01

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1388255_x_at	RT1-CE5	RT1 class I, CE5	309607	---	AJ243338	2.52	2.46	2.52	2.49	2.60	2.43	1.00	up	9.49E-01	9.85E-01	-	-
1394146_at	---	---	---	---	BG057548	2.33	2.30	2.33	2.33	2.33	2.30	1.00	down	7.94E-01	9.34E-01	-	-
1375281_at	Tbx2	T-box 2	303398	Rn.38282	AW533332	2.30	2.29	2.31	2.30	2.30	2.29	1.00	down	5.51E-01	8.95E-01	-	-
1392073_at	---	---	---	Rn.170996	BE106470	2.51	2.52	2.51	2.52	2.51	2.50	1.00	down	6.31E-01	8.95E-01	-	-
1393691_at	LOC688273	hypothetical protein LOC688273	688273	---	BG376718	2.33	2.32	2.34	2.33	2.34	2.32	1.00	down	6.93E-01	9.05E-01	-	-
1393982_at	Pole2	polymerase (DNA directed), epsilon 2 (p59 subunit)	299112	Rn.34652	AI070935	2.38	2.34	2.40	2.35	2.43	2.34	1.00	up	9.14E-01	9.74E-01	-	-
1374097_at	---	---	---	Rn.133959	AW251791	2.31	2.30	2.31	2.31	2.31	2.30	1.00	down	5.29E-01	8.95E-01	-	-
1378511_at	---	---	---	Rn.209767	BF390750	2.36	2.36	2.37	2.39	2.37	2.36	1.00	up	6.92E-01	9.05E-01	-	-
1383459_at	Lgi3	leucine-rich repeat LGI family, member 3	306013	Rn.50862	AI764525	2.38	2.37	2.39	2.37	2.41	2.37	1.00	up	8.03E-01	9.36E-01	-	-
1384085_at	Gtf2h5	general transcription factor IIH, polypeptide 5	502227	Rn.25310	AW144332	2.30	2.29	2.30	2.29	2.30	2.28	1.00	down	5.68E-01	8.95E-01	-	-
1387578_a_at	P2rx2	purinergic receptor P2X, ligand-gated ion channel, 2	114115	Rn.88799	AF028604	2.27	2.26	2.28	2.26	2.27	2.26	1.00	down	5.45E-01	8.95E-01	-	-
1368490_at	Cd14	CD14 molecule	60350	Rn.42942	NM_021744	2.37	2.37	2.39	2.37	2.38	2.37	1.00	down	4.62E-01	8.95E-01	-	-
1380482_at	---	---	---	Rn.205238	AI175691	2.31	2.30	2.32	2.30	2.31	2.30	1.00	down	5.63E-01	8.95E-01	-	-
1396577_at	---	---	---	Rn.205959	AI548703	2.41	2.40	2.42	2.40	2.42	2.39	1.00	down	7.22E-01	9.11E-01	-	-
1386358_at	---	---	---	---	AI639222	2.19	2.18	2.20	2.18	2.20	2.18	1.00	down	6.16E-01	8.95E-01	-	-
1380090_at	---	---	---	Rn.63824	BF407443	2.32	2.33	2.33	2.31	2.36	2.31	1.00	up	8.33E-01	9.47E-01	-	-
1369303_at	Crh	corticotropin releasing hormone	81648	Rn.10349	NM_031019	2.39	2.38	2.41	2.39	2.40	2.38	1.00	down	7.21E-01	9.11E-01	-	-
1374859_at	---	---	---	---	AI576252	2.40	2.38	2.41	2.38	2.40	2.41	1.00	up	7.64E-01	9.23E-01	-	-
1389825_at	LOC680117	Similar to T-cell leukemia homeobox protein 2 (Homeobox protein Hox-11L1)	680117	Rn.159786	AW533294	2.23	2.22	2.23	2.22	2.23	2.22	1.00	down	3.46E-01	8.95E-01	-	-
1385770_at	RGD1565726	similar to hypothetical protein A730098P15	363167	Rn.135672	BF415530	2.43	2.41	2.42	2.42	2.42	2.41	1.00	down	5.94E-01	8.95E-01	-	-
1385141_at	Olig3	oligodendrocyte transcription factor 3	293012	Rn.140572	BF397808	2.39	2.38	2.40	2.38	2.39	2.37	1.00	down	6.33E-01	8.95E-01	-	-
1392283_at	---	---	---	Rn.216879	BI288834	2.38	2.38	2.39	2.38	2.39	2.37	1.00	down	5.97E-01	8.95E-01	-	-
1387615_at	St8sia2	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 2	117523	Rn.44391	NM_057156	2.27	2.27	2.28	2.27	2.27	2.26	1.00	down	4.97E-01	8.95E-01	-	-
1381570_at	Nfkbid	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, de	308496	Rn.144998	BI293518	2.28	2.28	2.29	2.28	2.28	2.27	1.00	down	4.24E-01	8.95E-01	-	-
1369764_at	C4bpa	complement component 4 binding protein, alpha	24235	Rn.10408	NM_012516	2.37	2.35	2.37	2.36	2.37	2.35	1.00	down	7.21E-01	9.11E-01	-	-
1370760_a_at	Gad1	glutamate decarboxylase 1	24379	Rn.91245	M38350	2.34	2.33	2.35	2.33	2.35	2.32	1.00	down	7.15E-01	9.10E-01	-	-
1370788_at	Fgf4	fibroblast growth factor 4	116499	Rn.81223	AB078673	2.28	2.28	2.29	2.28	2.28	2.27	1.00	down	4.59E-01	8.95E-01	-	-
1378520_at	Bcl11b	B-cell CLL/lymphoma 11B (zinc finger protein)	314423	Rn.162897	BF398531	2.31	2.31	2.32	2.31	2.32	2.30	1.00	down	5.73E-01	8.95E-01	-	-
1368711_at	Foxa2	forkhead box A2	25099	Rn.10948	NM_012743	2.29	2.29	2.30	2.29	2.30	2.28	1.00	down	5.76E-01	8.95E-01	-	-
1398212_at	Olig2	Oligodendrocyte lineage transcription factor 2	304103	Rn.22121	BE106655	2.33	2.32	2.33	2.32	2.33	2.31	1.00	down	6.26E-01	8.95E-01	-	-
1372278_at	---	---	---	Rn.155733	BF404480	2.25	2.25	2.26	2.25	2.25	2.24	1.00	down	4.80E-01	8.95E-01	-	-
1378069_at	Pkn1	Protein kinase N1	29355	Rn.49880	BF411777	3.33	3.32	3.35	3.33	3.34	3.33	1.00	down	6.97E-01	9.07E-01	-	-
1378823_at	---	---	---	Rn.61261	BF409131	2.38	2.37	2.43	2.37	2.45	2.36	1.00	up	9.15E-01	9.75E-01	-	-
1384753_at	Fam71a	family with sequence similarity 71, member A	498311	Rn.59403	BF396537	2.44	2.42	2.46	2.43	2.45	2.42	1.00	down	8.13E-01	9.39E-01	-	-
1372147_at	Ndufs4	NADH dehydrogenase (ubiquinone) Fe-S protein 4	499529	Rn.203141	BM387802	9.72	9.71	9.73	9.72	9.72	9.70	1.00	down	6.99E-01	9.07E-01	-	-
1368966_at	Mybph	myosin binding protein H	83708	Rn.23666	NM_031813	2.33	2.31	2.33	2.32	2.33	2.31	1.00	down	6.99E-01	9.07E-01	-	-
1389810_at	Skiv2l	superkiller viralicidic activity 2-like 2 (S. cerevisiae)	365668	Rn.145315	BI275054	9.16	8.21	7.74	8.36	8.45	8.28	1.00	down	9.93E-01	9.98E-01	-	-
1387541_at	Ncan	neurocan	58982	Rn.10177	NM_031653	2.30	2.29	2.30	2.29	2.30	2.29	1.00	down	5.59E-01	8.95E-01	-	-
1373972_at	LOC685707	similar to neuron navigator 1	685707	Rn.154566	BF387266	2.26	2.25	2.26	2.25	2.26	2.25	1.00	down	4.82E-01	8.95E-01	-	-
1369731_at	Cnksr2	connector enhancer of kinase suppressor of Ras 2	59322	Rn.42893	AF102854	2.39	2.37	2.40	2.38	2.42	2.37	1.00	up	8.41E-01	9.50E-01	-	-
1388657_at	Dchs1	dachsous 1 (Drosophila)	308912	Rn.15768	AW253923	2.27	2.27	2.28	2.27	2.27	2.26	1.00	down	4.37E-01	8.95E-01	-	-
1380368_at	RGD1560470	similar to Gene model 996	362083	Rn.44904	BF403562	2.22	2.20	2.23	2.22	2.23	2.22	1.00	up	7.34E-01	9.15E-01	-	-
1396935_at	---	---	---	Rn.205865	AI410333	2.33	2.32	2.33	2.32	2.33	2.31	1.00	down	6.30E-01	8.95E-01	-	-
1389743_at	---	---	---	---	BF403162	2.49	2.48	2.51	2.49	2.52	2.48	1.00	up	8.06E-01	9.38E-01	-	-
1378125_at	Wdr91	WD repeat domain 91	312225	Rn.158722	AA998621	2.31	2.30	2.33	2.31	2.31	2.30	1.00	down	7.28E-01	9.13E-01	-	-
1380594_at	Scube1	signal peptide, CUB domain, EGF-like 1	315174	Rn.8673	AA957500	2.29	2.28	2.30	2.29	2.30	2.28	1.00	down	5.89E-01	8.95E-01	-	-
1397548_at	Hmha1	histocompatibility (minor) HA-1	314618	Rn.35286	BF417363	4.15	4.37	5.76	4.50	5.41	4.37	1.00	down	9.95E-01	9.98E-01	-	-
1373202_at	Gng3	guanine nucleotide binding protein (G protein), gamma 3	114117	Rn.198523	AI112577	2.29	2.28	2.28	2.28	2.29	2.27	1.00	down	5.47E-01	8.95E-01	-	-
1378628_at	---	---	---	Rn.61844	BF414451	2.62	2.61	2.63	2.61	2.72	2.54	1.00	up	9.48E-01	9.85E-01	-	-
1377582_at	Tox3	TOX high mobility group box family member 3	291908	Rn.41060	BE095938	2.40	2.39	2.42	2.40	2.42	2.38	1.00	down	8.19E-01	9.42E-01	-	-
1381894_at	OC678978 /// Phpr	hypothetical protein LOC678978 /// protein tyrosine phosphatase, non-recepto	246116 /// 67	Rn.41717	AI547542	2.26	2.26	2.27	2.26	2.27	2.26	1.00	down	5.18E-01	8.95E-01	-	-
1375389_at	Shox2	Short stature homeobox 2	25546	Rn.11258	AI103639	2.26	2.25	2.26	2.26	2.25	2.25	1.00	down	4.45E-01	8.95E-01	-	-
1380380_at	---	---	---	Rn.212680	BI296096	2.31	2.31	2.31	2.31	2.30	2.30	1.00	down	3.81E-01	8.95E-01	-	-
1389826_at	Cebpd	CCAAT/enhancer binding protein (C/EBP), delta	25695	Rn.202620	AI176576	2.22	2.21	2.22	2.21	2.23	2.21	1.00	up	6.57E-01	8.98E-01	-	-
1373735_at	---	---	---	Rn.41871	BG372418	2.96	2.62	2.62	2.59	3.03	2.56	1.00	down	9.85E-01	9.98E-01	-	-
1382457_at	Khdrbs3	KH domain containing, RNA binding, signal transduction associated 3	64015	Rn.54682	AI029816	2.36	2.35	2.37	2.35	2.36	2.35	1.00	down	6.43E-01	8.95E-01	-	-
1369425_at	Cdh13	cadherin 13	192248	Rn.23806	NM_138889	2.27	2.27	2.28	2.27	2.28	2.26	1.00	down	5.32E-01	8.95E-01	-	-
1387391_at	Cdkn1a	cyclin-dependent kinase inhibitor 1A (p21, Cip1)	114851	Rn.10089	U24174	2.31	2.30	2.32	2.30	2.31	2.30	1.00	down	5.21E-01	8.95E-01	-	-
1392749_at	Cntfr	ciliary neurotrophic factor receptor	313173	Rn.55036	BE109686	2.31	2.30	2.32	2.31	2.31	2.30	1.00	down	6.06E-01	8.95E-01	-	-
1397341_at	Pbk	PDZ binding kinase	290326	Rn.137333	BG663837	2.38	2.36	2.39	2.37	2.38	2.37	1.00	down	6.76E-01	9.02E-01	-	-
1370135_at	Cav2	caveolin 2	363425	Rn.81070	NM_131914	2.26	2.26	2.27	2.26	2.27	2.25	1.00	down	4.96E-01	8.95E-01	-	-
1380750_at	---	---	---	Rn.211906	BF398240	2.50	2.49	2.51	2.50	2.48	2.48	1.00	down	6.78E-01	9.02E-01	-	-
1380188_at	LOC689298	hypothetical protein LOC689298	689298	Rn.156563	BF407749	2.30	2.29	2.30	2.29	2.30	2.29	1.00	down	4.68E-01	8.95E-01	-	-
1369237_at	Slc6a7	solute carrier family 6 (neurotransmitter transporter, L-proline), member 7	117100	Rn.9663	NM_053996	2.47	2.45	2.50	2.46	2.49	2.46	1.00	down	8.53E-01	9.54E-01	-	-
1378678_at	---	---	---	Rn.210891	BF417886	2.35	2.34	2.35	2.35	2.36	2.33	1.00	down	6.65E-01	8.99E-01	-	-
1384932_at	Pflk1	PFTAIRE protein kinase 1	362316	Rn.12908	AI045232	2.25	2.25	2.26	2.25	2.25	2.24	1.00	down	4.93E-01	8.95E-01	-	-
1396094_at	Ahnak	AHNAK nucleoprotein	191572	Rn.112831	BG668757	2.37	2.36	2.37	2.37	2.38	2.35	1.00	down	6.21E-01	8.95E-01	-	-
1397098_at	Sdk2	Sidekick homolog 2 (chicken)	360652	Rn.49029	BF404299	2.24	2.23	2.24	2.23	2.25	2.23	1.00	up	6.72E-01	9.01E-01	-	-
1396120_at	---	---	---	Rn.63754	BF554238	2.27	2.26	2.28	2.27	2.27	2.26	1.00	down	4.97E-01	8.95E-01	-	-
1369033_at	Lhcgr	luteinizing hormone/choriogonadotropin receptor	25477	Rn.11216	NM_012978	2.32	2.31	2.32	2.31	2.32	2.30	1.00	down	5.45E-01	8.95E-01	-	-
1379064_at	---	---	---	Rn.212088	BI296614	2.33	2.32	2.34	2.33	2.36	2.32	1.00	up	8.14E-01	9.40E-01	-	-
1394411_at	RGD1560608	similar to novel protein	500724	Rn.53684	BF410745	2.53	2.50	2.52	2.51	2.56	2.49	1.00	up	8.80E-01	9.63E-01	-	-
1396681_at	---	---	---	Rn.207983	BF402663	2.47	2.47	2.47	2.46	2.48	2.45	1.00	down	6.57E-01	8.98E-01	-	-
1379382_at	---	---	---	Rn.6373	AI144865	2.29	2.28	2.29	2.28	2.29	2.28	1.00	down	5.30E-01	8.95E-01	-	-
1390948_at	Phrmx	gon hematopoietic expression	365390	Rn.154906	AI058307	2.34	2.33	2.35	2.33	2.35	2.32	1.00	down	7.16E-01	9.10E-01	-	-
1375142_at	Sv2b	Synaptic vesicle glycoprotein 2b	117556	Rn.58137	BI291337	2.34	2.33	2.35	2.33	2.35	2.32	1.00	down	6.98E-01	9.07E-01	-	-
1397858_at	---	---	---	Rn.168769	AI548704	2.62	2.57	2.70	2.64	2.72	2.53	1.00	up	9.59E-01	9.89E-01	-	-
1391597_at	Gpr75	G protein-coupled receptor 75	498434	Rn.140703	AW527416	2.30	2.29	2.31	2.30	2.31	2.29	1.00	down	6.28E-01	8.95E-01	-	-
1371162_at	Mrga10	nuclear receptor MrgA10 RF-amide G protein-coupled receptor	252960	Rn.81069	AJ311952	2.30	2.29	2.30	2.29	2.30	2.28	1.00	down	4.79E-01	8.95E-01	-	-
1393182_at	Cxcl3	chemokine (C-X-C motif) ligand 3	171551	Rn.10525	AW917501	2.32	2.31	2.32	2.31	2.32	2.30	1.00	down	5.92E-01	8.95E-01	-	-
1383895_at	Dynlrb2	dynein light chain roadblock-type 2	361415	Rn.27744	AI144946	2.41	2.41	2.42	2.40	2.43	2.41	1.00	down	6.47E-01	8.95E-01	-	-
1392263_at	Prkag2	protein kinase, AMP-activated, gamma 2 non-catalytic subunit	373545	Rn.51208	AI579640	2.31	2.30	2.31	2.30	2.31	2.30	1.00	down	3.82E-01	8.95E-01	-	-
1382545_at	---	---	---	Rn.16228	AI045469	2.27	2.27	2.27	2.27	2.27	2.26	1.00	down	3.80E-01	8.95E-01	-	-
1395140_at	---	---	---	Rn.206396	AW526814	2.41	2.41	2.42	2.41	2.41	2.40	1.00	down	4.42E-01	8.95E-01	-	-
1376379_a_at	RGD1309906	similar to RIKEN cDNA 2310004I24 gene	287406	Rn.163104	AW252141	2.40	2.38	2.47	2.44	2.42	2.37	1.00	down	9.18E-01	9.76E-01	-	-
1386224_at	---	---	---	Rn.163902	H33651	2.41	2.41	2.42	2.41	2.42	2.40	1.00	down	6.01E-01	8.95E-01	-	-
1368780_at	Adrb3	adrenergic, beta-3-, receptor	25645	Rn.10100	NM_013108	2.36	2.34	2.36	2.35	2.37	2.33	1.00	down	8.00E-01	9.35E-01	-	-
1369792_at	Gpr6	G protein-coupled receptor 6	83683	Rn.32092	U12006	2.41	2.40	2.42	2.40	2.41	2.40	1.00	down	5.63E-01	8.95E-01	-	-
1395789_at	---	---	---	Rn.153341	BM958510	2.44	2.42	2.45	2.44	2.45	2.42	1.00	down	7.80E-01	9.29E-01	-	-
1377165_at	---	---	---	Rn.122196	BF420864	2.24	2.24	2.25	2.24	2.24	2.23	1.00	down	5.15E-01	8.95E-01	-	-
1380908_at	---	---	---	Rn.203458	AA924563	2.31	2.31	2.32	2.31	2.32	2.30	1.00	down	5.54E-01	8.95E-01	-	-
1387068_at	Arc	activity-regulated cytoskeleton-associated protein	54323	Rn.10086	NM_019361	2.29	2.28	2.29	2.28	2.29	2.28	1.00	down	5.04E-01	8.95E-01	-	-
1387409_x_at	Nign3	neuroligin 3	171297	Rn.10263	NM_134336	2.29	2.29	2.30	2.29	2.29	2.28	1.00	down	5.57E-01	8.95E-01	-	-
1378764_at	---	---	---	Rn.41566	BE106826	2.33	2.32	2.34	2.32	2.33	2.32	1.00	down	5.90E-01	8.95E-01	-	-
1369615_at	Rap2a	RAS related protein 2a7	114560	Rn.11606	NM_053741	2.29	2.29	2.30	2.29	2.30	2.28	1.00	down	5.60E-01	8.95E-01	-	-
1370652_at	Ntrk2	neurotrophic tyrosine kinase, receptor, type 2	25054	Rn.11246	M55293	2.35	2.35	2.37	2.36	2.37	2.35	1.00	down	6.92E-01	9.05E-01	-	-
1377170_at	---	---	---	Rn.161091	AW534159	2.29	2.28	2.29	2.28	2.29	2.28	1.00	down	5.36E-01	8.95E-01	-	-
1385515_at	Adora3	adenosine A3 receptor	25370	Rn.10457	BG379920	2.51	2.50	2.53	2.51	2.56	2.47	1.00	down	9.02E-01	9.70E-01	-	-
1389697_at	---	---	---	Rn.124511	AW529759	2.40	2.40	2.41	2.42	2.40	2.39	1.00	up	7.18E-01	9.11E-01	-	-
1381540_at	LOC689019	hypothetical protein LOC689019	689019	Rn.16029	AI179073	2.38	2.38	2.39	2.38	2.38	2.37	1.00	down	4.98E-01	8.95E-01	-	-
1380758_at	---	---	---	Rn.209254	BF412419	2.36	2.36	2.38	2.36	2.37	2.36	1.00	down	5.96E-01	8.95E-01	-	-
1385232_at	Trim62	tripartite motif-containing 62	313045	Rn.20891	AI045540	2.33	2.32	2.33	2.32	2.33	2.31	1.00	down	6.40E-01	8.95E-01	-	-
1397162_x_at	Tpo	Thyroid peroxidase	54314	Rn.91199	M57705	2.60	2.58	2.67	2.58	2.67	2.58	1.00	down	9.29E-01	9.80E-01	-	-
1369595_at	Fgf23	fibroblast growth factor 23	170583	Rn.154421	NM_130754	2.32	2.31	2.33	2.32	2.32	2.31	1.00	down	5.59E-01	8.95E-01	-	-
1373700_at	---	---	---	Rn.176863	BI291459	2.30	2.29	2.30	2.30	2.30	2.29	1.00	down	5.38E-01	8.95E-01	-	-
1368502_at	Gas8	gastrin	25320	Rn.9754	NM_012849	2.36	2.35	2.37	2.35	2.36	2.34	1.00	down	6.74E-01	9.01E-01	-	-
1370798_a_at	Ngb	neuroglobin	85382	Rn.64645	AB056656	2.26	2.25	2.27	2.25	2.26	2.25	1.00	down	5.99E-01	8.95E-01	-	-
1391919_at	Tcerg1l	transcription elongation regulator 1-like	361669	Rn.45649	AW523472	2.31	2.30	2.31	2.30	2.31	2.30	1.00	down	5.19E-01	8.95E-01	-	-
1378529_at	---	---	---	Rn.115761	BE109895	2.37	2.36	2.37	2.36	2.37	2.36	1.00	down	3.55E-01	8.95E-01	-	-
1378035_at	---	---	---	Rn.211861	AI598512	2.32	2.31	2.33	2.31	2.32	2.31	1.00	down	5.82E-01	8.95E-01	-	-
1370749_at	V1rb7	vomeronasal 1 receptor, B7	286892	Rn.10227	U36786	2.29	2.28	2.29	2.28	2.29	2.28	1.00	down	5.84E-01	8.95E-01	-	-
1379507_at	---	---	---	Rn.160204	AW917933	2.40	2.39	2.42	2.40	2.41	2.39	1.00	down	7.34E-01	9.15E-01	-	-
1371155_at	Klrc1	killer cell lectin-like receptor subfamily C, member 1	29683	Rn.9895	AF021350	2.34	2.33	2.35	2.34	2.35	2.33	1.00	down	6.17E-01	8.95E-01	-	-
1378994_at	Osbpl10	Oxysterol binding protein-like 10	316039	Rn.205264	AI535127	2.44	2.44	2.45	2.44	2.46	2.44	1.00	up	6.85E-01	9.03E-01	-	-
1381319_at	---	---	---	Rn.206722	BF407155	2.31	2.30	2.31	2.31	2.31	2.30	1.00	down	5.73E-01	8.95E-01	-	-
1383581_at	LOC680531	similar to CG3880-PA	680531	Rn.42084	BI290662	2.26	2.26	2.27	2.26	2.27	2.26	1.00	down	4.24E-01	8.95E-01	-	-
1379387_at	---	---	---	Rn.105775	AI639103	2.39	2.38	2.42	2.40	2.39	2.39	1.00	down	7.77E-01	9.28E-01	-	-
1390303_at	---	---	---	Rn.64324	BF390840	2.32	2.32	2.33	2.32	2.33	2.31	1.00	down	6.04E-01	8.95E-01	-	-
1391087_at	Lrrc56	leucine rich repeat containing 56	365389	Rn.87507	AI236588	2.25	2.24	2.27	2.25	2.26	2.25	1.00	down	6.15E-01	8.95E-01	-	-
1370483_at	LOC679046 /// L	CD244 molecule, natural killer cell receptor 2B4 /// similar to transmembrane 5	679046 /// 68	Rn.53994	AF209406	2.47	2.47	2.50	2.48	2.49	2.46	1.00	down	7.97E-01	9.35E-01	-	-
1382937_at	Spdef	SAM pointed domain containing ets transcription factor	689210	Rn.55891	BE113837	2.31	2.30	2.33	2.31	2.33	2.30	1.00	down	7.53E-01	9.20E-01	-	-
1384982_at	---	---	---	---	BF397679	2.34	2.33	2.35	2.34	2.35	2.33	1.00	down	6.86E-01	9.04E-01	-	-
1378796_at	Omg	oligodendrocyte-myelin glycoprotein	450224	Rn.163139	AA964584	2.30	2.30	2.31	2.30	2.33	2.29	1.00	up	7.98E-01	9.35E-01	-	-
1369395_at	Tpc1808	tropic 1808	64560	Rn.127789	NM_022625	2.41	2.40	2.43	2.41	2.43	2.40	1.00	down	7.65E-01	9.23E-01	-	-
1397273_at	Ldb3	LIM domain binding 3	498587	Rn.219238	AW520906	2.30	2.29	2.30	2.29	2.30	2.28	1.00	down	5.21E-01	8.95E-01	-	-
1381372_at	Cep76	Centrosomal protein 76kDa	291540	Rn.98568	AI235395	2.25	2.25	2.26	2.25	2.25	2.24	1.00	down	4.37E-01	8.95E-01	-	-
1382677_at	---	---	---	Rn.204743	AA899419	2.30	2.29	2.31	2.30	2.30	2.28	1.00	down	5.40E-01	8.95E-01	-	-
1378997_at	Ephb6	Eph receptor B6	312275	Rn.125930	BM391684	2.38	2.37	2.39	2.38	2.39	2.37	1.00	down	6.91E-01	9.05E-01	-	-
1392340_at	RGD1565218	similar to Kelch-like protein 3	498697	Rn.198324	BF416150	2.34	2.33	2.35	2.34	2.35	2.33	1.00	down	6.42E-01	8.95E-01	-	-
1368301_at	Adora2a	adenosine A2a receptor	25369	Rn.11180	AF228684	2.30	2.30	2.31	2.30	2.31	2.29	1.00	down	6.23E-01	8.95E-01	-	-
1393312_at	---	---	---	Rn.32441	AA900283	2.31	2.30	2.32	2.31	2.32	2.30	1.00	down	6.35E-01	8.95E-01	-	-
1394528_at	---	---	---	Rn.211069	BF405166	2.35	2.35	2.36	2.35	2.36	2.34	1.00	down	6.54E-01	8.97E-01	-	-
1379720_at	---	---	---	Rn.169990	AW528715	2.34	2.34	2.35	2.34	2.35	2.34	1.00	down	5.61E-01	8.95E-01	-	-
1385988_at	Hmx1	H6 family homeobox 1	360960	Rn.24574	BF287243	2.28	2.27	2.29	2.28	2.29	2.27	1.00	down	6.33E-01	8.95E-01	-	-
1375379_at	Tap1	Transporter 1, ATP-binding cassette, sub-family B (MDR/TAP)	24811	Rn.10763	BI296734	2.36	2.36	2.37	2.36	2.37	2.35	1.00	down	5.32E-01	8.95E-01	-	-
1397437_at	Arid5a	AT rich interactive domain 5A (Mrf1 like)	316327	Rn.15775	AI715395	2.33	2.32	2.34	2.33	2.34	2.31	1.00	down	6.95E-01	9.06E-01	-	-
1381894_at	---	---	---	Rn.148873	AW552964	2.36	2.35	2.37	2.36	2.37	2.35	1.00	down	7.04E-01	9.07E-01	-	-
1387902_a_at	---	---	---	117925 /// Rn.126	L22655	2.35	2.34	2.36	2.34	2.37	2.32	1.00	down	8.30E-01	9.46E-01	-	-
1383319_at	Slc4a11	solute carrier family 4, sodium bicarbonate transporter-like, member 11	311423	Rn.162720	BI293444	2.25	2.25	2.25	2.25	2.25	2.24	1.00	down	3.96E-01	8.95E-01	-	-
1384054_at	Mrgprg	MAS-related GPR, member G	309133	Rn.112764	BF556686	2.43	2.41	2.44	2.42	2.44	2.41	1.00	down	7.85E-01	9.30E-01	-	-
1375149_at	Lrrc4b	leucine rich repeat containing 4B	360571	Rn.222207	AI145991	2.40	2.39	2.41	2.40	2.40	2.39	1.00	down	5.90E-01	8.95E-01	-	-
1375775_at	Odf3b	outer dense fiber of sperm tails 3B	500917	Rn.76400	BI296701	2.34

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1382766_at	Epor	erythropoietin receptor	24336	Rn.22394	BF288024	2.28	2.27	2.28	2.27	2.28	2.26	1.00	down	5.55E-01	8.95E-01	-	-
1391931_at	---	---	---	Rn.39209	BG372611	2.38	2.37	2.39	2.37	2.38	2.37	1.00	down	6.88E-01	9.04E-01	-	-
1369556_at	Ltb4r2	leukotriene B4 receptor 2	114098	Rn.74251	NM_053640	2.27	2.27	2.28	2.27	2.27	2.26	1.00	down	4.82E-01	8.95E-01	-	-
1386489_at	---	---	---	---	AA965259	2.30	2.30	2.32	2.30	2.31	2.30	1.00	down	6.07E-01	8.95E-01	-	-
1391692_at	---	---	---	Rn.205169	AI229519	2.33	2.32	2.33	2.32	2.33	2.31	1.00	down	6.94E-01	9.05E-01	-	-
1371277_at	Cdx1	caudal type homeo box 1	364883	---	M91450	2.35	2.34	2.35	2.34	2.35	2.34	1.00	down	4.28E-01	8.95E-01	-	-
1388275_at	Tcrb	T-cell receptor beta chain	24820	Rn.34871	AW919577	2.37	2.36	2.38	2.37	2.38	2.36	1.00	down	7.21E-01	9.11E-01	-	-
1390209_at	Syngr3	synaptogyrin 3	302975	Rn.6497	BE097982	2.33	2.32	2.34	2.33	2.34	2.32	1.00	down	6.98E-01	9.07E-01	-	-
1379993_at	Oaz3	ornithine decarboxylase antizyme 3	689588	Rn.43319	AW529628	2.31	2.30	2.32	2.31	2.32	2.30	1.00	down	6.25E-01	8.95E-01	-	-
1387743_at	Gpr20	G protein-coupled receptor 20	60667	Rn.138120	NM_022216	2.24	2.23	2.25	2.23	2.24	2.23	1.00	down	5.27E-01	8.95E-01	-	-
1378472_at	---	---	---	Rn.20751	BE108158	2.27	2.26	2.27	2.26	2.27	2.26	1.00	down	5.31E-01	8.95E-01	-	-
1370625_at	Faim2	Fas apoptotic inhibitory molecule 2	246274	Rn.162026	AF044201	2.28	2.28	2.29	2.28	2.28	2.27	1.00	down	4.95E-01	8.95E-01	-	-
1370494_at	Slc14a2	solute carrier family 14 (urea transporter), member 2	54302	Rn.10157	AF031642	2.33	2.33	2.34	2.33	2.34	2.32	1.00	down	5.08E-01	8.95E-01	-	-
1380037_at	---	---	---	Rn.81227	BI294354	2.32	2.31	2.33	2.32	2.34	2.31	1.00	up	6.86E-01	9.04E-01	-	-
1383006_at	---	---	---	Rn.151843	AW528365	2.47	2.44	2.46	2.45	2.50	2.42	1.00	down	8.88E-01	9.65E-01	-	-
1387373_at	Pde4dip	phosphodiesterase 4D interacting protein	64183	Rn.48693	NM_022382	2.42	2.41	2.44	2.37	2.54	2.37	1.00	up	9.53E-01	9.86E-01	-	-
1370125_at	Hapln1	hyaluronan and proteoglycan link protein 1	29331	Rn.50531	NM_019189	2.26	2.26	2.27	2.26	2.27	2.25	1.00	down	5.80E-01	8.95E-01	-	-
1392575_at	Znf654	zinc finger protein 654	288354	Rn.29452	BE108929	3.76	3.74	3.60	3.97	3.52	3.61	1.00	up	9.82E-01	9.94E-01	-	-
1389096_at	---	---	---	---	BI274243	2.38	2.36	2.39	2.37	2.39	2.37	1.00	down	7.55E-01	9.20E-01	-	-
1390677_at	Fibcd1	fibrinogen C domain containing 1	311861	Rn.47612	BF413126	2.35	2.35	2.35	2.35	2.35	2.34	1.00	down	4.03E-01	8.95E-01	-	-
1368871_at	Map3k1	mitogen activated protein kinase kinase kinase 1	116667	Rn.11081	NM_053887	2.39	2.38	2.40	2.38	2.40	2.38	1.00	down	7.16E-01	9.10E-01	-	-
1374271_at	---	---	---	Rn.129539	AW528864	2.37	2.36	2.38	2.37	2.38	2.36	1.00	down	7.12E-01	9.10E-01	-	-
1384158_at	---	---	---	Rn.166559	AW522416	2.44	2.43	2.45	2.44	2.47	2.42	1.00	up	8.08E-01	9.38E-01	-	-
1378865_at	---	---	---	Rn.46261	AI228240	2.36	2.34	2.37	2.35	2.36	2.35	1.00	down	6.94E-01	9.05E-01	-	-
1389887_at	---	---	---	Rn.204275	BF284592	2.34	2.33	2.35	2.34	2.35	2.33	1.00	down	5.84E-01	8.95E-01	-	-
1368632_at	Foxg1	forkhead box G1	24370	Rn.9864	NM_012560	2.43	2.41	2.45	2.43	2.45	2.41	1.00	down	8.47E-01	9.52E-01	-	-
1368205_at	Cfi	complement factor I	79126	Rn.7424	NM_024157	2.30	2.29	2.31	2.29	2.30	2.29	1.00	down	6.35E-01	8.95E-01	-	-
1396488_at	---	---	---	Rn.154001	BI291411	2.41	2.41	2.43	2.41	2.41	2.41	1.00	down	5.75E-01	8.95E-01	-	-
1369405_a_at	Chrnb4	cholinergic receptor, nicotinic, beta 4	25103	Rn.9695	X15834	2.29	2.28	2.29	2.28	2.29	2.27	1.00	down	5.55E-01	8.95E-01	-	-
1380927_at	---	---	---	Rn.162945	AW529115	2.27	2.27	2.28	2.27	2.28	2.26	1.00	down	5.56E-01	8.95E-01	-	-
1370730_a_at	Ghrhr	growth hormone releasing hormone receptor	25321	Rn.10936	AF400106	2.37	2.35	2.39	2.39	2.37	2.36	1.00	up	7.94E-01	9.34E-01	-	-
1369776_a_at	Shank2	SH3 and multiple ankyrin repeat domains 2	171093	Rn.14545	NM_133440	2.49	2.48	2.50	2.49	2.49	2.50	1.00	up	6.17E-01	8.95E-01	-	-
1395617_at	Cadm4	cell adhesion molecule 4	365216	Rn.198138	AA943034	2.27	2.27	2.28	2.27	2.28	2.26	1.00	down	5.73E-01	8.95E-01	-	-
1369178_a_at	P2rx1	purinergic receptor P2X, ligand-gated ion channel, 1	25505	Rn.91176	AF231010	2.28	2.27	2.29	2.28	2.28	2.27	1.00	down	5.49E-01	8.95E-01	-	-
1381493_x_at	---	---	---	---	AI137687	2.27	2.26	2.27	2.26	2.27	2.26	1.00	down	4.67E-01	8.95E-01	-	-
1389864_at	---	---	---	---	BF405086	2.31	2.30	2.32	2.31	2.31	2.30	1.00	down	6.19E-01	8.95E-01	-	-
1387467_at	Kcnj10	potassium inwardly-rectifying channel, subfamily J, member 10	29718	Rn.10196	NM_031602	2.40	2.40	2.41	2.40	2.41	2.39	1.00	down	5.92E-01	8.95E-01	-	-
1384973_at	Serpinb3	serine protease inhibitor B3	304688	Rn.213030	BM390580	2.28	2.27	2.29	2.28	2.28	2.27	1.00	down	5.28E-01	8.95E-01	-	-
1379208_at	---	---	---	Rn.91012	BE113484	2.38	2.37	2.39	2.37	2.39	2.37	1.00	down	7.01E-01	9.07E-01	-	-
1387419_at	Chrna7	cholinergic receptor, nicotinic, alpha 7	25302	Rn.9698	NM_012832	2.23	2.22	2.24	2.23	2.23	2.22	1.00	down	5.08E-01	8.95E-01	-	-
1394543_at	Anks1b	ankyrin repeat and sterile alpha motif domain containing 1B	314721	---	BF400104	2.34	2.34	2.35	2.34	2.35	2.33	1.00	down	5.50E-01	8.95E-01	-	-
1396204_at	---	---	---	---	Rn.199515	AI706471	2.28	2.28	2.29	2.28	2.29	2.27	1.00	down	4.86E-01	8.95E-01	-	-
1398135_at	---	---	---	---	---	AI511042	2.39	2.37	2.40	2.38	2.40	2.36	1.00	down	8.20E-01	9.42E-01	-	-
1378627_at	---	---	---	---	Rn.171722	BE120326	2.34	2.32	2.34	2.33	2.34	2.32	1.00	down	7.44E-01	9.17E-01	-	-
1387934_at	Bcan	brevican	25393	Rn.10315	U37142	2.36	2.35	2.40	2.40	2.36	2.35	1.00	down	8.78E-01	9.63E-01	-	-
1369648_at	Calcrl	calcitonin receptor-like	25029	Rn.11202	L27487	2.29	2.28	2.29	2.29	2.29	2.28	1.00	down	5.34E-01	8.95E-01	-	-
1391110_at	---	---	---	Rn.172702	BF393043	2.31	2.30	2.32	2.31	2.31	2.30	1.00	down	6.15E-01	8.95E-01	-	-
1395121_at	---	---	---	Rn.154383	BF394559	2.32	2.31	2.33	2.32	2.34	2.31	1.00	up	7.43E-01	9.17E-01	-	-
1392064_at	Dlx1	distal-less homeobox 1	296500	Rn.59152	BF400590	2.49	2.47	2.54	2.52	2.54	2.46	1.00	up	9.17E-01	9.75E-01	-	-
1385370_at	RGD1311142	similar to hypothetical protein FLJ32796	361564	Rn.82375	BE102234	2.25	2.24	2.26	2.25	2.25	2.24	1.00	down	5.49E-01	8.95E-01	-	-
1393805_at	Fa2h	fatty acid 2-hydroxylase	307855	Rn.67886	AW527783	2.48	2.47	2.49	2.46	2.50	2.47	1.00	down	7.75E-01	9.28E-01	-	-
1395369_at	---	---	---	Rn.55455	BI300958	2.30	2.30	2.31	2.30	2.31	2.29	1.00	down	5.59E-01	8.95E-01	-	-
1380423_at	---	---	---	Rn.199453	BF547213	2.37	2.37	2.38	2.37	2.39	2.36	1.00	up	7.49E-01	9.19E-01	-	-
1392226_at	---	---	---	---	AI234999	2.35	2.35	2.37	2.35	2.37	2.34	1.00	down	7.73E-01	9.26E-01	-	-
1387601_at	Dcx	doublecortin	84394	Rn.121471	NM_053379	2.32	2.31	2.33	2.31	2.32	2.31	1.00	down	5.03E-01	8.95E-01	-	-
1396724_at	---	---	---	Rn.155168	BF405918	2.46	2.43	2.46	2.44	2.47	2.44	1.00	up	7.83E-01	9.30E-01	-	-
1391742_at	---	---	---	Rn.202635	BI296945	2.32	2.31	2.33	2.32	2.32	2.31	1.00	down	5.30E-01	8.95E-01	-	-
1378935_at	Sox17	SRY (sex determining region Y)-box 17	312836	Rn.7884	AI235684	2.34	2.34	2.35	2.34	2.34	2.33	1.00	down	5.40E-01	8.95E-01	-	-
1374270_at	---	---	---	Rn.11914	AA964789	2.29	2.28	2.30	2.29	2.30	2.28	1.00	down	6.91E-01	9.05E-01	-	-
1396069_at	Utx	ubiquitously transcribed tetratricopeptide repeat, X chromosome	317178	Rn.105636	AI236941	2.27	2.27	2.28	2.27	2.28	2.26	1.00	down	5.17E-01	8.95E-01	-	-
1373289_at	Asb8	ankyrin repeat and SOCS box-containing protein 8	315287	Rn.98320	BI281935	5.37	4.74	5.71	5.46	4.98	5.38	1.00	up	9.92E-01	9.97E-01	-	-
1370094_at	Acrv1	acrosomal vesicle protein 1	60353	Rn.42946	NM_021747	2.32	2.32	2.33	2.32	2.33	2.31	1.00	down	5.78E-01	8.95E-01	-	-
1392852_at	Smoc1	SPARC related modular calcium binding 1	314280	Rn.55639	AI175880	2.35	2.35	2.36	2.35	2.38	2.34	1.00	up	8.01E-01	9.36E-01	-	-
1390420_at	Cpxm1	carboxypeptidase X (M14 family), member 1	296156	Rn.19382	AI577849	2.43	2.42	2.44	2.43	2.44	2.42	1.00	down	6.95E-01	9.06E-01	-	-
1397087_at	---	---	---	Rn.51499	BF414403	2.27	2.27	2.28	2.27	2.28	2.26	1.00	down	5.49E-01	8.95E-01	-	-
1370122_at	Rab27b	RAB27B, member RAS oncogene family	84590	Rn.112603	NM_053459	2.39	2.38	2.40	2.38	2.40	2.38	1.00	down	7.00E-01	9.07E-01	-	-
1374930_at	---	---	---	Rn.153650	BG378606	2.35	2.34	2.37	2.35	2.36	2.34	1.00	down	7.21E-01	9.11E-01	-	-
1387239_at	Phox2a	paired-like homeobox 2a	116648	Rn.2858	NM_053869	2.24	2.24	2.25	2.24	2.25	2.24	1.00	down	5.38E-01	8.95E-01	-	-
1369275_s_at	Cyp2a1 /// Cyp2a2	cytochrome P450 IIA1 (hepatic steroid hydroxylase IIA1) gene /// cytochrome	24894 /// 24895	Rn.9867	M12892	2.29	2.28	2.30	2.29	2.28	2.28	1.00	down	5.53E-01	8.95E-01	-	-
1380674_at	---	---	---	Rn.177625	BM385358	2.37	2.36	2.38	2.37	2.38	2.36	1.00	down	6.37E-01	8.95E-01	-	-
1386491_at	---	---	---	---	AA894070	2.33	2.32	2.34	2.32	2.33	2.32	1.00	down	5.53E-01	8.95E-01	-	-
1392804_at	Dnase1l2	deoxyribonuclease 1-like 2	681124	Rn.201776	BI274504	2.31	2.30	2.31	2.30	2.31	2.30	1.00	down	4.39E-01	8.95E-01	-	-
1369214_a_at	Cilta	class II transactivator	85483	Rn.162013	NM_053529	2.33	2.33	2.34	2.33	2.34	2.32	1.00	down	4.96E-01	8.95E-01	-	-
1381675_at	Fbxl7	F-box and leucine-rich repeat protein 7	361907	Rn.45065	BF414198	2.24	2.23	2.24	2.23	2.25	2.23	1.00	up	7.11E-01	9.10E-01	-	-
1381198_at	---	---	---	Rn.62509	BF414118	2.27	2.26	2.28	2.27	2.28	2.26	1.00	down	6.31E-01	8.95E-01	-	-
1382622_at	Cst7	cystatin F (leukocystatin)	296257	Rn.24282	AI502757	2.32	2.31	2.33	2.31	2.35	2.31	1.00	up	8.20E-01	9.42E-01	-	-
1391951_at	---	---	---	Rn.206282	BI296447	2.28	2.27	2.28	2.27	2.28	2.27	1.00	down	4.98E-01	8.95E-01	-	-
1387733_at	Drd3	dopamine receptor D3	29238	Rn.10356	NM_017140	2.34	2.33	2.35	2.34	2.35	2.33	1.00	down	6.31E-01	8.95E-01	-	-
1375824_at	---	---	---	Rn.60928	BF406232	2.33	2.32	2.34	2.32	2.33	2.32	1.00	down	5.48E-01	8.95E-01	-	-
1391740_at	---	---	---	Rn.35461	BE116140	2.30	2.29	2.34	2.29	2.35	2.29	1.00	up	9.00E-01	9.69E-01	-	-
1369563_at	Vax1	ventral anterior homeobox 1	64571	Rn.48764	NM_022636	2.46	2.44	2.46	2.45	2.45	2.44	1.00	down	6.99E-01	9.07E-01	-	-
1369366_at	Cntn5	contactin 5	114589	Rn.10643	NM_053746	2.30	2.29	2.30	2.29	2.30	2.29	1.00	down	5.81E-01	8.95E-01	-	-
1378337_at	Rbm20	RNA binding motif protein 20	309544	Rn.21596	BF284712	2.29	2.29	2.30	2.29	2.30	2.28	1.00	down	5.66E-01	8.95E-01	-	-
1371215_at	Fut2	fucosyltransferase 2 (secretor status included)	58924	Rn.10678	L26010	2.31	2.29	2.32	2.31	2.32	2.30	1.00	up	7.58E-01	9.21E-01	-	-
1386685_at	Sacs	spastic ataxia of Charlevoix-Saguenay (sacsin)	305940	Rn.206255	BF567998	2.39	2.39	2.40	2.39	2.41	2.37	1.00	down	7.41E-01	9.16E-01	-	-
1380080_at	---	---	---	Rn.207148	AW535933	2.26	2.25	2.27	2.26	2.27	2.25	1.00	down	5.95E-01	8.95E-01	-	-
1395270_x_at	Gabrd	gamma-aminobutyric acid (GABA) A receptor, delta	29689	Rn.10927	AI228492	2.30	2.29	2.31	2.30	2.31	2.29	1.00	down	6.34E-01	8.95E-01	-	-
1369142_at	Bglap	bone gamma-carboxyglutamate (gla) protein	25295	Rn.9722	NM_013414	2.39	2.37	2.39	2.39	2.39	2.38	1.00	up	6.57E-01	8.98E-01	-	-
1368945_at	Bmp2	bone morphogenetic protein 2	29373	Rn.90931	AA944827	2.35	2.35	2.36	2.35	2.38	2.32	1.00	down	8.35E-01	9.48E-01	-	-
1368182_at	Acsl6	acyl-CoA synthetase long-chain family member 6	117243	Rn.33697	NM_130739	2.39	2.38	2.41	2.40	2.40	2.37	1.00	down	8.32E-01	9.47E-01	-	-
1385815_at	Speg	SPEG complex locus	363256	Rn.11313	AI072733	2.20	2.19	2.20	2.20	2.20	2.19	1.00	down	4.02E-01	8.95E-01	-	-
1369350_at	Kcnq2	potassium voltage-gated channel, subfamily Q, member 2	170848	Rn.33317	NM_133322	2.36	2.36	2.37	2.36	2.37	2.35	1.00	down	6.59E-01	8.98E-01	-	-
1383802_at	---	---	---	Rn.204977	AW531948	2.38	2.38	2.39	2.40	2.39	2.37	1.00	down	7.17E-01	9.10E-01	-	-
1381439_at	---	---	---	---	AW534203	2.25	2.25	2.26	2.25	2.25	2.24	1.00	down	4.09E-01	8.95E-01	-	-
1372910_at	---	---	---	Rn.12954	AI408770	6.16	5.85	5.46	4.87	6.67	5.92	1.00	down	9.95E-01	9.98E-01	-	-
1377485_at	Gjc2	gap junction protein, gamma 2	497913	Rn.204000	AI144646	2.29	2.30	2.29	2.29	2.29	2.28	1.00	down	5.53E-01	8.95E-01	-	-
1394529_at	---	---	---	---	BE102606	2.39	2.38	2.39	2.38	2.41	2.38	1.00	up	7.66E-01	9.24E-01	-	-
1381954_at	Htra3	HtrA serine peptidase 3	360959	Rn.15228	AI011441	2.33	2.33	2.34	2.33	2.33	2.32	1.00	down	5.41E-01	8.95E-01	-	-
1379769_at	---	---	---	Rn.47296	AW529745	2.35	2.35	2.37	2.35	2.36	2.35	1.00	down	6.84E-01	9.03E-01	-	-
1369017_at	Lgals7	lectin, galactoside-binding, soluble, 7	29518	Rn.6336	NM_022582	2.28	2.28	2.29	2.28	2.29	2.27	1.00	down	5.80E-01	8.95E-01	-	-
1393250_at	---	---	---	---	BE095854	2.49	2.46	2.48	2.46	2.48	2.47	1.00	down	7.09E-01	9.09E-01	-	-
1396435_at	---	---	---	Rn.170213	AW914868	2.38	2.36	2.41	2.38	2.39	2.37	1.00	down	8.36E-01	9.48E-01	-	-
1394616_at	---	---	---	Rn.172053	BF287471	2.61	2.60	2.62	2.60	2.62	2.59	1.00	down	6.82E-01	9.03E-01	-	-
1369338_at	OC683548 /// Robo	similar to roundabout homolog 1 /// roundabout homolog 1 (Drosophila)	58946 /// 683548	Rn.44468	NM_022188	2.38	2.37	2.38	2.38	2.38	2.37	1.00	down	4.10E-01	8.95E-01	-	-
1385055_at	RGD1563458	similar to D0H6S2654E protein	306883	Rn.59400	BF399530	2.36	2.35	2.36	2.36	2.36	2.35	1.00	down	5.35E-01	8.95E-01	-	-
1396898_at	---	---	---	Rn.209688	BF390322	2.44	2.43	2.44	2.43	2.47	2.42	1.00	up	8.46E-01	9.52E-01	-	-
1387683_at	Crhr1	corticotropin releasing hormone receptor 1	58959	Rn.10499	NM_030999	2.38	2.38	2.39	2.38	2.39	2.38	1.00	down	5.90E-01	8.95E-01	-	-
1392254_at	Map4	microtubule-associated protein 4	367171	Rn.203122	AI408043	2.24	2.23	2.25	2.24	2.24	2.23	1.00	down	5.84E-01	8.95E-01	-	-
1390965_at	---	---	---	Rn.29057	AW142969	2.28	2.28	2.29	2.28	2.28	2.27	1.00	down	5.33E-01	8.95E-01	-	-
1394570_at	Xk	X-linked Kx blood group (McLeod syndrome) homolog	497078	Rn.211877	BF284360	2.49	2.46	2.51	2.48	2.48	2.48	1.00	down	8.14E-01	9.40E-01	-	-
1376398_at	---	---	---	Rn.164743	BF417784	2.32	2.31	2.33	2.32	2.33	2.31	1.00	down	7.32E-01	9.14E-01	-	-
1392080_at	e1s /// RGD15610	late cornified envelope 1S /// RGD1561089	499664 /// 686064	---	AA925824	2.29	2.28	2.30	2.29	2.29	2.28	1.00	down	5.53E-01	8.95E-01	-	-
1379999_at	LOC685601	similar to MICAL CG33208-PB, isoform B	685601	Rn.211296	AW530087	2.26	2.26	2.26	2.26	2.28	2.23	1.00	down	7.98E-01	9.35E-01	-	-
1390593_at	Zfp653	Zinc finger protein 653	300446	Rn.64371	BF419668	2.25	2.24	2.26	2.24	2.25	2.24	1.00	down	4.88E-01	8.95E-01	-	-
1368472_at	Celsr3	cadherin, EGF LAG seven-pass G-type receptor 3 (flamingo homolog, Droso	83466	Rn.14558	NM_031320	2.28	2.28	2.29	2.28	2.29	2.27	1.00	down	5.95E-01	8.95E-01	-	-
1393289_at	---	---	---	Rn.20373	AI072684	2.40	2.39	2.41	2.39	2.41	2.41	1.00	up	7.42E-01	9.17E-01	-	-
1398229_at	---	---	---	Rn.173252	BF415825	2.40	2.39	2.42	2.39	2.41	2.38	1.00	down	7.86E-01	9.31E-01	-	-
1381161_a_at	---	---	---	Rn.196112	BI301117	2.38	2.37	2.39	2.38	2.39	2.37	1.00	down	6.00E-01	8.95E-01	-	-
1397018_at	---	---	---	Rn.210635	BF399590	2.32	2.32	2.33	2.32	2.33	2.32	1.00	down	4.97E-01	8.95E-01	-	-
1369720_at	Myo1b	myosin Ib	117057	Rn.36339	NM_053986	2.32	2.31	2.33	2.32	2.32	2.31	1.00	down	5.52E-01	8.95E-01	-	-
1375169_at	Myo9b	myosin IXb	25486	Rn.33782	BF404391	2.41	2.41	2.43	2.41	2.42	2.41	1.00	down	7.45E-01	9.17E-01	-	-
1394823_at	---	---	---	---	AW921107	2.35	2.34	2.36	2.34	2.36	2.34	1.00	down	6.65E-01	8.99E-01	-	-
1392088_at	---	---	---	Rn.210607	BF399382	2.32	2.31	2.33	2.32	2.32	2.31	1.00	down	6.27E-01	8.95E-01	-	-
1393181_at	Nfasc	neurofascin	116690	Rn.3048	BG663084	2.32	2.31	2.33	2.32	2.32	2.31	1.00	down	5.75E-01	8.95E-01	-	-
1382295_at	---	---	---	Rn.149169	AW529753	2.32	2.31	2.32	2.31	2.32	2.31	1.00	down	6.03E-01	8.95E-01	-	-
1374594_at	LOC363060	similar to RIKEN cDNA 1600029D21	363060	Rn.39346	AI599133	2.35	2.34	2.35	2.34	2.35	2.34	1.00	down	5.39E-01	8.95E-01	-	-
1391920_at	RGD1564722	similar to C19orf36 protein	362832	Rn.11739	AA964213	2.31	2.30	2.32	2.31	2.31	2.30	1.00	down	5.85E-01	8.95E-01	-	-
1393018_at	---	---	---	---	AI071984	2.36	2.34	2.37	2.35	2.35	2.38	1.00	up	7.68E-01	9.24E-01	-	-
1397455_at	---	---	---	Rn.148135	BF389525	2.25	2.24	2.25	2.24	2.25	2.24	1.00	down	4.92E-01	8.95E-01	-	-
1368911_at	Kcnj8	potassium inwardly-rectifying channel, subfamily J, member 8	25472	Rn.118306	AB043636	2.42	2.42	2.43	2.41	2.43	2.41	1.00	down	6.31E-01	8.95E-01	-	-
1370733_at	Lipogenin	Lipogenin	252964	Rn.212748	AY057076	2.30	2.30	2.31	2.30	2.30	2.29	1.00	down	5.24E-01	8.95E-01	-	-
1394034_at	---	---	---	---	AI764372	2.29	2.28	2.30	2.29	2.28	2.28	1.00	down	5.33E-01	8.95E-01	-	-
1387749_at	Cd79b	Cd79b molecule, immunoglobulin-associated beta	171055	Rn.62607	NM_133533	2.37	2.36	2.38	2.37	2.38	2.35	1.00	down	7.15E-01	9.10E-01	-	-
1383567_at	---	---	---	Rn.221955	BI290183	2.29	2.28	2.29	2.29	2.29	2.28	1.00	down	5.47E-01	8.95E-01	-	-
1395204_at	---	---	---	Rn.119954	BM390675	2.69	2.65	2.71	2.68	2.70	2.66	1.00	down	8.78E-01	9.62E-01	-	-
1388047_at	Vom2r-ps45	vomeronasal 2 receptor, pseudogene 45	286982	Rn.10811	AF016183	2.53	2.51	2.56	2.49	2.59	2.50	1.00	down	9.25E-01	9.78E-01	-	-
1395317_at	---	---	---	Rn.140940	BF409510	2.30	2.30	2.30	2.30	2.30	2.29	1.00	down	4.27E-01	8.95E-01	-	-
1387923_at	Rnf112	ring finger protein 112	24916	Rn.7544	AF054586	2.28	2.28	2.29	2.28	2.29	2.28	1.00	down	5.02E-01	8.95E-01	-	-
1397993_at	---	---	---	Rn.61389	BF404649	2.32	2.31	2.33	2.32	2.33	2.31	1.00	down	6.13E-01	8.95E-01	-	-
1367952_at	Lrp2	low density lipoprotein-related protein 2	29216	Rn.26430	NM_030827	11.89	12.01	11.89	11.91	11.83	12.03	1.00	down	9.62E-01	9.89E-01	-	-
1376326_at	---	---	---	Rn.62778	BF404375	2.38	2.36	2.39	2.38	2.38	2.36	1.00	down	7.20E-01	9.11E-01	-	-
1379290_at	LOC300963	similar to centrosome protein Cep63	300963	Rn.198215	BI294016	6.50	6.60	5.48	6.83	5.34	6.42	1.00	up	9.95E-01	9.98E-01	-	-
1395804_at	LOC361016	Similar to RIKEN cDNA 4933406L09	361016	Rn.203376	BE109618	2.25	2.24	2.25	2.24	2.25	2.24	1.00	down	5.26E-01	8.95E-01	-	-
1396043_at	---	---	---	---	AW620327	2.55	2.54	2.57	2.55	2.58	2.54	1.00	up	7.97E-01	9.35E-01	-	-
1381957_at	---	---	---	---	AW529176	2.32	2.31	2.32	2.31	2.32

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)				REG	MTC
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval		
1383805_at	---	---	---	---	BG666454	2.33	2.32	2.33	2.32	2.33	2.32	1.00	down	5.94E-01	8.95E-01	-	-
1387603_at	Klrc2	killer cell lectin-like receptor subfamily C, member 2	29684	Rn.9894	NM_019261	2.32	2.31	2.33	2.32	2.33	2.31	1.00	down	7.39E-01	9.16E-01	-	-
1380981_at	Stxn2	Stonin 2	314349	Rn.199702	AW534519	2.58	2.57	2.59	2.57	2.58	2.58	1.00	down	6.91E-01	9.05E-01	-	-
1380851_at	Sema3f	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (se	315996	Rn.205616	BF417256	2.26	2.25	2.26	2.26	2.26	2.25	1.00	down	5.18E-01	8.95E-01	-	-
1371271_at	Olr416	olfactory receptor 416	296678	Rn.143025	U50947	2.29	2.29	2.30	2.29	2.29	2.28	1.00	down	5.29E-01	8.95E-01	-	-
1394922_at	---	---	---	Rn.154094	AI716205	2.28	2.27	2.29	2.28	2.28	2.27	1.00	down	5.30E-01	8.95E-01	-	-
1391907_at	Nags	N-acetylglutamate synthase	303563	Rn.23912	AI030790	2.28	2.27	2.29	2.27	2.28	2.27	1.00	down	6.51E-01	8.96E-01	-	-
1394402_at	---	---	---	---	BG381031	2.33	2.32	2.33	2.32	2.33	2.31	1.00	down	5.96E-01	8.95E-01	-	-
1395627_at	---	---	---	---	BF401766	2.37	2.36	2.38	2.37	2.37	2.35	1.00	down	7.19E-01	9.11E-01	-	-
1385257_at	LOC690206	hypothetical protein LOC690206	690206	Rn.126025	AI145717	2.37	2.36	2.38	2.37	2.38	2.36	1.00	down	6.95E-01	9.06E-01	-	-
1378174_at	---	---	---	---	BI274989	2.30	2.29	2.31	2.30	2.31	2.29	1.00	down	6.72E-01	9.01E-01	-	-
1393147_at	Clca5	chloride channel calcium activated 5	308016	Rn.48629	AW533569	2.31	2.31	2.33	2.31	2.32	2.30	1.00	down	6.42E-01	8.95E-01	-	-
1372989_at	Zdhhc14	zinc finger, DHHC-type containing 14	499014	Rn.18327	BI296586	2.43	2.43	2.47	2.44	2.46	2.43	1.00	up	8.41E-01	9.50E-01	-	-
1398563_at	---	---	---	Rn.208383	BE115879	2.76	2.70	2.88	2.91	2.78	2.64	1.00	down	9.73E-01	9.92E-01	-	-
1379875_at	---	---	---	Rn.208615	AA957406	2.31	2.31	2.32	2.31	2.32	2.30	1.00	down	5.39E-01	8.95E-01	-	-
1392022_at	---	---	---	Rn.156715	BF390674	2.52	2.52	2.52	2.52	2.55	2.51	1.00	up	7.81E-01	9.29E-01	-	-
1394799_at	---	---	---	Rn.205623	AI716831	2.28	2.27	2.28	2.27	2.28	2.27	1.00	down	4.05E-01	8.95E-01	-	-
1389942_at	Pqcp	Polyglutamine-containing protein	314329	Rn.15682	BF408366	2.26	2.26	2.27	2.26	2.26	2.26	1.00	down	4.57E-01	8.95E-01	-	-
1371252_at	Socs1	suppressor of cytokine signaling 1	252971	Rn.82754	BE100794	2.28	2.28	2.29	2.28	2.28	2.28	1.00	down	5.46E-01	8.95E-01	-	-
1385812_at	---	---	---	Rn.208137	BE110833	2.41	2.40	2.42	2.41	2.42	2.40	1.00	down	6.65E-01	8.99E-01	-	-
1380608_at	Hdac10	histone deacetylase 10	362981	Rn.107028	BM389241	2.34	2.33	2.35	2.34	2.32	2.32	1.00	down	7.03E-01	9.07E-01	-	-
1398053_at	---	---	---	Rn.209326	BF387612	2.42	2.40	2.43	2.41	2.43	2.40	1.00	down	7.94E-01	9.34E-01	-	-
1382066_at	R3hdm2	R3H domain containing 2	362894	Rn.203556	AI549105	2.31	2.30	2.31	2.31	2.31	2.30	1.00	down	3.23E-01	8.95E-01	-	-
1381856_at	---	---	---	---	BE102880	2.34	2.34	2.35	2.34	2.35	2.33	1.00	down	6.77E-01	9.02E-01	-	-
1385160_at	DC691926 /// Stab	similar to Stabilin-2 precursor (Hyaluronan receptor for endocytosis) /// stabili	282580 /// 691926	Rn.162931	BF401567	2.30	2.29	2.31	2.30	2.30	2.29	1.00	down	5.65E-01	8.95E-01	-	-
1397534_at	---	---	---	Rn.49800	AW918914	2.39	2.39	2.40	2.39	2.40	2.38	1.00	down	6.37E-01	8.95E-01	-	-
1381901_at	RGD1563109	RGD1563109	499586	Rn.203239	BE108013	2.31	2.30	2.31	2.30	2.31	2.30	1.00	down	4.39E-01	8.95E-01	-	-
1382608_at	Actl6b	actin-like 6B	288563	Rn.44972	BI281712	2.29	2.28	2.29	2.28	2.29	2.28	1.00	down	5.82E-01	8.95E-01	-	-
1387073_at	Snap25	synaptosomal-associated protein 25	25012	Rn.107689	NM_030991	2.33	2.31	2.33	2.31	2.35	2.31	1.00	up	8.17E-01	9.41E-01	-	-
1395453_at	RGD1560871	similar to plexin 1	362398	---	BF417952	2.29	2.28	2.29	2.28	2.29	2.27	1.00	down	6.43E-01	8.95E-01	-	-
1369089_at	Pkcg	protein kinase C, gamma	24681	Rn.9747	NM_012628	2.27	2.26	2.28	2.27	2.27	2.26	1.00	down	5.37E-01	8.95E-01	-	-
1382231_at	---	---	---	---	BF417649	2.33	2.33	2.33	2.32	2.33	2.32	1.00	down	3.63E-01	8.95E-01	-	-
1380080_at	Hey1	Hairy/enhancer-of-split related with YRPW motif 1	155437	Rn.98202	BE107815	2.37	2.37	2.38	2.37	2.38	2.36	1.00	down	6.07E-01	8.95E-01	-	-
1383493_at	---	---	---	Rn.167298	BE102202	2.37	2.35	2.39	2.36	2.39	2.35	1.00	down	8.68E-01	9.59E-01	-	-
1369901_at	Tubb3	tubulin, beta 3	246118	Rn.43958	NM_139254	2.35	2.34	2.35	2.35	2.35	2.33	1.00	down	6.29E-01	8.95E-01	-	-
1371165_a_at	Atp2a3	ATPase, Ca++ transporting, ubiquitous	25391	Rn.9920	AF458230	2.25	2.24	2.25	2.24	2.25	2.24	1.00	down	5.22E-01	8.95E-01	-	-
1397509_x_at	Rhox9	reproductive homeobox 9	298352	Rn.144519	BI289049	2.49	2.47	2.51	2.48	2.53	2.45	1.00	down	9.09E-01	9.72E-01	-	-
1382865_at	Tsga14	testis specific, 14	500069	Rn.162740	BM390858	2.48	2.48	2.48	2.47	2.50	2.47	1.00	up	7.63E-01	9.23E-01	-	-
1385435_at	Slc36a3	solute carrier family 36 (proton/amino acid symporter), member 3	303148	Rn.75959	BF412368	2.30	2.29	2.31	2.30	2.31	2.29	1.00	down	6.27E-01	8.95E-01	-	-
1380491_at	---	---	---	---	BF402629	2.37	2.36	2.37	2.36	2.37	2.35	1.00	down	6.89E-01	9.04E-01	-	-
1384051_at	---	---	---	Rn.26823	BF390066	2.34	2.32	2.34	2.33	2.34	2.33	1.00	down	6.53E-01	8.97E-01	-	-
1386340_at	---	---	---	---	BG057552	2.39	2.38	2.40	2.39	2.41	2.37	1.00	down	7.99E-01	9.35E-01	-	-
1397387_at	C1d	nuclear DNA binding protein	289810	Rn.102095	AA901254	2.42	2.41	2.42	2.41	2.42	2.41	1.00	down	4.13E-01	8.95E-01	-	-
1369440_at	Abcg8	ATP-binding cassette, sub-family G (WHITE), member 8	155192	Rn.161892	NM_130414	2.33	2.33	2.34	2.33	2.34	2.32	1.00	down	6.62E-01	8.98E-01	-	-
1381485_at	LOC683156	similar to testicular serine protease 2	683156	---	AF418149	2.26	2.26	2.27	2.26	2.27	2.26	1.00	down	5.53E-01	8.95E-01	-	-
1380882_at	---	---	---	Rn.209792	BF390857	2.49	2.48	2.49	2.48	2.49	2.48	1.00	down	4.95E-01	8.95E-01	-	-
1398258_at	Apod	apolipoprotein D	25239	Rn.11339	NM_012777	2.30	2.29	2.32	2.30	2.31	2.29	1.00	down	7.54E-01	9.20E-01	-	-
1375975_at	Ankrd26	ankyrin repeat domain 26	312667	Rn.198700	BF398567	2.36	2.35	2.36	2.35	2.36	2.35	1.00	down	5.61E-01	8.95E-01	-	-
1370658_a_at	St18	suppression of tumorigenicity 18	266680	Rn.91311	AF031942	2.26	2.25	2.26	2.25	2.26	2.25	1.00	down	5.39E-01	8.95E-01	-	-
1369164_a_at	Trpc4	transient receptor potential cation channel, subfamily C, member 4	84494	Rn.10853	AF288407	2.45	2.43	2.47	2.46	2.45	2.42	1.00	down	8.49E-01	9.53E-01	-	-
1389221_at	Mmd2	monocyte to macrophage differentiation-associated 2	304301	Rn.154557	BI286275	2.44	2.44	2.45	2.44	2.45	2.43	1.00	down	6.87E-01	9.04E-01	-	-
1385654_at	Sohlh1	spermatogenesis and oogenesis specific basic helix-loop-helix 1	362085	Rn.43879	AI548388	2.29	2.29	2.30	2.29	2.29	2.28	1.00	down	5.00E-01	8.95E-01	-	-
1385290_at	Tmco5a	transmembrane and coiled-coil domains 5A	499865	Rn.162673	BE119379	2.26	2.25	2.26	2.25	2.26	2.25	1.00	down	4.63E-01	8.95E-01	-	-
1392348_at	684392 /// LOC68	hypothetical protein LOC684392 /// similar to SON protein	684392 /// 685337	Rn.145078	BF418379	2.54	2.44	2.49	2.47	2.54	2.46	1.00	up	9.34E-01	9.81E-01	-	-
1382510_at	---	---	---	Rn.170932	BE105050	2.30	2.29	2.31	2.29	2.30	2.29	1.00	down	5.85E-01	8.95E-01	-	-
1368601_at	Slc6a3	solute carrier family 6 (neurotransmitter transporter, dopamine), member 3	24898	Rn.10093	M80233	2.35	2.35	2.36	2.35	2.37	2.34	1.00	down	7.11E-01	9.10E-01	-	-
1392002_at	Pcdhb22	protocadherin beta 22	307486	---	AI411977	2.38	2.38	2.39	2.38	2.39	2.38	1.00	up	5.09E-01	8.95E-01	-	-
1388010_at	---	---	---	Rn.160145	AF303035	2.41	2.40	2.41	2.40	2.41	2.39	1.00	down	6.34E-01	8.95E-01	-	-
1397732_at	---	---	---	Rn.209232	BF408724	2.25	2.24	2.25	2.24	2.25	2.24	1.00	down	5.38E-01	8.95E-01	-	-
1379240_at	---	---	---	---	AA893453	2.33	2.32	2.34	2.32	2.34	2.31	1.00	down	7.30E-01	9.14E-01	-	-
1369623_at	Morp1	morphine related protein-1	64548	Rn.127787	NM_022613	2.28	2.28	2.29	2.28	2.28	2.27	1.00	down	5.08E-01	8.95E-01	-	-
1390660_at	Tbx2	T-box 2	303398	Rn.38282	BE105596	2.30	2.29	2.31	2.30	2.31	2.29	1.00	down	6.72E-01	9.01E-01	-	-
1387302_at	Adcyap1r1	adenylate cyclase activating polypeptide 1 (pituitary) receptor type I	24167	Rn.88408	D16465	2.26	2.26	2.27	2.26	2.26	2.25	1.00	down	4.48E-01	8.95E-01	-	-
1379766_at	Sla	Src-like adaptor	338477	Rn.35223	AI500952	2.32	2.31	2.32	2.31	2.32	2.31	1.00	down	5.87E-01	8.95E-01	-	-
1397019_at	---	---	---	Rn.59637	BF400760	2.34	2.34	2.35	2.34	2.35	2.34	1.00	down	6.00E-01	8.95E-01	-	-
1387640_at	Fgf15	fibroblast growth factor 15	170582	Rn.81230	NM_130753	2.39	2.38	2.40	2.39	2.39	2.38	1.00	down	5.65E-01	8.95E-01	-	-
1396136_at	---	---	---	Rn.169944	BF386241	2.41	2.40	2.43	2.40	2.48	2.37	1.00	up	9.26E-01	9.79E-01	-	-
1376092_at	---	---	---	Rn.138001	BF396614	2.29	2.29	2.30	2.29	2.29	2.28	1.00	down	4.77E-01	8.95E-01	-	-
1390387_at	---	---	---	Rn.7922	BF396636	5.48	6.50	6.84	6.35	5.95	6.53	1.00	up	9.94E-01	9.98E-01	-	-
1368913_at	Csn2	casein beta	29173	Rn.10745	NM_017120	2.27	2.26	2.27	2.27	2.27	2.26	1.00	down	5.49E-01	8.95E-01	-	-
1378371_at	A2bp1	ataxin 2 binding protein 1	302920	Rn.92540	BE099730	2.36	2.35	2.36	2.35	2.36	2.35	1.00	down	4.95E-01	8.95E-01	-	-
1369750_at	Tshb	thyroid stimulating hormone, beta	25653	Rn.9966	M10902	2.41	2.40	2.42	2.40	2.42	2.40	1.00	down	7.58E-01	9.21E-01	-	-
1370169_at	Csde1	cold shock domain containing E1, RNA binding	117180	Rn.3562	BI289608	11.28	11.29	11.48	11.18	11.29	11.59	1.00	up	9.82E-01	9.95E-01	-	-
1390842_at	---	---	---	Rn.210117	BF394117	2.28	2.27	2.29	2.27	2.28	2.27	1.00	down	6.32E-01	8.95E-01	-	-
1380880_at	---	---	---	Rn.172985	BF400875	2.34	2.33	2.34	2.34	2.36	2.33	1.00	up	7.57E-01	9.21E-01	-	-
1390922_at	---	---	---	Rn.203615	AA957926	2.32	2.31	2.33	2.32	2.32	2.32	1.00	down	6.61E-01	8.98E-01	-	-
1374912_at	Klf2c	kinesin family member 2C	171529	Rn.152404	BI274467	2.36	2.35	2.37	2.36	2.37	2.35	1.00	down	6.46E-01	8.95E-01	-	-
1396431_at	---	---	---	Rn.211308	BF410221	2.29	2.28	2.30	2.29	2.30	2.29	1.00	down	6.44E-01	8.95E-01	-	-
1384861_at	---	---	---	Rn.15175	AW529591	2.29	2.28	2.30	2.28	2.29	2.28	1.00	down	5.41E-01	8.95E-01	-	-
1368135_at	Ninj2	ninjurin 2	59115	Rn.162768	NM_021595	2.40	2.40	2.41	2.40	2.41	2.40	1.00	down	5.88E-01	8.95E-01	-	-
1368755_at	Clec4f	C-type lectin domain family 4, member f	114598	Rn.9886	NM_053753	2.29	2.28	2.29	2.28	2.29	2.28	1.00	down	5.84E-01	8.95E-01	-	-
1389285_at	---	---	---	Rn.146354	AI229933	2.26	2.25	2.27	2.26	2.26	2.25	1.00	down	5.38E-01	8.95E-01	-	-
1394507_at	---	---	---	---	AI103591	2.34	2.33	2.35	2.33	2.35	2.33	1.00	down	6.83E-01	9.03E-01	-	-
1376105_at	Col14a1	collagen, type XIV, alpha 1	314981	Rn.99441	AI599143	2.34	2.33	2.35	2.34	2.34	2.33	1.00	down	6.70E-01	9.00E-01	-	-
1392151_at	---	---	---	Rn.46139	AW526257	2.40	2.39	2.40	2.40	2.43	2.38	1.00	up	8.35E-01	9.48E-01	-	-
1385180_at	---	---	---	Rn.151573	BF397451	2.44	2.43	2.45	2.43	2.44	2.43	1.00	down	5.94E-01	8.95E-01	-	-
1396643_at	---	---	---	Rn.210554	BF400061	2.33	2.33	2.34	2.33	2.32	2.32	1.00	down	4.78E-01	8.95E-01	-	-
1369422_at	Fap	fibroblast activation protein, alpha	192203	Rn.82756	NM_138850	2.32	2.32	2.33	2.32	2.32	2.31	1.00	down	5.78E-01	8.95E-01	-	-
1374173_at	---	---	---	Rn.3021	AA799841	3.59	3.72	3.52	3.48	3.73	3.61	1.00	down	9.74E-01	9.92E-01	-	-
1397352_at	---	---	---	Rn.133207	BF290961	2.33	2.31	2.33	2.32	2.33	2.31	1.00	down	7.25E-01	9.13E-01	-	-
1373008_x_at	Rtn4r	reticulon 4 receptor	113912	Rn.45686	BF386649	2.39	2.36	2.42	2.37	2.42	2.38	1.00	down	8.85E-01	9.64E-01	-	-
1370635_at	Defb22	defensin beta 22	171412	Rn.67074	AF329091	2.26	2.25	2.26	2.25	2.26	2.25	1.00	down	5.31E-01	8.95E-01	-	-
1382386_at	---	---	---	Rn.207657	AI176317	2.26	2.26	2.26	2.26	2.27	2.26	1.00	up	5.84E-01	8.95E-01	-	-
1384773_at	Ubtd2	ubiquitin domain containing 2	287178	Rn.95607	AI044323	2.37	2.36	2.36	2.36	2.37	2.35	1.00	down	5.47E-01	8.95E-01	-	-
1387449_at	Tshr	thyroid stimulating hormone receptor	25360	Rn.87913	NM_012888	2.43	2.41	2.43	2.42	2.44	2.40	1.00	down	8.12E-01	9.39E-01	-	-
1386387_at	Sox9	SRY-box containing gene 9	140586	Rn.95086	BE119829	2.43	2.42	2.46	2.43	2.45	2.42	1.00	down	8.45E-01	9.52E-01	-	-
1385600_at	---	---	---	Rn.216996	BF404816	2.45	2.44	2.45	2.46	2.45	2.44	1.00	up	6.40E-01	8.95E-01	-	-
1397398_at	---	---	---	Rn.208482	BG376725	2.27	2.26	2.27	2.26	2.27	2.26	1.00	down	5.22E-01	8.95E-01	-	-
1378460_at	---	---	---	Rn.208218	BG376867	2.38	2.36	2.39	2.37	2.38	2.37	1.00	down	7.14E-01	9.10E-01	-	-
1395000_at	---	---	---	Rn.176504	BG666908	2.38	2.37	2.39	2.37	2.39	2.36	1.00	down	7.42E-01	9.17E-01	-	-
1370546_at	Unc13c	unc-13 homolog C (C. elegans)	286931	Rn.11278	U75361	2.27	2.26	2.28	2.26	2.27	2.26	1.00	down	5.94E-01	8.95E-01	-	-
1384884_at	RGD1307595	similar to RIKEN cDNA 1700018B24	295019	Rn.46896	AW528484	2.32	2.31	2.33	2.32	2.33	2.31	1.00	down	6.55E-01	8.97E-01	-	-
1376063_at	Wnt6	wingless-type MMTV integration site family, member 6	316526	Rn.22149	AI599019	2.46	2.44	2.46	2.46	2.47	2.43	1.00	down	7.99E-01	9.35E-01	-	-
1395049_at	---	---	---	Rn.172519	BF391014	2.30	2.28	2.31	2.29	2.32	2.28	1.00	up	8.32E-01	9.47E-01	-	-
1387199_a_at	Arhgef9	Cdc42 guanine nucleotide exchange factor (GEF) 9	66013	Rn.163449	NM_023957	2.29	2.29	2.30	2.29	2.29	2.28	1.00	down	4.46E-01	8.95E-01	-	-
1383792_at	Syt1	synaptotagmin-like 1	297872	Rn.16862	BG378274	2.29	2.28	2.30	2.31	2.29	2.28	1.00	up	7.43E-01	9.17E-01	-	-
1369398_at	Naaladl1	N-acetylated alpha-linked acidic dipeptidase-like 1	83568	Rn.10856	NM_031759	2.35	2.34	2.36	2.34	2.35	2.33	1.00	down	6.61E-01	8.98E-01	-	-
1374800_at	---	---	---	Rn.66488	BI303627	9.31	9.08	9.20	9.05	8.91	9.64	1.00	up	9.89E-01	9.96E-01	-	-
1388205_at	---	---	---	Rn.32073	BI301318	2.39	2.38	2.40	2.38	2.40	2.37	1.00	down	7.84E-01	9.30E-01	-	-
1394407_at	---	---	---	Rn.28162	AW530287	3.76	4.53	4.18	4.13	3.87	4.46	1.00	down	9.91E-01	9.97E-01	-	-
1397889_at	---	---	---	---	BF409130	2.32	2.32	2.32	2.32	2.31	2.31	1.00	down	4.32E-01	8.95E-01	-	-
1369891_at	Batf3	basic leucine zipper transcription factor, ATF-like 3	60462	Rn.211982	NM_021865	2.25	2.25	2.26	2.25	2.26	2.24	1.00	down	5.26E-01	8.95E-01	-	-
1370702_at	Gabrr3	gamma-aminobutyric acid (GABA) receptor, rho 3	192258	Rn.10670	D50671	2.34	2.33	2.35	2.34	2.35	2.33	1.00	down	6.39E-01	8.95E-01	-	-
1389898_at	B4galt5	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 5	362275	Rn.107246	AA944170	2.30	2.30	2.30	2.30	2.29	2.29	1.00	down	4.49E-01	8.95E-01	-	-
1390925_a_at	Igsf3	immunoglobulin superfamily, member 3	295325	---	AI043758	2.46	2.43	2.44	2.43	2.49	2.42	1.00	up	8.83E-01	9.64E-01	-	-
1391930_at	---	---	---	---	AI408871	2.27	2.27	2.28	2.27	2.27	2.26	1.00	down	5.03E-01	8.95E-01	-	-
1391140_at	---	---	---	Rn.156248	BF403952	2.44	2.43	2.44	2.43	2.44	2.42	1.00	down	5.72E-01	8.95E-01	-	-
1369881_at	Gja6	gap junction protein, alpha 6	54256	Rn.209042	NM_019308	2.30	2.28	2.30	2.29	2.29	2.28	1.00	down	5.65E-01	8.95E-01	-	-
1369391_at	Grm8	glutamate receptor, metabotropic 8	60590	Rn.44420	NM_022202	2.29	2.28	2.29	2.28	2.29	2.27	1.00	down	6.29E-01	8.95E-01	-	-
1382451_at	Hebp2	heme binding protein 2	308632	Rn.106778	BM385477	2.31	2.30	2.31	2.30	2.32	2.29	1.00	down	7.19E-01	9.11E-01	-	-
1387166_at	Aipl1	aryl hydrocarbon receptor-interacting protein-like 1	59110	Rn.102037	NM_021590	2.39	2.37	2.39	2.38	2.39	2.37	1.00	down	7.36E-01	9.15E-01	-	-
1387333_at	Il5ra	interleukin 5 receptor, alpha	114103	Rn.67068	NM_053645	2.26	2.26	2.27	2.26	2.26	2.25	1.00	down	5.32E-01	8.95E-01	-	-
1391299_at	Itsn2	intersectin 2	313934	Rn.37673	AW251367	2.41	2.40	2.43	2.41	2.42	2.40	1.00	down	6.99E-01	9.07E-01	-	-
1391327_at	/// LOC687140 ///	similar to Reticulocalbin-1 precursor /// similar to Reticulocalbin-1 precursor ///	5 /// 687140 /// 68	Rn.109846	BF394271	2.13	2.14	2.13	2.13	2.13	2.13	1.00	down	3.96E-01	8.95E-01	-	-
1392880_at	---	---	---	---	BG665051	2.42	2.41	2.44	2.42	2.45	2.40	1.00	down	8.56E-01	9.55E-01	-	-
1396641_at	316460 /// LOC68	similar to CG18437-PA /// similar to CG18437-PA	316460 /// 689998	Rn.201770	BF394819	2.45	2.42	2.46	2.45	2.46	2.41	1.00	down	8.46E-01	9.52E-01	-	-
1375713_at	Hes5	Hairy and enhancer of split 5 (Drosophila)	79225	Rn.22422	AI599432	2.33	2.33	2.34	2.33	2.33	2.32	1.00	down	5.05E-01	8.95E-01	-	-
1379985_at	---	---	---	Rn.147509	AW530768	2.28	2.27	2.29	2.28	2.28	2.29	1.00	up	5.85E-01	8.95E-01	-	-
1387958_at	Akr1c18	aldo-keto reductase family 1, member C18	171516	Rn.10030	L32601	2.28	2.27	2.28	2.27	2.28	2.27	1.00	down	5.19E-01	8.95E-01	-	-
1388142_at	Vcan	versican	114122	Rn.35666	AA850991	2.43	2.41	2.44	2.42	2.43	2.41	1.00	down	7.94E-01	9.34E-01	-	-
1397650_at	---	---	---	Rn.50669	BF403165	2.38	2.37	2.38	2.37	2.38	2.37	1.00	down	3.76E-01	8.95E-01	-	-
1396632_at	---	---	---	Rn.173806	BF418074	2.30	2.29	2.30	2.30	2.29	2.29	1.00	down	5.09E-01	8.95E-01	-	-
1375084_at	Serinc2	serine incorporator 2	313057	Rn.144273	BF419780	2.33	2.32	2.34	2.32	2.34	2.31	1.00	down	7.37E-01	9.15E-01	-	-
1380849_at	---	---	---	Rn.50203	BE110106	2.28	2.27	2.29	2.28	2.28	2.27	1.00	down	5.43E-01	8.95E-01	-	-
1369584_at	Socs3	suppressor of cytokine signaling 3	89829	Rn.127801	NM_053565	2.27	2.26	2.28	2.27	2.26	2.27	1.00	down	5.16E-01	8.95E-01	-	-
1378522_at	---	---	---	Rn.200267	BG373062	2.98	3.17	3.15	3.09	3.29	2.93	1.00	up	9.79E-01	9.94E-01	-	-
1382145_at	Slc7a4	solute carrier family 7 (cationic amino acid transporter, y+ system), member 4	303787	Rn.47738	AW531444	2.34	2.35	2.37	2.35	2.36	2.34	1.00	down	7.02E-01	9.07E-01	-	-
1377567_at	RGD1565283	similar to novel protein	498274	Rn.38011	AW434728	2.46	2.44	2.48	2.46	2.49	2.45	1.00	up	8.62E-01	9.57E-01	-	-
1388263_at	Kcna6	potassium voltage gated channel, shaker related subfamily, member 6	64358	Rn.162791	AJ276137	2.31	2.30	2.31	2.30	2.31	2.30	1.00	down	5.40E-01	8.95E-01	-	-
1396953_at	---	---	---	Rn.210816	BF404609	2.47	2.45	2.49	2.47	2.49	2.47	1.00	up	8.16E-01	9.41E-01	-	-
1378597_at	---	---	---	Rn.210886	BF403721	2.37	2.37	2.37	2.37	2.37	2.36	1.00	down	5.95E-01	8.95E-01	-	-
1397494_at	---	---	---	Rn.216947	BF401060	2.33	2.32	2.34	2.33	2.34	2.32	1.00	down	7.33E-01	9.14E-01	-	-
1378130_at	Rnf12	ring finger protein, transmembrane 2	304521	Rn.28670	AI145935	2.45	2.45	2.46	2.47	2.46	2.45	1.00	up	5.84E-01	8.95E-01	-	-
1387044_at	Gpha2	glycoprotein hormone alpha 2	171158	Rn.22078	AF260741	2.24	2.24	2.25	2.24	2.25	2.24	1.00	down	5.55E-01	8.95E-01	-	-
1

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1379016_at	---	---	---	Rn.155286	BF412694	2.46	2.45	2.46	2.45	2.46	2.44	1.00	down	6.37E-01	8.95E-01	-	-
1367797_at	Men1	multiple endocrine neoplasia 1	29417	Rn.6775	NM_019208	2.72	2.61	2.61	2.50	2.62	2.84	1.00	up	9.77E-01	9.93E-01	-	-
1386208_at	---	---	---	Rn.135595	AI013238	2.44	2.40	2.43	2.41	2.42	2.45	1.00	up	8.62E-01	9.57E-01	-	-
1383773_at	---	---	---	Rn.13732	AI136301	2.24	2.24	2.25	2.24	2.25	2.23	1.00	down	5.47E-01	8.95E-01	-	-
1392070_at	Lix1l	Lix1 homolog (mouse)-like	499677	Rn.3632	AI112117	2.36	2.36	2.37	2.36	2.36	2.36	1.00	down	4.41E-01	8.95E-01	-	-
1379860_at	---	---	---	Rn.153604	AW527212	2.30	2.29	2.31	2.30	2.31	2.29	1.00	down	6.81E-01	9.03E-01	-	-
1371125_at	Kif2a	kinesin family member 2A	84391	Rn.218992	BF564995	2.43	2.43	2.44	2.43	2.43	2.42	1.00	down	4.65E-01	8.95E-01	-	-
1379872_at	---	---	---	Rn.216862	BG667371	2.25	2.24	2.25	2.25	2.25	2.24	1.00	down	5.03E-01	8.95E-01	-	-
1381475_at	Sdk2	sidekick homolog 2 (chicken)	360652	Rn.49029	BE108787	2.46	2.46	2.47	2.46	2.46	2.46	1.00	down	5.22E-01	8.95E-01	-	-
1369616_at	Fgf22	fibroblast growth factor 22	170579	Rn.198777	NM_130751	2.30	2.29	2.31	2.30	2.30	2.29	1.00	down	5.74E-01	8.95E-01	-	-
1368860_at	Phlda1	pleckstrin homology-like domain, family A, member 1	29380	Rn.40778	NM_017180	3.04	3.03	3.04	3.04	3.05	3.04	1.00	up	5.84E-01	8.95E-01	-	-
1378331_at	Mesdc2	Mesoderm development candidate 2	308796	Rn.41045	AI703716	2.35	2.35	2.36	2.35	2.36	2.34	1.00	down	6.01E-01	8.95E-01	-	-
1398043_at	rnase11 /// Rnase1	ribonuclease, RNase A family, 11 (non-active) /// ribonuclease, RNase A famil	364302 /// 497651	Rn.51424	BE110332	2.31	2.30	2.32	2.31	2.32	2.30	1.00	down	6.62E-01	8.98E-01	-	-
1378440_at	---	---	---	Rn.156139	BM385137	2.29	2.28	2.29	2.28	2.29	2.28	1.00	down	5.38E-01	8.95E-01	-	-
1373597_at	Pop7	processing of precursor 7, ribonuclease P/MRP subunit (S. cerevisiae)	288564	Rn.16344	AI102689	5.38	5.78	5.44	5.55	5.59	5.48	1.00	up	9.81E-01	9.94E-01	-	-
1394885_at	RGD1565482	RGD1565482	291535	Rn.162374	AI105003	2.33	2.32	2.34	2.33	2.34	2.32	1.00	up	7.05E-01	9.08E-01	-	-
1369132_at	Slc18a2	solute carrier family 18 (vesicular monoamine), member 2	25549	Rn.9686	M97381	2.29	2.28	2.30	2.29	2.29	2.28	1.00	down	5.21E-01	8.95E-01	-	-
1396858_at	---	---	---	Rn.206502	BF412454	2.31	2.31	2.32	2.31	2.32	2.30	1.00	down	6.95E-01	9.06E-01	-	-
1370761_at	Olr1361	olfactory receptor 1361	287000	Rn.44381	M64377	2.28	2.27	2.29	2.28	2.28	2.27	1.00	down	6.03E-01	8.95E-01	-	-
1391490_at	---	---	---	Rn.207865	BF394332	2.26	2.25	2.27	2.26	2.26	2.25	1.00	down	5.67E-01	8.95E-01	-	-
1372750_at	---	---	---	Rn.2743	AI102517	2.26	2.25	2.26	2.25	2.26	2.24	1.00	down	6.63E-01	8.99E-01	-	-
1397005_at	---	---	---	Rn.208083	BF393900	2.34	2.33	2.35	2.34	2.35	2.33	1.00	down	6.38E-01	8.95E-01	-	-
1396707_at	---	---	---	Rn.49945	BE108582	2.40	2.39	2.41	2.39	2.41	2.38	1.00	down	7.30E-01	9.14E-01	-	-
1390726_at	---	---	---	Rn.205659	BF393120	2.33	2.32	2.33	2.32	2.34	2.31	1.00	down	7.18E-01	9.11E-01	-	-
1376469_at	---	---	---	Rn.210005	BF392632	2.33	2.32	2.33	2.32	2.33	2.32	1.00	down	5.42E-01	8.95E-01	-	-
1390276_at	---	---	---	Rn.176869	BI296669	2.34	2.32	2.33	2.33	2.34	2.32	1.00	down	5.97E-01	8.95E-01	-	-
1379599_at	---	---	---	Rn.166230	AW142370	2.29	2.29	2.30	2.29	2.30	2.28	1.00	down	6.18E-01	8.95E-01	-	-
1391830_at	Cpne8	copine VIII	362988	Rn.11746	AI059204	2.63	2.62	2.65	2.62	2.64	2.63	1.00	down	7.56E-01	9.20E-01	-	-
1374248_at	Mybpc1	myosin binding protein C, slow type	362867	Rn.9153	BM389619	2.30	2.29	2.30	2.29	2.30	2.29	1.00	down	6.06E-01	8.95E-01	-	-
1395916_at	F8	coagulation factor VIII, procoagulant component	302470	Rn.95452	BF522383	2.35	2.34	2.35	2.35	2.35	2.34	1.00	down	5.99E-01	8.95E-01	-	-
1368371_at	Kcnq1	potassium voltage-gated channel, subfamily Q, member 1	84020	Rn.9779	NM_032073	2.42	2.40	2.44	2.41	2.43	2.40	1.00	down	8.14E-01	9.40E-01	-	-
1371141_at	Slc25a27	solute carrier family 25, member 27	85262	Rn.163043	AJ300164	2.36	2.34	2.39	2.35	2.40	2.33	1.00	down	8.97E-01	9.68E-01	-	-
1387688_at	Htr6	5-hydroxytryptamine (serotonin) receptor 6	64354	Rn.10552	L03202	2.29	2.28	2.30	2.29	2.30	2.28	1.00	down	6.22E-01	8.95E-01	-	-
1370772_a_at	Hfe	hemochromatosis	29199	Rn.42931	AF176534	2.35	2.34	2.36	2.35	2.36	2.34	1.00	down	6.46E-01	8.95E-01	-	-
1371157_at	Apob	apolipoprotein B (including Ag(x) antigen)	54225	Rn.33815	M14952	2.32	2.31	2.33	2.31	2.32	2.31	1.00	down	5.23E-01	8.95E-01	-	-
1375746_at	---	---	---	---	AW524548	2.33	2.32	2.33	2.32	2.33	2.31	1.00	down	6.09E-01	8.95E-01	-	-
1394923_at	LOC689619	similar to nuclear receptor interacting protein 2	689619	Rn.209630	AW528728	3.16	3.15	3.17	3.15	3.20	3.14	1.00	up	8.72E-01	9.60E-01	-	-
1385015_at	Zadh2	zinc binding alcohol dehydrogenase, domain containing 2	291403	Rn.12321	BM390024	2.37	2.36	2.38	2.37	2.37	2.36	1.00	down	4.83E-01	8.95E-01	-	-
1371158_at	Epha8	Eph receptor A8	60589	Rn.62934	X59290	2.32	2.31	2.32	2.31	2.32	2.30	1.00	down	6.67E-01	9.00E-01	-	-
1375589_at	Tmem8	transmembrane protein 8 (five membrane-spanning domains)	303004	Rn.21890	BF405194	2.28	2.28	2.29	2.31	2.29	2.26	1.00	up	8.55E-01	9.55E-01	-	-
1379184_at	---	---	---	Rn.137989	BI291332	2.35	2.34	2.36	2.34	2.36	2.33	1.00	down	7.55E-01	9.20E-01	-	-
1374380_at	---	---	---	Rn.146123	BF403474	2.30	2.29	2.31	2.30	2.30	2.29	1.00	down	5.84E-01	8.95E-01	-	-
1381342_at	Parvb	parvin, beta	362973	Rn.16709	BE109825	2.41	2.40	2.42	2.40	2.42	2.40	1.00	down	6.65E-01	8.99E-01	-	-
1381221_at	RGD1311300	similar to T cell receptor V delta 6	364378	Rn.105824	AI012548	2.43	2.42	2.44	2.43	2.46	2.40	1.00	down	8.58E-01	9.56E-01	-	-
1390424_at	---	---	---	Rn.199392	BF285207	2.36	2.36	2.38	2.37	2.38	2.36	1.00	down	7.16E-01	9.10E-01	-	-
1374907_at	Arhgef17	Rho guanine nucleotide exchange factor (GEF) 17	308862	Rn.106856	BI274338	2.40	2.42	2.44	2.42	2.45	2.40	1.00	up	8.45E-01	9.52E-01	-	-
1384064_at	Krt23	keratin 23 (histone deacetylase inducible)	287678	Rn.137736	AI502703	2.52	2.50	2.53	2.52	2.52	2.50	1.00	down	7.45E-01	9.18E-01	-	-
1391408_a_at	LOC684996	similar to chromosome 7 open reading frame 11	684996	Rn.30	AA891753	2.37	2.36	2.36	2.36	2.38	2.36	1.00	up	6.30E-01	8.95E-01	-	-
1369434_at	Dntttip1	Deoxynucleotidyltransferase, terminal, interacting protein 1	171437	Rn.82702	NM_134400	2.44	2.43	2.45	2.44	2.45	2.45	1.00	up	6.53E-01	8.97E-01	-	-
1385112_at	---	---	---	---	BF387696	2.43	2.42	2.44	2.42	2.44	2.41	1.00	down	7.81E-01	9.29E-01	-	-
1368005_at	Itpr3	inositol 1,4,5-trifosphate receptor, type 3	25679	Rn.11242	NM_013138	2.33	2.32	2.33	2.32	2.34	2.32	1.00	up	7.40E-01	9.16E-01	-	-
1387421_at	Kcnip3	Kv channel interacting protein 3, calsenilin	65199	Rn.74239	NM_032462	2.30	2.30	2.31	2.30	2.31	2.29	1.00	down	6.08E-01	8.95E-01	-	-
1379583_at	Afg3l1	AFG3(ATPase family gene 3)-like 1 (S. cerevisiae)	361436	Rn.41391	AI715295	3.14	3.43	2.80	3.20	3.04	3.14	1.00	up	9.87E-01	9.96E-01	-	-
1375765_at	Hpcal4	Hippocalcin-like 4	50872	Rn.34529	BI296503	2.33	2.33	2.34	2.33	2.34	2.32	1.00	down	6.93E-01	9.05E-01	-	-
1382566_at	Il7r	interleukin 7 receptor	294797	Rn.6633	AI071589	2.33	2.32	2.33	2.32	2.33	2.32	1.00	down	5.81E-01	8.95E-01	-	-
1375386_at	---	---	---	Rn.209303	BF406151	2.31	2.30	2.32	2.30	2.31	2.30	1.00	down	6.37E-01	8.95E-01	-	-
1391261_at	---	---	---	Rn.57680	BF394645	2.35	2.34	2.36	2.34	2.35	2.34	1.00	down	6.07E-01	8.95E-01	-	-
1377260_at	---	---	---	Rn.19097	AI170292	2.36	2.35	2.37	2.35	2.37	2.35	1.00	down	7.03E-01	9.07E-01	-	-
1368694_at	Psgb1	pregnancy-specific beta 1-glycoprotein	59313	Rn.42878	NM_021677	2.35	2.35	2.36	2.35	2.36	2.34	1.00	down	6.46E-01	8.95E-01	-	-
1375283_at	Scube1	Signal peptide, CUB domain, EGF-like 1	315174	Rn.8673	AA965236	2.37	2.36	2.37	2.36	2.38	2.36	1.00	down	6.73E-01	9.01E-01	-	-
1369853_at	Neurog3	neurogenin 3	60329	Rn.42927	NM_021700	2.29	2.28	2.29	2.28	2.29	2.28	1.00	down	5.22E-01	8.95E-01	-	-
1387628_at	Tas2r107	taste receptor, type 2, member 107	78981	Rn.48784	NM_023995	2.30	2.29	2.31	2.30	2.30	2.29	1.00	down	6.08E-01	8.95E-01	-	-
1375510_x_at	---	---	---	---	BF419823	2.27	2.27	2.28	2.27	2.27	2.26	1.00	down	5.41E-01	8.95E-01	-	-
1393994_at	Rpl13a	ribosomal protein L13A	317646	Rn.92211	BF522463	2.40	2.39	2.41	2.40	2.40	2.40	1.00	down	6.75E-01	9.01E-01	-	-
1395661_at	---	---	---	Rn.171223	BF388125	2.41	2.39	2.42	2.39	2.41	2.40	1.00	down	7.50E-01	9.19E-01	-	-
1370292_a_at	Crygc	crystallin, gamma C	24277	Rn.81172	J00717	2.36	2.34	2.36	2.35	2.36	2.35	1.00	down	6.98E-01	9.07E-01	-	-
1383036_at	---	---	---	Rn.166786	AI137547	2.49	2.47	2.50	2.48	2.50	2.47	1.00	down	8.20E-01	9.42E-01	-	-
1378513_at	Gmfb	Glia maturation factor, beta	81661	Rn.10454	BF415038	2.36	2.36	2.39	2.39	2.37	2.35	1.00	down	8.30E-01	9.47E-01	-	-
1380506_at	---	---	---	Rn.204009	AI043604	2.32	2.32	2.34	2.32	2.33	2.32	1.00	down	6.43E-01	8.95E-01	-	-
1384880_at	RGD1306704	hypothetical LOC295483	295483	Rn.154487	AW527941	2.29	2.29	2.30	2.29	2.30	2.28	1.00	down	5.35E-01	8.95E-01	-	-
1392395_at	---	---	---	Rn.47023	AW528834	2.50	2.50	2.50	2.49	2.52	2.48	1.00	down	8.21E-01	9.43E-01	-	-
1398003_at	---	---	---	Rn.208670	BF400768	2.39	2.39	2.42	2.41	2.40	2.38	1.00	down	8.13E-01	9.40E-01	-	-
1385816_at	Fam72a	Family with sequence similarity 72, member A	681249	Rn.212623	BI293456	2.42	2.40	2.43	2.41	2.43	2.40	1.00	down	7.92E-01	9.33E-01	-	-
1380571_at	---	---	---	Rn.169298	AW521312	2.38	2.37	2.38	2.37	2.38	2.37	1.00	down	6.24E-01	8.95E-01	-	-
1384779_at	Cplx3	complexin 3	501005	Rn.41338	AI716342	2.36	2.35	2.37	2.35	2.36	2.34	1.00	down	7.11E-01	9.10E-01	-	-
1368974_at	Gucy1a2	guanylate cyclase 1, soluble, alpha 2	66012	Rn.209304	NM_023956	2.32	2.32	2.34	2.32	2.33	2.32	1.00	down	6.44E-01	8.95E-01	-	-
1372492_at	Cldn10	claudin 10	290485	Rn.99994	AI412937	9.52	10.06	9.79	9.63	9.79	9.96	1.00	up	9.87E-01	9.96E-01	-	-
1382212_at	---	---	---	Rn.164647	AI385201	2.35	2.34	2.34	2.35	2.35	2.34	1.00	up	5.92E-01	8.95E-01	-	-
1387281_a_at	Prick	pregnancy upregulated non-ubiquitously expressed CaM kinase	29660	Rn.11178	D86556	2.31	2.31	2.32	2.31	2.34	2.30	1.00	up	8.03E-01	9.37E-01	-	-
1397451_at	---	---	---	Rn.16311	BI293050	2.32	2.31	2.33	2.31	2.32	2.31	1.00	down	6.42E-01	8.95E-01	-	-
1395447_at	Ermn	ermin, ERM-like protein	295619	Rn.20243	BF567711	2.32	2.31	2.33	2.31	2.33	2.31	1.00	down	7.25E-01	9.13E-01	-	-
1381547_at	---	---	---	Rn.161174	BI295803	2.27	2.27	2.28	2.27	2.27	2.27	1.00	down	5.43E-01	8.95E-01	-	-
1376122_at	---	---	---	Rn.209927	BF401577	2.48	2.46	2.50	2.48	2.49	2.47	1.00	down	8.36E-01	9.48E-01	-	-
1393536_at	LOC682473	hypothetical protein LOC682473	682473	---	AI144734	2.52	2.52	2.55	2.52	2.55	2.51	1.00	down	8.41E-01	9.50E-01	-	-
1369988_at	Epor	erythropoietin receptor	24336	Rn.22394	NM_017002	2.29	2.29	2.30	2.29	2.29	2.28	1.00	down	5.44E-01	8.95E-01	-	-
1396881_at	---	---	---	Rn.216795	BE103214	2.38	2.37	2.39	2.38	2.38	2.37	1.00	down	6.97E-01	9.07E-01	-	-
1387390_at	Gzmk	granzyme K	29165	Rn.11190	NM_017119	2.28	2.27	2.29	2.28	2.28	2.27	1.00	down	6.09E-01	8.95E-01	-	-
1372449_at	---	---	---	Rn.935	AW253616	2.56	2.42	2.42	2.41	2.57	2.41	1.00	down	9.67E-01	9.90E-01	-	-
1382408_at	RGD1561343	Similar to C20orf118	502689	Rn.203346	AI011879	2.29	2.28	2.29	2.28	2.29	2.28	1.00	down	6.21E-01	8.95E-01	-	-
1389690_at	RGD1311103	similar to RIKEN cDNA 2410146L05	301100	Rn.12843	AI233903	2.32	2.32	2.34	2.32	2.37	2.31	1.00	up	8.82E-01	9.64E-01	-	-
1368535_at	Hrk	harakiri, BCL2 interacting protein (contains only BH3 domain)	117271	Rn.89639	NM_057130	2.48	2.47	2.48	2.47	2.48	2.47	1.00	down	4.43E-01	8.95E-01	-	-
1381656_at	---	---	---	Rn.147716	BF401772	2.44	2.42	2.45	2.44	2.45	2.43	1.00	up	7.97E-01	9.34E-01	-	-
1397470_at	---	---	---	Rn.161400	BE099883	2.28	2.27	2.28	2.27	2.28	2.27	1.00	down	5.56E-01	8.95E-01	-	-
1389848_at	Arhgap23	Rho GTPase activating protein 23	303501	Rn.6554	BE097243	2.27	2.26	2.27	2.26	2.27	2.26	1.00	down	5.16E-01	8.95E-01	-	-
1368760_at	Cxcl2	chemokine (C-X-C motif) ligand 2	114105	Rn.10230	NM_053647	2.29	2.28	2.29	2.28	2.29	2.28	1.00	down	5.86E-01	8.95E-01	-	-
1380628_at	Krt34	keratin 34	303528	Rn.43921	BM385749	2.32	2.32	2.33	2.32	2.33	2.32	1.00	down	5.33E-01	8.95E-01	-	-
1394650_at	---	---	---	Rn.6554	BF284574	2.29	2.28	2.29	2.28	2.30	2.28	1.00	down	6.90E-01	9.05E-01	-	-
1394027_at	Nup62cl	nucleoporin 62 C-terminal like	300923	Rn.89460	AI179798	2.32	2.32	2.33	2.32	2.33	2.32	1.00	down	6.32E-01	8.95E-01	-	-
1375501_at	RGD1308106	LOC361719	361719	Rn.16874	AI600001	2.34	2.33	2.35	2.34	2.34	2.33	1.00	down	5.53E-01	8.95E-01	-	-
1391964_at	Rtel1	regulator of telomere elongation helicase 1	362288	Rn.98315	BI300993	2.40	2.39	2.40	2.38	2.40	2.41	1.00	up	7.32E-01	9.14E-01	-	-
1394378_at	Mettl1d1	methyltransferase 11 domain containing 1	305845	Rn.8815	BF561921	2.29	2.28	2.29	2.29	2.28	2.28	1.00	down	6.30E-01	8.95E-01	-	-
1397128_at	---	---	---	Rn.147710	BF392437	2.37	2.36	2.39	2.38	2.38	2.37	1.00	up	7.16E-01	9.10E-01	-	-
1387123_at	Cyp17a1	cytochrome P450, family 17, subfamily a, polypeptide 1	25146	Rn.10172	NM_012753	2.37	2.36	2.38	2.37	2.38	2.35	1.00	down	7.10E-01	9.09E-01	-	-
1388101_at	Dpysl3	dihydropyrimidinase-like 3	25418	Rn.93365	AF389425	2.31	2.30	2.32	2.30	2.31	2.30	1.00	down	6.55E-01	8.98E-01	-	-
1380103_at	---	---	---	Rn.204075	AI548379	2.27	2.27	2.27	2.27	2.27	2.26	1.00	down	5.27E-01	8.95E-01	-	-
1378660_at	Zfhx4	zinc finger homeobox 4	310250	Rn.133363	BF388630	2.35	2.34	2.36	2.35	2.35	2.33	1.00	down	6.88E-01	9.04E-01	-	-
1391187_at	Ppl	periplakin	302934	Rn.25259	BI303019	2.30	2.30	2.31	2.30	2.30	2.29	1.00	down	5.47E-01	8.95E-01	-	-
1398276_at	Dlg2	discs, large homolog 2 (Drosophila)	64053	Rn.202966	NM_022282	2.34	2.32	2.35	2.33	2.36	2.32	1.00	down	8.44E-01	9.52E-01	-	-
1380204_at	---	---	---	Rn.155994	BE116163	2.27	2.27	2.28	2.27	2.28	2.27	1.00	down	5.39E-01	8.95E-01	-	-
1386333_at	---	---	---	Rn.41237	AI044097	2.25	2.24	2.25	2.24	2.25	2.24	1.00	down	4.58E-01	8.95E-01	-	-
1393490_at	Cog7	component of oligomeric golgi complex 7	293456	Rn.23781	AI501671	2.34	2.33	2.34	2.33	2.34	2.33	1.00	down	5.00E-01	8.95E-01	-	-
1396679_at	---	---	---	Rn.210177	BF394899	2.40	2.39	2.40	2.40	2.39	2.39	1.00	down	5.44E-01	8.95E-01	-	-
1378553_at	LOC685756	Hypothetical protein LOC685756	685756	Rn.28477	AI227711	2.61	2.59	2.65	2.61	2.65	2.58	1.00	down	9.10E-01	9.73E-01	-	-
1368105_at	Tspan2	tetraspanin 2	64521	Rn.5872	AI228231	2.37	2.36	2.38	2.37	2.37	2.36	1.00	down	5.89E-01	8.95E-01	-	-
1375001_at	Cytl1	cytokine like 1	498392	Rn.8720	AA955251	2.31	2.30	2.31	2.30	2.31	2.30	1.00	down	5.16E-01	8.95E-01	-	-
1397081_at	---	---	---	---	BE120697	2.47	2.44	2.47	2.46	2.48	2.45	1.00	up	8.23E-01	9.43E-01	-	-
1371269_at	Olr857	olfactory receptor 857	366456	Rn.143179	AF029357	2.30	2.29	2.31	2.30	2.29	2.30	1.00	down	6.04E-01	8.95E-01	-	-
1397680_at	---	---	---	Rn.172096	BF288560	2.31	2.31	2.31	2.31	2.30	2.31	1.00	down	5.61E-01	8.95E-01	-	-
1380636_at	Alox12	arachidonate 12-lipoxygenase	287454	Rn.66513	BM390144	2.37	2.36	2.37	2.36	2.38	2.35	1.00	down	7.06E-01	9.08E-01	-	-
1398597_at	---	---	---	Rn.30788	AI044699	2.33	2.32	2.33	2.32	2.33	2.32	1.00	down	6.46E-01	8.95E-01	-	-
1368349_at	Fgfbp1	fibroblast growth factor binding protein 1	64535	Rn.6346	NM_022603	2.35	2.32	2.35	2.34	2.35	2.34	1.00	up	7.63E-01	9.23E-01	-	-
1378576_at	Sirt4	sirtuin (silent mating type information regulation 2 homolog) 4 (S. cerevisiae)	304539	Rn.92769	BI299039	2.38	2.37	2.39	2.37	2.38	2.39	1.00	down	6.97E-01	9.07E-01	-	-
1375482_at	RGD1560871	similar to plexin 1	362398	---	BE113029	2.27	2.26	2.28	2.27	2.28	2.26	1.00	down	6.14E-01	8.95E-01	-	-
1379498_at	---	---	---	Rn.57393	BF394165	2.34	2.33	2.34	2.33	2.34	2.33	1.00	down	5.41E-01	8.95E-01	-	-
1367862_at	Rrad	Ras-related associated with diabetes	83521	Rn.11189	NM_053338	2.36	2.35	2.36	2.36	2.36	2.35	1.00	down	5.33E-01	8.95E-01	-	-
1368307_at	Ggt7	gamma-glutamyltransferase 7	156275	Rn.15462	NM_130423	2.36	2.35	2.36	2.35	2.36	2.35	1.00	down	4.97E-01	8.95E-01	-	-
1374672_at	Tnni3k	TNNI3 interacting kinase	295531	Rn.3434	BI293080	2.36	2.34	2.37	2.35	2.38	2.35	1.00	up	8.34E-01	9.48E-01	-	-
1390595_at	---	---	---	Rn.88444	AW527996	2.34	2.34	2.35	2.34	2.35	2.34	1.00	down	6.16E-01	8.95E-01	-	-
1387387_at	Hpca	hippocalcin	29177	Rn.11019	NM_017122	2.27	2.26	2.27	2.26	2.27	2.26	1.00	down	5.78E-01	8.95E-01	-	-
1378923_at	Scarf2	scavenger receptor class F, member 2	287949	Rn.22134	AI710577	2.33	2.32	2.33	2.33	2.32	2.32	1.00	down	4.48E-01	8.95E-01	-	-
1369054_at	Rph3a	rabphilin 3A	171039	Rn.10976	NM_133518	2.50	2.47	2.51	2.49	2.51	2.48	1.00	up	8.44E-01	9.51E-01	-	-
1378461_at	---	---	---	---	BG376813	2.26	2.26	2.27	2.26	2.26	2.25	1.00	down	5.53E-01	8.95E-01	-	-
1378418_at	Tifab	TRAF-interacting protein with forkhead-associated domain, family member B	364674	Rn.160910	BI285027	2.61	2.56	2.62	2.60	2.61	2.59	1.00	up	8.79E-01	9.63E-01	-	-
1375826_at	Gpr61	G protein-coupled receptor 61	310780	Rn.49317	BF410192	2.33	2.32	2.33	2.32	2.33	2.31	1.00	down	7.12E-01	9.10E-01	-	-
1388037_at	Atp2b3	ATPase, Ca++ transporting, plasma membrane 3	29599	Rn.11053	J05087	2.31	2.30	2.31	2.30	2.31	2.30	1.00	down	5.54E-01	8.95E-01	-	-
1397971_at	---	---	---	Rn.137995	BE111159	2.49	2.47	2.52	2.48	2.56	2.45	1.00	up	9.35E-01	9.82E-01	-	-
1388221_at	Slc24a3	solute carrier family 24 (sodium/potassium/calcium exchanger), member 3	85267	Rn.206123	AY009158	2.34	2.34	2.35	2.34	2.35	2.33	1.00	down	6.47E-01	8.95E-01	-	-
1380512_at	Dpep2	dipeptidase 2	291984	Rn.20731	AI044125	2.30	2.30	2.31	2.30	2.33	2.29	1.00	up	8.39E-01	9.50E-01	-	-
1388284_at	---	---	---	---	AB003753	2.36	2.35	2.36	2.35	2.36	2.35	1.00	down	3.20E-01	8.95E-01	-	-
1370041_at	Stmn2	stathmin-like 2	84510	Rn.34335	BG668493	2.39	2.38	2.40	2.38	2.40	2.37	1.00	down	7.30E-01	9.14E-01	-	-
1392578_at	---	---	---	Rn.204270	AI070875	2.36	2.36	2.37	2.36	2.36	2.35	1.00	down	5.31E-01	8.95E-01	-	-
1392718_at	Fam38b	family with sequence similarity 38, member B	688934	Rn.163385	AA866357	2.33	2.32	2.34	2.32	2.33	2.32	1.00	down	6.74E-01	9.01E-01	-	-
1382098_at	---	---	---	---	AI228756	2.40	2.38	2.42	2.40	2.40	2.39	1.00	down	8.05E-01	9.37E-01	-	-
1381137_at	Dnajc7	DnaJ (Hsp40) homolog, subfamily C, member 7	303536	R

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1391013_at	Pcdh8	Protocadherin 8	64865	Rn.23337	AW523567	2.46	2.43	2.51	2.45	2.55	2.42	1.00	up	9.48E-01	9.85E-01	-	-
1375301_at	Hand1	heart and neural crest derivatives expressed 1	59112	Rn.39340	BI284322	2.40	2.39	2.40	2.40	2.41	2.38	1.00	down	8.06E-01	9.38E-01	-	-
1368759_at	Cacng2	calcium channel, voltage-dependent, gamma subunit 2	84347	Rn.72939	NM_053351	2.34	2.34	2.35	2.34	2.35	2.33	1.00	down	6.48E-01	8.98E-01	-	-
1380451_at	---	---	---	Rn.204197	AW915547	2.27	2.25	2.28	2.26	2.28	2.25	1.00	down	7.58E-01	9.21E-01	-	-
1376225_at	---	---	---	Rn.203707	BF411924	2.29	2.28	2.29	2.29	2.29	2.28	1.00	down	5.04E-01	8.95E-01	-	-
1375479_at	Magi3	Membrane associated guanylate kinase, WW and PDZ domain containing 3	245903	Rn.162623	AI555573	2.26	2.26	2.27	2.26	2.27	2.26	1.00	down	5.56E-01	8.95E-01	-	-
1387162_at	Tpsab1	tryptase alpha/beta 1	54211	Rn.10699	NM_019322	2.31	2.30	2.32	2.31	2.31	2.30	1.00	down	6.06E-01	8.95E-01	-	-
1376370_at	---	---	---	Rn.207738	BI299124	2.35	2.33	2.35	2.34	2.35	2.33	1.00	down	7.46E-01	9.18E-01	-	-
1370478_at	Myo16	myosin XVI	192253	Rn.207204	AY004215	2.31	2.30	2.31	2.30	2.31	2.29	1.00	down	6.36E-01	8.95E-01	-	-
1372289_at	Lbxcor1	LBXCOR1 homolog (mouse)	315748	Rn.58157	BF393969	2.30	2.30	2.31	2.30	2.31	2.29	1.00	down	6.42E-01	8.95E-01	-	-
1395042_at	---	---	---	Rn.204800	BF285153	2.26	2.25	2.26	2.25	2.26	2.25	1.00	down	5.40E-01	8.95E-01	-	-
1374869_at	---	---	---	Rn.7551	AA943361	2.31	2.30	2.31	2.30	2.31	2.29	1.00	down	6.48E-01	8.96E-01	-	-
1379680_at	---	---	---	Rn.38387	BI296059	2.45	2.44	2.46	2.44	2.45	2.45	1.00	down	6.30E-01	8.95E-01	-	-
1390191_at	---	---	---	Rn.24157	AI234119	2.28	2.28	2.29	2.28	2.29	2.27	1.00	down	6.30E-01	8.95E-01	-	-
1369587_at	Ereg	epiregulin	59325	Rn.42897	NM_021689	2.32	2.32	2.33	2.32	2.34	2.32	1.00	up	6.10E-01	8.95E-01	-	-
1399118_at	Msl1	male-specific lethal 1 homolog (Drosophila)	303514	Rn.22437	AI168933	5.15	4.84	4.72	4.88	4.95	4.87	1.00	down	9.83E-01	9.95E-01	-	-
1391239_at	RGD1306926	similar to hypothetical protein FLJ22175	303742	Rn.100769	BF412928	2.23	2.23	2.24	2.23	2.23	2.23	1.00	down	5.01E-01	8.95E-01	-	-
1394680_at	---	---	---	Rn.206617	AW528616	2.37	2.36	2.37	2.36	2.38	2.35	1.00	down	7.29E-01	9.13E-01	-	-
1394140_at	Krt31	keratin 31	450228	Rn.129815	AI639284	2.43	2.42	2.44	2.43	2.43	2.42	1.00	down	5.45E-01	8.95E-01	-	-
1390622_at	---	---	---	Rn.146585	BE113149	2.34	2.33	2.35	2.33	2.34	2.35	1.00	up	6.83E-01	9.03E-01	-	-
1376152_at	---	---	---	Rn.24516	AA819316	2.34	2.34	2.34	2.34	2.36	2.33	1.00	up	7.35E-01	9.15E-01	-	-
1381580_at	Trex2	three prime repair exonuclease 2	309275	Rn.63379	AF418169	2.26	2.25	2.26	2.26	2.26	2.25	1.00	down	5.78E-01	8.95E-01	-	-
1381183_at	---	---	---	---	BE102052	2.45	2.44	2.45	2.43	2.46	2.44	1.00	down	7.52E-01	9.20E-01	-	-
1370804_at	Gabarap	GABA(A) receptor-associated protein	58974	Rn.8411	AF161588	10.14	10.16	10.02	10.19	10.10	10.02	1.00	down	9.66E-01	9.90E-01	-	-
1370670_at	Zfp37	zinc finger protein 37	115768	Rn.29978	AF072439	2.51	2.51	2.52	2.51	2.52	2.50	1.00	down	6.80E-01	9.03E-01	-	-
1375227_at	---	---	---	Rn.172668	BF416235	2.38	2.37	2.40	2.38	2.39	2.37	1.00	down	7.43E-01	9.17E-01	-	-
1384311_at	Prdm5	PR domain containing 5	686788	Rn.171343	BE113214	2.24	2.23	2.24	2.24	2.24	2.23	1.00	down	6.07E-01	8.95E-01	-	-
1398017_at	---	---	---	Rn.61332	BF404952	2.32	2.32	2.33	2.32	2.33	2.32	1.00	down	5.09E-01	8.95E-01	-	-
1376886_at	---	---	---	Rn.154054	AW533838	2.37	2.36	2.38	2.36	2.37	2.36	1.00	down	6.69E-01	9.00E-01	-	-
1382532_at	Ela3b	elastase 3B, pancreatic	298567	Rn.11639	BF284283	2.27	2.26	2.27	2.26	2.27	2.26	1.00	down	6.04E-01	8.95E-01	-	-
1372708_at	---	---	---	---	BI296544	2.39	2.39	2.40	2.40	2.41	2.38	1.00	up	7.78E-01	9.28E-01	-	-
1387618_at	Bcl2l10	BCL2-like 10 (apoptosis facilitator)	114552	Rn.67084	NM_053733	2.25	2.24	2.25	2.25	2.25	2.24	1.00	down	6.19E-01	8.95E-01	-	-
1391260_at	---	---	---	Rn.12803	BF388662	2.42	2.40	2.43	2.42	2.42	2.41	1.00	up	7.94E-01	9.34E-01	-	-
1377010_at	RGD1565411	similar to 2610317D23Rik protein	363000	Rn.20937	BI274499	2.41	2.41	2.42	2.41	2.42	2.41	1.00	up	5.05E-01	8.95E-01	-	-
1382207_at	---	---	---	Rn.24014	BE097085	2.39	2.38	2.40	2.39	2.39	2.38	1.00	down	6.36E-01	8.95E-01	-	-
1385868_at	---	---	---	Rn.2798	AA875124	2.22	2.21	2.23	2.22	2.22	2.21	1.00	down	5.52E-01	8.95E-01	-	-
1376904_at	Tmem151a	transmembrane protein 151A	309158	Rn.100997	AI716115	2.29	2.30	2.30	2.29	2.30	2.29	1.00	down	3.05E-01	8.95E-01	-	-
1380635_at	---	---	---	---	BI275816	2.27	2.26	2.28	2.27	2.27	2.26	1.00	down	6.49E-01	8.96E-01	-	-
1392016_at	---	---	---	Rn.42884	AW533779	2.29	2.28	2.30	2.29	2.29	2.28	1.00	down	5.47E-01	8.95E-01	-	-
1398257_at	Mog	myelin oligodendrocyte glycoprotein	24558	Rn.9687	NM_022668	2.38	2.37	2.40	2.38	2.39	2.37	1.00	down	7.86E-01	9.31E-01	-	-
1395436_at	---	---	---	Rn.206728	BF415556	2.35	2.34	2.36	2.34	2.36	2.34	1.00	down	7.65E-01	9.23E-01	-	-
1369224_at	Cdh17	cadherin 17	117048	Rn.76726	NM_053977	2.28	2.27	2.28	2.28	2.28	2.26	1.00	down	5.82E-01	8.95E-01	-	-
1369787_at	---	---	---	---	M88096	2.43	2.42	2.44	2.43	2.45	2.43	1.00	up	6.72E-01	9.01E-01	-	-
1379082_at	RGD1307034	Similar to hypothetical protein CG003	304244	Rn.36184	BF409865	2.49	2.47	2.44	2.47	2.48	2.44	1.00	down	8.84E-01	9.64E-01	-	-
1385002_at	RGD1562639	similar to c-myc promoter binding protein	315756	Rn.21843	AI454987	2.41	2.40	2.42	2.40	2.41	2.40	1.00	down	6.62E-01	8.98E-01	-	-
1387711_at	Il10	interleukin 10	25325	Rn.9868	L02926	2.34	2.34	2.35	2.34	2.35	2.34	1.00	down	6.16E-01	8.95E-01	-	-
1395404_at	Fn3krp	fructosamine-3-kinase-related protein	303755	Rn.130706	BE110529	8.20	7.87	7.67	8.11	7.69	7.95	1.00	up	9.89E-01	9.96E-01	-	-
1382651_at	---	---	---	Rn.165520	AA998677	2.37	2.39	2.38	2.37	2.38	2.37	1.00	down	7.14E-01	9.10E-01	-	-
1378527_at	LOC303590	similar to cactin CG1676-PA	303590	Rn.156087	BF403857	2.36	2.35	2.36	2.35	2.37	2.35	1.00	up	7.29E-01	9.14E-01	-	-
1386809_at	Scrt1	scratch homolog 1, zinc finger protein (Drosophila)	366951	Rn.220523	BF558950	2.28	2.27	2.29	2.28	2.31	2.27	1.00	up	8.11E-01	9.39E-01	-	-
1379813_at	RGD1565689	RGD1565689	498958	Rn.199071	BE111288	2.54	2.54	2.55	2.54	2.55	2.53	1.00	down	5.82E-01	8.95E-01	-	-
1393864_at	---	---	---	---	BF390797	2.18	2.17	2.18	2.17	2.19	2.17	1.00	up	7.07E-01	9.08E-01	-	-
1385835_at	Plxdc1	plexin domain containing 1	303505	Rn.18110	AI030641	2.35	2.34	2.36	2.34	2.35	2.34	1.00	down	6.13E-01	8.95E-01	-	-
1395255_at	---	---	---	Rn.149098	AW526964	2.29	2.28	2.29	2.29	2.29	2.28	1.00	down	6.07E-01	8.95E-01	-	-
1398740_at	---	---	---	Rn.154086	BF396546	2.36	2.35	2.36	2.35	2.36	2.35	1.00	down	5.69E-01	8.95E-01	-	-
1390533_at	RGD1310448	similar to mKIAA1300 protein	311347	Rn.51378	BE112894	2.46	2.33	2.40	2.33	2.34	2.51	1.00	down	9.67E-01	9.90E-01	-	-
1377056_at	---	---	---	---	BF393907	2.37	2.36	2.39	2.37	2.38	2.36	1.00	down	7.53E-01	9.20E-01	-	-
1380872_at	---	---	---	Rn.134864	BF396681	2.50	2.50	2.52	2.52	2.52	2.49	1.00	up	8.18E-01	9.42E-01	-	-
1383794_at	RGD1311080	similar to RIKEN cDNA A930038C07	312401	Rn.162750	AI575277	2.28	2.27	2.29	2.28	2.29	2.27	1.00	down	6.32E-01	8.95E-01	-	-
1372165_at	---	---	---	Rn.137967	BF393140	2.33	2.33	2.34	2.33	2.33	2.33	1.00	down	4.47E-01	8.95E-01	-	-
1375515_at	---	---	---	Rn.63288	BF396077	2.30	2.29	2.31	2.30	2.31	2.29	1.00	down	7.38E-01	9.16E-01	-	-
1397282_at	---	---	---	Rn.206915	AW531746	2.31	2.31	2.32	2.31	2.31	2.31	1.00	down	4.84E-01	8.95E-01	-	-
1369017_at	Kcnh6	potassium voltage-gated channel, subfamily H (eag-related), member 6	116745	Rn.10875	NM_053937	2.34	2.33	2.35	2.33	2.34	2.33	1.00	down	6.40E-01	8.95E-01	-	-
1379426_at	---	---	---	Rn.204090	AW916940	2.34	2.34	2.35	2.34	2.35	2.34	1.00	down	5.18E-01	8.95E-01	-	-
1368797_at	Nr1i3	nuclear receptor subfamily 1, group I, member 3	65035	Rn.163229	NM_022941	2.32	2.31	2.32	2.31	2.34	2.31	1.00	up	7.66E-01	9.24E-01	-	-
1391428_at	---	---	---	Rn.28326	AI639162	2.48	2.47	2.48	2.47	2.49	2.46	1.00	down	7.62E-01	9.22E-01	-	-
1392886_a_at	Fcrla	Fc receptor-like A	304965	Rn.144949	AI453967	2.33	2.32	2.33	2.32	2.33	2.32	1.00	down	5.19E-01	8.95E-01	-	-
1382767_at	Rcn1	Reticulocalbin 1, EF-hand calcium binding domain	362182	Rn.103345	AI175752	2.52	2.51	2.52	2.51	2.52	2.51	1.00	down	3.23E-01	8.95E-01	-	-
1369717_at	Nmu	neuromedin U	63887	Rn.47720	M94555	2.29	2.28	2.30	2.28	2.28	2.28	1.00	down	6.27E-01	8.95E-01	-	-
1387707_at	Slc2a3	solute carrier family 2 (facilitated glucose transporter), member 3	25551	Rn.95055	NM_017102	2.32	2.31	2.33	2.31	2.32	2.31	1.00	down	6.51E-01	8.97E-01	-	-
1381303_at	---	---	---	Rn.171031	BE107070	2.49	2.46	2.52	2.47	2.58	2.43	1.00	up	9.52E-01	9.86E-01	-	-
1374023_at	---	---	---	---	AI071195	2.31	2.31	2.31	2.31	2.32	2.29	1.00	down	7.84E-01	9.30E-01	-	-
1383699_at	Rit2	Ras-like without CAAX 2	291713	Rn.106719	BG673521	2.30	2.29	2.31	2.29	2.30	2.29	1.00	down	6.22E-01	8.95E-01	-	-
1389018_at	---	---	---	---	BF411239	2.34	2.33	2.35	2.34	2.34	2.33	1.00	down	6.52E-01	8.97E-01	-	-
1381290_at	---	---	---	Rn.60229	AI101288	2.38	2.37	2.41	2.43	2.39	2.35	1.00	up	9.22E-01	9.77E-01	-	-
1397317_at	---	---	---	Rn.156068	BI296984	2.36	2.36	2.36	2.36	2.36	2.35	1.00	down	4.49E-01	8.95E-01	-	-
1384497_at	Klf7	Kruppel-like factor 7 (ubiquitous)	363243	Rn.219339	BG666291	2.27	2.26	2.28	2.27	2.27	2.26	1.00	down	5.87E-01	8.95E-01	-	-
1385836_at	---	---	---	---	AI454586	2.56	2.55	2.56	2.56	2.56	2.55	1.00	down	3.59E-01	8.95E-01	-	-
1387246_at	Vegfl1	von Ebners gland protein 1	65039	Rn.37454	NM_022945	2.36	2.37	2.38	2.36	2.39	2.36	1.00	down	7.88E-01	9.31E-01	-	-
1373683_at	Fyn	FYN oncogene related to SRC, FGR, YES	25150	Rn.19361	AI230396	2.46	2.43	2.45	2.44	2.46	2.43	1.00	down	8.11E-01	9.39E-01	-	-
1391720_at	---	---	---	Rn.146167	AW528396	2.35	2.34	2.36	2.34	2.36	2.34	1.00	down	7.04E-01	9.07E-01	-	-
1394408_at	RGD1563692	similar to hypothetical protein FLJ22671	501185	Rn.41540	AI717274	2.38	2.36	2.39	2.37	2.38	2.36	1.00	down	8.08E-01	9.38E-01	-	-
1378463_at	---	---	---	Rn.147670	BF405047	2.33	2.32	2.34	2.33	2.33	2.32	1.00	down	6.82E-01	9.03E-01	-	-
1385239_at	---	---	---	Rn.33362	AI045150	2.41	2.40	2.41	2.40	2.43	2.38	1.00	down	8.64E-01	9.58E-01	-	-
1378103_at	---	---	---	Rn.220218	AI406799	2.40	2.40	2.41	2.39	2.42	2.40	1.00	up	7.17E-01	9.10E-01	-	-
1382948_at	Arhgap28	Rho GTPase activating protein 28	301709	Rn.14693	BI296929	2.33	2.32	2.34	2.32	2.33	2.32	1.00	down	7.05E-01	9.08E-01	-	-
1394916_at	---	---	---	Rn.149245	AW526714	2.44	2.43	2.45	2.44	2.45	2.43	1.00	down	7.84E-01	9.30E-01	-	-
1380333_at	Ptpn22	protein tyrosine phosphatase, non-receptor type 22 (lymphoid)	295338	Rn.22891	AW915666	2.25	2.25	2.26	2.25	2.26	2.25	1.00	down	5.58E-01	8.95E-01	-	-
1375319_at	---	---	---	Rn.209318	BF406138	2.32	2.31	2.33	2.32	2.33	2.31	1.00	down	6.66E-01	8.96E-01	-	-
1389847_at	Notch4	Notch homolog 4 (Drosophila)	406162	Rn.12967	AA799611	2.38	2.38	2.39	2.38	2.40	2.38	1.00	up	6.92E-01	9.05E-01	-	-
1390654_at	---	---	---	Rn.147940	AA874809	2.31	2.30	2.32	2.31	2.31	2.30	1.00	down	5.51E-01	8.95E-01	-	-
1386545_at	Cops7b	COP9 constitutive photomorphogenic homolog subunit 7B (Arabidopsis)	363273	Rn.33834	BF549788	2.32	2.31	2.33	2.32	2.32	2.32	1.00	down	5.78E-01	8.95E-01	-	-
1380954_at	---	---	---	Rn.209089	BF386143	2.30	2.29	2.31	2.30	2.31	2.29	1.00	down	6.19E-01	8.95E-01	-	-
1381629_at	---	---	---	---	AI575874	2.43	2.42	2.43	2.43	2.45	2.42	1.00	up	7.37E-01	9.15E-01	-	-
1393872_at	RGD1562860	similar to RIKEN cDNA 2310045A20	360945	Rn.75246	BF401995	2.49	2.47	2.52	2.48	2.55	2.46	1.00	up	9.29E-01	9.80E-01	-	-
1387746_at	Olr414	olfactory receptor 414	56821	Rn.138116	NM_020106	2.29	2.28	2.30	2.29	2.29	2.28	1.00	down	6.06E-01	8.95E-01	-	-
1385557_at	---	---	---	---	AA925349	2.34	2.33	2.35	2.34	2.35	2.32	1.00	down	7.75E-01	9.27E-01	-	-
1385832_s_at	Sash3	SAM and SH3 domain containing 3	317578	Rn.15328	AA924459	2.23	2.22	2.24	2.24	2.23	2.22	1.00	up	7.29E-01	9.14E-01	-	-
1380711_at	---	---	---	Rn.210909	BF403307	2.31	2.30	2.32	2.31	2.32	2.30	1.00	down	7.32E-01	9.14E-01	-	-
1398650_at	683844 /// LOC68	similar to RING finger protein 11 (NEDD4 WW domain-binding protein 2) (Sid	683844 /// 689589	Rn.198287	AW529438	2.46	2.43	2.48	2.45	2.47	2.44	1.00	down	8.75E-01	9.61E-01	-	-
1388002_at	Taok1	TAO kinase 1	286993	Rn.30050	AF084205	3.68	4.50	4.13	4.03	3.88	4.39	1.00	down	9.92E-01	9.97E-01	-	-
1371061_at	Pou3f2	POU class 3 homeobox 2	29588	Rn.82733	BG380993	2.25	2.24	2.25	2.24	2.27	2.24	1.00	up	7.85E-01	9.30E-01	-	-
1387490_at	---	---	---	---	NM_022713	2.31	2.30	2.31	2.31	2.31	2.30	1.00	down	5.95E-01	8.95E-01	-	-
1396789_x_at	---	---	---	Rn.57555	BF391375	2.27	2.27	2.28	2.27	2.28	2.27	1.00	down	6.04E-01	8.95E-01	-	-
1368906_at	Pgk1	phosphoglycerate kinase 1	24644	Rn.108127	NM_053291	2.75	2.71	2.82	2.73	2.85	2.70	1.00	down	9.61E-01	9.89E-01	-	-
1374722_at	C1qtnf1	C1q and tumor necrosis factor related protein 1	303701	Rn.203149	BI296396	2.34	2.34	2.35	2.34	2.35	2.33	1.00	down	6.94E-01	9.05E-01	-	-
1394174_at	Defa-rs1	defensin alpha-related sequence 1	613220	Rn.122020	AI639089	2.37	2.34	2.37	2.36	2.37	2.34	1.00	down	8.22E-01	9.43E-01	-	-
1387709_at	Figf	c-fos induced growth factor	360457	Rn.10796	AY032728	2.41	2.40	2.42	2.41	2.42	2.40	1.00	down	7.15E-01	9.10E-01	-	-
1389437_at	Sall2	sal-like 2 (Drosophila)	305854	Rn.38075	BF392952	2.29	2.29	2.30	2.29	2.32	2.28	1.00	up	8.06E-01	9.38E-01	-	-
1396830_at	---	---	---	---	AW527558	2.26	2.25	2.27	2.26	2.25	2.26	1.00	down	6.19E-01	8.95E-01	-	-
1379907_at	---	---	---	Rn.172373	AI044838	2.30	2.29	2.30	2.29	2.30	2.29	1.00	down	6.32E-01	8.95E-01	-	-
1395390_at	---	---	---	Rn.26826	BM384238	2.28	2.28	2.29	2.28	2.29	2.27	1.00	down	5.74E-01	8.95E-01	-	-
1371077_at	Htr3b	5-hydroxytryptamine (serotonin) receptor 3b	58963	Rn.87106	AI575989	2.28	2.27	2.28	2.28	2.27	2.27	1.00	down	6.10E-01	8.95E-01	-	-
1398076_at	---	---	---	---	BF399749	2.28	2.27	2.28	2.27	2.28	2.27	1.00	down	5.24E-01	8.95E-01	-	-
1392071_at	---	---	---	Rn.209902	BF392945	2.28	2.27	2.28	2.28	2.28	2.27	1.00	down	6.19E-01	8.95E-01	-	-
1397566_at	Ube2s	ubiquitin-conjugating enzyme E2S	292588	Rn.102396	BF548706	2.27	2.27	2.28	2.27	2.27	2.27	1.00	down	3.70E-01	8.95E-01	-	-
1398216_at	---	---	---	Rn.210574	BF394439	2.37	2.36	2.37	2.36	2.38	2.35	1.00	down	7.42E-01	9.17E-01	-	-
1368956_at	Pcdh8	protocadherin 8	64865	Rn.23337	NM_022868	2.37	2.36	2.38	2.37	2.38	2.36	1.00	down	6.62E-01	8.98E-01	-	-
1395158_at	---	---	---	Rn.94034	BF391885	2.27	2.27	2.28	2.27	2.28	2.26	1.00	down	6.07E-01	8.95E-01	-	-
1376420_at	RGD1559885	similar to hypothetical gene supported by BC063892	500059	Rn.20360	BF419551	2.54	2.54	2.54	2.54	2.54	2.53	1.00	down	5.06E-01	8.95E-01	-	-
1396943_at	---	---	---	Rn.146762	AI547694	2.39	2.38	2.40	2.38	2.39	2.38	1.00	down	6.73E-01	9.01E-01	-	-
1381235_at	---	---	---	---	BE119846	2.29	2.29	2.30	2.31	2.30	2.28	1.00	up	7.16E-01	9.10E-01	-	-
1391489_at	Irgm	immunity-related GTPase family, M	303090	Rn.20356	AI407339	2.34	2.33	2.34	2.33	2.35	2.32	1.00	up	7.61E-01	9.22E-01	-	-
1388630_at	---	---	---	Rn.129573	BI296506	2.28	2.27	2.28	2.28	2.28	2.27	1.00	down	5.72E-01	8.95E-01	-	-
1368640_at	Spata19	spermatogenesis associated 19	171403	Rn.51863	NM_134384	2.35	2.33	2.35	2.34	2.35	2.33	1.00	down	6.94E-01	9.05E-01	-	-
1385373_at	---	---	---	Rn.203086	AA875324	2.42	2.42	2.42	2.42	2.44	2.42	1.00	up	7.19E-01	9.11E-01	-	-
1371114_at	Kcnj4	potassium inwardly-rectifying channel, subfamily J, member 4	116649	Rn.10197	X87635	2.27	2.26	2.27	2.27	2.27	2.26	1.00	down	6.02E-01	8.95E-01	-	-
1375837_at	---	---	---	Rn.161149	BF410412	2.38	2.37	2.39	2.38	2.39	2.37	1.00	down	7.33E-01	9.15E-01	-	-
1387579_at	---	---	---	---	NM_053737	2.35	2.34	2.36	2.35	2.36	2.34	1.00	down	7.17E-01	9.10E-01	-	-
1392709_at	---	---	---	---	BF286936	2.29	2.29	2.30	2.29	2.29	2.28	1.00	down	5.84E-01	8.95E-01	-	-
1381393_at	---	---	---	Rn.212342	BI301735	2.62	2.60	2.63	2.62	2.64	2.59	1.00	down	8.56E-01	9.55E-01	-	-
1387360_at	Stx1a	syntaxin 1A (brain)	116470	Rn.9943	NM_053788	2.31	2.31	2.32	2.31	2.32	2.30	1.00	down	6.86E-01	9.04E-01	-	-
1371068_at	cdha13 /// Pcdhac	protocadherin alpha 13 /// protocadherin alpha subfamily C, 2	116742 /// 393092	---	AW524833	2.36	2.36	2.37	2.36	2.36	2.35	1.00	down	5.54E-01	8.95E-01	-	-
1381866_at	---	---	---	Rn.59748	BF388061	2.25	2.24	2.25	2.24	2.25	2.24	1.00	down	5.60E-01	8.95E-01	-	-
1381499_at	---	---	---	Rn.78361	BM390226	2.40	2.41	2.42	2.39	2.41	2.43	1.00	up	7.96E-01	9.34E-01	-	-
1367920_at	S1pr2	sphingosine-1-phosphate receptor 2	29415	Rn.2491	NM_017192	2.30	2.29	2.30	2.29	2.30	2.28	1.00	down	6.36E-01	8.95E-01	-	-
1374871_at	Aarg1	asparaginase like 1	246307	Rn.22751	AI233343	9.80	10.67	10.30	10.13	10.08	10.55	1.00	down	9.82E-01	9.98E-01	-	-
1369977_at	Uchl1	ubiquitin carboxyl-terminal esterase L1 (ubiquitin thiolesterase)	29545	Rn.107213	NM_017237	2.40	2.39	2.41	2.40	2.41	2.39	1.00	down	7.66E-01	9.23E-01	-	-
1383249_at	---	---	---	Rn.25081	AW524109	2.30	2.30	2.32	2.30	2.31	2.29	1.00	down	7.19E-01	9.11E-01	-	-
1396169_at	---	---	---	Rn.74880	AI535351	2.45	2.44	2.46	2.45	2.51	2.40	1.00	up	9.26E-01	9.79E-01	-	-
1375017_at	---	---	---	Rn.73828	BI296120	2.38	2.38	2.39	2.38	2.39	2.36	1.00	down	7.82E-01	9.29E-01	-	-
1378056_at	Gmnn	geminin	291137	Rn.15438	BM391984	2.50	2.48	2.51	2.50	2.50	2.49	1.00	down	7.69E-01	9.25E-01	-	-
1395013_at	RGD1559610	similar to CGI-94 protein	313581	Rn.64865	AW531495	2.36	2.35	2.37	2.36	2.36	2.35	1.00	down	5.79E-01	8.95E-01	-	-
1380818_at	---	---	---	Rn.208951	BE121297	2.46	2.45	2.47	2.45	2.48	2.44	1.00	down	8.36E-01	9.48E-01	-	-
1392645_at	---	---	---	Rn.148526	AA998765	2.34	2.34	2.34	2.34	2.33	2.33	1.00	down	5.14E-01	8.95E-01	-	-
1370338_at	Hrh1	histamine receptor H 1	24448	Rn.81032	AF387884	2.46	2.45	2.47	2.44	2.48	2.45	1.00	down	8.18E-01	9.42E-01	-	-
1370270_at	Tcam1	testicular cell adhesion molecule 1	59305	Rn.125075	AB015749	2.27	2.26	2.27	2.26	2.27	2.26

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1381576_at	Pik3c2b	phosphoinositide-3-kinase, class 2, beta polypeptide	289021	Rn.72591	BE105801	2.40	2.39	2.42	2.39	2.41	2.39	1.00	down	8.06E-01	9.38E-01	-	-
1381114_at	RGD1562515	similar to RIKEN cDNA 4931417E11	500204	Rn.46644	BF387271	2.31	2.30	2.32	2.31	2.31	2.30	1.00	down	6.79E-01	9.02E-01	-	-
1369240_a_at	Avpr1b	arginine vasopressin receptor 1B	29462	Rn.10096	U27322	2.26	2.26	2.27	2.26	2.26	2.25	1.00	down	6.01E-01	8.95E-01	-	-
1377585_at	Vgll1	vestigial like 1 (Drosophila)	363508	Rn.106774	BI289790	2.44	2.42	2.44	2.43	2.45	2.41	1.00	down	8.37E-01	9.49E-01	-	-
1375742_at	Vash2	Vasohibin 2	498309	Rn.13814	AW434257	2.29	2.29	2.30	2.29	2.30	2.28	1.00	down	6.20E-01	8.95E-01	-	-
1380290_at	---	---	---	Rn.169231	AI013768	2.26	2.25	2.26	2.25	2.27	2.24	1.00	down	7.59E-01	9.21E-01	-	-
1369118_a_at	Gnrhr	gonadotropin releasing hormone receptor	81668	Rn.112595	NM_031038	2.24	2.24	2.25	2.24	2.24	2.23	1.00	down	5.42E-01	8.95E-01	-	-
1382822_at	---	---	---	Rn.199270	AI030124	2.24	2.23	2.24	2.24	2.24	2.23	1.00	down	5.71E-01	8.95E-01	-	-
1386261_x_at	Cav2	caveolin 2	363425	Rn.81070	AI406385	2.53	2.49	2.59	2.53	2.61	2.48	1.00	up	9.54E-01	9.86E-01	-	-
1377958_at	Lhfpl4	lipoma HMGIC fusion partner-like 4	353230	Rn.145133	AW550282	2.26	2.25	2.26	2.25	2.26	2.25	1.00	down	5.47E-01	8.95E-01	-	-
1396522_at	---	---	---	Rn.210599	BF409284	2.31	2.30	2.32	2.31	2.32	2.30	1.00	down	6.53E-01	8.97E-01	-	-
1384864_at	Dhh	desert hedgehog homolog (Drosophila)	84380	Rn.198251	AW529714	2.23	2.22	2.23	2.22	2.24	2.22	1.00	up	7.21E-01	9.11E-01	-	-
1394504_at	---	---	---	---	BE103949	2.25	2.24	2.26	2.25	2.25	2.24	1.00	down	5.94E-01	8.95E-01	-	-
1385524_at	Fam184a	family with sequence similarity 184, member A	361853	Rn.206410	AA925989	2.27	2.27	2.28	2.27	2.28	2.27	1.00	down	5.82E-01	8.95E-01	-	-
1370451_a_at	Cacna1c	calcium channel, voltage-dependent, L type, alpha 1C subunit	24239	Rn.9827	M59786	2.44	2.43	2.46	2.44	2.45	2.43	1.00	down	8.06E-01	9.38E-01	-	-
1385789_at	---	---	---	---	BF402317	2.32	2.32	2.33	2.32	2.33	2.32	1.00	down	5.24E-01	8.95E-01	-	-
1396372_at	---	---	---	Rn.62857	BF411657	2.46	2.43	2.47	2.45	2.46	2.44	1.00	up	8.33E-01	9.47E-01	-	-
1398656_at	---	---	---	---	AI576497	2.33	2.32	2.34	2.33	2.34	2.32	1.00	down	6.89E-01	9.04E-01	-	-
1384947_at	---	---	---	Rn.203563	BF556486	2.49	2.47	2.53	2.48	2.57	2.45	1.00	up	9.49E-01	9.85E-01	-	-
1381724_at	---	---	---	Rn.134723	BF392468	2.48	2.43	2.51	2.45	2.51	2.46	1.00	up	9.26E-01	9.79E-01	-	-
1393954_at	Chrdl2	chordin-like 2	308854	Rn.78674	BI286488	2.75	2.74	2.87	2.74	2.73	2.90	1.00	up	9.89E-01	9.91E-01	-	-
1377637_at	---	---	---	Rn.20376	AW916093	2.41	2.41	2.42	2.41	2.42	2.40	1.00	down	7.23E-01	9.12E-01	-	-
1369149_at	Limk1	LIM domain kinase 1	65172	Rn.11250	NM_031727	2.32	2.31	2.32	2.31	2.32	2.31	1.00	down	4.16E-01	8.95E-01	-	-
1371400_at	Thrsp	thyroid hormone responsive	25357	Rn.81140	AI169092	2.31	2.30	2.32	2.30	2.31	2.30	1.00	down	6.44E-01	8.95E-01	-	-
1388973_at	Col9a1	collagen, type IX, alpha 1	305104	Rn.90726	BM388861	2.35	2.34	2.36	2.35	2.37	2.34	1.00	up	7.95E-01	9.34E-01	-	-
1390769_at	LOC314140	ribose-phosphate pyrophosphokinase I -like	314140	Rn.91470	AI535312	2.51	2.52	2.57	2.53	2.54	2.50	1.00	down	9.00E-01	9.69E-01	-	-
1381425_at	---	---	---	---	AI454686	2.35	2.34	2.36	2.34	2.35	2.34	1.00	down	7.29E-01	9.14E-01	-	-
1398464_at	---	---	---	Rn.166622	AI575255	2.31	2.31	2.32	2.31	2.32	2.30	1.00	down	6.75E-01	9.01E-01	-	-
1387312_a_at	Gck	glucokinase	24385	Rn.10447	NM_012565	2.36	2.36	2.37	2.36	2.37	2.35	1.00	down	7.55E-01	9.20E-01	-	-
1384353_at	---	---	---	Rn.203901	AI028838	2.30	2.29	2.31	2.30	2.31	2.29	1.00	down	7.03E-01	9.07E-01	-	-
1378869_at	---	---	---	Rn.171730	BF413327	2.26	2.27	2.26	2.26	2.27	2.25	1.00	down	5.72E-01	8.95E-01	-	-
1393849_at	---	---	---	Rn.148035	AW521149	2.28	2.28	2.29	2.28	2.28	2.27	1.00	down	5.68E-01	8.95E-01	-	-
1395005_at	---	---	---	---	AI176817	2.29	2.28	2.29	2.28	2.30	2.27	1.00	down	7.24E-01	9.13E-01	-	-
1380211_at	---	---	---	Rn.106250	BE100946	2.35	2.34	2.36	2.35	2.36	2.34	1.00	down	6.38E-01	8.95E-01	-	-
1381301_at	---	---	---	---	BF417811	2.29	2.28	2.30	2.29	2.30	2.28	1.00	down	6.99E-01	9.07E-01	-	-
1377090_at	Dock6	dedicator of cytokinesis 6	367039	Rn.22443	AI102881	2.64	2.63	2.69	2.64	2.72	2.61	1.00	up	9.45E-01	9.84E-01	-	-
1367855_at	Scarb1	scavenger receptor class B, member 1	25073	Rn.88169	NM_031541	2.24	2.24	2.25	2.24	2.25	2.23	1.00	down	6.13E-01	8.95E-01	-	-
1384581_at	OC360902 /// RG	actin, gamma 1 /// similar to actin, gamma 2, smooth muscle, enteric /// simila	76 /// 360883 /// 36	Rn.160812	BI850151	2.28	2.27	2.28	2.28	2.28	2.27	1.00	down	4.70E-01	8.95E-01	-	-
1375134_at	Dda1	DET1 and DDB1 associated 1	688813	Rn.86998	AI603162	2.26	2.26	2.27	2.26	2.26	2.25	1.00	down	5.11E-01	8.95E-01	-	-
1396414_at	---	---	---	---	BF390501	2.23	2.23	2.24	2.23	2.24	2.23	1.00	down	4.79E-01	8.95E-01	-	-
1398829_at	Fkbp1a	FK506 binding protein 1a	25639	Rn.80611	AI598372	8.51	8.02	8.04	7.71	8.44	8.42	1.00	up	9.93E-01	9.98E-01	-	-
1387562_at	Padi3	peptidyl arginine deiminase, type III	29520	Rn.32094	NM_017230	2.33	2.32	2.34	2.33	2.33	2.32	1.00	down	6.97E-01	9.07E-01	-	-
1391191_at	Myg1	Melanocyte proliferating gene 1	300258	Rn.1226	BE100335	2.38	2.37	2.40	2.38	2.40	2.38	1.00	up	7.88E-01	9.31E-01	-	-
1368293_at	Cpz	carboxypeptidase Z	83575	Rn.11056	NM_031766	2.28	2.28	2.29	2.28	2.28	2.28	1.00	down	5.09E-01	8.95E-01	-	-
1380353_at	---	---	---	Rn.206202	AW523469	2.39	2.38	2.40	2.39	2.40	2.37	1.00	down	8.00E-01	9.35E-01	-	-
1368737_at	---	---	---	---	NM_022709	2.38	2.37	2.40	2.38	2.39	2.40	1.00	up	8.00E-01	9.35E-01	-	-
1371630_at	---	---	---	Rn.76502	BI291429	2.28	2.27	2.29	2.28	2.29	2.27	1.00	down	6.36E-01	8.95E-01	-	-
1380955_at	---	---	---	---	BE098501	2.28	2.28	2.29	2.28	2.29	2.28	1.00	down	5.84E-01	8.95E-01	-	-
1394632_at	---	---	---	Rn.146743	AA875589	2.37	2.36	2.38	2.36	2.37	2.36	1.00	down	7.10E-01	9.09E-01	-	-
1393291_at	LOC679949	similar to CG4502-PA, isoform A	679949	Rn.222110	AW914913	2.35	2.35	2.36	2.35	2.36	2.34	1.00	down	5.85E-01	8.95E-01	-	-
1391446_at	Ms4a1	membrane-spanning 4-domains, subfamily A, member 1	309217	Rn.16385	AA817742	2.26	2.26	2.27	2.26	2.26	2.25	1.00	down	5.64E-01	8.95E-01	-	-
1395597_at	---	---	---	---	AW921081	2.38	2.38	2.39	2.38	2.40	2.37	1.00	down	7.67E-01	9.24E-01	-	-
1383320_at	Lck	lymphocyte-specific protein tyrosine kinase	313050	Rn.22791	AI137137	2.35	2.34	2.36	2.35	2.35	2.34	1.00	down	6.99E-01	9.07E-01	-	-
1368804_at	Lif	leukemia inhibitory factor (cholinergic differentiation factor)	60584	Rn.44379	NM_022196	2.35	2.34	2.36	2.37	2.35	2.33	1.00	up	8.21E-01	9.43E-01	-	-
1368048_at	Serpina3k	serine (or cysteine) peptidase inhibitor, clade A, member 3K	24794	Rn.91257	NM_012857	2.34	2.33	2.34	2.33	2.34	2.32	1.00	down	7.14E-01	9.10E-01	-	-
1381945_at	---	---	---	Rn.155549	AI412432	2.38	2.37	2.39	2.37	2.38	2.37	1.00	down	7.13E-01	9.10E-01	-	-
1368689_at	Gjb5	gap junction protein, beta 5	29586	Rn.16074	NM_019241	2.39	2.39	2.41	2.39	2.42	2.37	1.00	down	8.79E-01	9.63E-01	-	-
1386467_at	---	---	---	---	H33140	2.49	2.47	2.49	2.48	2.49	2.48	1.00	down	7.07E-01	9.08E-01	-	-
1378892_at	---	---	---	Rn.205728	BF564915	2.36	2.35	2.37	2.35	2.36	2.35	1.00	down	7.20E-01	9.11E-01	-	-
1380094_at	---	---	---	Rn.146781	BI297316	2.33	2.32	2.33	2.32	2.33	2.31	1.00	down	6.08E-01	8.95E-01	-	-
1396765_at	RGD1564019	similar to GTPase activating RANGAP domain-like 3	499783	---	BF390955	2.37	2.36	2.38	2.37	2.38	2.36	1.00	down	7.54E-01	9.20E-01	-	-
1380461_at	---	---	---	Rn.148857	BF398551	2.30	2.29	2.31	2.30	2.31	2.29	1.00	down	7.80E-01	9.28E-01	-	-
1396361_at	---	---	---	---	BF393282	2.24	2.24	2.25	2.24	2.24	2.23	1.00	down	5.48E-01	8.95E-01	-	-
1386822_s_at	RGD1311823	Similar to RIKEN cDNA 1700016G05	362346	Rn.28920	BF288608	2.65	2.60	2.71	2.62	2.77	2.56	1.00	down	9.69E-01	9.91E-01	-	-
1390596_at	---	---	---	Rn.209770	BF390771	2.27	2.27	2.28	2.27	2.28	2.27	1.00	down	5.96E-01	8.95E-01	-	-
1392916_at	Map7	microtubule-associated protein 7	293016	Rn.23807	BM386695	8.97	8.74	9.45	9.18	8.61	9.39	1.00	up	9.93E-01	9.98E-01	-	-
1396978_at	---	---	---	Rn.60497	BF404424	2.28	2.27	2.29	2.28	2.28	2.27	1.00	down	5.74E-01	8.95E-01	-	-
1385659_at	LOC682861	similar to adenomatosis polyposis coli down-regulated 1	682861	---	AA966596	2.26	2.26	2.28	2.26	2.27	2.26	1.00	down	6.98E-01	9.07E-01	-	-
1381716_at	---	---	---	---	BE108564	2.30	2.29	2.30	2.30	2.29	2.29	1.00	down	6.15E-01	8.95E-01	-	-
1383483_at	Rab9b	RAB9B, member RAS oncogene family	367915	Rn.43853	BE106581	2.28	2.27	2.28	2.28	2.27	2.27	1.00	down	5.69E-01	8.95E-01	-	-
1384686_at	---	---	---	Rn.21956	AI071595	2.29	2.29	2.30	2.29	2.30	2.29	1.00	down	5.38E-01	8.95E-01	-	-
1398299_at	Arhgef11	Rho guanine nucleotide exchange factor (GEF) 11	78966	Rn.160580	NM_023982	2.46	2.45	2.46	2.46	2.45	2.45	1.00	down	5.14E-01	8.95E-01	-	-
1368693_at	Fgr	Gardner-Rasheed feline sarcoma viral (v-fgr) oncogene homolog	79113	Rn.11309	NM_024145	2.29	2.29	2.30	2.29	2.30	2.28	1.00	down	6.54E-01	8.97E-01	-	-
1397035_at	---	---	---	Rn.210628	BF399552	2.29	2.27	2.29	2.28	2.28	2.28	1.00	down	6.40E-01	8.95E-01	-	-
1376330_at	---	---	---	Rn.147324	BF393046	2.27	2.27	2.28	2.27	2.28	2.26	1.00	down	6.34E-01	8.95E-01	-	-
1381117_at	---	---	---	Rn.203357	BF388944	2.40	2.38	2.39	2.39	2.40	2.38	1.00	down	6.69E-01	9.00E-01	-	-
1369162_at	Gucy2c	guanylate cyclase 2C	25711	Rn.10931	NM_013170	2.35	2.34	2.36	2.34	2.36	2.33	1.00	down	7.46E-01	9.18E-01	-	-
1394596_at	---	---	---	Rn.160679	AW531463	2.40	2.39	2.40	2.39	2.39	2.39	1.00	down	5.49E-01	8.95E-01	-	-
1369351_at	Cntn3	contactin 3 (plasmacytoma associated)	54279	Rn.10043	NM_019329	2.26	2.25	2.27	2.26	2.26	2.25	1.00	down	6.35E-01	8.95E-01	-	-
1373318_at	---	---	---	Rn.212195	BI300650	2.34	2.33	2.35	2.34	2.36	2.33	1.00	up	8.14E-01	9.40E-01	-	-
1397521_at	Ilvbl	ilvB (bacterial acetolactate synthase)-like	362843	Rn.22332	BF281905	2.72	2.69	2.76	2.77	2.73	2.68	1.00	up	9.39E-01	9.83E-01	-	-
1376172_at	Abcg4	ATP-binding cassette, sub-family G (WHITE), member 4	300664	Rn.29008	BM390362	2.30	2.30	2.30	2.30	2.30	2.30	1.00	down	3.53E-01	8.95E-01	-	-
1373789_at	---	---	---	Rn.124702	AW254358	2.30	2.29	2.30	2.29	2.29	2.29	1.00	down	4.12E-01	8.95E-01	-	-
1377392_at	---	---	---	Rn.102398	BF389722	2.25	2.24	2.26	2.24	2.25	2.24	1.00	down	6.59E-01	8.98E-01	-	-
1390326_at	Ang1	angiogenin, ribonuclease A family, member 1	305843	Rn.206912	BF564217	2.38	2.37	2.39	2.37	2.39	2.36	1.00	down	7.81E-01	9.29E-01	-	-
1390089_at	---	---	---	Rn.200103	BF403804	2.34	2.33	2.35	2.33	2.34	2.34	1.00	down	7.44E-01	9.17E-01	-	-
1397140_at	---	---	---	---	BF390574	2.30	2.29	2.30	2.29	2.30	2.29	1.00	down	5.63E-01	8.95E-01	-	-
1384543_at	---	---	---	---	BF406553	2.26	2.26	2.27	2.26	2.26	2.25	1.00	down	5.85E-01	8.95E-01	-	-
1380662_at	---	---	---	---	BM386613	2.40	2.39	2.41	2.40	2.41	2.39	1.00	down	6.27E-01	8.95E-01	-	-
1368582_at	Slc7a3	solute carrier family 7 (cationic amino acid transporter, y+ system), member 3	29485	Rn.9804	NM_017217	2.27	2.27	2.28	2.27	2.28	2.26	1.00	down	6.41E-01	8.95E-01	-	-
1384865_at	---	---	---	---	AW535518	2.35	2.34	2.35	2.34	2.35	2.34	1.00	down	6.01E-01	8.95E-01	-	-
1391624_at	---	---	---	Rn.6394	BF283572	2.81	2.80	2.82	2.81	2.82	2.80	1.00	down	7.23E-01	9.12E-01	-	-
1378184_at	Cd200r2	Cd200 receptor 2	501779	Rn.24176	AI012281	2.33	2.32	2.34	2.32	2.34	2.32	1.00	down	7.11E-01	9.10E-01	-	-
1369609_at	Cldn11	claudin 11	84588	Rn.8282	NM_053457	2.28	2.27	2.28	2.28	2.30	2.27	1.00	up	7.99E-01	9.35E-01	-	-
1387731_at	Gja3	gap junction protein, alpha 3	79217	Rn.10345	NM_024376	2.36	2.35	2.37	2.35	2.36	2.35	1.00	down	7.45E-01	9.17E-01	-	-
1380183_at	E683849 /// Prss1	similar to protease, serine, 3 (mesotrypsin) /// similar to Anionic trypsin II prec	7 /// 362348 /// 408	Rn.34435	AI237604	2.23	2.23	2.25	2.24	2.25	2.23	1.00	up	7.75E-01	9.27E-01	-	-
1384627_at	RGD1559597	similar to RIKEN cDNA 2310057N15	501765	Rn.24526	AI598322	2.25	2.25	2.26	2.25	2.26	2.25	1.00	down	5.80E-01	8.95E-01	-	-
1378659_at	---	---	---	Rn.62224	BF413058	2.32	2.31	2.33	2.32	2.33	2.31	1.00	down	7.01E-01	9.07E-01	-	-
1387217_a_at	Ghrh	growth hormone releasing hormone	29446	Rn.10693	NM_031577	2.50	2.49	2.51	2.49	2.50	2.51	1.00	up	7.55E-01	9.20E-01	-	-
1371120_s_at	krb2 /// RGD1306	bradykinin receptor B2 /// similar to RIKEN cDNA 4933433P14 gene	25245 /// 362778	Rn.3701	X69681	2.33	2.32	2.34	2.33	2.34	2.32	1.00	down	6.38E-01	8.95E-01	-	-
1371097_at	---	---	---	---	AF053092	2.31	2.30	2.32	2.31	2.32	2.30	1.00	down	7.06E-01	9.08E-01	-	-
1370103_at	Hcn1	hyperpolarization-activated cyclic nucleotide-gated potassium channel 1	84390	Rn.21408	NM_053375	2.25	2.25	2.26	2.25	2.26	2.24	1.00	down	5.77E-01	8.95E-01	-	-
1386040_at	Klf2	Kruppel-like factor 2 (lung)	306330	Rn.92653	BF288243	2.25	2.24	2.26	2.25	2.25	2.24	1.00	down	6.03E-01	8.95E-01	-	-
1389224_at	---	---	---	Rn.211780	BI296652	2.35	2.34	2.36	2.35	2.36	2.34	1.00	down	7.16E-01	9.10E-01	-	-
1382973_at	Tessp2	testis serine protease 2	301027	Rn.32530	AA945921	2.32	2.31	2.33	2.31	2.33	2.31	1.00	down	7.32E-01	9.14E-01	-	-
1385190_at	---	---	---	Rn.66394	BG376453	2.34	2.33	2.34	2.34	2.35	2.32	1.00	up	7.29E-01	9.13E-01	-	-
1379145_at	---	---	---	Rn.207691	BF386266	2.33	2.32	2.33	2.32	2.33	2.32	1.00	down	6.42E-01	8.95E-01	-	-
1397219_at	---	---	---	Rn.55957	AW921479	2.32	2.31	2.32	2.31	2.32	2.30	1.00	down	6.90E-01	9.05E-01	-	-
1397668_at	---	---	---	Rn.147455	H34328	2.38	2.38	2.39	2.37	2.38	2.38	1.00	down	5.82E-01	8.95E-01	-	-
1383234_at	---	---	---	Rn.44010	BF405850	2.30	2.31	2.30	2.31	2.31	2.30	1.00	down	6.39E-01	8.95E-01	-	-
1396591_at	Pan2	PAN2 polyA specific ribonuclease subunit homolog (S. cerevisiae)	408200	Rn.9091	BI296487	2.40	2.39	2.40	2.39	2.41	2.38	1.00	down	7.88E-01	9.32E-01	-	-
1369207_at	Il7	interleukin 7	25647	Rn.10793	AF367210	2.50	2.47	2.50	2.48	2.51	2.48	1.00	up	8.47E-01	9.52E-01	-	-
1370507_at	Dlgap4	discs, large homolog-associated protein 4 (Drosophila)	286930	Rn.11279	U67140	3.52	3.02	3.46	3.44	3.42	3.92	1.00	down	9.97E-01	9.99E-01	-	-
1368373_at	Rgs7	regulator of G-protein signaling 7	54296	Rn.204219	NM_019343	2.25	2.25	2.26	2.25	2.25	2.24	1.00	down	5.74E-01	8.95E-01	-	-
1370093_at	Htr1f	5-hydroxytryptamine (serotonin) receptor 1F	60448	Rn.44301	NM_021857	2.39	2.38	2.40	2.38	2.40	2.37	1.00	down	7.89E-01	9.32E-01	-	-
1396570_at	---	---	---	Rn.132666	BF393250	2.40	2.39	2.41	2.39	2.40	2.40	1.00	down	5.92E-01	8.95E-01	-	-
1387463_at	Vcsa1	variable coding sequence A1	24867	Rn.9922	M63112	2.26	2.25	2.26	2.26	2.25	2.25	1.00	down	6.51E-01	8.96E-01	-	-
1398692_at	---	---	---	Rn.169071	BF287649	2.41	2.43	2.44	2.44	2.44	2.41	1.00	up	8.46E-01	9.52E-01	-	-
1384684_at	Zmiz1	zinc finger, MIZ-type containing 1	361103	Rn.1712	AI136711	2.27	2.26	2.27	2.27	2.27	2.26	1.00	down	5.27E-01	8.95E-01	-	-
1398290_at	Kcnk13	potassium channel, subfamily K, member 13	64120	Rn.53793	AF287301	2.27	2.27	2.28	2.27	2.28	2.27	1.00	down	6.19E-01	8.95E-01	-	-
1379389_at	---	---	---	Rn.205655	AI409738	2.36	2.34	2.37	2.35	2.37	2.34	1.00	down	8.47E-01	9.52E-01	-	-
1370847_at	Spon2	spondin 2, extracellular matrix protein	171569	Rn.6699	AA801238	2.30	2.29	2.30	2.29	2.30	2.29	1.00	down	5.80E-01	8.95E-01	-	-
1398226_at	---	---	---	Rn.153779	BF413171	2.45	2.43	2.46	2.44	2.47	2.42	1.00	down	8.67E-01	9.58E-01	-	-
1398686_at	---	---	---	Rn.152719	BF288090	2.38	2.38	2.39	2.37	2.39	2.38	1.00	down	6.81E-01	9.03E-01	-	-
1385530_at	Bcas3	breast carcinoma amplified sequence 3	363662	Rn.203379	AI136430	2.36	2.35	2.36	2.35	2.37	2.33	1.00	down	8.10E-01	9.39E-01	-	-
1394647_at	---	---	---	Rn.34167	AA819479	2.79	2.78	2.80	2.79	2.81	2.76	1.00	down	8.59E-01	9.56E-01	-	-
1377862_at	---	---	---	Rn.17298	BI276418	2.36	2.35	2.37	2.35	2.36	2.35	1.00	down	7.16E-01	9.10E-01	-	-
1393603_at	Camp	cathelicidin antimicrobial peptide	316010	Rn.33146	AA998531	2.32	2.31	2.32	2.31	2.32	2.30	1.00	down	6.69E-01	9.00E-01	-	-
1369578_at	Tas2r121	taste receptor, type 2, member 121	78983	Rn.48786	NM_023997	2.28	2.27	2.28	2.27	2.28	2.27	1.00	down	5.49E-01	8.95E-01	-	-
1393053_at	Man1c1	mannosidase, alpha, class 1C, member 1	362625	Rn.29300	AI179443	2.36	2.36	2.36	2.36	2.37	2.34	1.00	down	7.28E-01	9.13E-01	-	-
1390487_at	---	---	---	---	AW531732	2.23	2.23	2.23	2.23	2.23	2.22	1.00	down	4.78E-01	8.95E-01	-	-
1385695_at	Loxl3	lysyl oxidase-like 3	312478	Rn.180192	BI274399	2.35	2.35	2.36	2.35	2.36	2.34	1.00	down	5.91E-01	8.95E-01	-	-
1372226_at	---	---	---	Rn.24476	AI599349	2.28	2.27	2.28	2.27	2.28	2.27	1.00	down	6.78E-01	9.02E-01	-	-
1387285_at	Atp2b2	ATPase, Ca++ transporting, plasma membrane 2	24215	Rn.90982	NM_012508	2.31	2.30	2.32	2.31	2.32	2.30	1.00	down	7.40E-01	9.07E-01	-	-
1397981_at	---	---	---	Rn.155285	BF403833	2.28	2.28	2.29	2.28	2.29	2.27	1.00	down	6.92E-01	9.05E-01	-	-
1377348_at	---	---	---	Rn.210109	BF393968	2.39	2.37	2.38	2.37	2.40	2.37	1.00	up	8.20E-01	9.42E-01	-	-
1381778_at	---	---	---	Rn.52469	BI273900	2.55	2.47	2.62	2.55	2.66	2.55	1.00	up	8.50E-01	9.48E-01	-	-
1394602_at	---	---	---	---	BF414699	2.38	2.36	2.39	2.38	2.38	2.36	1.00	down	8.10E-01	9.39E-01	-	-
1390646_at	---	---	---	---	BE115520	2.25	2.24	2.25	2.25	2.25	2.24	1.00	down	5.74E-01	8.95E-01	-	-
1390639_at	---	---	---	Rn.12227	BM387719	2.31	2.30	2.32	2.31	2.31	2.30	1.00	down	5.63E-01	8.95E-01	-	-
1379458_at	Klhl14	kelch-like 14 (Drosophila)	364823	Rn.39343	AW533900	2.41	2.39	2.41	2.40	2.42	2.38	1.00	down	8.15E-01	9.40E-01	-	-
1379589_at	---	---	---	Rn.23179	AA957878	2.27	2.26	2.28	2.27	2.27	2.26	1.00	down	6.43E-01	8.95E-01	-	-
1394418_at	---	---	---	Rn.168257	BG375036	2.38	2.38	2.40	2.38	2.39	2.38	1.00	down	7.08E-01	9.09E-01	-	-
1382722_at	Scarf1	scavenger receptor class F, member 1	303313	Rn.130912	AI234675	2.27	2.26	2.27	2.27	2.27	2.26	1.00	down	6.12E-01	8.95E-01	-	-
1390196_at	Syn1	Synapsin I	24949	Rn.9923	BG378858	2.26	2.25	2.26	2.26	2.26	2.25	1.00	down	5.07E-01	8.95E-01	-	-
1369012_at	Inhba	inhibin beta-A	29200	Rn.9874	NM_017128	2.30	2.29	2.30	2.30	2.30

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)				REG	MTC
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval		
1385036_at	Sncaip	synuclein, alpha interacting protein	307309	Rn.208536	BE117744	2.47	2.45	2.50	2.45	2.54	2.43	1.00	up	9.43E-01	9.84E-01	-	-
1380923_at	---	---	---	Rn.209682	AI236047	2.39	2.37	2.39	2.41	2.38	2.37	1.00	up	8.45E-01	9.52E-01	-	-
1397751_at	---	---	---	Rn.28552	AI547518	2.45	2.46	2.46	2.45	2.45	2.45	1.00	down	4.94E-01	8.95E-01	-	-
1392569_at	---	---	---	Rn.201887	AA955871	2.43	2.42	2.44	2.42	2.45	2.40	1.00	down	8.52E-01	9.54E-01	-	-
1392139_at	---	---	---	Rn.146614	BE105731	2.37	2.36	2.37	2.36	2.37	2.35	1.00	down	7.45E-01	9.17E-01	-	-
1374358_at	RGD1307648	similar to CG13901-PA	294004	Rn.50057	BE098806	7.18	8.20	7.67	7.65	7.34	8.05	1.00	down	9.94E-01	9.98E-01	-	-
1387486_at	Trim9	tripartite motif-containing 9	155812	Rn.209223	NM_130420	2.51	2.48	2.51	2.49	2.53	2.46	1.00	down	9.13E-01	9.74E-01	-	-
1392857_at	Zscan20	zinc finger and SCAN domain containing 20	500549	Rn.205931	BG381246	2.45	2.49	2.46	2.44	2.41	2.55	1.00	up	9.55E-01	9.87E-01	-	-
1397560_at	---	---	---	Rn.166782	BF284722	2.27	2.26	2.27	2.26	2.27	2.25	1.00	down	6.56E-01	8.98E-01	-	-
1396838_at	---	---	---	---	AW529152	2.28	2.28	2.29	2.28	2.29	2.27	1.00	down	6.19E-01	8.95E-01	-	-
1387764_at	Cebpe	CCAAT/enhancer binding protein (C/EBP), epsilon	25410	Rn.44462	NM_017095	2.30	2.30	2.31	2.30	2.31	2.29	1.00	down	7.52E-01	9.20E-01	-	-
1378456_at	---	---	---	Rn.146546	AI411921	2.34	2.33	2.35	2.35	2.34	2.32	1.00	up	8.19E-01	9.42E-01	-	-
1378577_a_at	Mzf1	myeloid zinc finger 1	361508	Rn.205285	BF407188	2.36	2.37	2.40	2.37	2.39	2.37	1.00	down	8.55E-01	9.55E-01	-	-
1369585_at	Tore	tripanning orphan	64620	Rn.127790	NM_022679	2.28	2.28	2.29	2.28	2.29	2.27	1.00	down	6.67E-01	8.99E-01	-	-
1371261_at	Ptpn2	protein tyrosine phosphatase, non-receptor type 2	117063	Rn.33497	X92747	2.48	2.48	2.52	2.47	2.53	2.50	1.00	up	9.07E-01	9.71E-01	-	-
1374048_at	Nrtn	neurturin	84423	Rn.21952	AI598581	2.25	2.24	2.25	2.25	2.24	2.24	1.00	down	5.58E-01	8.95E-01	-	-
1394688_at	---	---	---	Rn.61595	BM388652	2.30	2.30	2.31	2.30	2.30	2.29	1.00	down	5.62E-01	8.95E-01	-	-
1388093_at	Tas2r126	taste receptor, type 2, member 126	246219	Rn.48794	AF240768	2.28	2.27	2.28	2.27	2.28	2.27	1.00	down	6.58E-01	8.98E-01	-	-
1391080_at	---	---	---	Rn.18547	BM390317	2.24	2.24	2.25	2.24	2.24	2.23	1.00	down	5.59E-01	8.95E-01	-	-
1384244_at	Hsd12	hydroxysteroid dehydrogenase like 2	313200	Rn.203984	AA964752	8.50	8.85	8.88	8.52	8.36	9.35	1.00	down	9.94E-01	9.98E-01	-	-
1380259_at	RGD1311358	similar to RIKEN cDNA 2410017P07	294519	Rn.72531	AI535549	2.56	2.57	2.58	2.57	2.62	2.51	1.00	down	9.34E-01	9.81E-01	-	-
1375693_at	---	---	---	---	AI029772	2.25	2.25	2.26	2.25	2.24	2.24	1.00	down	5.61E-01	8.95E-01	-	-
1378012_at	Sc65	synaptonemal complex protein SC65	59101	Rn.90100	BM389040	2.22	2.21	2.23	2.22	2.22	2.21	1.00	down	5.82E-01	8.95E-01	-	-
1393264_at	RGD1564833	similar to 9630058J23Rik protein	498207	Rn.140701	BG664142	2.51	2.52	2.54	2.53	2.55	2.49	1.00	down	8.89E-01	9.65E-01	-	-
1380337_at	LOC688390	Hypothetical protein LOC688390	688390	Rn.199078	AI454857	2.26	2.25	2.27	2.26	2.26	2.25	1.00	down	6.08E-01	8.95E-01	-	-
1375624_at	Irak4	interleukin-1 receptor-associated kinase 4	300177	Rn.61427	BF405951	2.22	2.21	2.23	2.22	2.22	2.21	1.00	down	7.04E-01	9.07E-01	-	-
1387097_at	Fut2	fucosyltransferase 2 (secretor status included)	58924	Rn.10631	NM_031635	2.31	2.30	2.32	2.30	2.32	2.30	1.00	down	6.94E-01	9.05E-01	-	-
1397151_at	---	---	---	Rn.207911	BE108017	2.40	2.39	2.42	2.40	2.41	2.38	1.00	down	8.31E-01	9.47E-01	-	-
1391668_at	---	---	---	---	AA964735	2.28	2.27	2.28	2.28	2.28	2.27	1.00	down	5.93E-01	8.95E-01	-	-
1382072_at	Olfml2a	olfactomedin-like 2A	296708	Rn.144357	AA944182	2.44	2.43	2.44	2.43	2.44	2.43	1.00	down	5.65E-01	8.95E-01	-	-
1389870_at	02-Mar	membrane-associated ring finger (C3HC4) 2	362849	Rn.145219	AI013040	2.31	2.40	2.33	2.41	2.32	2.32	1.00	down	9.49E-01	9.85E-01	-	-
1378573_at	---	---	---	---	BE109768	2.39	2.40	2.40	2.39	2.41	2.39	1.00	down	7.23E-01	9.12E-01	-	-
1375152_at	---	---	---	---	AI548389	2.45	2.44	2.50	2.45	2.52	2.44	1.00	up	9.34E-01	9.81E-01	-	-
1376759_at	---	---	---	---	BF406241	2.32	2.31	2.33	2.31	2.33	2.31	1.00	down	7.15E-01	9.10E-01	-	-
1392667_at	Vangl2	vang-like 2 (van gogh, Drosophila)	289229	Rn.198958	AI070793	2.36	2.35	2.36	2.35	2.37	2.35	1.00	down	7.19E-01	9.11E-01	-	-
1398748_at	---	---	---	Rn.126353	BF410456	2.26	2.25	2.26	2.25	2.26	2.25	1.00	down	6.54E-01	8.97E-01	-	-
1377024_at	Spink5	serine peptidase inhibitor, Kazal type 5	361319	Rn.106870	BM388334	2.35	2.34	2.36	2.34	2.35	2.34	1.00	down	7.38E-01	9.16E-01	-	-
1379504_at	---	---	---	Rn.16919	AW535155	2.31	2.31	2.32	2.31	2.32	2.30	1.00	down	6.45E-01	8.95E-01	-	-
1379602_at	---	---	---	---	AI010055	2.28	2.28	2.29	2.28	2.29	2.27	1.00	down	6.14E-01	8.95E-01	-	-
1368720_at	Tdo2	tryptophan 2,3-dioxygenase	64206	Rn.1029	NM_022403	2.33	2.32	2.34	2.32	2.34	2.32	1.00	down	7.35E-01	9.15E-01	-	-
1394890_at	---	---	---	---	AI234946	2.25	2.25	2.26	2.25	2.26	2.25	1.00	down	5.90E-01	8.95E-01	-	-
1397133_at	Tdrd1	tudor domain containing 1	292129	Rn.156064	BF412814	2.32	2.31	2.33	2.32	2.32	2.31	1.00	down	6.60E-01	8.98E-01	-	-
1368707_at	Itih4	inter alpha-trypsin inhibitor, heavy chain 4	54404	Rn.11308	NM_019369	2.40	2.39	2.40	2.39	2.41	2.38	1.00	down	7.54E-01	9.20E-01	-	-
1376684_at	Dlgap5	discs, large (Drosophila) homolog-associated protein 5	289997	Rn.3137	AA874827	2.27	2.26	2.27	2.26	2.27	2.26	1.00	down	5.98E-01	8.95E-01	-	-
1387810_at	Keap1	Kelch-like ECH-associated protein 1	117519	Rn.23467	BF414210	2.27	2.26	2.27	2.27	2.28	2.27	1.00	up	6.54E-01	8.97E-01	-	-
1387198_at	Inpp5d	inositol polyphosphate-5-phosphatase D	54259	Rn.10659	NM_019311	2.41	2.41	2.42	2.41	2.43	2.41	1.00	up	7.32E-01	9.14E-01	-	-
1394156_at	LOC683623	Similar to immunoglobulin superfamily, member 3	683623	Rn.165978	AI043758	2.56	2.54	2.55	2.54	2.56	2.53	1.00	down	8.20E-01	9.42E-01	-	-
1374902_at	Iqgap3	IQ motif containing GTPase activating protein 3	310621	Rn.17539	AI071398	2.27	2.27	2.28	2.27	2.26	2.26	1.00	down	5.54E-01	8.95E-01	-	-
1382690_at	Cgm4	carcinoembryonic antigen gene family 4	24257	Rn.25934	AI070180	2.23	2.23	2.24	2.23	2.24	2.23	1.00	down	5.72E-01	8.95E-01	-	-
1386596_at	Spdya	Speedy homolog A (Xenopus laevis)	192209	Rn.19576	BF563673	2.25	2.25	2.26	2.25	2.26	2.24	1.00	down	6.45E-01	8.95E-01	-	-
1382172_at	---	---	---	---	AI228660	2.41	2.39	2.41	2.39	2.41	2.40	1.00	down	6.73E-01	9.01E-01	-	-
1371339_at	Tnni1	troponin I type 1 (skeletal, slow)	29388	Rn.4035	AI559017	2.35	2.35	2.36	2.35	2.35	2.34	1.00	down	5.66E-01	8.95E-01	-	-
1387376_at	Aox1	aldehyde oxidase 1	54349	Rn.15681	NM_019363	2.42	2.41	2.42	2.43	2.42	2.41	1.00	up	6.67E-01	8.99E-01	-	-
1396641_at	---	---	---	---	BF397278	2.28	2.27	2.28	2.27	2.28	2.27	1.00	down	5.88E-01	8.95E-01	-	-
1380972_at	---	---	---	---	AI176450	2.39	2.38	2.40	2.39	2.42	2.38	1.00	up	8.39E-01	9.50E-01	-	-
1389901_at	Dlg4	discs, large homolog 4 (Drosophila)	29495	Rn.9765	BI298083	2.26	2.26	2.27	2.26	2.26	2.26	1.00	down	5.68E-01	8.95E-01	-	-
1387321_at	Atp1b4	ATPase, (Na+)/K+ transporting, beta 4 polypeptide	84396	Rn.160581	NM_053381	2.37	2.36	2.38	2.37	2.38	2.36	1.00	down	7.64E-01	9.23E-01	-	-
1379806_at	---	---	---	Rn.12685	BF550836	2.39	2.39	2.39	2.39	2.41	2.39	1.00	up	7.28E-01	9.13E-01	-	-
1389946_at	RGD1559923	Similar to chromosome 14 open reading frame 35	498489	Rn.15205	BF289341	2.40	2.37	2.41	2.39	2.40	2.38	1.00	down	8.15E-01	9.40E-01	-	-
1388042_at	Kcnh8	potassium voltage-gated channel, subfamily H (eag-related), member 8	246325	Rn.30029	AF061957	2.53	2.52	2.53	2.52	2.53	2.52	1.00	down	6.45E-01	8.95E-01	-	-
1391850_at	---	---	---	Rn.213938	BE116159	2.44	2.44	2.45	2.44	2.45	2.44	1.00	down	6.60E-01	8.98E-01	-	-
1376854_at	---	---	---	Rn.14682	BE110028	2.32	2.31	2.33	2.33	2.32	2.31	1.00	down	7.61E-01	9.22E-01	-	-
1395180_s_at	---	---	---	Rn.200238	AW535140	2.59	2.53	2.62	2.56	2.64	2.56	1.00	up	9.48E-01	9.85E-01	-	-
1395056_at	---	---	---	Rn.82216	BM389046	2.26	2.25	2.26	2.25	2.26	2.25	1.00	down	6.15E-01	8.95E-01	-	-
1391853_at	---	---	---	Rn.147112	AA998997	2.30	2.32	2.30	2.30	2.31	2.30	1.00	down	7.18E-01	9.11E-01	-	-
1383990_at	---	---	---	---	AW534014	2.27	2.27	2.28	2.27	2.27	2.27	1.00	down	3.97E-01	8.95E-01	-	-
1368316_at	Aqp8	aquaporin 8	29172	Rn.6315	NM_019158	2.25	2.24	2.26	2.25	2.25	2.24	1.00	down	6.08E-01	8.95E-01	-	-
1392114_at	---	---	---	Rn.130321	AI555339	2.35	2.34	2.36	2.34	2.36	2.35	1.00	up	6.75E-01	9.01E-01	-	-
1395403_at	Stac3	SH3 and cysteine rich domain 3	362895	Rn.38689	BM385735	2.49	2.48	2.49	2.48	2.49	2.48	1.00	down	5.39E-01	8.95E-01	-	-
1369618_at	Il13	interleukin 13	116553	Rn.9921	NM_053828	2.29	2.29	2.30	2.29	2.32	2.28	1.00	up	8.29E-01	9.46E-01	-	-
1379121_at	Rilpl1	Rab interacting lysosomal protein-like 1	304469	Rn.62627	BE102420	2.22	2.22	2.23	2.22	2.24	2.22	1.00	up	7.51E-01	9.19E-01	-	-
1395201_at	Sspn	Sarcospan	500364	Rn.22364	BE114807	2.47	2.46	2.52	2.47	2.48	2.50	1.00	down	9.04E-01	9.71E-01	-	-
1373325_at	---	---	---	Rn.145388	AF413609	2.29	2.30	2.30	2.31	2.29	2.28	1.00	down	8.03E-01	9.36E-01	-	-
1384430_at	Dph3	DPH3, KTI11 homolog (S. cerevisiae)	680594	Rn.3536	BF390040	2.43	2.39	2.40	2.40	2.41	2.40	1.00	down	8.39E-01	9.50E-01	-	-
1388543_at	Pisqdc1a	phosphatidic acid phosphatase type 2 domain containing 1A	309014	Rn.53410	BI291257	2.26	2.25	2.27	2.26	2.26	2.25	1.00	down	5.80E-01	8.95E-01	-	-
1369389_at	Znf483	zinc finger protein 483	170955	Rn.211991	NM_133422	2.33	2.32	2.33	2.32	2.33	2.31	1.00	down	6.90E-01	9.05E-01	-	-
1379688_at	---	---	---	---	BM389813	2.36	2.35	2.37	2.36	2.37	2.34	1.00	down	8.23E-01	9.43E-01	-	-
1394638_at	Bcl9	B-cell CLL/lymphoma 9	310704	Rn.264	BE096307	2.34	2.34	2.34	2.34	2.34	2.33	1.00	down	5.43E-01	8.95E-01	-	-
1398021_at	81935 /// RGD156	similar to Ral guanine nucleotide dissociation stimulator (RalGEF) (RalGDS)	502047 /// 502055	Rn.43644	AI411984	2.41	2.39	2.41	2.40	2.43	2.39	1.00	up	8.54E-01	9.55E-01	-	-
1380613_at	---	---	---	Rn.209330	BM390334	2.51	2.50	2.52	2.50	2.54	2.50	1.00	up	8.72E-01	9.60E-01	-	-
1395727_at	Rabggta	Rab geranylgeranyltransferase, alpha subunit	58983	Rn.29434	BF291124	2.38	2.36	2.39	2.38	2.39	2.36	1.00	down	8.39E-01	9.50E-01	-	-
1379071_at	B4galt2	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 2	313536	Rn.219217	BF388558	2.55	2.55	2.55	2.54	2.57	2.54	1.00	down	8.14E-01	9.40E-01	-	-
1386540_at	---	---	---	Rn.163608	BG666051	2.30	2.30	2.31	2.30	2.30	2.30	1.00	down	5.25E-01	8.95E-01	-	-
1398737_at	---	---	---	Rn.210547	BF403341	2.36	2.35	2.36	2.35	2.36	2.35	1.00	down	6.70E-01	9.00E-01	-	-
1390363_at	Map6d1	MAP6 domain containing 1	363823	Rn.39369	AI556913	2.25	2.24	2.26	2.25	2.25	2.24	1.00	down	6.05E-01	8.95E-01	-	-
1389630_at	---	---	---	Rn.18224	AI168941	2.41	2.37	2.42	2.41	2.45	2.39	1.00	up	8.76E-01	9.61E-01	-	-
1383434_at	Pycr1	pyrroline-5-carboxylate reductase 1	287877	Rn.99704	AA997640	2.43	2.42	2.46	2.43	2.45	2.42	1.00	down	8.57E-01	9.55E-01	-	-
1372599_at	Mgst2	microsomal glutathione S-transferase 2	295037	Rn.7854	BI290559	2.35	2.34	2.36	2.34	2.35	2.34	1.00	down	6.26E-01	8.95E-01	-	-
1392354_at	---	---	---	Rn.205947	AW529939	2.43	2.42	2.45	2.42	2.48	2.39	1.00	down	9.29E-01	9.80E-01	-	-
1380991_at	Ptar1	Protein prenyltransferase alpha subunit repeat containing 1	286972	Rn.107234	AI145767	2.31	2.30	2.31	2.30	2.31	2.30	1.00	down	4.67E-01	8.95E-01	-	-
1381911_at	Lmod3	Leiomodin 3 (fetal)	500267	Rn.91424	AW251138	2.31	2.30	2.31	2.30	2.32	2.30	1.00	up	7.18E-01	9.11E-01	-	-
1391529_at	Gpx4	glutathione peroxidase 4	29328	Rn.3647	AI073125	2.42	2.42	2.42	2.42	2.42	2.41	1.00	down	5.11E-01	8.95E-01	-	-
1387842_at	Syt8	synaptotagmin VIII	60566	Rn.46519	NM_053325	2.28	2.27	2.28	2.27	2.27	2.27	1.00	down	5.33E-01	8.95E-01	-	-
1379988_a_at	LOC305633	similar to Antxr2 protein	305633	Rn.203300	AI236937	2.28	2.28	2.29	2.28	2.29	2.28	1.00	down	5.16E-01	8.95E-01	-	-
1368353_at	Gfap	glial fibrillary acidic protein	24387	Rn.91512	NM_017009	2.24	2.24	2.25	2.24	2.25	2.24	1.00	down	5.71E-01	8.95E-01	-	-
1376742_at	---	---	---	---	BF396436	2.45	2.44	2.46	2.45	2.44	2.44	1.00	down	6.41E-01	8.95E-01	-	-
1379175_at	---	---	---	Rn.209439	BF388224	2.35	2.34	2.35	2.34	2.36	2.34	1.00	up	7.75E-01	9.27E-01	-	-
1370409_at	Slc38a1	solute carrier family 38, member 1	170567	Rn.162022	AF075704	2.22	2.22	2.23	2.22	2.23	2.22	1.00	down	5.39E-01	8.95E-01	-	-
1379629_at	---	---	---	Rn.156475	BE118613	2.30	2.30	2.31	2.30	2.31	2.29	1.00	down	5.99E-01	8.95E-01	-	-
1394796_at	Mark4	MAP/microtubule affinity-regulating kinase 4	680407	Rn.98278	AA964964	2.31	2.30	2.32	2.31	2.31	2.30	1.00	down	6.04E-01	8.95E-01	-	-
1387155_at	Pcsk2	proprotein convertase subtilisin/kexin type 2	25121	Rn.89052	NM_012746	2.38	2.36	2.41	2.37	2.41	2.36	1.00	down	8.95E-01	9.67E-01	-	-
1386122_at	Wnt8b	wingless-type MMTV integration site family, member 8B	293990	Rn.58872	BI397665	2.31	2.30	2.31	2.30	2.31	2.30	1.00	down	6.49E-01	8.96E-01	-	-
1368717_at	Faah	fatty acid amide hydrolase	29347	Rn.89110	NM_024132	2.40	2.41	2.42	2.42	2.42	2.38	1.00	down	8.73E-01	9.61E-01	-	-
1379468_at	---	---	---	Rn.148577	BI281734	2.31	2.30	2.32	2.31	2.31	2.30	1.00	down	6.79E-01	9.02E-01	-	-
1378788_at	Znf474	zinc finger protein 474	307310	Rn.163374	AW535970	2.54	2.53	2.55	2.54	2.55	2.52	1.00	down	8.08E-01	9.38E-01	-	-
1369831_at	Bcan	brevican	25393	Rn.10315	NM_012916	2.24	2.24	2.25	2.24	2.24	2.23	1.00	down	5.12E-01	8.95E-01	-	-
1369916_at	Klrh1	killer cell lectin-like receptor subfamily H, member 1	246043	Rn.83604	NM_139187	2.33	2.32	2.34	2.33	2.34	2.32	1.00	down	7.80E-01	9.28E-01	-	-
1378234_at	---	---	---	Rn.205565	BF524457	2.65	2.64	2.65	2.64	2.65	2.64	1.00	down	6.14E-01	8.95E-01	-	-
1394716_at	---	---	---	---	AI011137	2.35	2.34	2.35	2.34	2.35	2.34	1.00	down	5.96E-01	8.95E-01	-	-
1378832_at	---	---	---	---	BF386602	3.07	2.72	2.96	2.99	2.90	2.88	1.00	up	9.82E-01	9.94E-01	-	-
1385412_at	---	---	---	---	AI556003	2.38	2.38	2.39	2.38	2.38	2.37	1.00	down	5.37E-01	8.95E-01	-	-
1368978_at	Scrg1	scrapie responsive gene 1	64458	Rn.7724	NM_033499	2.32	2.31	2.32	2.31	2.32	2.30	1.00	down	7.04E-01	9.07E-01	-	-
1369507_at	V1r5	vomeronasal 1 receptor, B5	497787	Rn.10142	NM_133301	2.37	2.35	2.38	2.37	2.38	2.35	1.00	down	8.53E-01	9.54E-01	-	-
1398467_at	---	---	---	Rn.154666	BF396823	2.41	2.40	2.41	2.41	2.41	2.40	1.00	down	5.78E-01	8.95E-01	-	-
1373847_at	Tm4sf1	transmembrane 4 L six family member 1	295061	Rn.24712	AW435343	2.35	2.35	2.36	2.35	2.36	2.35	1.00	down	5.83E-01	8.95E-01	-	-
1384825_at	LOC499089	similar to pregnancy-specific glycoprotein 25	499089	Rn.161809	AI178814	2.40	2.39	2.42	2.40	2.42	2.38	1.00	down	8.56E-01	9.55E-01	-	-
1382559_at	Pax9	paired box 9	362741	Rn.82416	AA957339	2.56	2.54	2.56	2.55	2.56	2.56	1.00	up	7.33E-01	9.14E-01	-	-
1387431_at	Kab	KARP-1 binding protein 1	171457	Rn.6424	NM_134416	2.54	2.53	2.56	2.58	2.56	2.50	1.00	up	9.28E-01	9.80E-01	-	-
1398158_at	---	---	---	Rn.211053	BF405012	2.30	2.30	2.31	2.31	2.31	2.29	1.00	up	8.04E-01	9.37E-01	-	-
1374991_at	Ydjc	YdjC homolog (bacterial)	287938	Rn.144719	BE107630	2.45	2.43	2.49	2.44	2.48	2.45	1.00	down	9.02E-01	9.70E-01	-	-
1377205_at	RGD1308759	similar to KIAA0892 protein	290668	Rn.49215	BE107410	2.30	2.30	2.31	2.30	2.31	2.29	1.00	down	5.49E-01	8.95E-01	-	-
1397061_at	---	---	---	---	BF394045	2.32	2.31	2.33	2.32	2.32	2.32	1.00	down	6.88E-01	9.04E-01	-	-
1381020_at	---	---	---	---	BE102110	2.32	2.31	2.33	2.34	2.33	2.31	1.00	up	8.09E-01	9.38E-01	-	-
1379610_at	---	---	---	Rn.64135	BF409025	2.34	2.33	2.35	2.34	2.34	2.34	1.00	down	6.32E-01	8.95E-01	-	-
1379030_at	---	---	---	---	AI549346	2.30	2.29	2.31	2.29	2.30	2.29	1.00	down	6.29E-01	8.95E-01	-	-
1368902_at	Pak3	p21 protein (Cdc42/Rac)-activated kinase 3	29433	Rn.10128	NM_019210	2.27	2.27	2.28	2.27	2.28	2.26	1.00	down	6.84E-01	9.03E-01	-	-
1379617_at	---	---	---	Rn.167240	BF288779	2.30	2.29	2.31	2.30	2.30	2.29	1.00	down	6.81E-01	9.03E-01	-	-
1384130_at	RGD1560171	similar to PRO0149 protein	367949	Rn.96135	AA875572	2.40	2.40	2.41	2.40	2.41	2.39	1.00	down	6.67E-01	8.99E-01	-	-
1368851_at	Ets1	v-ets erythroblastosis virus E26 oncogene homolog 1 (avian)	24356	Rn.88756	NM_012555	2.69	2.68	2.69	2.68	2.69	2.67	1.00	down	7.36E-01	9.15E-01	-	-
1380114_at	---	---	---	Rn.43878	BI289106	2.32	2.30	2.32	2.31	2.32	2.30	1.00	down	7.00E-01	9.07E-01	-	-
1393540_at	---	---	---	Rn.203434	AA924346	2.30	2.30	2.31	2.30	2.30	2.29	1.00	down	6.13E-01	8.95E-01	-	-
1397107_at	---	---	---	Rn.207987	BE114486	2.31	2.31	2.37	2.31	2.36	2.30	1.00	down	9.25E-01	9.78E-01	-	-
1382311_at	Tifa	TRAF-interacting protein with forkhead-associated domain	310877	Rn.136924	BM384466	2.30	2.29	2.31	2.30	2.30	2.30	1.00	down	5.93E-01	8.95E-01	-	-
1378713_at	---	---	---	Rn.211170	BF406829	2.41	2.40	2.63	2.64	2.41	2.39	1.00	up	9.82E-01	9.95E-01	-	-
1373360_at	---	---	---	Rn.209821	BF398966	2.39	2.38	2.39	2.38	2.40	2.37	1.00	down	8.33E-01	9.47E-01	-	-
1378792_at	RGD1564091	similar to Kiaa0575	500633	---	BE105401	2.40	2.39	2.40	2.39	2.40	2.39	1.00	down	6.23E-01	8.95E-01	-	-
1380988_at	---	---	---	Rn.63301	BF405096	2.38	2.36	2.39	2.37	2.40	2.36	1.00	down	8.63E-01	9.58E-01	-	-
1388243_at	Gpr176	G protein-coupled receptor 176	117257	Rn.44656	BG663422	2.37	2.36	2.38	2.36	2.38	2.36	1.00	down	7.39E-01	9.16E-01	-	-
1375786_at	---	---	---	---	BF413396	2.28	2.28	2.29	2.28	2.29	2.28	1.00	down	6.23E-01	8.95E-01	-	-
1382669_at	Bin2a	bone-galactosidase-like protein	494244	Rn.16177	AI045311	2.30	2.29	2.31	2.30	2.31	2.29	1.00	down	6.67E-01	8.99E-01	-	-
1390198_at	Suv420h1	suppressor of variegation 4-20 homolog 1 (Drosophila)	361688	Rn.203473	AW523642	4.01	4.46	4.10	3.98	4.21	4.39	1.00	up	9.89E-01	9.96E-01	-	-
1385914_at	Irx5	Iroquois homeobox 5	498918	Rn.141335	AI714147	2.56	2.56	2.57	2.56	2.56	2.55	1.00	down	5.84E-01	8.95E-01	-	-
1388496_at	Flnc	filamin C, gamma (actin binding protein 280)	362332	Rn.22352	AI103600	2.39	2.38	2.39	2.39	2.39	2.38	1.00	down	6.75E-01	9.01E-01	-	-
1386948_at	Nes	nestin	25491	Rn.9701	NM_012987	2.40	2.40	2.39	2.39	2.41	2.39	1.00	down	6.87E-01	9.04E-01	-	-
1371222_at	Lepr	le

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1386189_at	---	---	---	Rn.133717	AI639145	2.29	2.28	2.28	2.28	2.29	2.27	1.00	down	5.40E-01	8.95E-01	-	-
1387226_at	Ina	internexin neuronal intermediate filament protein, alpha	24503	Rn.88941	NM_019128	2.36	2.36	2.37	2.36	2.37	2.36	1.00	down	5.89E-01	8.95E-01	-	-
1376139_at	Plxna3	plexin A3	309280	Rn.21101	BI295513	2.27	2.27	2.28	2.27	2.27	2.28	1.00	up	5.73E-01	8.95E-01	-	-
1377426_at	---	---	---	Rn.202483	BF403541	2.29	2.29	2.30	2.29	2.30	2.28	1.00	down	7.48E-01	9.18E-01	-	-
1397064_at	---	---	---	Rn.147520	BE114456	2.31	2.30	2.32	2.30	2.32	2.30	1.00	down	7.80E-01	9.28E-01	-	-
1387224_at	Dgkb	diacylglycerol kinase, beta	54248	Rn.11413	NM_019304	2.30	2.29	2.31	2.30	2.31	2.29	1.00	down	7.69E-01	9.24E-01	-	-
1384736_at	---	---	---	Rn.23120	AA956799	2.29	2.28	2.29	2.28	2.30	2.28	1.00	up	7.50E-01	9.19E-01	-	-
1387320_a_at	Lrrc7	leucine rich repeat containing 7	117284	Rn.89629	AF266164	2.38	2.37	2.40	2.38	2.39	2.37	1.00	down	7.59E-01	9.22E-01	-	-
1392058_at	Txnl1	thioredoxin-like 1	140922	Rn.40430	BF400044	2.40	2.42	2.44	2.42	2.43	2.41	1.00	up	8.54E-01	9.55E-01	-	-
1369817_at	Hand2	heart and neural crest derivatives expressed 2	84637	Rn.41057	NM_022696	2.40	2.39	2.42	2.40	2.41	2.39	1.00	down	8.12E-01	9.39E-01	-	-
1388928_at	Cfl2	cofilin 2, muscle	366624	Rn.101880	BF399310	5.79	5.85	6.56	5.52	6.16	6.52	1.00	down	9.95E-01	9.98E-01	-	-
1393979_at	---	---	---	---	AA875203	2.24	2.23	2.24	2.24	2.24	2.23	1.00	down	5.92E-01	8.95E-01	-	-
1395301_x_at	LOC685157	similar to paired immunoglobin-like type 2 receptor beta	685157	Rn.154833	AI555307	2.26	2.26	2.27	2.26	2.27	2.25	1.00	down	6.40E-01	8.95E-01	-	-
1375611_at	---	---	---	Rn.23602	AI112487	2.30	2.29	2.30	2.30	2.30	2.29	1.00	down	6.28E-01	8.95E-01	-	-
1397567_at	---	---	---	Rn.43132	BI273995	2.25	2.24	2.25	2.24	2.25	2.24	1.00	down	6.05E-01	8.95E-01	-	-
1375262_at	Egln1	EGL nine homolog 1 (C. elegans)	308913	Rn.44718	AW252715	2.28	2.28	2.29	2.28	2.29	2.27	1.00	down	6.67E-01	8.99E-01	-	-
1377411_at	---	---	---	Rn.60219	BF404135	2.36	2.35	2.37	2.35	2.37	2.35	1.00	down	7.72E-01	9.28E-01	-	-
1395691_at	Klhl22	Kelch-like 22 (Drosophila)	303792	Rn.23143	BF416203	2.26	2.26	2.26	2.25	2.26	2.25	1.00	down	4.67E-01	8.95E-01	-	-
1378617_at	Trerf1	transcriptional regulating factor 1	316219	Rn.91677	BM390846	2.33	2.32	2.33	2.33	2.33	2.32	1.00	down	5.28E-01	8.95E-01	-	-
1396556_at	---	---	---	Rn.52205	BF413386	2.40	2.38	2.40	2.39	2.41	2.37	1.00	down	8.54E-01	9.55E-01	-	-
1393667_at	Zmat4	zinc finger, matrin type 4	684961	Rn.61258	BE106620	2.28	2.27	2.29	2.28	2.28	2.27	1.00	down	7.27E-01	9.13E-01	-	-
1378957_at	RGD1564776	Similar to ornithine decarboxylase-like protein	500550	Rn.6427	AA849112	2.31	2.31	2.32	2.31	2.32	2.31	1.00	down	6.04E-01	8.95E-01	-	-
1391575_at	Hapln4	hyaluronan and proteoglycan link protein 4	361129	Rn.98352	BG380566	2.27	2.26	2.27	2.27	2.27	2.25	1.00	down	7.12E-01	9.10E-01	-	-
1383468_at	---	---	---	Rn.22683	BM958512	2.38	2.36	2.39	2.37	2.39	2.36	1.00	down	8.52E-01	9.54E-01	-	-
1378135_at	---	---	---	Rn.41204	AI710574	2.35	2.34	2.36	2.35	2.36	2.34	1.00	down	7.60E-01	9.22E-01	-	-
1387565_at	Trpv6	transient receptor potential cation channel, subfamily V, member 6	114246	Rn.205943	NM_053686	2.34	2.33	2.34	2.34	2.34	2.33	1.00	down	6.18E-01	8.95E-01	-	-
1393355_at	Grm5	glutamate receptor, metabotropic 5	24418	Rn.29972	NM_017012	2.32	2.31	2.32	2.31	2.32	2.31	1.00	down	6.78E-01	9.02E-01	-	-
1396532_at	---	---	---	Rn.154216	BG662870	2.36	2.36	2.37	2.36	2.37	2.35	1.00	down	7.18E-01	9.11E-01	-	-
1377036_at	---	---	---	Rn.203304	BE102350	2.31	2.30	2.31	2.30	2.31	2.31	1.00	up	6.24E-01	8.95E-01	-	-
1380253_at	---	---	---	Rn.148854	BE102139	2.56	2.54	2.62	2.56	2.63	2.55	1.00	up	9.44E-01	9.84E-01	-	-
1384704_at	---	---	---	---	BE112917	2.23	2.23	2.24	2.23	2.24	2.22	1.00	down	6.04E-01	8.95E-01	-	-
1381300_at	RGD1562390	similar to RGD, leucine-rich repeat, tropomodulin and proline-rich containing p	307797	Rn.154883	AI234603	2.56	2.50	2.52	2.50	2.58	2.49	1.00	up	9.41E-01	9.83E-01	-	-
1381249_at	---	---	---	Rn.169275	BF390089	2.37	2.37	2.37	2.37	2.37	2.37	1.00	down	4.15E-01	8.95E-01	-	-
1387922_at	Crispld2	cysteine-rich secretory protein LCCL domain containing 2	171547	Rn.4346	AF1096874	2.37	2.36	2.38	2.37	2.38	2.37	1.00	down	7.15E-01	9.10E-01	-	-
1369836_at	Ifit1	interferon-induced protein with tetratricopeptide repeats 1	56824	Rn.48677	NM_020096	2.23	2.22	2.23	2.22	2.23	2.22	1.00	down	5.76E-01	8.95E-01	-	-
1377177_at	Irx1	iroquois homeobox 1	306659	Rn.46018	BE099446	2.41	2.41	2.41	2.40	2.41	2.40	1.00	down	4.23E-01	8.95E-01	-	-
1397367_at	LOC689663	hypothetical protein LOC689663	689663	Rn.167316	AI501213	2.29	2.29	2.30	2.29	2.30	2.28	1.00	down	6.41E-01	8.95E-01	-	-
1397360_at	Clec3a	C-type lectin domain family 3, member a	365009	Rn.82624	BM389024	2.49	2.46	2.52	2.47	2.55	2.44	1.00	down	9.51E-01	9.86E-01	-	-
1387694_at	Cnga4	cyclic nucleotide gated channel alpha 4	85258	Rn.91104	U12425	2.36	2.35	2.36	2.35	2.36	2.34	1.00	down	7.36E-01	9.15E-01	-	-
1376048_at	Guca1b	guanylate cyclase activator 1B	316218	Rn.38113	BG373370	2.46	2.44	2.46	2.46	2.47	2.42	1.00	up	8.83E-01	9.64E-01	-	-
1378090_at	---	---	---	Rn.7558	BE109128	2.29	2.29	2.30	2.29	2.30	2.28	1.00	down	7.19E-01	9.11E-01	-	-
1385056_at	Msh5	mutS homolog 5 (E. coli)	294252	Rn.44043	BG372572	2.45	2.44	2.46	2.44	2.45	2.44	1.00	down	7.14E-01	9.10E-01	-	-
1381323_at	Rbbp5	retinoblastoma binding protein 5	304794	Rn.11774	BG381396	4.28	4.89	6.03	5.49	5.00	4.72	1.00	up	9.97E-01	9.98E-01	-	-
1397683_at	Wdr55	WD repeat domain 55	307494	Rn.162302	BM386779	2.44	2.42	2.45	2.43	2.44	2.42	1.00	down	8.14E-01	9.40E-01	-	-
1398165_at	---	---	---	Rn.147547	BF399452	2.25	2.25	2.26	2.25	2.26	2.25	1.00	down	6.04E-01	8.95E-01	-	-
1369544_a_at	Hoxa1	homeo box A1	25607	Rn.9780	U93093	2.24	2.23	2.24	2.24	2.24	2.23	1.00	down	5.73E-01	8.95E-01	-	-
1369827_at	Clstn3	calsyntenin 3	171393	Rn.162785	NM_134376	2.26	2.26	2.27	2.26	2.27	2.25	1.00	down	6.00E-01	8.95E-01	-	-
1370561_at	A3galt2	alpha 1,3-galactosyltransferase 2	171553	Rn.37737	AF248543	2.30	2.30	2.30	2.30	2.30	2.29	1.00	down	5.42E-01	8.95E-01	-	-
1396981_at	Panx1	Pannexin 1	315435	Rn.204521	BM390744	2.31	2.31	2.32	2.31	2.32	2.31	1.00	down	5.00E-01	8.95E-01	-	-
1395467_at	Cpne6	copine VI	691478	Rn.99541	AI145705	2.44	2.42	2.45	2.44	2.45	2.44	1.00	up	7.88E-01	9.24E-01	-	-
1369859_at	Nr5a1	nuclear receptor subfamily 5, group A, member 1	83826	Rn.6586	NM_053344	2.33	2.32	2.33	2.32	2.33	2.32	1.00	down	6.11E-01	8.95E-01	-	-
1393590_at	Col23a1	collagen, type XXIII, alpha 1	353303	Rn.206241	AW524253	2.29	2.28	2.29	2.28	2.29	2.28	1.00	down	5.66E-01	8.95E-01	-	-
1396506_at	---	---	---	---	AT006336	2.39	2.37	2.39	2.38	2.39	2.38	1.00	down	7.68E-01	9.24E-01	-	-
1382116_at	RGD1563510	similar to RIKEN cDNA 8430427H17 gene	362240	Rn.162697	AW529348	2.34	2.33	2.34	2.34	2.34	2.32	1.00	down	7.37E-01	9.15E-01	-	-
1388183_at	Csn1s1	casein alpha s1	24284	Rn.10744	J00710	2.32	2.31	2.33	2.31	2.32	2.30	1.00	down	7.83E-01	9.30E-01	-	-
1374643_at	Fat4	FAT tumor suppressor homolog 4 (Drosophila)	310341	Rn.30629	BF288461	2.36	2.34	2.35	2.35	2.38	2.33	1.00	up	8.77E-01	9.62E-01	-	-
1378171_at	---	---	---	Rn.204859	BF409060	2.31	2.31	2.32	2.31	2.31	2.31	1.00	down	5.81E-01	8.95E-01	-	-
1392200_a_at	Fam132a	family with sequence similarity 132, member A	313774	Rn.16254	AI045555	2.53	2.82	2.57	2.52	2.90	2.51	1.00	up	9.88E-01	9.98E-01	-	-
1380524_at	Krt86	keratin 86	407760	Rn.12519	AA997356	2.82	2.82	2.83	2.82	2.83	2.82	1.00	down	5.21E-01	8.95E-01	-	-
1389741_at	Lass4	LAG1 homolog, ceramide synthase 4	304208	Rn.128409	BE111727	2.35	2.34	2.36	2.35	2.35	2.34	1.00	down	6.35E-01	8.95E-01	-	-
1370445_at	Pla1a	phospholipase A1 member A	85311	Rn.10696	D88666	2.28	2.28	2.29	2.28	2.29	2.27	1.00	down	7.20E-01	9.11E-01	-	-
1370472_a_at	Kcnma1	potassium large conductance calcium-activated channel, subfamily M, alpha	81731	Rn.30616	AF135285	2.38	2.37	2.39	2.38	2.39	2.37	1.00	down	7.77E-01	9.28E-01	-	-
1384162_at	Csmp2	cysteine-serine-rich nuclear protein 2	315308	Rn.24286	BI285660	2.28	2.27	2.28	2.27	2.28	2.26	1.00	down	7.22E-01	9.12E-01	-	-
1378866_at	---	---	---	Rn.202781	BF401176	2.34	2.33	2.34	2.33	2.34	2.33	1.00	down	6.83E-01	9.03E-01	-	-
1396544_at	Rspo3	R-spondin 3 homolog (Xenopus laevis)	498997	Rn.15751	BF399557	2.32	2.32	2.33	2.32	2.33	2.31	1.00	down	7.79E-01	9.28E-01	-	-
1388079_at	Cacng8	calcium channel, voltage-dependent, gamma subunit 8	140729	Rn.207527	AF361346	2.35	2.34	2.35	2.34	2.35	2.34	1.00	down	7.02E-01	9.07E-01	-	-
1396605_at	Mov10l1	Mov10l1, Moloney leukemia virus 10-like 1, homolog (mouse)	300141	Rn.53760	BE121147	2.41	2.39	2.42	2.40	2.42	2.40	1.00	down	8.24E-01	9.44E-01	-	-
1384965_at	Stk	STE20-like kinase (yeast)	54308	Rn.33275	BI281936	2.53	2.74	3.15	2.83	2.58	2.99	1.00	down	9.91E-01	9.97E-01	-	-
1395028_at	---	---	---	Rn.61209	BF387787	2.26	2.26	2.27	2.26	2.25	2.25	1.00	down	6.20E-01	8.95E-01	-	-
1388289_s_at	Fshb	follicle stimulating hormone, beta polypeptide	25447	Rn.92303	D00577	2.55	2.51	2.56	2.53	2.56	2.52	1.00	down	9.09E-01	9.72E-01	-	-
1368489_at	Fosl1	fos-like antigen 1	25445	Rn.11306	NM_012953	2.26	2.26	2.26	2.26	2.26	2.25	1.00	down	6.14E-01	8.95E-01	-	-
1387723_at	Sema3a	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (se	29751	Rn.44410	NM_017310	2.43	2.42	2.44	2.42	2.44	2.42	1.00	down	7.74E-01	9.26E-01	-	-
1368445_at	Shank1	SH3 and multiple ankyrin repeat domains 1	78957	Rn.144602	NM_031751	2.20	2.19	2.20	2.19	2.20	2.19	1.00	down	5.11E-01	8.95E-01	-	-
1394960_at	Sdr42e1	short chain dehydrogenase/reductase family 42E, member 1	307897	Rn.32783	AA955070	2.25	2.24	2.25	2.24	2.25	2.24	1.00	down	6.18E-01	8.95E-01	-	-
1391122_at	---	---	---	Rn.161005	BE110610	2.35	2.34	2.35	2.34	2.35	2.34	1.00	down	7.34E-01	9.15E-01	-	-
1387899_at	Crmp1	collapsin response mediator protein 1	25415	Rn.11379	U52102	2.43	2.43	2.44	2.43	2.44	2.42	1.00	down	7.16E-01	9.10E-01	-	-
1381082_at	RGD1564357	RGD1564357	502306	Rn.59107	BF398539	2.38	2.37	2.39	2.38	2.38	2.37	1.00	down	7.20E-01	9.11E-01	-	-
1390920_at	---	---	---	---	AI145802	2.26	2.26	2.27	2.26	2.27	2.26	1.00	down	5.87E-01	8.95E-01	-	-
1392118_at	---	---	---	Rn.3109	BE099845	2.33	2.33	2.34	2.34	2.35	2.33	1.00	up	7.41E-01	9.17E-01	-	-
1380043_at	LOC688890	hypothetical protein LOC688890	688890	Rn.168767	AA944436	2.32	2.31	2.33	2.32	2.33	2.31	1.00	down	7.09E-01	9.09E-01	-	-
1381015_at	---	---	---	Rn.153888	BM386901	2.38	2.37	2.39	2.38	2.39	2.37	1.00	down	8.03E-01	9.37E-01	-	-
1371577_at	Ndufs1	NADH dehydrogenase (ubiquinone) Fe-S protein 1	301458	Rn.1467	AI171362	8.56	8.73	8.57	8.73	8.20	8.93	1.00	up	9.92E-01	9.97E-01	-	-
1388248_at	---	---	---	Rn.202941	L26293	2.41	2.40	2.42	2.40	2.43	2.39	1.00	down	8.50E-01	9.53E-01	-	-
1381415_at	---	---	---	---	AI070192	2.24	2.24	2.25	2.24	2.24	2.23	1.00	down	5.50E-01	8.95E-01	-	-
1389236_at	Mybphl	myosin binding protein H-like	310782	Rn.139442	AI104915	2.32	2.32	2.33	2.32	2.33	2.31	1.00	down	6.87E-01	9.04E-01	-	-
1393530_at	---	---	---	Rn.16787	AI044044	2.29	2.28	2.29	2.28	2.29	2.28	1.00	down	6.44E-01	8.95E-01	-	-
1383143_at	Ephb2	Eph receptor B2	313633	Rn.27233	BF549473	2.28	2.27	2.28	2.27	2.28	2.27	1.00	down	6.44E-01	8.95E-01	-	-
1395960_at	LOC688276	similar to epidermodysplasia verruciformis 2	688276	Rn.216854	BI301495	2.44	2.44	2.48	2.43	2.49	2.43	1.00	down	9.17E-01	9.75E-01	-	-
1369053_at	Syt2	synaptotagmin II	24805	Rn.88574	NM_012665	2.27	2.27	2.28	2.27	2.28	2.26	1.00	down	6.85E-01	9.03E-01	-	-
1385813_at	RGD1310251	similar to RIKEN cDNA 2010001M09	291675	Rn.19595	AI069938	2.30	2.30	2.31	2.30	2.30	2.29	1.00	down	5.99E-01	8.95E-01	-	-
1369910_at	Prthr	prolactin releasing hormone receptor	246075	Rn.138127	NM_139193	2.32	2.32	2.33	2.32	2.35	2.31	1.00	up	8.62E-01	9.57E-01	-	-
1370352_at	/// Es22 /// rCG_4	carboxylesterase-like 1 /// esterase 22 /// carboxylesterase ES-4	5372 /// 29225 /// 5	Rn.82692	AB023630	11.41	11.36	11.25	11.22	11.56	11.50	1.00	down	9.85E-01	9.96E-01	-	-
1381440_at	---	---	---	---	AI548182	2.51	2.50	2.52	2.51	2.52	2.50	1.00	down	7.74E-01	9.28E-01	-	-
1394628_at	---	---	---	---	AI234854	2.38	2.37	2.38	2.37	2.39	2.37	1.00	up	7.17E-01	9.10E-01	-	-
1385041_at	Sorcs3	sortilin-related VPS10 domain containing receptor 3	294043	Rn.46999	BF409626	2.29	2.29	2.30	2.29	2.29	2.28	1.00	down	6.32E-01	8.95E-01	-	-
1391645_at	---	---	---	Rn.205509	BF393822	2.39	2.36	2.39	2.38	2.39	2.36	1.00	down	8.56E-01	9.55E-01	-	-
1371142_at	Cyp2g1	cytochrome P450, subfamily 2G, polypeptide 1	25251	Rn.10909	M33296	2.28	2.28	2.28	2.27	2.30	2.27	1.00	up	7.87E-01	9.31E-01	-	-
1388980_at	MGC72560	hypothetical LOC308869	308869	Rn.121836	BG381728	7.61	7.89	7.91	7.69	7.42	8.29	1.00	down	9.93E-01	9.98E-01	-	-
1382450_at	---	---	---	Rn.48596	AA998804	2.26	2.26	2.27	2.26	2.26	2.25	1.00	down	6.03E-01	8.95E-01	-	-
1373987_at	Kcnip2	Kv channel-interacting protein 2	56817	Rn.98394	AI410448	2.33	2.32	2.33	2.32	2.34	2.31	1.00	down	7.99E-01	9.35E-01	-	-
1381406_at	RGD1561734	Similar to KIAA1913	501201	Rn.121539	AI763954	2.24	2.24	2.24	2.24	2.24	2.23	1.00	down	5.05E-01	8.95E-01	-	-
1388596_at	Coil1	coactosin-like 1 (Dictyostelium)	361422	Rn.98506	AI411057	9.17	10.16	9.71	9.56	9.78	9.69	1.00	down	9.94E-01	9.98E-01	-	-
1378023_at	---	---	---	Rn.204947	AW532259	2.31	2.30	2.31	2.30	2.31	2.30	1.00	down	6.55E-01	8.98E-01	-	-
1392577_at	Map3k3	mitogen activated protein kinase kinase kinase 3	303604	Rn.72680	AA925300	2.40	2.39	2.41	2.40	2.41	2.39	1.00	down	7.17E-01	9.10E-01	-	-
1376522_at	---	---	---	Rn.212200	BI291288	2.32	2.32	2.32	2.32	2.32	2.31	1.00	down	4.89E-01	8.95E-01	-	-
1397712_at	Esco1	establishment of cohesion 1 homolog 1 (S. cerevisiae)	680014	Rn.19439	BF290256	2.73	2.59	3.01	2.68	2.74	2.90	1.00	down	9.87E-01	9.98E-01	-	-
1392735_at	---	---	---	Rn.92773	AI229265	2.37	2.36	2.37	2.37	2.39	2.35	1.00	up	8.48E-01	9.53E-01	-	-
1388283_at	RT1-CE3	RT1 class I, CE3	414793	---	AB002169	2.31	2.30	2.32	2.30	2.32	2.30	1.00	down	7.59E-01	9.21E-01	-	-
1397992_at	---	---	---	Rn.59916	BF402133	2.26	2.26	2.27	2.26	2.26	2.26	1.00	down	6.20E-01	8.95E-01	-	-
1377615_at	Tmem130	transmembrane protein 130	304280	Rn.25814	AI112395	2.31	2.31	2.32	2.31	2.32	2.30	1.00	down	6.21E-01	8.95E-01	-	-
1376713_at	Mta1	metastasis associated 1	64520	Rn.5840	BF420125	2.49	2.47	2.53	2.53	2.49	2.48	1.00	up	9.22E-01	9.77E-01	-	-
1376752_at	---	---	---	Rn.160839	AW918585	2.33	2.32	2.33	2.32	2.33	2.32	1.00	down	6.93E-01	9.05E-01	-	-
1369805_at	Scl5	synaptonemal complex protein SC65	59101	Rn.90100	NM_021581	2.24	2.23	2.24	2.24	2.24	2.23	1.00	down	5.93E-01	8.95E-01	-	-
1389495_at	---	---	---	Rn.63615	BF394211	2.47	2.45	2.47	2.46	2.51	2.43	1.00	up	9.29E-01	9.80E-01	-	-
1381752_at	---	---	---	Rn.203961	BE106899	2.33	2.35	2.34	2.37	2.34	2.32	1.00	up	8.86E-01	9.65E-01	-	-
1385453_at	---	---	---	Rn.23179	AI145167	2.48	2.47	2.52	2.47	2.53	2.46	1.00	down	9.32E-01	9.81E-01	-	-
1368636_at	Cyp27b1	cytochrome P450, family 27, subfamily b, polypeptide 1	114700	Rn.10847	NM_053763	2.23	2.23	2.24	2.23	2.24	2.23	1.00	down	5.75E-01	8.95E-01	-	-
1372385_at	---	---	---	---	AA957292	2.26	2.25	2.26	2.25	2.26	2.25	1.00	down	6.24E-01	8.95E-01	-	-
1367786_at	Psmb8	proteasome (prosome, macropain) subunit, beta type 8 (large multifunctional	24968	Rn.203098	NM_080767	2.30	2.29	2.31	2.30	2.31	2.30	1.00	up	6.68E-01	9.00E-01	-	-
1396008_at	---	---	---	Rn.147863	BF411771	2.43	2.41	2.47	2.42	2.47	2.40	1.00	down	9.33E-01	9.81E-01	-	-
1385703_at	Ccdc25	coiled-coil domain containing 25	361059	Rn.136803	AA818737	2.46	2.44	2.49	2.45	2.48	2.44	1.00	down	9.03E-01	9.70E-01	-	-
1390618_at	---	---	---	Rn.210135	BF394265	2.44	2.41	2.44	2.43	2.44	2.43	1.00	up	8.36E-01	9.48E-01	-	-
1390484_at	Mrpl12	Mitochondrial ribosomal protein L12	303746	Rn.105932	AI176750	2.53	2.52	2.54	2.52	2.54	2.52	1.00	down	7.52E-01	9.20E-01	-	-
1374881_at	---	---	---	Rn.15089	BF405945	2.37	2.36	2.39	2.37	2.38	2.37	1.00	down	7.98E-01	9.35E-01	-	-
1391754_at	Oas1i	2' -5' oligoadenylate synthetase 1I	304507	Rn.203133	BM391818	2.29	2.29	2.30	2.29	2.30	2.29	1.00	down	6.22E-01	8.95E-01	-	-
1392113_at	---	---	---	Rn.147502	BF419649	2.43	2.42	2.43	2.42	2.44	2.42	1.00	up	7.94E-01	9.34E-01	-	-
1379197_at	Cacna1h	Calcium channel, voltage-dependent, T type, alpha 1H subunit	114862	Rn.49178	BF414167	2.36	2.36	2.37	2.37	2.37	2.35	1.00	down	7.32E-01	9.14E-01	-	-
1387930_at	Reg3a	regenerating islet-derived 3 alpha	171162	Rn.11222	L10229	2.34	2.33	2.35	2.34	2.35	2.33	1.00	down	7.34E-01	9.15E-01	-	-
1368224_at	Serpina3n	serine (or cysteine) peptidase inhibitor, clade A, member 3N	24795	Rn.202939	NM_031531	2.29	2.28	2.29	2.28	2.29	2.28	1.00	down	7.30E-01	9.14E-01	-	-
1370587_at	Grik3	glutamate receptor, ionotropic, kainate 3	298521	Rn.92477	M83552	2.29	2.28	2.30	2.29	2.30	2.28	1.00	down	7.42E-01	9.17E-01	-	-
1368455_at	Nkg7	natural killer cell group 7 sequence	171062	Rn.20448	NM_133540	2.30	2.30	2.31	2.30	2.31	2.30	1.00	down	5.99E-01	8.95E-01	-	-
1376466_at	---	---	---	Rn.171664	BF419536	2.46	2.45	2.46	2.45	2.53	2.40	1.00	up	9.51E-01	9.86E-01	-	-
1369189_at	Ppyr1	pancreatic polypeptide receptor 1	29471	Rn.10574	NM_031581	2.20	2.20	2.20	2.20	2.19	2.19	1.00	down	5.50E-01	8.95E-01	-	-
1375499_at	---	---	---	Rn.153868	BI299782	2.44	2.42	2.44	2.43	2.43	2.43	1.00	down	7.43E-01	9.17E-01	-	-
1392704_at	---	---	---	Rn.203910	AI029221	2.33	2.32	2.34	2.33	2.34	2.32	1.00	down	7.42E-01	9.17E-01	-	-
1369121_at	Gdf9	growth differentiation factor 9	59304	Rn.42874	NM_021672	2.27	2.26	2.27	2.27	2.27	2.26	1.00	down	5.76E-01	8.95E-01	-	-
1379789_at	---	---	---	Rn.17519	BF410639	2.29	2.28	2.29	2.29	2.29	2.28	1.00	down	6.40E-01	8.95E-01	-	-
1395313_s_at	Anxa3	Annexin A3	25291	Rn.6589	AI179982	2.22	2.19	2.21	2.20	2.22	2.20	1.00	up	8.02E-01	9.36E-01	-	-
1387344_at	Aldh6a1	aldehyde dehydrogenase 6 family, member A1	81708	Rn.2098	AI407458	11.76	11.92	11.92	11.83	11.84	11.92	1.00	down	9.71E-01	9.91E-01	-	-
1367781_at	Plp	prolactin induced protein	64673	Rn.78367	NM_022708	2.42	2.39	2.44	2.42	2.42	2.42	1.00	up	8.84E-01	9.64E-01	-	-
1391010_at	Dpys3	dihydropyrimidinase-like 3	25418	Rn.93365	AI059953	2.34	2.34	2.35	2.34	2.35	2.34	1.00	down	5.78E-01	8.95E-01	-	-
1381287_at	---	---	---	Rn.190267	BE099909	2.29	2.28	2.29	2.28	2.29	2.28	1.00	down

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1369314_at	Fgf5	fibroblast growth factor 5	60662	Rn.44445	NM_022211	2.37	2.35	2.37	2.36	2.38	2.35	1.00	up	8.39E-01	9.50E-01	-	-
1370716_at	Smad9	SMAD family member 9	85435	Rn.10862	AF012347	2.28	2.27	2.28	2.27	2.28	2.27	1.00	down	5.92E-01	8.95E-01	-	-
1375804_at	Gjc2	Gap junction protein, gamma 2	497913	Rn.203090	AI227657	2.17	2.16	2.17	2.16	2.17	2.16	1.00	down	5.21E-01	8.95E-01	-	-
1369553_at	Hsd17b3	hydroxysteroid (17-beta) dehydrogenase 3	117182	Rn.10895	NM_054007	2.28	2.28	2.29	2.28	2.28	2.27	1.00	down	6.32E-01	8.95E-01	-	-
1376871_at	C685305 /// LOC	similar to paired immunoglobin-like type 2 receptor beta /// similar to paired im	69 /// 681182 /// 68	Rn.144010	AA891475	2.56	2.55	2.56	2.56	2.57	2.55	1.00	up	7.54E-01	9.20E-01	-	-
1378865_at	---	---	---	Rn.147347	AW253888	2.45	2.43	2.46	2.45	2.46	2.43	1.00	down	8.43E-01	9.51E-01	-	-
1374794_at	Kif15	kinesin family member 15	353302	Rn.45205	BF396282	2.46	2.44	2.47	2.45	2.46	2.44	1.00	down	8.01E-01	9.36E-01	-	-
1392526_at	---	---	---	Rn.96146	AA901274	2.23	2.23	2.24	2.23	2.23	2.23	1.00	down	5.21E-01	8.95E-01	-	-
1369367_at	Trpc2	transient receptor potential cation channel, subfamily C, member 2	64573	Rn.220468	NM_022638	2.28	2.28	2.29	2.28	2.29	2.27	1.00	down	7.31E-01	9.14E-01	-	-
1368505_at	Rgs4	regulator of G-protein signaling 4	29480	Rn.11065	U27767	2.31	2.30	2.32	2.32	2.31	2.29	1.00	up	8.28E-01	9.45E-01	-	-
1395230_at	---	---	---	Rn.173885	AI112506	2.25	2.25	2.25	2.25	2.24	2.24	1.00	down	5.76E-01	8.95E-01	-	-
1397702_at	---	---	---	---	BF551921	2.88	4.06	3.51	3.49	3.49	3.48	1.00	up	9.95E-01	9.98E-01	-	-
1387323_at	Klkb1	kallikrein B, plasma 1	25048	Rn.9880	NM_012726	2.38	2.37	2.40	2.37	2.41	2.36	1.00	down	8.93E-01	9.67E-01	-	-
1373722_at	Kif20a	kinesin family member 20A	361308	Rn.101107	BE111697	2.40	2.38	2.40	2.39	2.41	2.38	1.00	down	8.14E-01	9.40E-01	-	-
1397106_at	---	---	---	Rn.207435	BE101327	2.37	2.36	2.38	2.36	2.38	2.36	1.00	down	8.13E-01	9.40E-01	-	-
1391082_at	---	---	---	Rn.199653	BE106201	2.35	2.34	2.35	2.34	2.35	2.34	1.00	down	6.57E-01	8.98E-01	-	-
1390346_at	RGD1308165	Similar to hypothetical protein MGC17337	362516	Rn.22294	AA859181	2.33	2.33	2.34	2.33	2.34	2.33	1.00	down	7.00E-01	9.07E-01	-	-
1380327_at	---	---	---	Rn.205913	AI408747	2.54	2.87	2.52	2.88	2.46	2.59	1.00	up	9.89E-01	9.97E-01	-	-
1388242_at	Gpr176	G protein-coupled receptor 176	117257	Rn.44656	BG663422	2.35	2.34	2.35	2.34	2.35	2.33	1.00	down	7.94E-01	9.34E-01	-	-
1374799_at	Ncapd2	non-SMC condensin I complex, subunit D2	362438	Rn.7870	AI407418	2.35	2.35	2.37	2.36	2.37	2.34	1.00	down	8.01E-01	9.36E-01	-	-
1368927_at	Fam62a	family with sequence similarity 62 (C2 domain containing), member A	29579	Rn.11636	NM_017249	2.33	2.32	2.34	2.33	2.34	2.32	1.00	down	7.40E-01	9.16E-01	-	-
1378649_at	---	---	---	Rn.6308	AA800285	2.29	2.28	2.30	2.29	2.30	2.28	1.00	down	6.98E-01	9.07E-01	-	-
1370681_at	Pacs1	phosphofurin acidic cluster sorting protein 1	171444	Rn.154425	AF076184	2.30	2.30	2.31	2.30	2.30	2.30	1.00	down	6.10E-01	8.95E-01	-	-
1371837_at	Ddx5	DEAD (Asp-Glu-Ala-Asp) box polypeptide 5	287765	Rn.162208	AA851926	9.55	10.08	9.71	9.81	9.55	9.97	1.00	down	9.91E-01	9.97E-01	-	-
1396338_at	---	---	---	---	BF416353	2.58	2.58	2.59	2.58	2.60	2.58	1.00	up	7.97E-01	9.34E-01	-	-
1379246_at	RGD1308742	similar to Complement C5 precursor	362120	Rn.23009	AI169938	2.29	2.28	2.30	2.29	2.29	2.28	1.00	down	6.91E-01	9.05E-01	-	-
1391053_at	Dus3l	dihydrouridine synthase 3-like (S. cerevisiae)	301122	Rn.42187	BF408838	2.28	2.27	2.29	2.28	2.28	2.27	1.00	down	6.50E-01	8.98E-01	-	-
1380391_at	Sfrs7	splicing factor, arginine/serine-rich 7	362687	Rn.218757	BE119019	2.34	2.33	2.34	2.33	2.34	2.33	1.00	down	4.68E-01	8.95E-01	-	-
1381938_at	Usp13	Ubiquitin specific protease 13 (isopeptidase T-3)	310306	Rn.16802	BE120581	2.23	2.23	2.24	2.23	2.23	2.23	1.00	down	4.69E-01	8.95E-01	-	-
1380958_at	Wnt7a	wingless-type MMTV integration site family, member 7A	114850	Rn.160583	BG671935	2.31	2.30	2.31	2.31	2.32	2.29	1.00	down	8.11E-01	9.39E-01	-	-
1377568_at	Zfpm2	zinc finger protein, multitype 2	314930	Rn.135463	BE098911	2.30	2.29	2.30	2.29	2.30	2.29	1.00	down	6.77E-01	9.02E-01	-	-
1376372_at	---	---	---	Rn.200250	BI301069	2.31	2.30	2.31	2.31	2.31	2.30	1.00	down	5.85E-01	8.95E-01	-	-
1380151_at	---	---	---	Rn.154057	BG374625	2.39	2.38	2.40	2.39	2.40	2.37	1.00	down	7.95E-01	9.34E-01	-	-
1368855_at	Ighm2	immunoglobulin mu binding protein 2	29532	Rn.23984	NM_031586	2.28	2.28	2.29	2.28	2.29	2.27	1.00	down	6.50E-01	8.98E-01	-	-
1380798_at	Nfkbiz	Nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, ze	304005	Rn.58420	BF395369	2.45	2.45	2.45	2.45	2.44	2.44	1.00	down	4.42E-01	8.95E-01	-	-
1397144_at	---	---	---	Rn.146803	BE109216	2.41	2.40	2.43	2.41	2.44	2.38	1.00	down	9.12E-01	9.74E-01	-	-
1398529_at	LOC686048	similar to butyrophilin-like 7	686048	Rn.39183	AI566622	2.29	2.29	2.30	2.29	2.30	2.29	1.00	down	7.15E-01	9.10E-01	-	-
1367949_at	Penk1	proenkephalin 1	29237	Rn.10015	NM_017139	2.29	2.28	2.29	2.29	2.29	2.28	1.00	down	5.86E-01	8.95E-01	-	-
1378533_at	Notch4	Notch homolog 4 (Drosophila)	406162	Rn.12967	BE113482	2.47	2.47	2.48	2.47	2.48	2.46	1.00	down	6.43E-01	8.95E-01	-	-
1379277_at	---	---	---	Rn.164561	AI573341	6.10	6.88	8.10	6.72	7.19	7.18	1.00	up	9.97E-01	9.99E-01	-	-
1398509_at	---	---	---	Rn.167122	AI170370	2.81	2.76	2.76	2.77	2.78	2.79	1.00	up	8.97E-01	9.68E-01	-	-
1376405_at	---	---	---	Rn.207344	BF404837	2.54	2.51	2.54	2.55	2.55	2.49	1.00	up	9.24E-01	9.78E-01	-	-
1379714_at	rCG_43687	hypothetical protein LOC688459	688459	Rn.161109	AI230650	2.25	2.25	2.26	2.25	2.26	2.24	1.00	down	6.36E-01	8.95E-01	-	-
1390742_at	---	---	---	---	BF404359	2.43	2.42	2.44	2.42	2.46	2.41	1.00	up	8.85E-01	9.64E-01	-	-
1384094_at	---	---	---	Rn.98037	BF414316	2.37	2.36	2.37	2.37	2.38	2.35	1.00	down	8.24E-01	9.44E-01	-	-
1379975_at	---	---	---	Rn.206671	AW529144	2.31	2.30	2.31	2.30	2.31	2.30	1.00	down	6.28E-01	8.95E-01	-	-
1396645_at	---	---	---	Rn.171598	BE109893	2.42	2.40	2.42	2.41	2.43	2.40	1.00	down	8.45E-01	9.52E-01	-	-
1369521_at	RGD69425	ubiquitin-conjugating enzyme	79435	Rn.113868	NM_031001	2.32	2.31	2.33	2.32	2.32	2.31	1.00	down	6.76E-01	9.02E-01	-	-
1380000_at	---	---	---	---	AI071500	2.25	2.24	2.26	2.25	2.25	2.24	1.00	down	6.19E-01	8.95E-01	-	-
1392814_at	---	---	---	Rn.166555	AA893234	2.32	2.31	2.32	2.31	2.32	2.31	1.00	down	6.26E-01	8.95E-01	-	-
1378045_at	C1ql1	complement component 1, q subcomponent-like 1	368688	Rn.105544	AI070110	2.37	2.36	2.37	2.36	2.37	2.36	1.00	down	7.00E-01	9.07E-01	-	-
1379966_at	---	---	---	Rn.206810	AW530531	2.22	2.21	2.22	2.21	2.22	2.21	1.00	down	5.10E-01	8.95E-01	-	-
1392732_at	Nusap1	nucleolar and spindle associated protein 1	311336	Rn.106933	AI711233	2.37	2.36	2.37	2.36	2.38	2.36	1.00	down	7.67E-01	9.24E-01	-	-
1368184_at	Psmd9	proteasome (prosome, macropain) 26S subunit, non-ATPase, 9	161475	Rn.24127	NM_130430	4.05	4.28	3.81	4.35	3.55	4.25	1.00	up	9.94E-01	9.98E-01	-	-
1370257_at	Pla2g1b	phospholipase A2, group IB, pancreas	25526	Rn.4283	AI234860	2.51	2.45	2.48	2.55	2.47	2.43	1.00	up	9.56E-01	9.87E-01	-	-
1378083_at	---	---	---	Rn.38231	BE106666	2.33	2.32	2.34	2.33	2.34	2.32	1.00	down	7.57E-01	9.21E-01	-	-
1395690_at	---	---	---	Rn.62262	BF413156	2.23	2.22	2.23	2.22	2.23	2.22	1.00	down	6.04E-01	8.95E-01	-	-
1370763_at	Olr1496	olfactory receptor 1496	404968	Rn.113469	M64385	2.29	2.28	2.29	2.29	2.29	2.28	1.00	down	6.79E-01	9.02E-01	-	-
1369186_at	Casp1	caspase 1	25166	Rn.37508	D85899	2.36	2.34	2.39	2.36	2.37	2.36	1.00	up	8.89E-01	9.65E-01	-	-
1389533_at	Fbln2	fibulin 2	282583	Rn.7350	AA944398	2.29	2.28	2.29	2.28	2.29	2.28	1.00	down	6.75E-01	9.01E-01	-	-
1391159_at	Obsl1	Obscurin-like 1	363259	Rn.776	AW525294	2.21	2.21	2.21	2.21	2.21	2.20	1.00	down	5.42E-01	8.95E-01	-	-
1392280_at	Tlr2	toll-like receptor 2	315353	Rn.46387	AW526982	2.41	2.40	2.42	2.40	2.42	2.40	1.00	down	8.04E-01	9.37E-01	-	-
1382864_at	Palmd	palmdelphin	310811	Rn.24602	AI231808	2.37	2.36	2.38	2.36	2.38	2.36	1.00	down	8.26E-01	9.45E-01	-	-
1375318_at	---	---	---	Rn.8304	AI555848	2.30	2.30	2.31	2.30	2.31	2.30	1.00	down	4.81E-01	8.95E-01	-	-
1373759_at	---	---	---	Rn.32994	BF522317	2.41	2.40	2.42	2.40	2.42	2.40	1.00	down	8.09E-01	9.38E-01	-	-
1396546_at	---	---	---	Rn.208609	BE119757	2.33	2.32	2.34	2.33	2.34	2.31	1.00	down	8.33E-01	9.47E-01	-	-
1396597_at	---	---	---	Rn.173091	BF405040	2.28	2.27	2.28	2.28	2.28	2.27	1.00	down	7.42E-01	9.17E-01	-	-
1368914_at	Runx1	runt related transcription factor 1	50662	Rn.11201	NM_017325	2.35	2.34	2.35	2.34	2.35	2.34	1.00	down	5.44E-01	8.95E-01	-	-
1377227_at	---	---	---	Rn.23610	BG378045	2.25	2.24	2.25	2.24	2.25	2.24	1.00	down	6.25E-01	8.95E-01	-	-
1390495_at	---	---	---	Rn.40976	BI294144	2.24	2.23	2.25	2.24	2.24	2.23	1.00	down	6.67E-01	8.99E-01	-	-
1380560_at	---	---	---	Rn.148289	BI289499	2.30	2.29	2.30	2.30	2.30	2.29	1.00	down	6.38E-01	8.95E-01	-	-
1393535_at	---	---	---	Rn.155828	AI010250	2.35	2.34	2.36	2.35	2.36	2.35	1.00	up	7.11E-01	9.09E-01	-	-
1375578_at	---	---	---	---	AI502009	2.43	2.43	2.47	2.46	2.46	2.42	1.00	up	9.04E-01	9.70E-01	-	-
1383684_at	Asf1b	ASF1 anti-silencing function 1 homolog B (S. cerevisiae)	304648	Rn.899	BI288761	2.41	2.39	2.41	2.40	2.41	2.39	1.00	down	8.13E-01	9.40E-01	-	-
1381005_at	LOC691889	similar to ATPase, aminophospholipid transporter-like, class I, type 8A, memb	691889	---	BE106535	2.27	2.26	2.28	2.27	2.29	2.26	1.00	up	8.23E-01	9.43E-01	-	-
1395734_at	Palmd	palmdelphin	310811	Rn.24602	AW919178	2.40	2.39	2.40	2.39	2.40	2.38	1.00	down	7.71E-01	9.25E-01	-	-
1395246_at	---	---	---	Rn.204803	AI104783	10.13	10.06	9.37	9.79	9.76	10.01	1.00	down	9.93E-01	9.98E-01	-	-
1380130_at	---	---	---	Rn.92597	AW434319	2.33	2.33	2.34	2.33	2.34	2.33	1.00	down	6.97E-01	9.07E-01	-	-
1395731_at	---	---	---	Rn.145699	BF291205	2.55	2.54	2.59	2.68	2.52	2.48	1.00	down	9.73E-01	9.92E-01	-	-
1368656_at	Scg3	secretogranin III	116635	Rn.11093	NM_053856	2.41	2.41	2.42	2.41	2.42	2.40	1.00	down	7.54E-01	9.20E-01	-	-
1368359_a_at	Vgf	VGF nerve growth factor inducible	29461	Rn.9704	NM_030997	2.36	2.34	2.35	2.34	2.38	2.34	1.00	up	8.85E-01	9.64E-01	-	-
1373865_at	Snap91	synaptosomal-associated protein 91	65178	Rn.11022	BF281248	2.42	2.40	2.44	2.41	2.43	2.41	1.00	down	8.54E-01	9.55E-01	-	-
1378835_at	---	---	---	Rn.204674	AI145398	2.75	2.48	2.48	2.78	2.48	2.44	1.00	down	9.88E-01	9.96E-01	-	-
1378648_at	---	---	---	Rn.144919	BF404852	2.38	2.37	2.38	2.37	2.38	2.37	1.00	down	6.40E-01	8.95E-01	-	-
1375198_at	LOC690139	similar to RNA binding motif protein 24	690139	Rn.199020	AW520820	2.35	2.34	2.35	2.35	2.35	2.34	1.00	down	7.08E-01	9.08E-01	-	-
1378417_at	---	---	---	Rn.205470	BI285847	2.29	2.28	2.30	2.29	2.29	2.28	1.00	down	6.53E-01	8.97E-01	-	-
1393539_at	Dsc1	desmocollin 1	291759	Rn.21711	AI044004	2.26	2.26	2.27	2.26	2.26	2.25	1.00	down	6.59E-01	8.98E-01	-	-
1392821_at	RGD1308195	similar to secreted Ly6/uPAR related protein 2	315074	Rn.24786	AI234147	2.23	2.22	2.23	2.22	2.23	2.22	1.00	down	6.15E-01	8.95E-01	-	-
1370578_at	RGD621098	similar to RIKEN cDNA D230025D16Rik	207123	Rn.9778	U92010	2.41	2.40	2.41	2.40	2.42	2.39	1.00	down	8.06E-01	9.38E-01	-	-
1395368_at	---	---	---	Rn.170867	BF408886	2.50	2.44	2.52	2.44	2.57	2.43	1.00	down	9.68E-01	9.91E-01	-	-
1386364_at	Nup37	Nucleoporin 37	299706	Rn.135562	H31217	2.33	2.32	2.34	2.33	2.34	2.32	1.00	down	7.70E-01	9.25E-01	-	-
1378900_at	Gcn5l2	GCN5 general control of amino acid synthesis-like 2 (yeast)	303539	Rn.53502	BF415195	2.53	2.43	2.43	2.44	2.54	2.42	1.00	up	9.66E-01	9.90E-01	-	-
1383335_at	Rapgef1	Rap guanine nucleotide exchange factor (GEF)-like 1	303515	Rn.17949	AI197215	2.28	2.28	2.29	2.29	2.28	2.28	1.00	down	5.92E-01	8.95E-01	-	-
1398085_at	---	---	---	Rn.211167	BF408166	2.40	2.38	2.41	2.41	2.41	2.38	1.00	up	8.70E-01	9.60E-01	-	-
1371550_at	Tsc22d4	TSC22 domain family, member 4	684980	Rn.21359	AW553431	2.70	3.22	3.71	3.13	3.23	3.27	1.00	up	9.94E-01	9.98E-01	-	-
1380734_at	---	---	---	Rn.212521	BM390049	2.23	2.23	2.23	2.23	2.23	2.22	1.00	down	5.16E-01	8.95E-01	-	-
1387699_at	Cnga2	cyclic nucleotide gated channel alpha 2	25411	Rn.10384	AF126808	2.26	2.25	2.26	2.25	2.26	2.24	1.00	down	7.46E-01	9.18E-01	-	-
1373891_at	Zcchc12	zinc finger, CCHC domain containing 12	313436	Rn.23849	AI101009	2.28	2.28	2.29	2.28	2.29	2.28	1.00	down	6.51E-01	8.96E-01	-	-
1390938_at	Arhgap28	Rho GTPase activating protein 28	301709	Rn.14693	BI276015	2.27	2.26	2.28	2.27	2.28	2.27	1.00	down	7.03E-01	9.07E-01	-	-
1396707_at	---	---	---	Rn.59285	BF404674	2.42	2.39	2.43	2.41	2.46	2.37	1.00	up	9.38E-01	9.82E-01	-	-
1385912_at	Dusp15	dual specificity phosphatase-like 15	362238	Rn.58260	AI412854	2.34	2.33	2.35	2.33	2.36	2.32	1.00	down	8.51E-01	9.53E-01	-	-
1368985_at	Grin2a	glutamate receptor, ionotropic, N-methyl D-aspartate 2A	24409	Rn.9710	AF001423	2.43	2.41	2.43	2.44	2.42	2.40	1.00	down	8.74E-01	9.61E-01	-	-
1395234_at	---	---	---	---	AI178199	2.29	2.29	2.30	2.30	2.30	2.29	1.00	up	8.70E-01	9.00E-01	-	-
1377761_at	Gfpt2	glutamine-fructose-6-phosphate transaminase 2	360518	Rn.16089	BI296057	2.28	2.27	2.28	2.28	2.28	2.27	1.00	down	6.29E-01	8.95E-01	-	-
1383848_at	Adrb1	Adrenergic, beta-1-, receptor	24925	Rn.87064	BE098191	2.47	2.47	2.47	2.47	2.47	2.46	1.00	down	5.41E-01	8.95E-01	-	-
1392082_a_at	Cd7	Cd7 molecule	303747	Rn.8175	BI295048	2.30	2.29	2.30	2.29	2.30	2.29	1.00	down	6.83E-01	9.03E-01	-	-
1385075_at	Ccdc32	coiled-coil domain containing 32	296081	Rn.154291	BE101529	2.33	2.30	2.34	2.32	2.33	2.31	1.00	up	8.80E-01	9.63E-01	-	-
1388223_at	Gnat3	guanine nucleotide binding protein, alpha transducing 3	286924	Rn.10456	X65747	2.53	2.49	2.53	2.51	2.56	2.48	1.00	down	9.40E-01	9.83E-01	-	-
1392307_at	---	---	---	Rn.156059	BI300978	2.17	2.16	2.17	2.16	2.17	2.16	1.00	down	6.04E-01	8.95E-01	-	-
1384863_at	Zfp84	zinc finger protein 84	308482	Rn.203644	AW527181	2.36	2.53	2.37	2.36	2.57	2.53	1.00	down	9.78E-01	9.93E-01	-	-
1391232_at	---	---	---	Rn.156761	BG381215	2.29	2.28	2.29	2.28	2.29	2.28	1.00	down	7.04E-01	9.07E-01	-	-
1383426_at	Pstpip1	proline-serine-threonine phosphatase-interacting protein 1	300732	Rn.6937	BI290159	2.58	2.61	2.66	2.65	2.61	2.59	1.00	up	9.38E-01	9.82E-01	-	-
1369887_at	Nfl4	neurofilin 4	25730	Rn.44225	NM_013184	2.28	2.28	2.29	2.28	2.29	2.27	1.00	down	6.85E-01	9.03E-01	-	-
1375410_at	LOC365344	Similar to testes-specific heterogenous nuclear ribonucleoprotein G-T	365344	Rn.196146	BF411840	2.22	2.21	2.22	2.21	2.22	2.23	1.00	up	7.65E-01	9.23E-01	-	-
1376334_at	RGD1308101	similar to hypothetical protein FLJ20276	679640	Rn.58227	BF394214	2.20	2.20	2.21	2.20	2.20	2.20	1.00	down	6.25E-01	8.95E-01	-	-
1396559_at	---	---	---	---	BF396596	2.39	2.38	2.41	2.40	2.40	2.37	1.00	down	8.84E-01	9.64E-01	-	-
1378015_at	Cd21b	chemokine (C-C motif) ligand 21b (serine)	298006	Rn.39658	BI282920	2.26	2.25	2.26	2.26	2.26	2.25	1.00	down	8.69E-01	9.00E-01	-	-
1383985_at	Cdh15	cadherin 15	361432	Rn.18406	AW523000	2.22	2.21	2.22	2.22	2.22	2.21	1.00	down	5.98E-01	8.95E-01	-	-
1385583_at	Tyr	tyrosinase	308800	Rn.38928	AI578193	2.26	2.26	2.27	2.26	2.27	2.26	1.00	down	6.68E-01	9.00E-01	-	-
1393971_at	---	---	---	Rn.48527	AW535616	2.30	2.29	2.32	2.30	2.33	2.29	1.00	up	8.84E-01	9.64E-01	-	-
1379050_at	---	---	---	Rn.101964	AW532022	2.33	2.32	2.33	2.33	2.32	2.32	1.00	down	6.26E-01	8.95E-01	-	-
1387607_at	Npffr2	neuropeptide FF receptor 2	78964	Rn.64524	NM_023980	2.27	2.27	2.28	2.27	2.27	2.27	1.00	down	6.55E-01	8.98E-01	-	-
1370784_a_at	Cacng6	calcium channel, voltage-dependent, gamma subunit 6	140727	Rn.91033	AF361344	2.33	2.32	2.34	2.33	2.33	2.32	1.00	down	6.75E-01	9.01E-01	-	-
1382036_at	Tln1	talin 1	313494	Rn.7715	AA900870	2.32	2.31	2.34	2.33	2.33	2.30	1.00	down	8.53E-01	9.55E-01	-	-
1398581_at	---	---	---	Rn.8623	AA956307	2.22	2.21	2.23	2.22	2.22	2.21	1.00	down	6.63E-01	8.98E-01	-	-
1374744_at	---	---	---	Rn.209980	BF392285	2.48	2.46	2.52	2.47	2.54	2.45	1.00	down	9.49E-01	9.85E-01	-	-
1395657_at	---	---	---	Rn.55765	BF289401	2.41	2.39	2.42	2.40	2.44	2.39	1.00	up	9.05E-01	9.71E-01	-	-
1387710_at	Oxtr	oxytocin receptor	25342	Rn.6841	L81169	2.29	2.28	2.29	2.29	2.29	2.28	1.00	down	7.17E-01	9.10E-01	-	-
1397694_at	Elmod3	ELMO/CED-12 domain containing 3	297342	Rn.203170	BF288347	2.37	2.36	2.39	2.38	2.38	2.35	1.00	down	8.58E-01	9.56E-01	-	-
1375012_at	Pdzk4	PDZ domain containing 4	293856	Rn.28086	BF398627	2.30	2.29	2.31	2.29	2.31	2.29	1.00	down	7.97E-01	9.34E-01	-	-
1368920_at	Slit3	slit homolog 3 (Drosophila)	83467	Rn.12298	NM_031321	2.24	2.23	2.24	2.23	2.24	2.23	1.00	down	6.07E-01	8.95E-01	-	-
1385331_at	RGD1562911	similar to hypothetical protein MGC45441	500534	Rn.144397	AA819842	2.48	2.47	2.48	2.48	2.49	2.47	1.00	down	7.16E-01	9.10E-01	-	-
1379345_at	Col15a1	collagen, type XV, alpha 1	298069	Rn.31832	BM386752	2.44	2.45	2.47	2.43	2.48	2.45	1.00	down	9.03E-01	9.70E-01	-	-
1392450_at	---	---	---	---	BF419910	2.24	2.24	2.25	2.24	2.25	2.24	1.00	down	5.35E-01	8.95E-01	-	-
1380361_at	---	---	---	Rn.169117	AI547532	2.41	2.41	2.41	2.41	2.41	2.40	1.00	down	5.87E-01	8.95E-01	-	-
1386529_at	---	---	---	Rn.160464	BF564309	2.38	2.36	2.38	2.37	2.38	2.37	1.00	down	7.45E-01	9.17E-01	-	-
1375153_at	Sox2	SRY (sex determining region Y)-box 2	499593	Rn.219221	AI111954	2.54	2.53	2.54	2.53	2.59	2.49	1.00	up	9.44E-01	9.84E-01	-	-
1395308_at	Tmem127	transmembrane protein 127	311405	Rn.19881	BE097976	2.26	2.25	2.26	2.25	2.26	2.25	1.00	down	5.81E-01	8.95E-01	-	-
1376905_at	---	---	---	Rn.3706	BI304147	2.30	2.30	2.31	2.30	2.31	2.29	1.00	down	7.30E-01	9.14E-01	-	-
1387954_a_at	Grip2	glutamate receptor interacting protein 2	171571	Rn.15680	AF090113	2.32	2.29	2.31	2.33	2.31	2.29	1.00	up	8.87E-01	9.65E-01	-	-
1373219_at	Snai1	snail homolog 1 (Drosophila)	116490	Rn.8008	AA946199	2.35	2.34	2.36	2.36	2.35	2.34	1.00	up	8.97E-01	9.34E-01	-	-
1394113_at	Cdc20	cell division cycle 20 homolog (S. cerevisiae)	64515	Rn.9262	BI850139	2.41	2.40	2.43	2.43	2.41	2.39	1.00	down	8.94E-01	9.67E-01	-	-
1385220_at	Zwilch	Zwilch, kinetochore associated, homolog (Drosophila)	691493	Rn.204979	BG377563	2.56	2.56	2.59	2.57	2.57	2.56	1.00	down	8.31E-01	9.47E-01	-	-
1397135_at	--

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1378131_at	RGD1560736	similar to solute carrier family 9 (sodium/hydrogen exchanger), isoform 9	363115	---	AI045015	2.40	2.39	2.40	2.39	2.42	2.39	1.00	up	8.32E-01	9.47E-01	-	-
1389607_at	Rcor2	REST corepressor 2	305811	Rn.209048	BF285211	2.26	2.26	2.27	2.26	2.27	2.25	1.00	down	6.66E-01	8.99E-01	-	-
1386390_at	---	---	---	---	AI639354	2.28	2.27	2.28	2.27	2.28	2.27	1.00	down	6.91E-01	9.05E-01	-	-
1395635_at	Tnfrsf26	tumor necrosis factor receptor superfamily, member 26	361685	Rn.162508	BE098317	2.39	2.36	2.40	2.38	2.40	2.38	1.00	up	8.73E-01	9.61E-01	-	-
1375446_at	Znf498 /// Znf655	zinc finger protein 498 /// zinc finger protein 655	360764 /// 363872	Rn.6640	BE104397	2.41	2.40	2.41	2.40	2.41	2.40	1.00	down	7.23E-01	9.12E-01	-	-
1398963_at	Taf10	TAF10 RNA polymerase II, TATA box binding protein (TBP)-associated factor	293345	Rn.144795	BM392226	8.16	8.27	9.05	8.86	8.17	8.45	1.00	down	9.95E-01	9.98E-01	-	-
1387997_at	Hcn4	hyperpolarization activated cyclic nucleotide-gated potassium channel 4	59266	Rn.41082	AF247453	2.31	2.31	2.31	2.31	2.31	2.30	1.00	down	6.12E-01	8.95E-01	-	-
1391966_at	---	---	---	Rn.49501	BG380804	2.35	2.35	2.36	2.37	2.36	2.35	1.00	up	7.25E-01	9.13E-01	-	-
1368417_at	Syt5	synaptotagmin V	54309	Rn.11030	NM_019350	2.25	2.24	2.25	2.24	2.25	2.24	1.00	down	6.24E-01	8.95E-01	-	-
1386356_at	---	---	---	Rn.135073	AI639400	2.35	2.34	2.36	2.34	2.36	2.34	1.00	down	8.07E-01	9.38E-01	-	-
1383562_at	Cldn18	claudin 18	315953	Rn.105888	AA901239	2.46	2.46	2.47	2.46	2.46	2.46	1.00	down	5.10E-01	8.95E-01	-	-
1394497_at	679869 /// LOC68	similar to transcription factor 7-like 2, T-cell specific, HMG-box /// similar to Tra	679869 /// 683733	Rn.105849	AI535239	2.47	2.45	2.47	2.46	2.47	2.47	1.00	up	7.80E-01	9.28E-01	-	-
1368585_at	Cartpt	CART prepropeptide	29131	Rn.89164	NM_017110	2.25	2.24	2.25	2.24	2.25	2.24	1.00	down	5.89E-01	8.95E-01	-	-
1377144_at	RGD1564982	RGD1564982	308556	Rn.3332	AA944584	2.23	2.22	2.23	2.23	2.23	2.22	1.00	down	6.21E-01	8.95E-01	-	-
1387423_at	Lhcgr	luteinizing hormone/choriogonadotropin receptor	25477	Rn.11216	NM_012978	2.26	2.25	2.26	2.26	2.26	2.25	1.00	down	6.55E-01	8.97E-01	-	-
1373724_at	Krt4	keratin 4	315323	Rn.100688	BI274589	2.25	2.25	2.25	2.25	2.25	2.24	1.00	down	6.62E-01	8.98E-01	-	-
1381603_at	LOC502684	hypothetical protein LOC502684	502684	Rn.206234	AW524138	2.40	2.39	2.41	2.40	2.41	2.38	1.00	down	8.36E-01	9.48E-01	-	-
1380439_at	---	---	---	---	AI548395	2.28	2.27	2.28	2.27	2.28	2.26	1.00	down	7.55E-01	9.20E-01	-	-
1374226_at	Col7a1	procollagen, type VII, alpha 1	301012	Rn.24307	AI408498	2.32	2.32	2.33	2.32	2.33	2.32	1.00	down	6.62E-01	8.98E-01	-	-
1393980_at	---	---	---	Rn.120503	AW522502	2.43	2.43	2.44	2.43	2.44	2.43	1.00	down	6.35E-01	8.95E-01	-	-
1376929_at	Tpm3	Tropomyosin 3, gamma	117557	Rn.37575	BF544829	2.37	2.37	2.37	2.37	2.36	2.36	1.00	down	6.78E-01	9.02E-01	-	-
1382449_at	Rassf1	Ras association (RalGDS/AF-6) domain family member 1	363140	Rn.83042	AI230845	2.36	2.35	2.37	2.36	2.37	2.35	1.00	down	7.97E-01	9.35E-01	-	-
1397544_at	---	---	---	Rn.216824	BF404617	2.30	2.29	2.30	2.30	2.30	2.30	1.00	down	4.31E-01	8.95E-01	-	-
1381615_at	---	---	---	Rn.1973	AA819292	2.50	2.48	2.51	2.48	2.53	2.48	1.00	up	9.20E-01	9.76E-01	-	-
1377050_at	---	---	---	Rn.147428	BF395777	2.32	2.32	2.38	2.39	2.33	2.32	1.00	up	9.45E-01	9.84E-01	-	-
1392037_at	---	---	---	Rn.43297	BM383048	2.28	2.27	2.28	2.28	2.28	2.27	1.00	down	6.97E-01	9.07E-01	-	-
1382502_at	RGD1311517	similar to RIKEN cDNA 9430015G10	313775	Rn.83717	BF286888	2.34	2.33	2.34	2.34	2.34	2.33	1.00	down	6.43E-01	8.95E-01	-	-
1395050_at	---	---	---	---	BE098619	2.30	2.29	2.31	2.29	2.30	2.29	1.00	down	7.71E-01	9.25E-01	-	-
1392312_at	---	---	---	---	BG375255	2.30	2.29	2.30	2.29	2.30	2.30	1.00	down	6.46E-01	8.95E-01	-	-
1386785_a_at	---	---	---	Rn.202616	BF559982	2.41	2.40	2.43	2.41	2.42	2.40	1.00	down	8.55E-01	9.55E-01	-	-
1391537_at	Sertad4	SERTA domain containing 4	360899	Rn.101908	AW251654	2.37	2.35	2.38	2.37	2.37	2.37	1.00	up	7.73E-01	9.26E-01	-	-
1388220_at	Pou2f3	POU class 2 homeobox 3	116544	Rn.81060	L23863	2.19	2.18	2.19	2.19	2.19	2.18	1.00	down	5.53E-01	8.95E-01	-	-
1388222_at	Tert	telomerase reverse transcriptase	301965	Rn.48802	AF247818	2.32	2.31	2.33	2.31	2.35	2.30	1.00	up	9.14E-01	9.74E-01	-	-
1391569_at	---	---	---	Rn.208849	AF406435	2.24	2.23	2.24	2.23	2.24	2.23	1.00	down	6.16E-01	8.95E-01	-	-
1396345_at	Galnt1	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltran	79214	Rn.10266	BF403604	2.27	2.26	2.28	2.27	2.29	2.26	1.00	up	8.47E-01	9.52E-01	-	-
1387287_a_at	Abcc9	ATP-binding cassette, sub-family C (CFTR/MRP), member 9	25560	Rn.10528	D83598	2.28	2.28	2.29	2.28	2.28	2.28	1.00	down	6.10E-01	8.95E-01	-	-
1384178_at	Lrrc4b	leucine rich repeat containing 4B	308571	Rn.22207	BF546934	2.29	2.29	2.30	2.29	2.30	2.29	1.00	down	6.09E-01	8.95E-01	-	-
1374099_at	Nrap	nebulin-related anchoring protein	307982	Rn.35092	BM386665	2.27	2.27	2.28	2.27	2.28	2.27	1.00	down	6.96E-01	9.06E-01	-	-
1374619_at	Tusc5	tumor suppressor candidate 5	360576	Rn.18571	BM386662	2.27	2.26	2.27	2.27	2.27	2.26	1.00	down	6.29E-01	8.95E-01	-	-
1377052_at	---	---	---	Rn.38919	AW533469	2.61	2.57	2.63	2.61	2.61	2.60	1.00	up	9.13E-01	9.74E-01	-	-
1386186_s_at	---	---	---	---	H31802	2.28	2.27	2.29	2.28	2.28	2.27	1.00	down	6.79E-01	9.02E-01	-	-
1397727_at	---	---	---	Rn.47889	BE100341	2.30	2.29	2.31	2.30	2.30	2.29	1.00	down	6.83E-01	9.03E-01	-	-
1397404_at	---	---	---	Rn.56026	AI233732	2.35	2.34	2.35	2.34	2.35	2.34	1.00	down	6.79E-01	9.02E-01	-	-
1391782_at	---	---	---	---	AI555247	2.35	2.34	2.35	2.34	2.35	2.34	1.00	down	6.63E-01	8.99E-01	-	-
1387994_at	Hsd17b6	hydroxysteroid (17-beta) dehydrogenase 6	286964	Rn.10857	U89282	2.28	2.27	2.29	2.28	2.29	2.27	1.00	down	7.55E-01	9.20E-01	-	-
1395588_at	---	---	---	Rn.147759	AI715259	2.51	2.49	2.51	2.49	2.51	2.50	1.00	down	8.33E-01	9.47E-01	-	-
1384953_at	Ptprm	Protein tyrosine phosphatase, receptor type, M	29616	Rn.205336	BF547294	2.39	2.38	2.41	2.39	2.42	2.38	1.00	up	8.86E-01	9.65E-01	-	-
1369359_at	Il9r	interleukin 9 receptor	24500	Rn.10045	NM_017021	2.25	2.24	2.25	2.24	2.25	2.24	1.00	down	6.32E-01	8.95E-01	-	-
1390071_at	Arhgap23	Rho GTPase activating protein 23	303501	Rn.6554	AI575729	2.27	2.27	2.27	2.27	2.27	2.26	1.00	down	4.94E-01	8.95E-01	-	-
1385311_at	Slco5a1	solute carrier organic anion transporter family, member 5A1	312907	Rn.49225	BI274649	2.31	2.30	2.32	2.30	2.33	2.30	1.00	up	8.67E-01	9.59E-01	-	-
1395428_at	RGD1563533	similar to novel protein	313713	Rn.91524	BE097105	2.29	2.28	2.29	2.28	2.29	2.28	1.00	down	7.30E-01	9.14E-01	-	-
1382949_at	Rdh12	retinol dehydrogenase 12 (all-trans/9-cis/11-cis)	314264	Rn.148972	BM386727	2.40	2.39	2.41	2.40	2.41	2.39	1.00	down	8.26E-01	9.45E-01	-	-
1370794_at	Spag11b	sperm associated antigen 11B	246305	Rn.81215	AF217088	2.45	2.43	2.47	2.44	2.46	2.44	1.00	down	8.83E-01	9.64E-01	-	-
1397911_at	---	---	---	Rn.50847	BE115009	2.24	2.24	2.24	2.24	2.24	2.23	1.00	down	5.03E-01	8.95E-01	-	-
1379927_at	---	---	---	Rn.204482	AI113197	2.29	2.28	2.29	2.28	2.29	2.28	1.00	down	7.17E-01	9.10E-01	-	-
1394595_at	Stim1	stromal interaction molecule 1	361618	Rn.106771	AI763957	2.40	2.38	2.41	2.40	2.41	2.39	1.00	up	8.40E-01	9.50E-01	-	-
1379155_at	---	---	---	---	BF404422	2.35	2.33	2.35	2.34	2.35	2.34	1.00	down	8.01E-01	9.35E-01	-	-
1385345_at	---	---	---	Rn.123987	BE099947	2.26	2.25	2.26	2.25	2.27	2.24	1.00	down	7.86E-01	9.31E-01	-	-
1381756_at	Adh6a	alcohol dehydrogenase 6A (class V)	295498	Rn.137460	BI294834	2.28	2.28	2.29	2.28	2.28	2.28	1.00	down	6.47E-01	8.95E-01	-	-
1380238_at	---	---	---	Rn.203685	BE117357	2.43	2.42	2.43	2.42	2.43	2.42	1.00	down	6.72E-01	9.01E-01	-	-
1369524_at	Zic1	Zic family member 1 (odd-paired homolog, Drosophila)	64618	Rn.161923	NM_022677	2.36	2.35	2.36	2.35	2.36	2.35	1.00	down	5.96E-01	8.95E-01	-	-
1369150_at	Pdk4	pyruvate dehydrogenase kinase, isozyme 4	89813	Rn.30070	NM_053551	2.36	2.36	2.37	2.36	2.37	2.35	1.00	down	6.94E-01	9.05E-01	-	-
1387927_a_at	Olfm1	olfactomedin 1	93667	Rn.11005	U03415	2.28	2.28	2.29	2.28	2.29	2.28	1.00	down	7.02E-01	9.07E-01	-	-
1399116_at	Luc7l2	LUC7-like 2 (S. cerevisiae)	312251	Rn.18604	AI171781	8.89	9.24	9.25	9.10	9.00	9.28	1.00	down	9.89E-01	9.96E-01	-	-
1374946_at	---	---	---	Rn.8952	BI296261	2.48	2.76	2.48	2.48	2.49	2.75	1.00	down	9.88E-01	9.86E-01	-	-
1370703_at	Mrgprf	MAS-related GPR, member F	266762	Rn.9848	M35297	2.38	2.37	2.39	2.37	2.39	2.37	1.00	down	8.56E-01	9.55E-01	-	-
1375002_at	---	---	---	Rn.172715	BF393014	2.32	2.31	2.34	2.32	2.34	2.31	1.00	down	8.73E-01	9.61E-01	-	-
1370372_at	Rasd2	RASD family, member 2	171099	Rn.115571	BF404624	2.25	2.25	2.26	2.25	2.26	2.25	1.00	down	6.62E-01	8.98E-01	-	-
1369884_at	Fat2	FAT tumor suppressor homolog 2 (Drosophila)	85048	Rn.13761	NM_022954	2.36	2.35	2.36	2.37	2.35	2.35	1.00	down	7.27E-01	9.13E-01	-	-
1381068_at	RGD1307155	similar to CG18661-PA	302998	Rn.202598	BF391448	2.22	2.22	2.23	2.22	2.23	2.22	1.00	down	5.96E-01	8.95E-01	-	-
1367809_at	Prl4a1	prolactin family 4, subfamily a, member 1	24656	Rn.11230	NM_017036	2.33	2.32	2.34	2.32	2.34	2.32	1.00	down	7.85E-01	9.30E-01	-	-
1397393_at	---	---	---	Rn.177258	AI231774	2.35	2.34	2.36	2.35	2.36	2.34	1.00	down	8.02E-01	9.36E-01	-	-
1391037_at	Vwa5b2	von Willebrand factor A domain containing 5B2	303812	Rn.63842	BF412161	2.49	2.48	2.49	2.48	2.49	2.48	1.00	down	4.96E-01	8.95E-01	-	-
1392689_at	Aloxe3	arachidonate lipoxygenase 3	287424	Rn.8716	AI105029	2.31	2.31	2.32	2.31	2.33	2.29	1.00	down	8.33E-01	9.47E-01	-	-
1395738_at	---	---	---	Rn.173328	AW143035	2.37	2.36	2.37	2.37	2.39	2.36	1.00	up	8.23E-01	9.43E-01	-	-
1380061_at	Ppp2ca	Protein phosphatase 2 (formerly 2A), catalytic subunit, alpha isoform	24672	Rn.1271	BF418702	2.36	2.36	2.37	2.36	2.37	2.36	1.00	down	7.92E-01	9.33E-01	-	-
1387043_at	Lypd3	Ly6/Plaur domain containing 3	60378	Rn.38434	NM_021759	2.35	2.33	2.35	2.34	2.35	2.33	1.00	down	7.78E-01	9.28E-01	-	-
1393578_at	---	---	---	Rn.14748	AA892301	2.29	2.28	2.29	2.29	2.30	2.28	1.00	up	7.94E-01	9.34E-01	-	-
1369538_at	Cdk5r1	cyclin-dependent kinase 5, regulatory subunit 1 (p35)	116671	Rn.11213	NM_053891	2.35	2.35	2.37	2.36	2.36	2.35	1.00	down	7.64E-01	9.23E-01	-	-
1387756_s_at	Hemgn	hemogen	113882	Rn.22633	NM_133294	2.37	2.36	2.37	2.36	2.37	2.36	1.00	down	6.27E-01	8.95E-01	-	-
1387795_at	Pola2	polymerase (DNA directed), alpha 2	85242	Rn.205002	NM_053480	2.40	2.39	2.41	2.39	2.41	2.40	1.00	down	8.40E-01	9.50E-01	-	-
1368800_at	Cd40lg	CD40 ligand	84349	Rn.44218	NM_053353	2.35	2.34	2.36	2.35	2.35	2.34	1.00	down	6.94E-01	9.05E-01	-	-
1396636_at	---	---	---	Rn.173104	BF400225	2.32	2.31	2.32	2.32	2.32	2.31	1.00	down	7.36E-01	9.15E-01	-	-
1396847_at	---	---	---	Rn.35151	AI454925	2.22	2.22	2.23	2.22	2.23	2.22	1.00	down	5.74E-01	8.95E-01	-	-
1380003_at	---	---	---	Rn.154019	BI281665	2.29	2.29	2.30	2.29	2.30	2.29	1.00	down	7.15E-01	9.10E-01	-	-
1389752_at	Sorcs3	sortilin-related VPS10 domain containing receptor 3	294043	Rn.46899	BE109861	2.24	2.24	2.24	2.24	2.24	2.23	1.00	down	6.04E-01	8.95E-01	-	-
1393907_at	Pyy	peptide YY (mapped)	287730	Rn.13173	AA998735	2.27	2.27	2.28	2.27	2.28	2.26	1.00	down	7.11E-01	9.09E-01	-	-
1393486_at	Cyp46a1	cytochrome P450, family 46, subfamily a, polypeptide 1	362782	Rn.203681	AI111519	2.34	2.34	2.35	2.34	2.36	2.33	1.00	up	8.55E-01	9.55E-01	-	-
1375492_at	Suf1	sulfatase 1	171396	Rn.161961	BF409823	2.40	2.38	2.40	2.39	2.40	2.38	1.00	down	8.32E-01	9.47E-01	-	-
1380973_at	---	---	---	Rn.153609	BG376835	2.34	2.33	2.34	2.33	2.35	2.33	1.00	down	7.96E-01	9.34E-01	-	-
1375203_at	---	---	---	---	AI144889	2.26	2.25	2.26	2.26	2.26	2.25	1.00	down	6.44E-01	8.95E-01	-	-
1369462_at	Gad2	glutamate decarboxylase 2	24380	Rn.29951	NM_012563	2.35	2.34	2.35	2.36	2.36	2.33	1.00	up	8.57E-01	9.55E-01	-	-
1383873_at	Rspo3	R-spondin 3 homolog (Xenopus laevis)	498997	Rn.15751	BG377729	2.23	2.23	2.23	2.23	2.23	2.23	1.00	down	5.32E-01	8.95E-01	-	-
1395773_at	---	---	---	---	BF288487	2.49	2.48	2.54	2.49	2.55	2.47	1.00	down	9.52E-01	9.86E-01	-	-
1397961_x_at	Csde1	cold shock domain containing E1, RNA binding	117180	Rn.3562	AI010663	2.26	2.26	2.26	2.26	2.26	2.26	1.00	down	5.22E-01	8.95E-01	-	-
1379022_at	Adamts8	ADAM metallopeptidase with thrombospondin type 1 motif, 8	300475	Rn.100730	AI577318	2.33	2.31	2.34	2.32	2.34	2.32	1.00	up	8.62E-01	9.57E-01	-	-
1369037_at	---	---	---	---	NM_019349	2.26	2.26	2.27	2.26	2.27	2.26	1.00	down	6.58E-01	8.98E-01	-	-
1393616_at	---	---	---	Rn.199302	AI059202	2.34	2.33	2.35	2.34	2.34	2.33	1.00	down	7.51E-01	9.19E-01	-	-
1379381_at	---	---	---	Rn.16740	AI045321	2.54	2.53	2.54	2.53	2.54	2.53	1.00	down	5.56E-01	8.95E-01	-	-
1390927_at	LOC654482	hypothetical protein LOC654482	654482	Rn.162979	AI176779	2.38	2.38	2.39	2.38	2.39	2.39	1.00	up	7.31E-01	9.14E-01	-	-
1380295_at	---	---	---	Rn.56993	BF389710	2.30	2.29	2.31	2.29	2.31	2.29	1.00	down	7.78E-01	9.28E-01	-	-
1379947_at	---	---	---	Rn.203486	AA925321	2.43	2.46	2.42	2.41	2.50	2.40	1.00	up	9.56E-01	9.87E-01	-	-
1381228_at	---	---	---	Rn.207299	BE097136	2.51	2.49	2.52	2.49	2.53	2.50	1.00	down	8.96E-01	9.69E-01	-	-
1371138_at	Trdn	triadin	59299	Rn.41863	AJ243303	2.34	2.33	2.34	2.34	2.36	2.33	1.00	up	8.60E-01	9.57E-01	-	-
1394777_at	---	---	---	---	AI228857	2.36	2.35	2.37	2.36	2.37	2.35	1.00	down	7.68E-01	9.24E-01	-	-
1371082_at	Arr3	arrestin 3, retinal (X-arrestin)	171107	Rn.20297	AI112106	2.48	2.47	2.48	2.48	2.47	2.47	1.00	down	7.51E-01	9.19E-01	-	-
1382695_at	Lrrn4cl	LRRN4 C-terminal like	690329	Rn.198538	BF523738	2.26	2.25	2.27	2.26	2.26	2.25	1.00	down	7.17E-01	9.10E-01	-	-
1396350_at	---	---	---	---	BE097744	2.44	2.44	2.45	2.44	2.45	2.43	1.00	down	7.24E-01	9.12E-01	-	-
1398280_at	Impg1	interphotoreceptor matrix proteoglycan 1	66014	Rn.64488	NM_023958	2.46	2.43	2.48	2.46	2.47	2.44	1.00	down	9.10E-01	9.73E-01	-	-
1382950_at	---	---	---	Rn.15220	AA901350	2.47	2.55	2.48	2.48	2.48	2.44	1.00	down	9.69E-01	9.91E-01	-	-
1390405_at	---	---	---	Rn.199161	AA942765	2.35	2.34	2.35	2.34	2.35	2.34	1.00	down	7.07E-01	9.08E-01	-	-
1370748_at	---	---	---	---	AF093625	2.35	2.35	2.36	2.35	2.36	2.35	1.00	down	7.59E-01	9.21E-01	-	-
1377409_at	Mocs3	Molybdenum cofactor synthesis 3	311655	Rn.35140	BE114634	2.25	2.24	2.25	2.24	2.25	2.24	1.00	down	6.54E-01	8.97E-01	-	-
1368145_at	Pcp4	Purkinje cell protein 4	25510	Rn.9736	NM_013002	2.37	2.36	2.37	2.36	2.38	2.35	1.00	down	8.54E-01	9.55E-01	-	-
1371017_at	---	---	---	---	Z27087	2.21	2.20	2.21	2.20	2.21	2.20	1.00	down	5.72E-01	8.95E-01	-	-
1382541_at	Alk	anaplastic lymphoma kinase	266802	Rn.202143	BE103034	2.32	2.31	2.32	2.32	2.32	2.31	1.00	down	7.09E-01	9.09E-01	-	-
1378876_at	---	---	---	Rn.13662	BI295030	2.32	2.31	2.32	2.32	2.32	2.31	1.00	down	5.95E-01	8.95E-01	-	-
1396221_at	B3galt6	UDP-Gal:betaGal beta 1,3-galactosyltransferase, polypeptide 6	298690	Rn.219787	H31609	2.48	2.47	2.49	2.48	2.50	2.47	1.00	up	8.69E-01	9.59E-01	-	-
1384223_at	---	---	---	Rn.24193	AA819618	2.35	2.35	2.36	2.35	2.35	2.35	1.00	down	6.44E-01	8.95E-01	-	-
1395646_at	Letmd1	LETM1 domain containing 1	681352	Rn.102946	AW550447	2.33	2.31	2.33	2.33	2.33	2.31	1.00	down	8.00E-01	9.35E-01	-	-
1379762_at	---	---	---	Rn.156089	AA849027	2.29	2.29	2.29	2.29	2.29	2.29	1.00	down	4.39E-01	8.95E-01	-	-
1379373_at	---	---	---	Rn.22959	AI556457	2.35	2.34	2.35	2.34	2.35	2.34	1.00	down	7.42E-01	9.17E-01	-	-
1371151_at	Cpa3	carboxypeptidase A3, mast cell	54242	Rn.10700	U67914	2.34	2.34	2.35	2.34	2.35	2.34	1.00	down	7.92E-01	9.33E-01	-	-
1380645_at	---	---	---	Rn.146813	BF396136	2.25	2.24	2.25	2.24	2.25	2.24	1.00	down	6.55E-01	8.98E-01	-	-
1381653_at	---	---	---	Rn.172900	BF386457	2.45	2.43	2.46	2.44	2.45	2.44	1.00	down	8.06E-01	9.38E-01	-	-
1381160_at	---	---	---	Rn.169977	AW522852	2.50	2.44	2.53	2.48	2.54	2.45	1.00	down	9.58E-01	9.89E-01	-	-
1370867_at	Gnb2	guanine nucleotide binding protein (G protein), beta polypeptide 2	81667	Rn.1155	BM384381	4.09	4.09	4.18	4.09	4.18	4.08	1.00	down	9.65E-01	9.90E-01	-	-
1387274_at	Dlx5	distal-less homeobox 5	25431	Rn.11248	NM_012943	2.29	2.28	2.29	2.28	2.29	2.28	1.00	down	7.07E-01	9.08E-01	-	-
1383035_at	Ffar2	free fatty acid receptor 2	292794	Rn.17909	AI012890	2.23	2.23	2.24	2.23	2.25	2.23	1.00	up	7.25E-01	9.13E-01	-	-
1393374_at	---	---	---	Rn.212402	BM386110	2.36	2.36	2.37	2.36	2.37	2.36	1.00	down	7.17E-01	9.10E-01	-	-
1382383_at	---	---	---	---	AI103351	2.33	2.32	2.33	2.32	2.33	2.33	1.00	down	5.57E-01	8.95E-01	-	-
1371218_a_at	Nrg1	neuregulin 1	112400	Rn.37438	AF194443	2.27	2.27	2.28	2.27	2.28	2.27	1.00	down	6.55E-01	8.97E-01	-	-
1368198_at	Oprk1	opioid receptor, kappa 1	29335	Rn.89571	L22536	2.25	2.24	2.25	2.25	2.25	2.24	1.00	down	7.11E-01	9.09E-01	-	-
1368110_a_at	Syngap1	synaptic Ras GTPase activating protein 1 homolog (rat)	192117	Rn.9808	NM_053442	2.40	2.39	2.41	2.43	2.41	2.37	1.00	up	9.17E-01	9.75E-01	-	-
1387575_at	Rbbp9	retinoblastoma binding protein 9	29459	Rn.162693	NM_019219	2.62	2.54	2.66	2.61	2.66	2.54	1.00	down	9.69E-01	9.91E-01	-	-
1388181_at	LOC641523	immunoglobulin delta heavy chain constant region	641523	Rn.10956	J00741	2.37	2.36	2.37	2.36	2.37	2.35	1.00	down	7.82E-01	9.29E-01	-	-
1393513_at	---	---	---	Rn.170960	AI071445	2.30	2.30	2.32	2.30	2.31	2.30	1.00	down	7.54E-01	9.20E-01	-	-
1386121_at	RGD1566266	similar to hypothetical protein FLJ21127	304486	Rn.12905	BF561671	2.40	2.38	2.41	2.40	2.40	2.37	1.00	down	8.82E-01	9.64E-01	-	-
1396092_at	Nkiras1	NFKB inhibitor interacting Ras-like 1	305751	Rn.98363	BG667897	2.37	2.36	2.38	2.37	2.38	2.37	1.00	down	7.49E-01	9.19E-01	-	-
1396635_at	---	---	---	---	BF409915	2.57	2.54	2.60	2.58	2.59	2.53	1.00	down	9.32E-01	9.81E-01	-	-
1379355_at	Man2a2	mannosidase 2, alpha 2	308757	Rn.41796	BM392046	2.52	2.51	2.53	2.51	2.53	2.53	1.00	up	8.31E-01	9.47E-01	-	-
1387466_a_at	Htr7	5-hydroxytryptamine (serotonin) receptor 7	65032	Rn.87132	U68490	2.33	2.33	2.34	2.33	2.34	2.32	1.00	down	8.21E-01	9.43E-01	-	-
1392350_at	---	---	---	Rn.216787	AW525149	2.29	2.28	2.30	2.29	2.29	2.28	1.00	down	6.72E-01	9.01E-01	-	-
1380160_at

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1368500_a_at	Rgs9	regulator of G-protein signaling 9	29481	Rn.10903	NM_019224	2.35	2.35	2.37	2.35	2.36	2.35	1.00	down	7.93E-01	9.34E-01	-	-
1397478_at	Phb2	Prohibitin 2	114766	Rn.64535	AI030187	2.33	2.32	2.33	2.33	2.33	2.32	1.00	down	5.56E-01	8.95E-01	-	-
1398002_at	---	---	---	Rn.61465	BF409649	2.34	2.34	2.35	2.34	2.35	2.33	1.00	down	8.08E-01	9.38E-01	-	-
1391396_at	Eftud2	Elongation factor Tu GTP binding domain containing 2	287739	Rn.62495	AI136358	2.33	2.33	2.34	2.33	2.34	2.32	1.00	down	7.17E-01	9.10E-01	-	-
1389119_at	Xirp1	xin actin-binding repeat containing 1	316071	Rn.27588	AI105018	2.47	2.45	2.47	2.46	2.48	2.44	1.00	down	8.83E-01	9.64E-01	-	-
1380489_at	---	---	---	Rn.7020	BF389269	2.64	2.60	2.81	2.71	2.71	2.63	1.00	down	9.79E-01	9.94E-01	-	-
1390703_at	---	---	---	Rn.205602	AW251303	2.41	2.40	2.42	2.41	2.42	2.40	1.00	down	8.34E-01	9.48E-01	-	-
1367928_at	Myh7	myosin, heavy chain 7, cardiac muscle, beta	29557	---	BF395647	2.44	2.34	2.42	2.41	2.42	2.37	1.00	up	9.56E-01	9.87E-01	-	-
1374386_at	---	---	---	Rn.2569	AI412423	2.45	2.43	2.45	2.44	2.45	2.42	1.00	down	8.68E-01	9.59E-01	-	-
1377587_at	Ankrd60	ankyrin repeat domain 60	296417	Rn.62712	BF400794	2.32	2.31	2.33	2.33	2.33	2.31	1.00	down	8.07E-01	9.38E-01	-	-
1368148_at	Ngfr	nerve growth factor receptor (TNFR superfamily, member 16)	24596	Rn.10980	NM_012610	2.35	2.34	2.36	2.35	2.36	2.35	1.00	down	7.81E-01	9.29E-01	-	-
1393924_s_at	---	---	---	---	BF553036	2.28	2.27	2.28	2.28	2.28	2.27	1.00	down	7.03E-01	9.07E-01	-	-
1393272_at	---	---	---	Rn.204026	AI044383	2.38	2.38	2.39	2.38	2.39	2.37	1.00	down	7.21E-01	9.11E-01	-	-
1382342_at	---	---	---	Rn.16167	BI281174	2.46	2.45	2.47	2.46	2.45	2.45	1.00	down	7.47E-01	9.18E-01	-	-
1393767_at	---	---	---	Rn.130983	AA866293	2.39	2.38	2.39	2.39	2.39	2.38	1.00	down	6.66E-01	8.99E-01	-	-
1397578_at	Smyd1	SET and MYND domain containing 1	297333	Rn.203854	BE099423	2.34	2.33	2.36	2.35	2.35	2.33	1.00	down	8.54E-01	9.55E-01	-	-
1370515_x_at	Syt7	synaptotagmin VII	59267	Rn.91884	AI713274	2.34	2.34	2.35	2.35	2.34	2.33	1.00	down	7.60E-01	9.22E-01	-	-
1369428_a_at	Htr3a	5-hydroxytryptamine (serotonin) receptor 3a	79246	Rn.55109	U28430	2.27	2.26	2.27	2.26	2.27	2.26	1.00	down	7.03E-01	9.07E-01	-	-
1377017_at	---	---	---	Rn.174538	BE110143	2.27	2.26	2.27	2.26	2.27	2.26	1.00	down	6.69E-01	9.00E-01	-	-
1385234_at	---	---	---	Rn.21107	AI095587	2.34	2.33	2.35	2.34	2.36	2.32	1.00	down	8.60E-01	9.57E-01	-	-
1399685_at	Mta3	metastasis associated 1 family, member 3	298763	Rn.94848	BE106310	2.25	2.24	2.25	2.25	2.25	2.24	1.00	down	6.51E-01	8.96E-01	-	-
1376510_at	---	---	---	Rn.216603	AI072079	2.28	2.28	2.29	2.28	2.29	2.28	1.00	down	6.51E-01	8.97E-01	-	-
1380715_at	---	---	---	Rn.146937	BF400683	2.26	2.25	2.26	2.25	2.26	2.25	1.00	down	6.79E-01	9.02E-01	-	-
1375443_at	LOC691093	similar to gene trap ROSA b-geo 22	691093	Rn.22319	BF400690	2.27	2.26	2.27	2.26	2.27	2.26	1.00	down	5.77E-01	8.95E-01	-	-
1391088_at	Cdh11	Cadherin 11	84407	Rn.8900	BF414005	2.27	2.26	2.28	2.27	2.28	2.26	1.00	down	8.20E-01	9.42E-01	-	-
1380308_at	---	---	---	Rn.160009	AI072778	2.35	2.34	2.36	2.35	2.36	2.35	1.00	up	7.39E-01	9.16E-01	-	-
1384979_at	Gpr50	G protein-coupled receptor 50	117097	Rn.92385	BI289437	2.31	2.30	2.32	2.31	2.31	2.30	1.00	down	7.61E-01	9.22E-01	-	-
1394175_at	---	---	---	---	AI639194	2.32	2.31	2.33	2.32	2.33	2.31	1.00	down	7.72E-01	9.26E-01	-	-
1369987_at	Nkx2-5	NK2 transcription factor related, locus 5 (Drosophila)	114109	Rn.6179	NM_053651	2.21	2.21	2.21	2.21	2.21	2.21	1.00	down	5.54E-01	8.95E-01	-	-
1381437_at	---	---	---	---	AW253656	2.27	2.27	2.28	2.27	2.27	2.27	1.00	down	5.99E-01	8.95E-01	-	-
1383994_at	Syt3	Synaptotagmin III	25731	Rn.48884	BI289342	2.27	2.27	2.26	2.27	2.27	2.26	1.00	down	6.78E-01	9.02E-01	-	-
1388901_at	Fkbp5	FK506 binding protein 5	361810	Rn.144288	AW534837	8.74	7.07	8.34	8.85	6.92	8.37	1.00	down	9.98E-01	9.99E-01	-	-
1393467_at	Pcsk5	proprotein convertase subtilisin/kexin type 5	116548	Rn.104002	BF549923	2.44	2.43	2.46	2.44	2.46	2.42	1.00	down	8.94E-01	9.67E-01	-	-
1386379_at	---	---	---	Rn.163252	AI172246	2.44	2.43	2.47	2.46	2.45	2.42	1.00	down	9.15E-01	9.75E-01	-	-
1381849_at	LOC688749	similar to Tubby-related protein 3 (Tubby-like protein 3)	688749	Rn.8754	BE110844	2.28	2.27	2.28	2.28	2.28	2.28	1.00	up	6.52E-01	8.97E-01	-	-
1397053_at	---	---	---	Rn.206307	AW526050	2.29	2.29	2.30	2.29	2.30	2.29	1.00	down	6.94E-01	9.06E-01	-	-
1376743_at	---	---	---	Rn.38776	BE113293	2.23	2.23	2.24	2.23	2.24	2.23	1.00	down	6.59E-01	8.98E-01	-	-
1370416_at	Mxd3	Max dimerization protein 3	252915	Rn.10274	U45986	2.38	2.37	2.39	2.38	2.38	2.37	1.00	down	7.49E-01	9.19E-01	-	-
1370744_at	Gpr26	G protein-coupled receptor 26	192153	Rn.48779	AF208288	2.31	2.30	2.31	2.30	2.31	2.30	1.00	down	7.73E-01	9.26E-01	-	-
1384976_at	Tcfap2e	transcription factor AP-2, epsilon	313596	Rn.145085	BM389824	2.27	2.26	2.28	2.27	2.29	2.26	1.00	up	8.27E-01	9.45E-01	-	-
1392419_at	RGD1311870	similar to RIKEN cDNA 4930546C01	298563	Rn.61927	BF411806	2.52	2.47	2.54	2.48	2.59	2.45	1.00	down	9.86E-01	9.91E-01	-	-
1396179_at	LOC684425	similar to Adenylosuccinate synthetase isozyme 1 (Adenylosuccinate synthet	684425	---	BF406314	2.40	2.39	2.41	2.40	2.43	2.39	1.00	up	8.86E-01	9.65E-01	-	-
1381593_x_at	RT1-Ba	RT1 class II, locus Ba	309621	Rn.25717	AW528743	2.22	2.21	2.22	2.22	2.22	2.21	1.00	down	6.59E-01	8.98E-01	-	-
1385778_at	---	---	---	Rn.133713	BF409913	2.39	2.38	2.42	2.39	2.43	2.37	1.00	down	9.27E-01	9.79E-01	-	-
1387883_at	Kcnv1	potassium channel, subfamily V, member 1	60326	Rn.42829	BF391696	2.29	2.29	2.30	2.29	2.32	2.28	1.00	up	8.69E-01	9.59E-01	-	-
1382369_at	---	---	---	Rn.24710	AI233268	2.38	2.37	2.39	2.37	2.39	2.37	1.00	down	8.38E-01	9.49E-01	-	-
1386860_at	Mfge8	milk fat globule-EGF factor 8 protein	25277	Rn.3742	NM_012811	2.40	2.39	2.40	2.39	2.40	2.40	1.00	up	5.56E-01	8.95E-01	-	-
1389691_at	Znf575	zinc finger protein 575	308430	Rn.24529	AI230862	2.19	2.19	2.19	2.19	2.19	2.19	1.00	down	5.41E-01	8.95E-01	-	-
1384800_at	Zic3	Zic family member 3 (odd-paired homolog, Drosophila)	367944	Rn.64713	BE101902	2.20	2.19	2.20	2.19	2.20	2.19	1.00	down	6.54E-01	8.97E-01	-	-
1384533_at	---	---	---	---	AW527248	2.39	2.38	2.39	2.38	2.40	2.38	1.00	down	8.32E-01	9.47E-01	-	-
1387004_at	Nbl1	neuroblastoma, suppression of tumorigenicity 1	50594	Rn.4073	NM_031609	2.40	2.38	2.39	2.39	2.39	2.39	1.00	down	7.15E-01	9.10E-01	-	-
1381213_at	Nflx	nuclear factor I/X (CCAAT-binding transcription factor)	81524	Rn.56776	BE117138	2.24	2.24	2.25	2.24	2.24	2.24	1.00	down	6.30E-01	8.95E-01	-	-
1377491_at	---	---	---	---	BE112929	2.23	2.23	2.24	2.23	2.23	2.22	1.00	down	6.54E-01	8.97E-01	-	-
1392034_at	---	---	---	Rn.56681	BE099812	2.30	2.30	2.31	2.30	2.30	2.29	1.00	down	6.39E-01	8.95E-01	-	-
1393802_x_at	Gsg1	germ cell associated 1	312793	Rn.68598	BE102118	2.18	2.18	2.18	2.18	2.18	2.17	1.00	down	5.47E-01	8.95E-01	-	-
1390192_at	Slc27a3	solute carrier family 27 (fatty acid transporter), member 3	295219	Rn.22977	BF406261	2.31	2.30	2.31	2.32	2.31	2.30	1.00	up	7.09E-01	9.09E-01	-	-
1393807_at	---	---	---	Rn.107603	BF396605	2.28	2.27	2.29	2.28	2.28	2.27	1.00	down	6.99E-01	9.07E-01	-	-
1378909_at	---	---	---	Rn.146228	BE120180	2.40	2.39	2.42	2.39	2.43	2.38	1.00	down	9.15E-01	9.75E-01	-	-
1397054_at	---	---	---	Rn.114416	BF563234	2.37	2.33	2.35	2.32	2.41	2.33	1.00	up	9.51E-01	9.86E-01	-	-
1395576_at	---	---	---	Rn.206493	BI295834	2.34	2.33	2.35	2.34	2.34	2.33	1.00	down	7.47E-01	9.18E-01	-	-
1376735_at	---	---	---	---	BF414136	2.57	2.58	2.59	2.58	2.59	2.58	1.00	up	7.75E-01	9.27E-01	-	-
1381107_at	---	---	---	Rn.208744	BF387958	2.38	2.37	2.38	2.38	2.39	2.37	1.00	up	7.79E-01	9.28E-01	-	-
1393934_at	---	---	---	---	AA874877	2.41	2.41	2.42	2.41	2.41	2.41	1.00	down	5.55E-01	8.95E-01	-	-
1379311_at	Arid5a	AT rich interactive domain 5A (Mrf1 like)	316327	Rn.15775	AI177813	2.35	2.34	2.35	2.34	2.35	2.34	1.00	down	6.93E-01	9.05E-01	-	-
1378095_at	---	---	---	Rn.147995	BI297467	2.25	2.24	2.26	2.25	2.26	2.25	1.00	down	7.10E-01	9.09E-01	-	-
1383979_at	Mogat2	monoacylglycerol O-acyltransferase 2	681211	Rn.19175	BM392389	2.32	2.32	2.33	2.33	2.32	2.32	1.00	up	7.50E-01	9.19E-01	-	-
1390885_at	---	---	---	Rn.35036	AW535696	2.32	2.32	2.33	2.33	2.32	2.32	1.00	up	6.67E-01	8.99E-01	-	-
1384981_at	Cd6	Cd6 molecule	25752	Rn.57336	BM384254	2.39	2.38	2.39	2.38	2.40	2.37	1.00	down	8.61E-01	9.57E-01	-	-
1382881_at	Raver1	ribonucleoprotein, PTB-binding 1	298705	Rn.105739	BI290218	2.29	2.28	2.29	2.29	2.30	2.29	1.00	up	7.72E-01	9.26E-01	-	-
1379955_at	Ptchd2	patched domain containing 2	313705	Rn.103010	BE096222	2.38	2.38	2.39	2.38	2.38	2.38	1.00	down	6.21E-01	8.95E-01	-	-
1385749_at	---	---	---	Rn.57932	BF392886	2.38	2.37	2.40	2.38	2.38	2.38	1.00	down	8.09E-01	9.38E-01	-	-
1395820_at	Rnf150	ring finger protein 150	364983	Rn.205688	BF388337	2.45	2.44	2.45	2.44	2.45	2.44	1.00	down	7.27E-01	9.13E-01	-	-
1383371_at	Srcrb4d	scavenger receptor cysteine rich domain containing, group B (4 domains)	304401	Rn.35187	AI712305	2.91	2.51	2.65	2.83	2.63	2.62	1.00	up	9.90E-01	9.97E-01	-	-
1388270_at	Hbe1	hemoglobin, epsilon 1	293267	Rn.191853	BE107364	2.41	2.40	2.41	2.40	2.41	2.40	1.00	down	7.77E-01	9.28E-01	-	-
1397976_at	RGD1560556	similar to C14orf25 protein	366631	Rn.95516	BF408806	2.73	2.67	2.72	2.69	2.87	2.56	1.00	down	9.84E-01	9.95E-01	-	-
1375151_at	RGD1565168	Similar to RAP2A, member of RAS oncogene family	366733	Rn.8473	BF284007	2.21	2.20	2.21	2.20	2.21	2.20	1.00	down	6.23E-01	8.95E-01	-	-
1379751_at	Tox3	TOX high mobility group box family member 3	291908	Rn.41060	BF554367	2.30	2.29	2.31	2.30	2.30	2.29	1.00	down	7.81E-01	9.29E-01	-	-
1392583_at	---	---	---	Rn.165579	AI008140	2.25	2.25	2.26	2.25	2.26	2.25	1.00	down	7.34E-01	9.15E-01	-	-
1378217_at	Zfhx2	zinc finger homeobox 2	305888	Rn.161359	BI284196	2.34	2.32	2.34	2.33	2.34	2.32	1.00	down	7.45E-01	9.17E-01	-	-
1371268_at	Olr1641	olfactory receptor 1641	290050	Rn.142431	U50949	2.30	2.29	2.31	2.30	2.30	2.29	1.00	down	7.19E-01	9.11E-01	-	-
1394998_at	---	---	---	Rn.172508	BI301433	2.36	2.35	2.38	2.36	2.38	2.35	1.00	down	8.88E-01	9.65E-01	-	-
1380873_at	---	---	---	Rn.172382	BI295852	2.34	2.33	2.35	2.33	2.35	2.34	1.00	up	8.00E-01	9.35E-01	-	-
1382624_at	---	---	---	---	AA858768	2.34	2.33	2.35	2.34	2.34	2.33	1.00	down	7.08E-01	9.09E-01	-	-
1377853_at	Tshz3	teashirt zinc finger homeobox 3	308523	Rn.9411	AI599177	2.36	2.35	2.37	2.36	2.37	2.36	1.00	up	7.70E-01	9.25E-01	-	-
1397807_at	---	---	---	Rn.172621	BF412350	2.47	2.46	2.48	2.47	2.47	2.46	1.00	down	7.55E-01	9.20E-01	-	-
1383569_at	Pmpcb	peptidase (mitochondrial processing) beta	64198	Rn.841	AA925804	2.39	2.40	2.39	2.39	2.40	2.38	1.00	down	7.33E-01	9.15E-01	-	-
1398150_at	---	---	---	---	BF404612	2.34	2.33	2.34	2.33	2.34	2.33	1.00	down	7.15E-01	9.10E-01	-	-
1374899_at	Fam70b	family with sequence similarity 70, member B	290877	Rn.8443	BM383043	2.22	2.22	2.23	2.22	2.23	2.22	1.00	down	5.77E-01	8.95E-01	-	-
1381712_at	---	---	---	Rn.216858	BE102603	2.36	2.36	2.37	2.36	2.37	2.36	1.00	down	6.96E-01	9.06E-01	-	-
1370205_at	Slco1c1	solute carrier organic anion transporter family, member 1c1	84511	Rn.45744	BE118954	2.40	2.39	2.41	2.39	2.41	2.39	1.00	down	8.04E-01	9.37E-01	-	-
1369356_at	Gucy2f	guanylate cyclase 2F	116556	Rn.10061	NM_053831	2.38	2.37	2.39	2.38	2.39	2.37	1.00	down	8.38E-01	9.49E-01	-	-
1384844_at	RGD1564005	similar to novel protein	360575	Rn.19412	AI060280	2.23	2.23	2.23	2.23	2.23	2.22	1.00	down	6.68E-01	9.00E-01	-	-
1396990_at	---	---	---	---	BF396608	2.38	2.41	2.39	2.40	2.40	2.40	1.00	up	8.50E-01	9.53E-01	-	-
1393079_at	Siae	sialic acid acetylesterase	363045	Rn.21775	AI111605	3.53	2.74	2.73	2.72	3.42	2.86	1.00	up	9.96E-01	9.98E-01	-	-
1397651_at	---	---	---	Rn.209716	AI591591	2.24	2.24	2.25	2.24	2.25	2.24	1.00	down	3.84E-01	8.95E-01	-	-
1386241_at	---	---	---	---	BG153317	2.47	2.43	2.46	2.43	2.51	2.41	1.00	down	9.57E-01	9.88E-01	-	-
1393547_at	Rnf182	ring finger protein 182	498726	Rn.141306	BE101549	2.35	2.34	2.36	2.34	2.35	2.34	1.00	down	7.84E-01	9.30E-01	-	-
1385992_at	---	---	---	---	AI406700	2.26	2.25	2.26	2.26	2.25	2.25	1.00	down	6.82E-01	9.03E-01	-	-
1381047_at	---	---	---	---	BE097624	2.38	2.37	2.39	2.38	2.39	2.37	1.00	down	8.00E-01	9.35E-01	-	-
1390015_at	---	---	---	---	BF396129	2.39	2.38	2.40	2.38	2.40	2.37	1.00	down	8.52E-01	9.54E-01	-	-
1395838_at	---	---	---	Rn.172789	BF394890	2.29	2.29	2.30	2.29	2.30	2.28	1.00	down	7.54E-01	9.20E-01	-	-
1396611_at	Cul4b	cullin 4B	302502	Rn.21178	BG671713	2.38	2.38	2.39	2.37	2.38	2.39	1.00	down	7.79E-01	9.28E-01	-	-
1377374_at	---	---	---	Rn.28718	AI146055	2.27	2.26	2.28	2.27	2.28	2.26	1.00	down	7.69E-01	9.24E-01	-	-
1393384_at	LOC682006	hypothetical protein LOC682006	682006	---	BF393809	2.31	2.31	2.32	2.31	2.31	2.30	1.00	down	6.50E-01	8.96E-01	-	-
1368850_at	Csnk1g3	casein kinase 1, gamma 3	64823	Rn.10084	BE111111	2.40	2.17	2.66	2.40	2.40	2.42	1.00	down	9.90E-01	9.97E-01	-	-
1390890_at	---	---	---	Rn.13158	AI460854	2.37	2.36	2.38	2.37	2.38	2.36	1.00	down	8.41E-01	9.50E-01	-	-
1398301_at	31563135 /// RGD	hypothetical LOC364105 /// similar to ribosomal protein L36 /// hypothetical ge	364105 /// 366485	Rn.1439	AI009003	2.35	2.36	2.37	2.35	2.37	2.35	1.00	down	7.56E-01	9.20E-01	-	-
1374951_at	Obscn	obscurin, cytoskeletal calmodulin and titin-interacting RhoGEF	338458	Rn.45300	BF404478	2.33	2.32	2.34	2.33	2.34	2.32	1.00	down	8.42E-01	9.51E-01	-	-
1373873_at	---	---	---	Rn.14050	AI175346	2.30	2.29	2.30	2.29	2.31	2.28	1.00	down	8.25E-01	9.45E-01	-	-
1369043_at	Gabrd	gamma-aminobutyric acid (GABA) A receptor, delta	29689	Rn.10927	NM_017289	2.28	2.27	2.29	2.28	2.28	2.27	1.00	down	7.09E-01	9.09E-01	-	-
1379231_at	Sptb	Spectrin, beta, erythrocytic	314251	Rn.63940	BF418950	2.28	2.28	2.29	2.28	2.28	2.27	1.00	down	6.87E-01	9.04E-01	-	-
1397416_at	---	---	---	Rn.57152	BG672308	2.43	2.42	2.44	2.43	2.43	2.42	1.00	down	7.09E-01	9.09E-01	-	-
1378398_at	RGD1563060	similar to AVLV472	291808	Rn.137959	BM385071	2.26	2.25	2.26	2.25	2.26	2.24	1.00	down	7.65E-01	9.23E-01	-	-
1385065_at	---	---	---	Rn.14719	AA891903	2.40	2.39	2.43	2.39	2.41	2.41	1.00	up	9.02E-01	9.70E-01	-	-
1371256_at	Ptpn18	protein tyrosine phosphatase, non-receptor type 18	301333	Rn.9310	BM386565	2.32	2.31	2.32	2.31	2.32	2.31	1.00	down	5.28E-01	8.95E-01	-	-
1387506_at	Foxa3	forkhead box A3	25100	Rn.10949	NM_017077	2.34	2.32	2.34	2.33	2.34	2.32	1.00	down	8.31E-01	9.47E-01	-	-
1380364_at	RGD1561115	similar to Gene model 1568	298560	Rn.141508	AI575320	2.23	2.23	2.24	2.23	2.23	2.23	1.00	down	6.35E-01	8.95E-01	-	-
1389501_at	LOC688297	similar to Retinal rod rhodopsin-sensitive cGMP 3,5-cyclic phosphodiesterase	688297	---	BG371889	2.24	2.23	2.24	2.23	2.24	2.23	1.00	down	5.92E-01	8.95E-01	-	-
1390573_a_at	Nfatc4	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 4	305897	Rn.23727	BG377358	2.20	2.20	2.21	2.20	2.21	2.20	1.00	down	5.46E-01	8.95E-01	-	-
1369107_at	Sftpa1	surfactant protein A1	24773	Rn.11343	BI295853	2.45	2.44	2.46	2.44	2.47	2.43	1.00	down	8.93E-01	9.67E-01	-	-
1391546_at	Kcnq2	potassium voltage-gated channel, subfamily Q, member 2	170848	Rn.33317	AI412209	2.26	2.25	2.26	2.25	2.26	2.25	1.00	down	6.76E-01	9.01E-01	-	-
1382885_at	Ebf4	Early B-cell factor 4	680751	Rn.46878	AW534013	2.32	2.31	2.33	2.31	2.32	2.33	1.00	up	8.15E-01	9.40E-01	-	-
1393665_at	---	---	---	Rn.206344	AW526330	2.47	2.45	2.49	2.46	2.49	2.45	1.00	down	9.17E-01	9.75E-01	-	-
1374317_at	Pik3r6	phosphoinositide-3-kinase, regulatory subunit 6	497932	Rn.58070	BM383924	2.31	2.30	2.32	2.31	2.34	2.30	1.00	up	8.87E-01	9.65E-01	-	-
1376361_at	---	---	---	Rn.172531	BF406226	2.46	2.45	2.47	2.45	2.48	2.45	1.00	up	8.65E-01	9.58E-01	-	-
1368629_at	Reg1a	regenerating islet-derived 1 alpha	24714	Rn.11332	NM_012641	2.32	2.32	2.40	2.40	2.32	2.31	1.00	down	9.67E-01	9.90E-01	-	-
1393049_at	Myo1g	myosin IG	289785	Rn.198974	BF417582	2.38	2.37	2.38	2.38	2.38	2.37	1.00	down	7.09E-01	9.09E-01	-	-
1369659_at	Cga	glycoprotein hormones, alpha subunit	116700	Rn.10589	NM_053918	2.23	2.23	2.24	2.23	2.24	2.23	1.00	down	6.72E-01	9.01E-01	-	-
1397936_at	Foxr1	forkhead box R1	315601	Rn.198806	BF415706	2.26	2.25	2.26	2.25	2.26	2.25	1.00	down	7.03E-01	9.07E-01	-	-
1379906_at	Atp1b2	ATPase, Na+/K+ transporting, beta 2 polypeptide	24214	Rn.10624	BM385311	2.53	2.52	2.53	2.54	2.52	2.53	1.00	up	7.23E-01	9.12E-01	-	-
1391906_at	Cort /// Kif1b	cortistatin /// kinesin family member 1B	117548 /// 25305	Rn.6526	BE113001	2.53	2.85	2.42	2.33	2.33	3.14	1.00	up	9.95E-01	9.98E-01	-	-
1370070_at	Synj1	synaptojanin 1	85238	Rn.22685	NM_053476	3.88	3.75	3.99	3.88	3.88	3.86	1.00	down	9.80E-01	9.94E-01	-	-
1396300_at	---	---	---	Rn.167353	AI548714	2.58	2.56	2.57	2.57	2.59	2.55	1.00	down	8.83E-01	9.64E-01	-	-
1391683_at	---	---	---	Rn.166989	BF410646	2.34	2.33	2.35	2.34	2.37	2.33	1.00	up	8.93E-01	9.67E-01	-	-
1397423_at	---	---	---	Rn.79309	BI292177	2.35	2.34	2.36	2.35	2.37	2.34	1.00	down	8.67E-01	9.59E-01	-	-
1388599_at	---	---	---	Rn.107201	BE107098	2.29	2.28	2.29	2.28	2.29	2.28	1.00	down	6.32E-01	8.95E-01	-	-
1379897_at	---	---	---	Rn.168080	AI535567	2.39	2.38	2.40	2.38	2.41	2.37	1.00	down	8.93E-01	9.67E-01	-	-
1385604_at	LOC685734	similar to erythrocyte membrane protein band 4.1 like 4B isoform 2	685734	Rn.207907	BE108011	2.37	2.36	2.39	2.37	2.39	2.35	1.00	down	9.00E-01	9.69E-01	-	-
1396290_at	---	---	---	---	BG380538	2.41	2.40	2.42	2.40	2.42	2.40	1.00	down	8.67E-01	9.58E-01	-	-
1368581_at	Sdc3	syndecan 3	116873	Rn.10504	U73184	2.30	2.30	2.31	2.30	2.31	2.30	1.00	down	6.74E-01	9.01E-01	-	-
1398416_at	Rnase n	ribonuclease type III, nuclear	310159	Rn.41113	AI008376	2.48	2.47	2.49	2.48	2.49	2.46	1.00	down	8.42E-01	9.51E-01	-	-
1396260_at	---	---	---	---	BE108054	2.41	2.41	2.41	2.41	2.43	2.40	1.00	up	8.32E-01	9.47E-01	-	-
1384906_at	Dlk2	delta-like 2 homolog (Drosophila)	316232	Rn.202372	AI577346	2.34	2.33	2.34	2.33	2.34	2.32	1.00	down	8.13E-01	9.39E-01	-	-
1391688_at	Map3k14	mitogen-activated protein kinase kinase kinase 14	360640	Rn.47167	BM385156	2.64	2.62	2.67	2.68	2.64	2.62	1.00	up	9.36E-01	9.82E-01	-	-
1391896_at

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1393066_at	---	---	---	Rn.212219	AI070787	2.42	2.41	2.42	2.41	2.42	2.40	1.00	down	7.95E-01	9.34E-01	-	-
1397873_at	---	---	---	Rn.199136	AI502924	2.42	2.42	2.43	2.42	2.43	2.42	1.00	down	6.59E-01	8.98E-01	-	-
1398604_at	Osbp2	oxysterol binding protein 2	305475	Rn.40484	AI112698	2.21	2.21	2.21	2.21	2.21	2.20	1.00	down	6.14E-01	8.95E-01	-	-
1387203_at	Gckr	glucokinase regulatory protein	25658	Rn.7863	NM_013120	2.26	2.25	2.26	2.25	2.26	2.25	1.00	down	6.84E-01	9.03E-01	-	-
1390630_at	---	---	---	Rn.160378	BE112446	2.28	2.27	2.29	2.28	2.29	2.27	1.00	down	7.48E-01	9.18E-01	-	-
1369721_at	Strn	striatin, calmodulin binding protein	29149	Rn.37469	NM_019148	2.40	2.40	2.40	2.40	2.41	2.40	1.00	down	4.31E-01	8.95E-01	-	-
1392540_at	---	---	---	Rn.167243	AI236936	2.28	2.27	2.29	2.28	2.29	2.27	1.00	down	8.08E-01	9.38E-01	-	-
1369322_at	Kcne2	potassium voltage-gated channel, Isk-related subfamily, gene 2	171138	Rn.48691	NM_133603	2.34	2.33	2.34	2.34	2.34	2.33	1.00	down	7.37E-01	9.16E-01	-	-
1384061_at	---	---	---	Rn.203931	AI029659	2.44	2.41	2.48	2.43	2.50	2.40	1.00	up	9.63E-01	9.89E-01	-	-
1391900_at	---	---	---	Rn.146764	AW534091	2.39	2.38	2.41	2.39	2.40	2.38	1.00	down	8.72E-01	9.61E-01	-	-
1370868_at	Krt1	keratin 1	300250	Rn.31789	X54806	2.28	2.28	2.29	2.28	2.29	2.28	1.00	down	7.16E-01	9.10E-01	-	-
1374391_at	Sln	sarcolipin	367086	Rn.16457	BF408611	2.33	2.32	2.34	2.33	2.35	2.31	1.00	down	8.74E-01	9.61E-01	-	-
1397839_at	Rab15	RAB15, member RAS oncogene family	299156	Rn.24234	BF554320	2.26	2.24	2.25	2.24	2.26	2.24	1.00	down	8.13E-01	9.40E-01	-	-
1377041_at	Mfng	MFNG O-fucosylpeptide 3-beta-N-acetylglucosaminyltransferase	315119	Rn.102109	AA891664	2.30	2.29	2.30	2.30	2.31	2.29	1.00	down	7.51E-01	9.19E-01	-	-
1385442_at	---	---	---	Rn.121179	AW529552	2.29	2.29	2.29	2.29	2.30	2.28	1.00	down	7.43E-01	9.17E-01	-	-
1393417_at	---	---	---	Rn.200292	BF522397	2.28	2.27	2.28	2.27	2.29	2.27	1.00	down	7.62E-01	9.22E-01	-	-
1385247_at	Ugt2b	UDP glycosyltransferase 2 family, polypeptide B	24862	Rn.2521	AA858993	2.41	2.40	2.43	2.41	2.45	2.39	1.00	up	9.40E-01	9.83E-01	-	-
1371492_at	Apobec2	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 2	301226	Rn.163040	BF285350	2.30	2.30	2.31	2.30	2.31	2.30	1.00	down	7.46E-01	9.18E-01	-	-
1376809_at	Fbrsl1	fibrosin-like 1	304572	Rn.24267	BI288660	2.63	2.46	2.55	2.54	2.56	2.54	1.00	down	9.74E-01	9.92E-01	-	-
1382218_at	Ldlr	low density lipoprotein receptor	300438	Rn.10483	X13722	2.36	2.35	2.36	2.35	2.36	2.35	1.00	down	6.54E-01	8.97E-01	-	-
1379944_at	---	---	---	Rn.21640	BE112610	2.32	2.32	2.33	2.32	2.32	2.32	1.00	down	4.64E-01	8.95E-01	-	-
1390314_at	---	---	---	Rn.206611	BF400220	2.25	2.25	2.26	2.25	2.26	2.25	1.00	down	7.85E-01	9.30E-01	-	-
1369672_at	Alox5ap	arachidonate 5-lipoxygenase activating protein	29624	Rn.18399	NM_017260	2.39	2.39	2.40	2.40	2.40	2.38	1.00	down	8.34E-01	9.48E-01	-	-
1395578_at	---	---	---	Rn.27883	BF419340	2.36	2.36	2.37	2.36	2.37	2.36	1.00	down	6.67E-01	8.99E-01	-	-
1375734_at	Fam65a	Family with sequence similarity 65, member A	291974	Rn.105873	BF419022	2.39	2.38	2.43	2.39	2.40	2.40	1.00	down	9.12E-01	9.74E-01	-	-
1387719_at	Clcn1	chloride channel 1	25688	Rn.10440	NM_013147	2.29	2.29	2.30	2.29	2.30	2.28	1.00	down	7.67E-01	9.24E-01	-	-
1390007_at	---	---	---	Rn.53291	BE121293	2.27	2.26	2.27	2.27	2.27	2.26	1.00	down	7.33E-01	9.14E-01	-	-
1398320_at	Pfkfb2	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 2	24640	Rn.44844	BM986214	2.33	2.32	2.34	2.33	2.33	2.32	1.00	down	7.90E-01	9.32E-01	-	-
1373988_at	LOC690073	similar to neuroblastoma-amplified protein	690073	Rn.21749	BM387458	2.48	2.55	2.49	2.48	2.58	2.47	1.00	up	9.69E-01	9.91E-01	-	-
1387846_at	Cacna1f	calcium channel, voltage-dependent, L type, alpha 1F subunit	114493	Rn.39125	NM_053701	2.31	2.31	2.32	2.31	2.32	2.31	1.00	down	6.74E-01	9.01E-01	-	-
1391015_at	Ccdc69	coiled-coil domain containing 69	497906	Rn.138612	AI548779	2.44	2.42	2.44	2.43	2.46	2.42	1.00	up	9.15E-01	9.75E-01	-	-
1395188_at	---	---	---	---	BF393262	2.27	2.26	2.27	2.26	2.27	2.26	1.00	down	7.39E-01	9.16E-01	-	-
1381467_at	---	---	---	Rn.161078	AI598594	2.32	2.32	2.34	2.32	2.33	2.31	1.00	down	8.60E-01	9.57E-01	-	-
1381281_at	---	---	---	Rn.202054	BF415733	2.54	2.49	2.57	2.53	2.54	2.52	1.00	down	9.46E-01	9.84E-01	-	-
1391713_at	RGD1308958	similar to chromosome 9 open reading frame 5	298020	Rn.39293	BE112609	2.32	2.31	2.32	2.31	2.32	2.31	1.00	down	7.26E-01	9.13E-01	-	-
1368950_a_at	Grin2d	glutamate receptor, ionotropic, N-methyl D-aspartate 2D	24412	Rn.91209	D13213	2.35	2.35	2.36	2.35	2.36	2.35	1.00	up	7.34E-01	9.15E-01	-	-
1397760_at	---	---	---	Rn.173319	BI290156	2.30	2.29	2.31	2.30	2.31	2.30	1.00	up	7.12E-01	9.10E-01	-	-
1369288_at	Pitx1	paired-like homeodomain 1	113983	Rn.74240	NM_053624	2.26	2.25	2.27	2.26	2.26	2.26	1.00	down	7.72E-01	9.26E-01	-	-
1387257_at	Sct	secretin	24769	Rn.9919	NM_022670	2.48	2.48	2.49	2.48	2.48	2.48	1.00	down	5.56E-01	8.95E-01	-	-
1376378_at	---	---	---	Rn.209160	BF393577	2.33	2.32	2.33	2.31	2.33	2.35	1.00	up	8.84E-01	9.64E-01	-	-
1380041_at	---	---	---	Rn.167922	BF396849	2.29	2.29	2.30	2.29	2.30	2.28	1.00	down	7.83E-01	9.30E-01	-	-
1397995_at	---	---	---	Rn.199937	BF386447	2.30	2.30	2.30	2.32	2.31	2.29	1.00	up	8.73E-01	9.61E-01	-	-
1371947_at	Ndn	necdin homolog (mouse)	308690	Rn.3096	BG671865	2.39	2.37	2.41	2.38	2.41	2.37	1.00	down	9.18E-01	9.76E-01	-	-
1390227_at	Pcp4l1	Purkinje cell protein 4-like 1	685448	Rn.155340	AI101017	2.43	2.41	2.44	2.42	2.45	2.41	1.00	up	9.07E-01	9.72E-01	-	-
1371234_at	Fgb	fibrinogen beta chain	24366	Rn.11416	M35602	2.29	2.28	2.30	2.29	2.32	2.28	1.00	up	9.02E-01	9.70E-01	-	-
1384835_at	---	---	---	Rn.216765	AI547468	2.38	2.37	2.40	2.41	2.39	2.36	1.00	up	9.17E-01	9.75E-01	-	-
1369267_at	Gabrg3	gamma-aminobutyric acid (GABA) A receptor, gamma 3	79211	Rn.10369	NM_024370	2.28	2.27	2.28	2.27	2.28	2.27	1.00	down	7.88E-01	9.31E-01	-	-
1378462_at	---	---	---	Rn.36309	BE107396	2.35	2.33	2.36	2.34	2.35	2.34	1.00	down	8.65E-01	9.58E-01	-	-
1393381_at	---	---	---	Rn.148804	AA924139	2.30	2.29	2.31	2.30	2.31	2.29	1.00	down	7.70E-01	9.25E-01	-	-
1395669_at	---	---	---	---	AW434878	2.29	2.28	2.29	2.29	2.29	2.27	1.00	down	8.19E-01	9.42E-01	-	-
1369079_at	Nxph1	neurexophilin 1	25501	Rn.10610	NM_012994	2.34	2.33	2.35	2.34	2.34	2.33	1.00	down	7.50E-01	9.19E-01	-	-
1382367_at	---	---	---	Rn.204940	AI228502	2.29	2.29	2.30	2.29	2.29	2.29	1.00	down	4.16E-01	8.95E-01	-	-
1396665_at	---	---	---	---	BE115250	2.45	2.45	2.46	2.45	2.46	2.45	1.00	down	7.12E-01	9.10E-01	-	-
1372938_at	Smarce1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin,	303518	Rn.8513	AI575671	7.32	6.93	6.21	6.66	6.78	7.01	1.00	down	9.96E-01	9.98E-01	-	-
1376809_at	Rasl10a	RAS-like, family 10, member A	364190	Rn.50230	AI412686	2.28	2.27	2.27	2.27	2.28	2.27	1.00	down	6.90E-01	9.05E-01	-	-
1368357_at	Kcnh4	potassium voltage-gated channel, subfamily H (eag-related), member 4	114032	Rn.30035	NM_053630	2.28	2.28	2.28	2.28	2.27	1.00	down	7.41E-01	9.16E-01	-	-
1387751_at	Wap	whey acidic protein	114596	Rn.9978	NM_053751	2.27	2.26	2.28	2.27	2.29	2.26	1.00	up	8.57E-01	9.55E-01	-	-
1387208_at	Ngb	neuroglobin	85382	Rn.64645	NM_033359	2.25	2.24	2.25	2.25	2.25	2.24	1.00	down	6.75E-01	9.01E-01	-	-
1391012_at	RGD1562089	similar to hypothetical protein MGC27770	315145	Rn.24714	BF283210	2.35	2.34	2.35	2.34	2.35	2.34	1.00	down	5.33E-01	8.95E-01	-	-
1381492_at	---	---	---	---	AI137687	2.27	2.26	2.27	2.26	2.27	2.26	1.00	down	7.67E-01	9.24E-01	-	-
1378774_at	---	---	---	Rn.45809	BE115264	2.29	2.28	2.29	2.29	2.29	2.28	1.00	down	7.12E-01	9.10E-01	-	-
1396572_at	RGD1565096	similar to TSG118.1	499255	Rn.162451	BE107002	2.26	2.25	2.26	2.26	2.25	2.25	1.00	down	6.99E-01	9.07E-01	-	-
1397901_at	---	---	---	Rn.145857	BI298378	2.37	2.37	2.37	2.37	2.37	2.37	1.00	down	5.99E-01	8.95E-01	-	-
1371054_at	Pnmt	phenylethanolamine-N-methyltransferase	24661	Rn.202604	BF408734	2.38	2.37	2.39	2.38	2.39	2.37	1.00	up	8.54E-01	9.55E-01	-	-
1388062_at	Mapk15	mitogen-activated protein kinase 15	286997	Rn.42898	AF078798	2.17	2.16	2.17	2.16	2.17	2.16	1.00	down	5.66E-01	8.95E-01	-	-
1394666_at	Neb	nebulin	311029	Rn.134031	AI549596	2.37	2.36	2.38	2.37	2.39	2.35	1.00	down	8.97E-01	9.68E-01	-	-
1395722_at	Trove2	TROVE domain family, member 2	304833	Rn.146598	BF288345	2.27	2.27	2.29	2.27	2.29	2.26	1.00	down	8.55E-01	9.55E-01	-	-
1394634_at	Dnajc10	DnaJ (Hsp40) homolog, subfamily C, member 10	295690	Rn.8642	AI176634	2.29	2.28	2.30	2.28	2.29	2.29	1.00	down	7.64E-01	9.23E-01	-	-
1369253_at	Kremen1	kringle containing transmembrane protein 1	114107	Rn.90021	NM_053649	2.39	2.38	2.39	2.38	2.38	2.38	1.00	down	8.22E-01	9.43E-01	-	-
1373896_at	Syt1	synaptotagmin I	25716	Rn.216272	AA943569	2.26	2.26	2.27	2.26	2.27	2.26	1.00	down	6.99E-01	9.07E-01	-	-
1397922_at	---	---	---	---	BF393925	2.48	2.45	2.52	2.45	2.57	2.44	1.00	up	9.73E-01	9.92E-01	-	-
1398171_at	Ggn	gametogenetin	292765	Rn.52869	BF406300	2.27	2.26	2.27	2.26	2.27	2.26	1.00	down	5.75E-01	8.95E-01	-	-
1398094_at	RGD1311343	similar to RIKEN cDNA 4930524B15	360506	Rn.145140	BE102480	2.16	2.16	2.16	2.16	2.16	2.14	1.00	down	6.09E-01	8.95E-01	-	-
1397421_at	---	---	---	Rn.168795	AI549253	2.23	2.23	2.24	2.23	2.24	2.23	1.00	down	7.40E-01	9.16E-01	-	-
1377168_at	Cpne9	copine family member IX	297516	Rn.87286	AI412673	2.41	2.40	2.41	2.40	2.41	2.40	1.00	down	6.44E-01	8.95E-01	-	-
1391794_at	---	---	---	Rn.199899	BI300542	2.40	2.38	2.40	2.39	2.40	2.39	1.00	down	8.28E-01	9.45E-01	-	-
1376412_at	---	---	---	Rn.207716	BF410759	2.33	2.32	2.34	2.33	2.34	2.32	1.00	down	8.40E-01	9.50E-01	-	-
1379753_at	Pex5l	peroxisomal biogenesis factor 5-like	286937	Rn.207886	BE121134	2.36	2.35	2.38	2.35	2.39	2.34	1.00	down	9.18E-01	9.76E-01	-	-
1375747_at	Acap2	ArfGAP with coiled-coil, ankyrin repeat and PH domains 2	619382	Rn.208307	BF390818	2.29	2.29	2.30	2.29	2.30	2.28	1.00	down	8.05E-01	9.37E-01	-	-
1392679_at	Znf787	zinc finger protein 787	365176	Rn.23427	AW525036	2.33	2.32	2.33	2.33	2.33	2.32	1.00	down	7.64E-01	9.23E-01	-	-
1394531_at	---	---	---	Rn.206326	AW526150	2.38	2.37	2.39	2.37	2.38	2.38	1.00	down	8.39E-01	9.50E-01	-	-
1397395_at	---	---	---	Rn.199486	AI555034	2.31	2.31	2.32	2.31	2.32	2.31	1.00	down	7.53E-01	9.20E-01	-	-
1397315_at	---	---	---	Rn.168081	AI554978	2.37	2.36	2.38	2.37	2.38	2.36	1.00	down	8.55E-01	9.55E-01	-	-
1389882_at	Ier5	immediate early response 5	498256	Rn.8590	AI180270	2.16	2.16	2.17	2.17	2.16	2.16	1.00	up	6.39E-01	8.95E-01	-	-
1389992_at	RGD1307493	similar to membrane protein expressed in epithelial-like lung adenocarcinoma	303317	---	BF392822	2.38	2.37	2.39	2.37	2.40	2.37	1.00	down	8.67E-01	9.59E-01	-	-
1383784_at	---	---	---	---	BI289438	2.41	2.40	2.42	2.40	2.41	2.41	1.00	down	8.27E-01	9.45E-01	-	-
1380777_at	---	---	---	Rn.210624	BF399517	2.37	2.36	2.38	2.37	2.39	2.36	1.00	up	8.90E-01	9.66E-01	-	-
1379748_at	H28	Histocompatibility 28	310968	Rn.16644	AA819629	2.41	2.39	2.40	2.40	2.41	2.39	1.00	down	8.55E-01	9.55E-01	-	-
1391152_at	685769 /// LOC68	similar to RIKEN cDNA 4930555G01 /// similar to Discs large homolog 5 (Plac	680281 /// 685769	Rn.78670	AI412781	2.44	2.43	2.45	2.44	2.46	2.41	1.00	down	9.21E-01	9.77E-01	-	-
1378955_at	St6galnac2	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosami	303692	Rn.53257	BE119519	2.23	2.23	2.24	2.23	2.24	2.23	1.00	down	6.91E-01	9.05E-01	-	-
1377128_at	F8a1	coagulation factor VIII-associated (intronic transcript) 1	501661	Rn.41311	AI412407	2.14	2.14	2.15	2.14	2.14	2.14	1.00	down	5.87E-01	8.95E-01	-	-
1397345_at	---	---	---	Rn.209080	AI011553	2.34	2.32	2.35	2.34	2.34	2.33	1.00	down	8.74E-01	9.61E-01	-	-
1380523_at	Fbxo15	F-box protein 15	361354	Rn.24143	AI145917	2.56	2.57	2.59	2.58	2.58	2.57	1.00	down	8.85E-01	9.64E-01	-	-
1379570_at	RGD1562841	Similar to fibrillarin	363563	Rn.50690	AI578255	2.29	2.29	2.30	2.29	2.30	2.29	1.00	down	6.88E-01	9.04E-01	-	-
1395566_at	---	---	---	Rn.169435	AW524204	2.55	2.55	2.56	2.55	2.56	2.55	1.00	up	5.54E-01	8.95E-01	-	-
1379444_at	---	---	---	Rn.44024	BF283694	2.32	2.32	2.33	2.32	2.33	2.31	1.00	down	7.50E-01	9.19E-01	-	-
1397435_at	---	---	---	Rn.208988	BF394050	2.39	2.38	2.39	2.38	2.42	2.37	1.00	up	9.23E-01	9.77E-01	-	-
1385182_at	Pkp1	plakophilin 1	304822	Rn.123811	BG371843	2.29	2.29	2.30	2.29	2.30	2.29	1.00	down	7.49E-01	9.19E-01	-	-
1396508_at	---	---	---	Rn.147893	BF392880	2.60	2.56	2.60	2.59	2.61	2.56	1.00	down	9.33E-01	9.81E-01	-	-
1370836_at	Serpina4	serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antit	246328	Rn.11152	U51017	2.36	2.36	2.37	2.37	2.36	2.36	1.00	down	6.88E-01	9.04E-01	-	-
1374726_at	Fndc1	fibronectin type III domain containing 1	308099	Rn.20633	AI411941	3.22	3.76	2.82	3.24	3.15	3.43	1.00	up	9.96E-01	9.98E-01	-	-
1375648_at	RGD1307966	similar to hypothetical protein	287736	---	BE113026	2.23	2.23	2.24	2.23	2.24	2.23	1.00	down	6.33E-01	8.95E-01	-	-
1377134_at	Kdm5b	lysine (K)-specific demethylase 5B	304809	Rn.22866	AI454378	2.30	2.29	2.30	2.29	2.30	2.29	1.00	down	7.63E-01	9.23E-01	-	-
1368686_at	Ambp	alpha-1-microglobulin/bikunin precursor	25377	Rn.18721	NM_012901	2.50	2.69	2.50	2.49	2.51	2.71	1.00	up	9.87E-01	9.96E-01	-	-
1391341_at	Plxdc1	plexin domain containing 1	303505	Rn.18110	BM389038	2.24	2.24	2.25	2.24	2.25	2.24	1.00	down	6.75E-01	9.01E-01	-	-
1385279_at	---	---	---	Rn.133660	AA866259	2.45	2.43	2.46	2.44	2.47	2.43	1.00	up	9.16E-01	9.75E-01	-	-
1391929_at	---	---	---	Rn.59088	AI231461	2.32	2.32	2.33	2.32	2.32	2.31	1.00	down	7.18E-01	9.11E-01	-	-
1368663_at	LOC56764	dnaj-like protein	56764	Rn.92862	AI138041	2.34	2.33	2.35	2.33	2.35	2.33	1.00	down	8.39E-01	9.50E-01	-	-
1381932_at	Fam46a	family with sequence similarity 46, member A	300870	Rn.788	AI136660	2.24	2.23	2.24	2.23	2.24	2.23	1.00	down	6.30E-01	8.95E-01	-	-
1391748_at	P42pop	Myb protein P42POP	499090	Rn.63885	AI044898	2.17	2.17	2.18	2.17	2.17	2.16	1.00	down	5.85E-01	8.95E-01	-	-
1395729_at	---	---	---	Rn.60088	BF402821	2.26	2.26	2.27	2.26	2.27	2.26	1.00	down	6.39E-01	8.95E-01	-	-
1391502_at	---	---	---	Rn.169408	AI170453	2.32	2.31	2.33	2.32	2.33	2.31	1.00	down	8.55E-01	9.55E-01	-	-
1369911_at	Cxcr5	chemokine (C-X-C motif) receptor 5	29363	Rn.127121	NM_053303	2.28	2.27	2.28	2.28	2.29	2.27	1.00	down	7.90E-01	9.33E-01	-	-
1381648_at	Dna2	DNA replication helicase 2 homolog (yeast)	309762	Rn.208052	BF397798	2.35	2.34	2.35	2.34	2.37	2.33	1.00	up	9.00E-01	9.69E-01	-	-
1392292_at	Kctd5	potassium channel tetramerisation domain containing 5	287109	Rn.161259	BM386143	2.43	2.43	2.43	2.43	2.43	2.43	1.00	up	5.93E-01	8.95E-01	-	-
1383404_at	---	---	---	Rn.168799	BI295203	2.34	2.32	2.33	2.34	2.33	2.32	1.00	down	8.54E-01	9.55E-01	-	-
1395119_at	---	---	---	Rn.17727	BI290674	2.37	2.35	2.38	2.36	2.39	2.35	1.00	down	9.09E-01	9.73E-01	-	-
1376359_at	Ms4a8a	membrane-spanning 4-domains, subfamily A, member 8A	361733	Rn.136564	BG375355	2.39	2.39	2.40	2.39	2.40	2.39	1.00	down	6.90E-01	9.05E-01	-	-
1392302_at	---	---	---	Rn.172366	BI288847	2.30	2.29	2.30	2.30	2.30	2.29	1.00	down	7.27E-01	9.13E-01	-	-
1396518_at	---	---	---	Rn.208637	BF396059	2.33	2.31	2.33	2.32	2.33	2.32	1.00	down	8.37E-01	9.49E-01	-	-
1381942_at	Hic1	hypermethylated in cancer 1	303310	Rn.11570	AA963505	2.22	2.22	2.22	2.22	2.22	2.22	1.00	down	5.56E-01	8.95E-01	-	-
1382750_at	---	---	---	Rn.20961	AI058503	2.40	2.44	2.42	2.42	2.42	2.41	1.00	down	8.96E-01	9.67E-01	-	-
1396864_at	LOC366300	hypothetical LOC366300	366300	Rn.203101	AI501493	2.22	2.21	2.22	2.21	2.22	2.21	1.00	down	6.22E-01	8.95E-01	-	-
1397424_at	Sypo2	Synaptopodin 2	499702	Rn.205751	BM389876	2.27	2.27	2.28	2.27	2.28	2.27	1.00	down	7.37E-01	9.16E-01	-	-
1370654_at	Slc6a17	solute carrier family 6 (neurotransmitter transporter), member 17	613226	Rn.186904	L06434	2.30	2.29	2.30	2.29	2.30	2.29	1.00	down	7.67E-01	9.24E-01	-	-
1387030_at	Abcc5	ATP-binding cassette, sub-family C (CFTR/MRP), member 5	116721	Rn.9491	NM_053924	2.32	2.32	2.33	2.32	2.33	2.31	1.00	down	7.18E-01	9.11E-01	-	-
1380592_at	---	---	---	Rn.168184	BI280752	2.32	2.31	2.33	2.32	2.33	2.31	1.00	down	7.98E-01	9.35E-01	-	-
1394349_at	---	---	---	---	BF288777	2.29	2.29	2.30	2.29	2.29	2.29	1.00	down	6.29E-01	8.95E-01	-	-
1371149_at	Adam18	ADAM metallopeptidase domain 18	57029	Rn.42923	Y11490	2.29	2.28	2.30	2.29	2.29	2.29	1.00	down	7.21E-01	9.11E-01	-	-
1385441_at	Vpreb3	pre-B lymphocyte 3	365550	Rn.90200	AW524286	2.26	2.25	2.27	2.26	2.26	2.25	1.00	down	7.75E-01	9.27E-01	-	-
1395482_at	---	---	---	---	BI300477	2.59	2.54	2.61	2.57	2.62	2.54	1.00	down	9.62E-01	9.89E-01	-	-
1393498_at	---	---	---	---	AI237455	2.29	2.28	2.30	2.29	2.30	2.28	1.00	down	8.51E-01	9.54E-01	-	-
1397246_at	Ntrk2	neurotrophic tyrosine kinase, receptor, type 2	25054	Rn.11246	BE102996	2.32	2.32	2.33	2.32	2.33	2.32	1.00	down	7.06E-01	9.08E-01	-	-
1372335_at	LOC682105	similar to receptor expression enhancing protein 2	682105	Rn.201567	BE114641	2.30	2.29	2.30	2.30	2.29	2.30	1.00	up	7.15E-01	9.10E-01	-	-
1396012_at	---	---	---	---	BF395845	2.33	2.32	2.33	2.33	2.32	2.33	1.00	down	7.54E-01	9.20E-01	-	-
1391310_at	RGD1307525	Similar to intracellular protein transport like (XM453)	308053	Rn.38655	AI555036	2.23	2.22	2.23	2.22	2.23	2.22	1.00	down	6.69E-01	9.00E-01	-	-
1392028_at	LOC679290	hypothetical protein LOC679290	679290	---	BI285481	2.21	2.21	2.22	2.21	2.22	2.21	1.00	down	7.06E-01	9.09E-01	-	-
1372737_at	Ldb3	LIM domain binding 3	498587	Rn.219238	BF395095	2.24	2.23	2.24	2.23	2.24	2.23	1.00	down	7.09E-01	9.09E-01	-	-
1391795_at	---	---	---	Rn.147793	AW535137	2.20	2.20	2.21	2.20	2.21	2.20	1.00	down	7.35E-01	9.15E-01	-	-
1390490_at	Mllt1	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila);	301119	Rn.33401	AI501092	2.29	2.28	2.29	2.31	2.29	2.27	1.00	up	9.06E-01	9.71E-01	-	-
1391641_at	---	---	---	---	AI598332	2.45	2.45	2.47	2.45	2.48	2.44	1.00	down	9.09E-01	9.72E-01	-	-
1391842_at	---	---	---	---	AI136544	2.66	2.62	2.65	2.65	2.65	2.64	1.00	up	8.98E-01	9.68E-01	-	-
1385457_x_at	---	---	---	Rn.114311	AI715357	2.41	2.40	2.42	2.41	2.43	2.40	1.00	up	8.89E-01	9.65E-01	-	-
1376478_at	---	---	---	Rn.208953	BF401684	2.26	2.25	2.26	2.25	2.26	2.25	1.00	down	7.08E-01	9.08E-01	-

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1383370_at	Fam5b	family with sequence similarity 5, member B	286895	Rn.22596	BF393519	2.37	2.36	2.38	2.37	2.46	2.27	1.00	down	9.79E-01	9.94E-01	-	-
1375233_at	---	---	---	Rn.66604	BI296668	2.29	2.28	2.30	2.29	2.30	2.28	1.00	down	7.91E-01	9.33E-01	-	-
1390182_at	---	---	---	Rn.6580	BF394624	2.36	2.34	2.36	2.35	2.36	2.35	1.00	up	8.53E-01	9.55E-01	-	-
1369005_at	Kcnq3	potassium voltage-gated channel, subfamily Q, member 3	29682	Rn.205060	NM_031597	2.27	2.27	2.28	2.27	2.28	2.27	1.00	down	7.16E-01	9.10E-01	-	-
1385071_at	RGD1563955	similar to transmembrane serine protease 9	363274	Rn.121154	AI070366	2.22	2.22	2.23	2.22	2.23	2.22	1.00	down	6.84E-01	9.03E-01	-	-
1390559_at	---	---	---	Rn.96943	AI144863	2.39	2.38	2.39	2.39	2.39	2.38	1.00	down	7.16E-01	9.10E-01	-	-
1396894_at	---	---	---	---	AW533825	2.30	2.29	2.30	2.29	2.30	2.28	1.00	down	8.33E-01	9.47E-01	-	-
1370387_at	Cyp3a9	cytochrome P450, family 3, subfamily a, polypeptide 9	171352	Rn.10489	U46118	2.42	2.42	2.43	2.42	2.43	2.42	1.00	down	7.41E-01	9.16E-01	-	-
1368493_at	Lim2	lens intrinsic membrane protein 2	114903	Rn.9688	NM_053771	2.32	2.31	2.32	2.31	2.32	2.31	1.00	down	7.22E-01	9.12E-01	-	-
1380942_at	---	---	---	Rn.169413	AW520594	2.34	2.33	2.34	2.33	2.35	2.33	1.00	up	8.63E-01	9.57E-01	-	-
1373587_at	Gnat1	guanine nucleotide binding protein, alpha transducing 1	363143	Rn.8781	AI412496	2.33	2.32	2.33	2.32	2.34	2.31	1.00	down	8.76E-01	9.62E-01	-	-
1384727_at	---	---	---	---	AI227982	2.34	2.33	2.34	2.34	2.35	2.33	1.00	down	8.41E-01	9.50E-01	-	-
1370079_at	Rhd	Rh blood group, D antigen	60414	Rn.1943	NM_022505	2.33	2.33	2.34	2.33	2.34	2.32	1.00	down	7.55E-01	9.20E-01	-	-
1392041_at	RGD1565959	RGD1565959	301230	Rn.92071	BE109924	2.28	2.27	2.28	2.27	2.28	2.27	1.00	down	6.82E-01	9.03E-01	-	-
1375831_at	LOC365344	similar to testes-specific heterogenous nuclear ribonucleoprotein G-T	365344	Rn.196146	AW528794	2.19	2.19	2.19	2.19	2.19	2.19	1.00	down	6.66E-01	8.99E-01	-	-
1397474_at	---	---	---	---	AI549177	2.34	2.34	2.35	2.34	2.35	2.33	1.00	down	8.28E-01	9.45E-01	-	-
1370874_at	Prl3b1	Prolactin family 3, subfamily b, member 1	24283	Rn.9749	BI283832	2.40	2.39	2.41	2.39	2.42	2.39	1.00	down	9.01E-01	9.69E-01	-	-
1370918_a_at	Atp5c1	ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptid	116550	Rn.63959	BI275939	12.04	11.94	12.05	11.96	12.01	12.06	1.00	up	9.76E-01	9.93E-01	-	-
1369436_at	Chrna10	cholinergic receptor, nicotinic, alpha 10	64574	Rn.48767	NM_022639	2.41	2.41	2.42	2.41	2.42	2.41	1.00	down	7.94E-01	9.34E-01	-	-
1390619_at	---	---	---	Rn.216881	AI178473	2.53	2.78	2.54	2.63	2.80	2.43	1.00	up	9.92E-01	9.97E-01	-	-
1395187_at	---	---	---	Rn.169846	AW531976	2.43	2.40	2.44	2.42	2.44	2.41	1.00	down	9.12E-01	9.74E-01	-	-
1376232_at	---	---	---	Rn.45164	AW521352	2.35	2.34	2.35	2.34	2.36	2.34	1.00	down	8.61E-01	9.57E-01	-	-
1379512_at	---	---	---	Rn.146682	BF396579	2.63	2.61	2.68	2.63	2.66	2.63	1.00	down	9.52E-01	9.86E-01	-	-
1390843_at	Ccdc102a	coiled-coil domain containing 102A	361363	Rn.41567	AI229827	2.34	2.35	2.57	2.56	2.36	2.34	1.00	down	9.89E-01	9.98E-01	-	-
1395709_at	---	---	---	---	BG378609	2.35	2.34	2.36	2.37	2.35	2.33	1.00	up	9.06E-01	9.71E-01	-	-
1387548_at	Has2	hyaluronan synthase 2	25694	Rn.87393	NM_013153	2.35	2.34	2.35	2.34	2.36	2.33	1.00	down	8.81E-01	9.63E-01	-	-
1398271_at	Polo	piccolo (presynaptic cytomatrix protein)	56768	Rn.53925	AF134789	2.34	2.34	2.35	2.34	2.35	2.33	1.00	down	7.63E-01	9.23E-01	-	-
1392039_at	---	---	---	Rn.177094	AI007657	2.42	2.41	2.43	2.41	2.43	2.41	1.00	down	8.66E-01	9.58E-01	-	-
1369498_at	Mc5r	melanocortin 5 receptor	25726	Rn.9673	NM_013182	2.34	2.34	2.36	2.37	2.35	2.33	1.00	up	9.09E-01	9.73E-01	-	-
1387752_s_at	Htr2a	5-hydroxytryptamine (serotonin) receptor 2A	29595	Rn.214221	NM_021862	2.42	2.41	2.45	2.41	2.46	2.40	1.00	down	9.47E-01	9.85E-01	-	-
1384919_at	---	---	---	Rn.204309	AI071689	2.39	2.39	2.40	2.39	2.40	2.38	1.00	down	8.58E-01	9.55E-01	-	-
1391197_at	---	---	---	---	BF399523	2.33	2.32	2.33	2.32	2.33	2.32	1.00	down	7.17E-01	9.10E-01	-	-
1387400_at	---	---	---	---	AF001423	2.39	2.38	2.39	2.38	2.40	2.37	1.00	down	8.69E-01	9.59E-01	-	-
1381045_at	---	---	---	---	BI276129	2.29	2.28	2.30	2.29	2.29	2.28	1.00	down	7.56E-01	9.20E-01	-	-
1369815_at	Ccl3	chemokine (C-C motif) ligand 3	25542	Rn.10139	U22414	2.27	2.27	2.28	2.27	2.28	2.26	1.00	down	7.63E-01	9.22E-01	-	-
1377423_at	---	---	---	Rn.161396	AW526335	2.33	2.32	2.34	2.33	2.34	2.32	1.00	down	8.16E-01	9.41E-01	-	-
1370755_at	Cacng4	calcium channel, voltage-dependent, gamma subunit 4	140725	Rn.162211	AF361341	2.25	2.24	2.25	2.25	2.25	2.24	1.00	down	7.44E-01	9.17E-01	-	-
1389151_at	Adam19	a disintegrin and metallopeptidase domain 19 (meltrin beta)	303068	Rn.163114	AI103449	2.25	2.24	2.25	2.24	2.25	2.24	1.00	down	5.84E-01	8.95E-01	-	-
1382632_at	Robo2	roundabout, axon guidance receptor, homolog 2 (Drosophila)	84409	Rn.24350	AI069991	2.38	2.36	2.38	2.37	2.38	2.37	1.00	down	8.45E-01	9.52E-01	-	-
1373686_at	Serpina6	serine (or cysteine) peptidase inhibitor, clade A, member 6	299270	Rn.2374	AA893495	2.30	2.29	2.31	2.30	2.30	2.29	1.00	down	7.99E-01	9.35E-01	-	-
1375158_at	---	---	---	Rn.206190	BI291441	2.54	2.54	2.54	2.54	2.54	2.53	1.00	down	6.59E-01	8.98E-01	-	-
1379238_at	Cldspl	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phos	301056	Rn.37030	BE112261	2.43	2.41	2.44	2.42	2.44	2.42	1.00	down	9.08E-01	9.72E-01	-	-
1396097_at	---	---	---	Rn.156055	BG376872	2.44	2.42	2.45	2.43	2.47	2.41	1.00	down	9.46E-01	9.84E-01	-	-
1386106_at	Zcchc24	zinc finger, CCHC domain containing 24	361104	Rn.219261	BF288435	2.61	2.60	2.63	2.61	2.64	2.60	1.00	up	9.36E-01	9.82E-01	-	-
1392167_at	---	---	---	Rn.199794	BE104899	2.41	2.40	2.41	2.40	2.41	2.40	1.00	down	7.27E-01	9.13E-01	-	-
1377150_at	---	---	---	Rn.211910	BF420136	2.34	2.34	2.35	2.34	2.35	2.34	1.00	up	7.82E-01	9.29E-01	-	-
1376564_at	Sptbn4	spectrin, beta, non-erythrocytic 4	308458	Rn.63104	AW527595	2.56	2.53	2.55	2.54	2.58	2.54	1.00	up	9.34E-01	9.81E-01	-	-
1387414_at	Duox2	dual oxidase 2	79107	Rn.55542	NM_024141	2.36	2.34	2.36	2.35	2.36	2.34	1.00	down	8.70E-01	9.60E-01	-	-
1391869_at	LOC686314	similar to dachshund b	686314	---	AW532427	2.20	2.19	2.20	2.19	2.20	2.19	1.00	down	6.14E-01	8.95E-01	-	-
1370486_a_at	Iiig9	IIIG9 protein	252958	Rn.45119	AY032665	2.29	2.29	2.29	2.29	2.29	2.29	1.00	down	6.59E-01	8.98E-01	-	-
1393925_at	---	---	---	Rn.212955	BM388014	2.24	2.23	2.24	2.24	2.24	2.23	1.00	down	6.95E-01	9.06E-01	-	-
1385640_at	Pcsk9	proprotein convertase subtilisin/kexin type 9	298296	Rn.19195	AI059511	2.34	2.33	2.35	2.33	2.34	2.34	1.00	down	8.31E-01	9.47E-01	-	-
1369383_a_at	Gabre	gamma-aminobutyric acid (GABA) A receptor, epsilon	65191	Rn.54455	NM_023091	2.33	2.32	2.34	2.33	2.34	2.33	1.00	down	8.44E-01	9.51E-01	-	-
1390876_at	Hsppd2a	histidine acid phosphatase domain containing 2A	311355	Rn.46305	BM386308	2.63	2.64	2.99	2.97	2.64	2.66	1.00	up	9.93E-01	9.98E-01	-	-
1384871_at	Osbp8	oxysterol binding protein-like 6	311129	Rn.15167	AA901035	2.42	2.42	2.43	2.42	2.42	2.42	1.00	down	8.01E-01	9.36E-01	-	-
1381926_at	LOC685079	similar to Protein SYS1 homolog	685079	Rn.31818	AA964273	2.05	2.05	2.05	2.05	2.05	2.05	1.00	down	5.66E-01	8.95E-01	-	-
1376514_at	---	---	---	Rn.209941	BF409548	2.25	2.25	2.25	2.25	2.25	2.24	1.00	down	7.27E-01	9.13E-01	-	-
1393931_at	RGD1311447	LOC363276	363276	Rn.82859	AI031033	2.40	2.39	2.40	2.39	2.41	2.39	1.00	up	8.67E-01	9.58E-01	-	-
1375475_at	---	---	---	Rn.208145	BE111304	2.39	2.38	2.40	2.39	2.40	2.37	1.00	down	9.03E-01	9.70E-01	-	-
1368462_at	Itpka	inositol 1,4,5-trisphosphate 3-kinase A	81677	Rn.9877	NM_031045	2.37	2.36	2.37	2.37	2.37	2.36	1.00	down	7.83E-01	9.30E-01	-	-
1373258_at	Ctsf	cathepsin F	361704	Rn.25087	AI169359	5.30	5.90	5.10	5.26	5.28	5.75	1.00	down	9.96E-01	9.98E-01	-	-
1396396_at	---	---	---	---	AW528330	2.47	2.42	2.51	2.44	2.54	2.41	1.00	down	9.76E-01	9.93E-01	-	-
1388349_at	Ckmt2	creatine kinase, mitochondrial 2, sarcomeric	688698	Rn.202308	AA799557	2.34	2.34	2.36	2.36	2.35	2.33	1.00	down	8.98E-01	9.68E-01	-	-
1379164_at	---	---	---	Rn.207364	BE117672	2.35	2.34	2.36	2.34	2.35	2.34	1.00	down	8.18E-01	9.42E-01	-	-
1378670_at	---	---	---	Rn.148962	AW526307	2.31	2.31	2.31	2.30	2.33	2.30	1.00	up	8.86E-01	9.65E-01	-	-
1373414_at	Tmem59l	transmembrane protein 59-like	306349	Rn.203070	BG380515	2.22	2.22	2.23	2.22	2.24	2.22	1.00	up	8.65E-01	9.58E-01	-	-
1378921_at	---	---	---	Rn.51120	BF407470	2.45	2.44	2.45	2.45	2.46	2.42	1.00	down	9.12E-01	9.74E-01	-	-
1387254_at	Ghrl	ghrelin/obestatin preproppeptide	59301	Rn.42103	NM_021669	2.27	2.26	2.27	2.27	2.27	2.26	1.00	up	8.02E-01	9.36E-01	-	-
1396788_at	---	---	---	Rn.57539	BF391375	2.27	2.27	2.28	2.27	2.28	2.27	1.00	down	7.37E-01	9.16E-01	-	-
1396963_at	---	---	---	Rn.209721	BF404522	2.27	2.26	2.28	2.27	2.28	2.26	1.00	down	8.49E-01	9.53E-01	-	-
1379275_at	Snx10	sorting nexin 10	297096	Rn.44192	AI007889	2.40	2.39	2.41	2.40	2.42	2.38	1.00	down	9.08E-01	9.72E-01	-	-
1376010_at	Prpf4b	PRP4 pre-mRNA processing factor 4 homolog B (yeast)	291078	Rn.32654	BM384201	5.60	6.23	6.31	6.29	5.87	5.98	1.00	down	9.96E-01	9.98E-01	-	-
1383980_at	---	---	---	Rn.49623	BI293388	2.31	2.29	2.30	2.30	2.29	2.29	1.00	down	8.39E-01	9.50E-01	-	-
1397673_at	---	---	---	Rn.206219	AW523660	2.31	2.30	2.31	2.30	2.32	2.29	1.00	down	8.78E-01	9.62E-01	-	-
1390575_at	B3galtl	beta 1,3-galactosyltransferase-like	689765	Rn.49884	BF282989	2.33	2.32	2.34	2.32	2.33	2.32	1.00	down	8.61E-01	9.57E-01	-	-
1378412_at	---	---	---	---	BE098862	2.25	2.25	2.24	2.25	2.25	2.24	1.00	up	6.50E-01	8.96E-01	-	-
1387207_at	Gja5	gap junction protein, alpha 5	50563	Rn.88300	M83092	2.46	2.45	2.46	2.45	2.46	2.45	1.00	down	7.93E-01	9.34E-01	-	-
1378228_at	OC683953 /// Prrt	similar to NG5 protein /// proline-rich transmembrane protein 1	406167 /// 683953	Rn.144293	BF567990	2.24	2.24	2.25	2.24	2.25	2.24	1.00	down	7.10E-01	9.09E-01	-	-
1369575_at	Tas2r114	taste receptor, type 2, member 114	78982	Rn.48785	NM_023996	2.37	2.36	2.39	2.37	2.38	2.37	1.00	up	8.58E-01	9.56E-01	-	-
1370869_at	Bcat1	branched chain aminotransferase 1, cytosolic	29592	Rn.8273	AI102790	2.33	2.33	2.34	2.33	2.34	2.33	1.00	down	8.05E-01	9.37E-01	-	-
1376479_at	Mast3	Microtubule associated serine/threonine kinase 3	688540	Rn.155444	AI045461	2.56	2.55	2.66	2.53	2.55	2.69	1.00	down	9.83E-01	9.95E-01	-	-
1387750_at	Twist1	twist homolog 1 (Drosophila)	85489	Rn.161904	NM_053530	2.35	2.34	2.36	2.35	2.36	2.34	1.00	down	7.86E-01	9.31E-01	-	-
1381688_a_at	---	---	---	Rn.155356	BF415390	2.23	2.22	2.23	2.22	2.23	2.22	1.00	down	7.79E-01	9.28E-01	-	-
1393660_at	Acer1	alkaline ceramidase 1	301118	Rn.126384	BM386815	2.38	2.36	2.38	2.38	2.38	2.36	1.00	down	8.99E-01	9.69E-01	-	-
1380960_at	Coro2a	coronin, actin binding protein 2A	313235	Rn.196722	BF412996	2.35	2.34	2.35	2.34	2.36	2.33	1.00	down	9.10E-01	9.73E-01	-	-
1375576_at	Ddx28	DEAD (Asp-Glu-Ala-Asp) box polypeptide 28	364995	Rn.140812	BE113025	2.30	2.30	2.32	2.30	2.31	2.30	1.00	down	8.74E-01	9.61E-01	-	-
1382442_at	06-Sep	septin 6	691335	Rn.48945	BF288000	2.37	2.36	2.38	2.37	2.38	2.36	1.00	down	8.33E-01	9.47E-01	-	-
1381891_at	Ptpn14	Protein tyrosine phosphatase, non-receptor type 14	305064	Rn.61069	AI070060	2.33	2.32	2.34	2.32	2.34	2.32	1.00	down	8.92E-01	9.67E-01	-	-
1397297_at	---	---	---	Rn.129187	AI176747	2.36	2.36	2.37	2.36	2.36	2.36	1.00	down	6.53E-01	8.97E-01	-	-
1379032_at	---	---	---	Rn.204262	BG372658	2.28	2.27	2.28	2.28	2.29	2.27	1.00	up	8.22E-01	9.43E-01	-	-
1380792_at	---	---	---	Rn.147615	BF406244	2.52	2.48	2.55	2.52	2.54	2.50	1.00	down	9.56E-01	9.87E-01	-	-
1370850_at	Scn3b	sodium channel, voltage-gated, type III, beta	246956	Rn.3402	AA885184	2.32	2.32	2.33	2.32	2.33	2.32	1.00	down	7.20E-01	9.11E-01	-	-
1385794_at	MGC94891	hypothetical protein LOC681210	681210	Rn.143810	BF403295	2.37	2.37	2.38	2.37	2.38	2.36	1.00	down	8.45E-01	9.52E-01	-	-
1389610_at	---	---	---	Rn.153883	AW520754	2.60	2.59	2.60	2.59	2.60	2.59	1.00	down	7.17E-01	9.10E-01	-	-
1397998_at	---	---	---	Rn.216978	BF400054	2.23	2.23	2.23	2.23	2.23	2.23	1.00	down	6.74E-01	9.01E-01	-	-
1370011_at	Ak1	adenylate kinase 1	24183	Rn.105715	NM_024349	2.31	2.30	2.32	2.32	2.31	2.29	1.00	down	8.65E-01	9.58E-01	-	-
1396271_at	---	---	---	Rn.212105	BG378842	2.39	2.37	2.39	2.38	2.40	2.38	1.00	down	8.71E-01	9.60E-01	-	-
1382650_at	---	---	---	---	AA850953	2.57	2.55	2.59	2.56	2.58	2.56	1.00	down	9.07E-01	9.72E-01	-	-
1378829_at	LOC691729	Similar to spermatogenesis associated 5-like 1	691729	Rn.151898	BE107177	2.27	2.26	2.27	2.27	2.27	2.26	1.00	down	7.19E-01	9.11E-01	-	-
1388020_a_at	Pde1c	phosphodiesterase 1C	81742	Rn.10289	AF328800	2.29	2.28	2.29	2.28	2.29	2.28	1.00	down	8.08E-01	9.38E-01	-	-
1376308_at	---	---	---	---	BF400741	2.37	2.37	2.39	2.37	2.40	2.36	1.00	down	9.19E-01	9.76E-01	-	-
1395786_at	Mll4	myeloid/lymphoid or mixed-lineage leukemia 4	361543	Rn.57787	BE126851	2.39	2.38	2.40	2.39	2.41	2.36	1.00	down	9.34E-01	9.81E-01	-	-
1398037_at	---	---	---	Rn.172358	BF390325	2.47	2.44	2.46	2.45	2.48	2.45	1.00	up	9.24E-01	9.78E-01	-	-
1371283_at	---	---	---	---	M34001	2.38	2.38	2.38	2.38	2.38	2.37	1.00	down	7.26E-01	9.13E-01	-	-
1368638_at	Npffr1	neuropeptide FF receptor 1	64107	Rn.64483	NM_022291	2.33	2.32	2.33	2.33	2.33	2.32	1.00	down	7.42E-01	9.17E-01	-	-
1382723_at	Kcnk2	potassium channel, subfamily K, member 2	170899	Rn.21984	AI071739	2.17	2.17	2.17	2.17	2.17	2.16	1.00	down	6.01E-01	8.95E-01	-	-
1377001_at	Nrcam	neuronal cell adhesion molecule	497815	Rn.10691	AI406747	2.30	2.29	2.31	2.29	2.31	2.29	1.00	down	8.90E-01	9.66E-01	-	-
1369786_at	Chrm5	cholinergic receptor, muscarinic 5	53949	Rn.44293	M22926	2.30	2.29	2.30	2.30	2.30	2.29	1.00	down	7.48E-01	9.18E-01	-	-
1385642_at	---	---	---	Rn.20665	AI071886	2.22	2.22	2.23	2.22	2.22	2.21	1.00	down	7.37E-01	9.16E-01	-	-
1379084_at	---	---	---	Rn.147975	BF396266	2.39	2.38	2.39	2.39	2.40	2.38	1.00	up	8.81E-01	9.64E-01	-	-
1386053_at	RGD1564163	Similar to RIKEN cDNA 1700025K23	500554	Rn.6676	AA800971	2.31	2.30	2.31	2.31	2.31	2.30	1.00	up	8.22E-01	9.43E-01	-	-
1396588_at	---	---	---	Rn.202030	BF405168	2.30	2.29	2.30	2.29	2.30	2.29	1.00	down	7.65E-01	9.23E-01	-	-
1395842_at	---	---	---	Rn.204525	AI136504	2.45	2.43	2.48	2.44	2.51	2.41	1.00	down	9.67E-01	9.91E-01	-	-
1397465_at	Rangap1	RAN GTPase activating protein 1	362965	Rn.107099	BF406475	2.20	2.19	2.20	2.20	2.20	2.19	1.00	down	6.43E-01	8.95E-01	-	-
1381039_at	Dnah1	dynein, axonemal, heavy chain 1	171339	Rn.136817	BF416970	2.35	2.35	2.36	2.35	2.36	2.35	1.00	down	7.28E-01	9.13E-01	-	-
1387220_at	Mcpt9	mast cell protease 9	54272	Rn.10651	NM_019323	2.64	2.58	2.66	2.63	2.71	2.55	1.00	up	9.81E-01	9.94E-01	-	-
1396808_at	---	---	---	Rn.204515	AI501314	2.38	2.37	2.39	2.38	2.39	2.37	1.00	up	8.66E-01	9.58E-01	-	-
1385843_at	---	---	---	---	BM386971	2.23	2.23	2.24	2.23	2.25	2.23	1.00	up	8.44E-01	9.52E-01	-	-
1395068_at	RGD1566029	similar to mKIAA1644 protein	500913	Rn.208958	BE121345	2.31	2.31	2.32	2.31	2.32	2.31	1.00	down	8.44E-01	9.52E-01	-	-
1398313_a_at	Kcnk3	potassium channel, subfamily K, member 3	29553	Rn.15536	AW435212	2.25	2.25	2.26	2.25	2.26	2.25	1.00	down	7.80E-01	9.28E-01	-	-
1394825_at	---	---	---	---	BF291173	2.25	2.25	2.26	2.25	2.26	2.25	1.00	down	5.66E-01	8.95E-01	-	-
1377174_at	Sbf1	SET binding factor 1	300147	Rn.7632	AW434982	2.28	2.28	2.29	2.28	2.30	2.27	1.00	up	8.65E-01	9.58E-01	-	-
1377199_at	---	---	---	---	BI274530	2.29	2.28	2.29	2.29	2.29	2.28	1.00	down	8.28E-01	9.46E-01	-	-
1377481_at	---	---	---	---	BF396092	2.38	2.37	2.38	2.37	2.38	2.38	1.00	down	7.93E-01	9.34E-01	-	-
1383663_at	---	---	---	Rn.216539	AI044443	2.53	2.52	2.53	2.53	2.53	2.52	1.00	down	7.32E-01	9.14E-01	-	-
1396926_at	Vac14	Vac14 homolog (S. cerevisiae)	307842	Rn.46366	BF563155	2.29	2.29	2.30	2.29	2.30	2.29	1.00	down	8.03E-01	9.36E-01	-	-
1381360_at	---	---	---	Rn.49629	BE097516	2.23	2.23	2.24	2.23	2.24	2.23	1.00	down	7.40E-01	9.16E-01	-	-
1393485_at	---	---	---	Rn.204376	AI716589	2.20	2.19	2.20	2.19	2.20	2.19	1.00	down	6.77E-01	9.02E-01	-	-
1376667_at	Cyp26b1	cytochrome P450, family 26, subfamily b, polypeptide 1	312495	Rn.19898	BE105541	2.47	2.47	2.50	2.46	2.50	2.47	1.00	down	9.29E-01	9.80E-01	-	-
1383254_at	---	---	---	---	BF403169	2.47	2.42	2.49	2.46	2.53	2.39	1.00	down	9.77E-01	9.93E-01	-	-
1393122_at	---	---	---	---	BG380561	2.65	2.64	2.65	2.64	2.66	2.65	1.00	up	8.11E-01	9.39E-01	-	-
1387577_at	Neurod2	neurogenic differentiation 2	54276	Rn.10724	NM_019326	2.21	2.20	2.21	2.21	2.20	2.20	1.00	down	6.87E-01	9.04E-01	-	-
1369917_at	Nradd	neurotrophin receptor associated death domain	246143	Rn.40242	NM_139259	2.28	2.27	2.28	2.27	2.29	2.27	1.00	up	8.64E-01	9.58E-01	-	-
1391287_at	---	---	---	---	BF406805	2.57	2.56	2.57	2.57	2.57	2.56	1.00	down	5.44E-01	8.95E-01	-	-
1377726_at	Trim25	tripartite motif-containing 25	494338	Rn.34382	BI293740	7.81	6.30	5.70	7.62	5.43	6.75	1.00	down	9.99E-01	1.00E+00	-	-
1380621_at	Fes	feline sarcoma oncogene	361597	Rn.27239	BI289400	2.40	2.39	2.41	2.40	2.41	2.39	1.00	up	8.61E-01	9.57E-01	-	-
1378882_at	---	---	---	Rn.173172	BF418273	2.41	2.40	2.43	2.41	2.45	2.39	1.00	up	9.47E-01	9.85E-01	-	-
1391712_at	---	---	---	---	BM387888	2.38	2.37	2.39	2.38	2.39	2.38	1.00	up	8.21E-01	9.43E-01	-	-
1390975_at	---	---	---	---	BE111775	2.33	2.32	2.34	2.32	2.35	2.32	1.00	up	9.10E-01	9.73E-01	-	-
1398148_at	---	---	---	Rn.146473	BF406137	2.42	2.41	2.43	2.41	2.45	2.40	1.00	down	9.32E-01	9.81E-01	-	-
1388004_at	Gpr37l1	G protein-coupled receptor 37-like 1	252939	Rn.144679	AF087947	2.21	2.20	2.21	2.20	2.21	2.20	1.00	down	7.19E-01	9.11E-01	-	-
1394699_at	RGD1564677	similar to transcription factor ONECUT2	307376	Rn.32723	BG671896	2.33	2.32	2.34	2.33	2.34	2.32	1.00	down	8.37E-01	9.49E-01	-	-
1396809_at	---	---	---	Rn.147014	AI712958	2.34	2.33	2.35	2.34	2.35	2.32	1.00	down	9.00E-01	9.69E-01	-	-
1386119_at	LOC689147	Hypothetical protein LOC689147	689147	Rn.118853	BF393607	2.42	2.40	2.43	2.44	2.43	2.39	1.00	up	9.37E-01	9.82E-01	-	-
1377505_at	---	---	---	---	BI296695	2.74	2.65	2.72	2.71	2.72	2.67	1.00

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1396394_at	---	---	---	---	AW527140	2.31	2.31	2.32	2.30	2.33	2.30	1.00	down	8.92E-01	9.67E-01	-	-
1390890_at	Sval1	seminal vesicle antigen-like 1	680174	Rn.220735	NM_133292	2.38	2.37	2.39	2.37	2.40	2.36	1.00	down	9.19E-01	9.76E-01	-	-
1369370_s_at	Trpv1 /// Trpv4	transient receptor potential cation channel, subfamily V, member 1 /// transien	66026 /// 83810	Rn.64508	NM_023970	2.76	2.92	2.77	2.75	2.77	2.92	1.00	down	9.87E-01	9.98E-01	-	-
1384921_at	Ctxn2	cortexin 2	100302373	---	AW524713	2.37	2.36	2.38	2.37	2.38	2.37	1.00	up	8.56E-01	9.55E-01	-	-
1374290_at	---	---	---	Rn.14810	AI408191	2.33	2.32	2.33	2.33	2.34	2.32	1.00	down	8.08E-01	9.38E-01	-	-
1396735_at	---	---	---	Rn.210594	BF403265	2.30	2.30	2.31	2.30	2.31	2.29	1.00	down	8.84E-01	9.64E-01	-	-
1377658_at	Afap1l1	actin filament associated protein 1-like 1	291565	Rn.199131	AI170431	2.36	2.35	2.36	2.36	2.37	2.36	1.00	up	8.39E-01	9.50E-01	-	-
1380476_at	---	---	---	---	AI715469	2.13	2.13	2.14	2.13	2.13	2.13	1.00	down	6.75E-01	9.01E-01	-	-
1394119_at	---	---	---	Rn.203158	AA891233	2.24	2.24	2.25	2.24	2.25	2.24	1.00	down	7.81E-01	9.29E-01	-	-
1373635_at	P42pop	Myb protein P42POP	499090	Rn.63885	BF393090	2.28	2.28	2.29	2.28	2.29	2.27	1.00	down	7.92E-01	9.33E-01	-	-
1391111_at	---	---	---	Rn.146286	BE109670	2.35	2.35	2.36	2.35	2.36	2.35	1.00	up	8.21E-01	9.43E-01	-	-
1384540_at	Lrfn3	leucine rich repeat and fibronectin type III domain containing 3	308495	Rn.219796	BE101066	2.34	2.34	2.35	2.34	2.35	2.34	1.00	down	7.07E-01	9.08E-01	-	-
1384235_at	---	---	---	Rn.32931	BM386899	2.34	2.34	2.35	2.34	2.34	2.34	1.00	down	7.94E-01	9.34E-01	-	-
1393771_at	Scgb3a1	secretoglobin, family 3A, member 1	338418	Rn.30648	AI011836	2.31	2.30	2.31	2.30	2.31	2.30	1.00	down	8.17E-01	9.41E-01	-	-
1374096_at	---	---	---	Rn.39176	BF411381	2.30	2.30	2.31	2.30	2.30	2.30	1.00	down	6.22E-01	8.95E-01	-	-
1383488_at	LOC687536	similar to Forkhead box protein F1 (Forkhead-related protein FKHL5) (Forkhe	687536	---	AA817785	2.27	2.26	2.27	2.26	2.28	2.26	1.00	up	8.71E-01	9.60E-01	-	-
1384993_at	RGD1309847	similar to peptidylglycine alpha-amidating monooxygenase COOH-terminal in	308894	Rn.73147	BG376804	2.43	2.39	2.45	2.36	2.44	2.48	1.00	down	9.75E-01	9.92E-01	-	-
1393645_at	Mageb16	melanoma antigen family B, 16	317274	Rn.78836	BI288003	2.31	2.30	2.31	2.30	2.31	2.30	1.00	down	7.47E-01	9.18E-01	-	-
1381710_at	---	---	---	Rn.216586	BE098789	2.37	2.36	2.37	2.38	2.37	2.35	1.00	down	8.95E-01	9.67E-01	-	-
1391590_at	RGD1560927	RGD1560927	501507	Rn.19283	BF282295	2.28	2.27	2.28	2.28	2.28	2.27	1.00	down	7.65E-01	9.23E-01	-	-
1384722_at	Bpil1	bactericidal/permeability-increasing protein-like 1	296290	Rn.162713	BI279481	2.43	2.42	2.43	2.42	2.43	2.42	1.00	down	8.31E-01	9.47E-01	-	-
1368171_at	Lox	lysyl oxidase	24914	Rn.11372	BI304009	2.37	2.36	2.38	2.36	2.37	2.37	1.00	down	8.80E-01	9.63E-01	-	-
1381188_at	---	---	---	Rn.156406	BF390117	2.49	2.46	2.52	2.49	2.51	2.48	1.00	up	9.43E-01	9.84E-01	-	-
1388066_at	Insrr	insulin receptor-related receptor	60663	Rn.44446	M90661	2.44	2.43	2.45	2.43	2.47	2.41	1.00	down	9.48E-01	9.85E-01	-	-
1384338_at	Cdc45l	CDC45 cell division cycle 45-like (S. cerevisiae)	287961	Rn.98535	AW525128	2.46	2.44	2.46	2.45	2.48	2.42	1.00	down	9.45E-01	9.84E-01	-	-
1385535_at	---	---	---	---	AA866223	2.49	2.47	2.55	2.48	2.55	2.47	1.00	up	9.72E-01	9.92E-01	-	-
1369221_at	Ppp2r2a	protein phosphatase 2 (formerly 2A), regulatory subunit B, alpha isoform	117104	Rn.81155	NM_053999	2.28	2.27	2.28	2.27	2.29	2.27	1.00	up	8.92E-01	9.66E-01	-	-
1396655_at	Kcnj9	potassium inwardly-rectifying channel, subfamily J, member 9	116560	---	BF400896	2.41	2.39	2.41	2.40	2.41	2.39	1.00	down	8.83E-01	9.64E-01	-	-
1385743_at	Cklf	chemokine-like factor	245978	Rn.81197	BF388856	2.63	2.63	2.64	2.63	2.73	2.53	1.00	down	9.84E-01	9.95E-01	-	-
1388021_at	Sfrp4	secreted frizzled-related protein 4	89803	Rn.10788	AF220608	2.31	2.30	2.31	2.30	2.32	2.29	1.00	down	9.10E-01	9.73E-01	-	-
1368565_at	Slc1a3	solute carrier family 1 (glial high affinity glutamate transporter), member 3	29483	Rn.34134	NM_019225	2.44	2.43	2.45	2.43	2.44	2.43	1.00	down	8.43E-01	9.51E-01	-	-
1369833_at	Adam2	ADAM metallopeptidase domain 2	56806	Rn.42917	NM_020077	2.33	2.31	2.34	2.33	2.33	2.32	1.00	down	8.63E-01	9.57E-01	-	-
1369835_at	Omp	olfactory marker protein	24612	Rn.9720	NM_012616	2.31	2.30	2.32	2.31	2.31	2.30	1.00	down	8.30E-01	9.46E-01	-	-
1368580_at	Sdc3	syndecan 3	116873	Rn.10504	U73184	2.26	2.25	2.26	2.26	2.26	2.26	1.00	up	7.85E-01	9.30E-01	-	-
1396920_at	Gpr176	G protein-coupled receptor 176	117257	Rn.44656	AW532852	2.10	2.10	2.11	2.10	2.11	2.10	1.00	down	6.97E-01	9.07E-01	-	-
1383681_at	---	---	---	Rn.24848	BI289508	2.41	2.41	2.41	2.41	2.41	2.41	1.00	down	5.81E-01	8.95E-01	-	-
1369010_at	Chek2	Chk2 checkpoint homolog (S. pombe)	114212	Rn.163213	NM_053677	2.36	2.37	2.37	2.38	2.37	2.36	1.00	up	8.89E-01	9.66E-01	-	-
1378317_at	Krt78	keratin 78	685672	Rn.40671	BI282595	2.58	2.58	2.59	2.58	2.60	2.57	1.00	up	9.16E-01	9.75E-01	-	-
1381676_at	Nrxn3	neurexin 3	116508	Rn.10926	BF416388	2.43	2.40	2.46	2.45	2.44	2.40	1.00	up	9.59E-01	9.89E-01	-	-
1395348_at	Ttyh3	tweety homolog 3 (Drosophila)	304315	Rn.37666	AW143673	2.30	2.30	2.30	2.31	2.30	2.30	1.00	up	7.69E-01	9.24E-01	-	-
1374017_at	Trim72	tripartite motif-containing 72	363777	Rn.23565	BI289517	2.35	2.34	2.36	2.34	2.36	2.34	1.00	down	8.88E-01	9.65E-01	-	-
1384980_at	---	---	---	---	BM387361	2.42	2.41	2.42	2.43	2.42	2.40	1.00	up	9.11E-01	9.73E-01	-	-
1397073_at	---	---	---	Rn.171527	BE117296	2.37	2.36	2.38	2.36	2.39	2.35	1.00	down	9.27E-01	9.79E-01	-	-
1382958_at	Ucp3	uncoupling protein 3 (mitochondrial, proton carrier)	25708	Rn.9902	BI274655	2.22	2.22	2.23	2.22	2.22	2.22	1.00	down	7.74E-01	9.26E-01	-	-
1381125_at	---	---	---	Rn.203696	AI229425	2.47	2.45	2.49	2.46	2.49	2.45	1.00	down	9.47E-01	9.85E-01	-	-
1385301_at	---	---	---	---	BG378711	2.33	2.32	2.34	2.34	2.34	2.32	1.00	down	8.68E-01	9.59E-01	-	-
1384361_at	Mal2	mal, T-cell differentiation protein 2	362911	Rn.103382	BF555523	2.48	2.46	2.52	2.47	2.54	2.44	1.00	down	9.73E-01	9.92E-01	-	-
1381090_at	---	---	---	Rn.170576	BE096310	2.39	2.38	2.40	2.39	2.40	2.38	1.00	down	8.82E-01	9.64E-01	-	-
1385608_at	---	---	---	Rn.146615	BF404154	2.75	2.72	2.76	2.75	2.76	2.73	1.00	up	9.33E-01	9.81E-01	-	-
1391563_at	Mum1l1	melanoma associated antigen (mutated) 1-like 1	501630	Rn.12231	AA963184	2.34	2.33	2.35	2.35	2.35	2.33	1.00	up	9.15E-01	9.75E-01	-	-
1397984_at	---	---	---	Rn.62438	BF413720	2.19	2.19	2.20	2.19	2.19	2.19	1.00	down	7.44E-01	9.17E-01	-	-
1385040_at	Fbxo17	F-box protein 17	292757	Rn.53606	BE120593	2.34	2.33	2.34	2.34	2.35	2.33	1.00	down	8.36E-01	9.48E-01	-	-
1369155_at	Cntn4	contactin 4	116658	Rn.10117	NM_053879	2.36	2.35	2.37	2.36	2.37	2.35	1.00	down	8.83E-01	9.64E-01	-	-
1379054_at	---	---	---	Rn.209936	BF391881	2.59	2.57	2.64	2.60	2.66	2.55	1.00	up	9.74E-01	9.92E-01	-	-
1391662_at	RGD1311517	similar to RIKEN cDNA 9430015G10	313775	Rn.83717	AI104367	2.32	2.31	2.33	2.32	2.32	2.32	1.00	down	8.12E-01	9.39E-01	-	-
1398433_at	---	---	---	Rn.22419	BG378056	2.35	2.35	2.36	2.35	2.37	2.34	1.00	down	8.77E-01	9.62E-01	-	-
1388891_at	Parvb	Parvin, beta	362973	Rn.16709	BG374285	2.35	2.34	2.36	2.35	2.36	2.33	1.00	down	9.12E-01	9.74E-01	-	-
1375327_at	Leng8	leukocyte receptor cluster (LRC) member 8	361506	Rn.217745	BF403319	2.15	2.15	2.15	2.15	2.15	2.15	1.00	down	5.76E-01	8.95E-01	-	-
1395219_at	---	---	---	---	BE096754	2.40	2.39	2.40	2.39	2.41	2.38	1.00	down	9.04E-01	9.71E-01	-	-
1395136_at	---	---	---	Rn.52464	BE115145	2.47	2.58	2.48	2.50	2.57	2.45	1.00	up	9.81E-01	9.94E-01	-	-
1376381_at	Xkr5	XK, Kell blood group complex subunit-related family, member 5	497083	Rn.33372	AW252094	2.55	2.55	2.55	2.55	2.56	2.54	1.00	down	8.08E-01	9.38E-01	-	-
1380559_at	---	---	---	---	AI030465	2.38	2.37	2.38	2.37	2.39	2.36	1.00	down	9.15E-01	9.75E-01	-	-
1389477_at	---	---	---	Rn.35620	BI278855	2.46	2.45	2.46	2.46	2.47	2.45	1.00	up	8.41E-01	9.50E-01	-	-
1368846_at	Camkv	CaM kinase-like vesicle-associated	79011	Rn.9958	AI412410	2.39	2.36	2.40	2.37	2.39	2.38	1.00	down	9.28E-01	9.80E-01	-	-
1368610_at	Mcas2	mast cell antigen 32	59105	Rn.40569	NM_021585	2.39	2.38	2.40	2.39	2.41	2.38	1.00	down	9.18E-01	9.76E-01	-	-
1394598_at	---	---	---	Rn.146794	AA956038	2.28	2.28	2.28	2.28	2.28	2.27	1.00	down	7.70E-01	9.25E-01	-	-
1383412_at	---	---	---	Rn.92861	AI070450	2.50	2.47	2.50	2.49	2.51	2.48	1.00	down	9.36E-01	9.82E-01	-	-
1369545_at	Egr3	early growth response 3	25148	Rn.44371	NM_017086	2.40	2.39	2.40	2.40	2.40	2.39	1.00	down	7.21E-01	9.11E-01	-	-
1381731_at	---	---	---	Rn.210180	BF396462	2.30	2.29	2.31	2.30	2.31	2.29	1.00	down	8.83E-01	9.64E-01	-	-
1387338_s_at	Bcl2l11	BCL2-like 11 (apoptosis facilitator)	64547	Rn.82709	NM_022612	2.52	2.48	2.52	2.50	2.47	2.47	1.00	down	9.66E-01	9.90E-01	-	-
1395059_at	Shroom3	shroom family member 3	305230	Rn.15243	BE112187	2.42	2.41	2.43	2.41	2.43	2.42	1.00	up	8.80E-01	9.63E-01	-	-
1381746_at	---	---	---	Rn.210610	BF419533	2.33	2.32	2.33	2.33	2.34	2.31	1.00	down	8.78E-01	9.62E-01	-	-
1373817_at	Ing4	inhibitor of growth family, member 4	297597	Rn.48967	BM391761	3.52	3.46	3.44	3.42	3.58	3.42	1.00	up	9.84E-01	9.95E-01	-	-
1373288_at	St5	suppression of tumorigenicity 5	308944	Rn.39696	BG373023	2.37	2.37	2.38	2.38	2.38	2.37	1.00	up	8.17E-01	9.41E-01	-	-
1383201_at	---	---	---	Rn.222010	BI289300	7.04	6.97	6.91	6.97	6.79	7.15	1.00	down	9.82E-01	9.97E-01	-	-
1378810_at	---	---	---	Rn.208271	BE114206	2.46	2.45	2.49	2.46	2.48	2.46	1.00	down	9.32E-01	9.81E-01	-	-
1374013_at	C1qtnf5	C1q and tumor necrosis factor related protein 5	315598	Rn.99884	BI278078	2.20	2.19	2.20	2.20	2.20	2.19	1.00	down	7.14E-01	9.10E-01	-	-
1394425_at	---	---	---	Rn.207476	BE101933	2.38	2.37	2.39	2.38	2.39	2.37	1.00	down	8.90E-01	9.66E-01	-	-
1369823_at	Sebox	SEBOX homeobox	58922	Rn.211992	NM_023951	2.58	2.54	2.56	2.59	2.56	2.54	1.00	up	9.52E-01	9.86E-01	-	-
1392691_at	RGD1305211	Similar to RIKEN cDNA 2610209A20	365314	Rn.22440	AI599130	2.26	2.25	2.26	2.25	2.26	2.25	1.00	down	7.85E-01	9.30E-01	-	-
1376915_at	LOC679931	Hypothetical protein LOC679931	679931	Rn.198125	AW913994	2.35	2.35	2.36	2.41	2.36	2.30	1.00	up	9.73E-01	9.92E-01	-	-
1379083_at	Adat3	adenosine deaminase, tRNA-specific 3, TAD3 homolog (S. cerevisiae)	100125374	Rn.203784	AI029510	2.19	2.18	2.19	2.19	2.19	2.18	1.00	down	6.55E-01	8.98E-01	-	-
1369021_at	Hcrtr1	hypocretin (orexin) receptor 1	25593	Rn.88262	NM_013064	2.25	2.24	2.26	2.25	2.25	2.24	1.00	down	8.09E-01	9.38E-01	-	-
1389928_at	---	---	---	Rn.202057	BI296691	2.39	2.37	2.38	2.38	2.39	2.37	1.00	down	8.96E-01	9.67E-01	-	-
1383758_at	---	---	---	---	AA924804	2.43	2.41	2.44	2.42	2.45	2.40	1.00	down	9.44E-01	9.84E-01	-	-
1385310_at	---	---	---	Rn.150426	BI295907	2.54	2.53	2.56	2.61	2.55	2.46	1.00	down	9.79E-01	9.94E-01	-	-
1396575_at	Arhgap20	Rho GTPase activating protein 20	367085	Rn.20805	AI576265	2.22	2.22	2.22	2.22	2.22	2.22	1.00	down	7.58E-01	9.21E-01	-	-
1384943_at	RGD1563888	similar to DNA segment, Chr 16, ERATO Doi 472, expressed	360692	Rn.146501	AI137629	2.37	2.36	2.38	2.37	2.39	2.36	1.00	up	9.11E-01	9.73E-01	-	-
1391337_at	---	---	---	Rn.207446	BE116623	2.29	2.28	2.29	2.29	2.30	2.28	1.00	down	8.14E-01	9.40E-01	-	-
1381645_at	Tdrkh	tudor and KH domain containing	310652	Rn.98848	BE097207	2.39	2.38	2.40	2.38	2.40	2.38	1.00	down	8.80E-01	9.63E-01	-	-
1398193_at	---	---	---	Rn.208281	BE114283	2.34	2.32	2.34	2.33	2.34	2.33	1.00	up	8.79E-01	9.63E-01	-	-
1390936_at	Lgl4	Leucine-rich repeat LGI family, member 4	361549	Rn.143830	BE120691	2.37	2.36	2.39	2.38	2.38	2.35	1.00	down	9.32E-01	9.81E-01	-	-
1385622_at	---	---	---	---	BE119164	2.40	2.39	2.41	2.40	2.43	2.38	1.00	up	9.40E-01	9.83E-01	-	-
1374759_at	Galntl1	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltrar	362760	Rn.40168	AI600037	2.34	2.33	2.35	2.34	2.35	2.34	1.00	up	8.80E-01	9.63E-01	-	-
1391067_at	---	---	---	Rn.15097	BF389648	2.45	2.45	2.46	2.45	2.49	2.42	1.00	down	9.58E-01	9.88E-01	-	-
1371063_at	Sh3gl2	SH3-domain GRB2-like 2	116743	Rn.10787	AF009903	2.40	2.39	2.42	2.40	2.41	2.40	1.00	down	8.87E-01	9.65E-01	-	-
1368203_at	Scnn1a	sodium channel, nonvoltage-gated, type I, alpha	25122	Rn.9808	NM_031548	2.37	2.34	2.37	2.36	2.38	2.33	1.00	down	9.43E-01	9.84E-01	-	-
1393541_at	---	---	---	Rn.24023	AI146150	2.36	2.35	2.37	2.36	2.36	2.36	1.00	up	8.64E-01	9.58E-01	-	-
1378082_at	---	---	---	Rn.46402	BF411790	2.35	2.34	2.36	2.34	2.36	2.35	1.00	down	8.88E-01	9.65E-01	-	-
1380809_at	---	---	---	Rn.154153	BM388375	2.32	2.31	2.33	2.31	2.34	2.31	1.00	down	8.29E-01	9.80E-01	-	-
1384643_at	---	---	---	Rn.199297	AI071465	2.38	2.37	2.39	2.38	2.39	2.37	1.00	down	8.76E-01	9.62E-01	-	-
1387700_at	Cckar	cholecystokinin A receptor	24889	Rn.10184	M88096	2.29	2.29	2.30	2.30	2.30	2.28	1.00	down	8.61E-01	9.57E-01	-	-
1380855_at	---	---	---	Rn.12903	BM390807	2.39	2.38	2.39	2.38	2.39	2.38	1.00	down	8.10E-01	9.39E-01	-	-
1391381_at	---	---	---	Rn.172287	BF410362	2.36	2.35	2.36	2.35	2.37	2.34	1.00	down	8.93E-01	9.67E-01	-	-
1391385_at	---	---	---	---	AW535948	2.15	2.15	2.15	2.15	2.16	2.15	1.00	up	8.08E-01	9.38E-01	-	-
1393640_at	---	---	---	Rn.40663	BF542956	2.39	2.38	2.41	2.41	2.39	2.39	1.00	down	9.16E-01	9.75E-01	-	-
1391334_at	---	---	---	Rn.124241	BE106273	2.50	2.49	2.51	2.50	2.51	2.49	1.00	down	9.07E-01	9.72E-01	-	-
1371841_at	Mtpn	myotrophin	79215	Rn.3239	AI228667	9.42	9.43	9.46	9.38	9.41	9.52	1.00	up	9.80E-01	9.94E-01	-	-
1379631_at	Csf1	colony stimulating factor 1 (macrophage)	78965	Rn.83632	AI071665	2.35	2.35	2.35	2.35	2.35	2.35	1.00	down	6.65E-01	8.99E-01	-	-
1396798_at	---	---	---	Rn.202779	BF386659	2.31	2.30	2.31	2.31	2.32	2.30	1.00	down	8.53E-01	9.55E-01	-	-
1371553_at	Mrpl36	mitochondrial ribosomal protein L36	364656	Rn.7601	BF288120	9.00	9.77	9.44	9.23	9.24	9.74	1.00	up	9.97E-01	9.99E-01	-	-
1368557_s_at	Vegp1 /// Vegp2	von Ebners gland protein 1 /// von Ebners gland protein 2	65039 /// 94106	Rn.11217	NM_022945	2.55	2.49	2.60	2.54	2.56	2.53	1.00	down	9.73E-01	9.92E-01	-	-
1371848_at	LOC687711	similar to small nuclear ribonucleoprotein D3	687711	---	AA799526	7.40	8.12	7.78	7.17	7.93	8.20	1.00	down	9.98E-01	9.99E-01	-	-
1394309_at	Tekt5	tektin 5	363538	Rn.145418	BF563936	2.39	2.38	2.40	2.39	2.40	2.38	1.00	up	9.03E-01	9.70E-01	-	-
1395135_at	Wbscr27	Williams Beuren syndrome chromosome region 27	688407	Rn.163207	AW528720	2.25	2.24	2.25	2.24	2.25	2.24	1.00	down	7.56E-01	9.21E-01	-	-
1396924_at	Mpped1	Metallophosphoesterase domain containing 1	362971	Rn.19156	BF399805	2.10	2.10	2.11	2.10	2.10	2.10	1.00	down	6.59E-01	8.98E-01	-	-
1383775_at	---	---	---	Rn.206011	BF386414	2.29	2.28	2.29	2.28	2.29	2.27	1.00	down	8.20E-01	9.42E-01	-	-
1396516_at	---	---	---	---	BE120213	2.38	2.36	2.38	2.37	2.39	2.36	1.00	up	9.30E-01	9.80E-01	-	-
1380314_at	RGD1563072	similar to hypothetical protein FLJ38984	313595	Rn.9381	BI290787	2.36	2.35	2.36	2.35	2.36	2.36	1.00	down	8.15E-01	9.40E-01	-	-
1372574_at	Tead2	TEA domain family member 2	308582	Rn.13042	AW142018	2.24	2.24	2.24	2.24	2.24	2.24	1.00	down	6.82E-01	9.03E-01	-	-
1398059_at	---	---	---	Rn.199465	AI501546	2.38	2.38	2.39	2.37	2.41	2.37	1.00	down	9.46E-01	9.84E-01	-	-
1395788_at	---	---	---	Rn.57702	BF392117	2.46	2.45	2.49	2.45	2.51	2.43	1.00	down	9.68E-01	9.91E-01	-	-
1393510_at	Golsyn	Golgi-localized protein	500865	Rn.99794	AW524463	2.37	2.35	2.37	2.36	2.37	2.36	1.00	down	8.72E-01	9.60E-01	-	-
1391120_at	---	---	---	Rn.63637	BF405020	2.32	2.31	2.32	2.31	2.32	2.30	1.00	down	8.73E-01	9.61E-01	-	-
1380010_at	---	---	---	Rn.170611	BE097232	2.40	2.38	2.40	2.39	2.40	2.39	1.00	up	8.49E-01	9.53E-01	-	-
1372687_at	Crct1	cysteine-rich C-terminal 1	688401	---	BI278186	2.36	2.35	2.36	2.35	2.36	2.35	1.00	down	7.54E-01	9.20E-01	-	-
1370104_at	Pde9b	phosphodiesterase 9H, cGMP-specific, cone, gamma	114248	Rn.21249	NM_053688	2.24	2.23	2.25	2.24	2.24	2.23	1.00	down	8.18E-01	9.42E-01	-	-
1375312_at	---	---	---	Rn.187635	BF419911	2.27	2.27	2.28	2.27	2.28	2.26	1.00	down	8.18E-01	9.42E-01	-	-
1391775_at	Zpbp2	zona pellucida binding protein 2	363676	Rn.51329	BE107879	2.37	2.37	2.38	2.37	2.38	2.36	1.00	down	8.87E-01	9.65E-01	-	-
1398114_at	---	---	---	Rn.208696	BF564763	2.33	2.33	2.34	2.35	2.34	2.32	1.00	up	9.22E-01	9.77E-01	-	-
1396378_at	---	---	---	Rn.210838	BF412429	2.32	2.31	2.32	2.31	2.32	2.31	1.00	down	8.52E-01	9.54E-01	-	-
1380731_at	Mgat5b	mannosyl (alpha-1,6-)-glycoprotein beta-1,6-N-acetyl-glucosaminyltransferase	303693	Rn.50582	BI290520	2.31	2.30	2.31	2.31	2.30	2.30	1.00	up	8.60E-01	9.57E-01	-	-
1378789_at	---	---	---	Rn.209353	BF404861	2.35	2.34	2.35	2.37	2.35	2.32	1.00	up	9.40E-01	9.83E-01	-	-
1368346_at	B3galt4	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 4	171079	Rn.24575	NM_133553	2.92	3.00	2.93	2.92	2.93	3.00	1.00	up	9.77E-01	9.93E-01	-	-
1391967_at	---	---	---	Rn.66354	BM389832	2.29	2.28	2.30	2.29	2.29	2.28	1.00	down	8.74E-01	9.61E-01	-	-
1396818_at	---	---	---	Rn.204408	AI111504	2.36	2.35	2.36	2.36	2.37	2.35	1.00	up	8.77E-01	9.62E-01	-	-
1398405_at	06-Sep	septin 6	691335	Rn.48945	BI289917	2.29	2.28	2.29	2.28	2.29	2.28	1.00	down	8.01E-01	9.36E-01	-	-
1390009_at	Ints6	Integrator complex subunit 6	361057	Rn.202377	AW523412	2.37	2.36	2.37	2.37	2.37	2.36	1.00	down	7.28E-01	9.13E-01	-	-
1380227_at	---	---	---	Rn.209685	BF409095	2.42	2.40	2.43	2.41	2.45	2.40	1.00	down	9.49E-01	9.85E-01	-	-
1384942_at	Lrfn5	leucine rich repeat and fibronectin type III domain containing 5	314164	Rn.16847	AA818417	2.33	2.32	2.33	2.32	2.34	2.32	1.00	up	8.81E-01	9.64E-01	-	-
1397488_at	Ibtlf /// RGD15639	RAB interacting factor /// similar to Mss4 protein	304807 /// 499636	Rn.129601	BF386747	2.39	2.38	2.42	2.39	2.42	2.37	1.00	up	9.51E-01	9.86E-01	-	-
1387157_at	Pmfbp1	polyamine modulated factor 1 binding protein 1	171414	Rn.51502	NM_134393	2.23	2.23	2.23	2.23	2.24	2.22	1.00	down	8.27E-01	9.45E-01	-	-
1384955_at	---	---	---	Rn.19592	AI069925	2.40	2.29	2.34	2.33	2.33	2.36	1.00	up	9.75E-01	9.92E-01	-	-
1387690_at	Casp3	caspase 3, apoptosis related cysteine protease	25402	Rn.10562	U84410	2.33	2.32	2.33	2.32

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)				REG	MTC
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval		
1385211_at	RGD1310951	similar to RIKEN cDNA E130308A19	313202	Rn.214130	BE116091	2.35	2.35	2.36	2.35	2.36	2.35	1.00	up	8.24E-01	9.44E-01	-	-
1391541_at	---	---	---	Rn.34081	BF401158	2.29	2.29	2.30	2.29	2.31	2.28	1.00	down	9.05E-01	9.71E-01	-	-
1390826_at	---	---	---	Rn.143757	BM386821	2.39	2.38	2.39	2.38	2.40	2.37	1.00	down	9.19E-01	9.76E-01	-	-
1369044_a_at	Pde4b	phosphodiesterase 4B, cAMP specific	24626	Rn.37733	AF202733	2.40	2.39	2.41	2.39	2.42	2.38	1.00	up	9.44E-01	9.84E-01	-	-
1369863_at	Adh4	alcohol dehydrogenase 4 (class II), pi polypeptide	29646	Rn.98159	NM_017270	2.52	2.51	2.52	2.51	2.52	2.51	1.00	down	8.84E-01	9.64E-01	-	-
1369810_at	Dmd	dystrophin, muscular dystrophy	24907	Rn.10307	NM_012698	2.39	2.38	2.40	2.39	2.41	2.38	1.00	up	9.37E-01	9.82E-01	-	-
1367849_at	Sdc1	syndecan 1	25216	Rn.11176	NM_013026	2.38	2.35	2.38	2.37	2.37	2.36	1.00	down	9.20E-01	9.76E-01	-	-
1374811_at	---	---	---	Rn.2356	AA858705	2.48	2.47	2.47	2.48	2.47	2.47	1.00	down	8.83E-01	9.64E-01	-	-
1381664_at	---	---	---	---	BF403849	2.41	2.40	2.42	2.40	2.44	2.39	1.00	up	9.52E-01	9.86E-01	-	-
1391810_at	Rbm20	RNA binding motif protein 20	309544	Rn.21596	BI280157	2.36	2.35	2.37	2.35	2.37	2.35	1.00	down	9.18E-01	9.76E-01	-	-
1376838_at	Rnf207	ring finger protein 207	691246	Rn.155693	AW525290	2.19	2.18	2.19	2.19	2.19	2.18	1.00	down	7.46E-01	9.18E-01	-	-
1381670_at	---	---	---	Rn.62139	BF412681	2.54	2.49	2.54	2.52	2.53	2.52	1.00	up	9.46E-01	9.85E-01	-	-
1380761_at	---	---	---	Rn.199816	BE107402	2.36	2.35	2.37	2.36	2.37	2.35	1.00	down	9.07E-01	9.72E-01	-	-
1375493_at	Vangl2	vang-like 2 (van gogh, Drosophila)	289229	Rn.198958	BE104373	2.51	2.48	2.52	2.53	2.52	2.47	1.00	up	9.65E-01	9.90E-01	-	-
1377410_at	E2f8	E2F transcription factor 8	308607	Rn.15287	AI231053	2.41	2.41	2.42	2.40	2.44	2.40	1.00	up	9.32E-01	9.81E-01	-	-
1383259_at	---	---	---	Rn.16404	BF412819	2.39	2.38	2.40	2.38	2.40	2.39	1.00	down	9.11E-01	9.73E-01	-	-
1396360_at	Akr1b1	Aldo-keto reductase family 1, member B1 (aldose reductase)	24192	Rn.107801	BI283535	2.29	2.28	2.30	2.29	2.29	2.30	1.00	down	8.87E-01	9.65E-01	-	-
1379903_at	---	---	---	Rn.98831	AI059853	2.34	2.33	2.36	2.34	2.37	2.33	1.00	up	9.44E-01	9.84E-01	-	-
1384095_at	Myrip	myosin VIIA and Rab interacting protein	360034	Rn.161974	BF524140	2.32	2.31	2.33	2.32	2.33	2.32	1.00	down	8.62E-01	9.57E-01	-	-
1387572_at	Psd	pleckstrin and Sec7 domain containing	171381	Rn.64489	NM_134370	2.36	2.35	2.36	2.36	2.36	2.34	1.00	down	8.87E-01	9.65E-01	-	-
1369271_at	Prkab2	protein kinase, AMP-activated, beta 2 non-catalytic subunit	64562	Rn.207202	NM_022627	2.32	2.31	2.32	2.32	2.33	2.31	1.00	down	8.88E-01	9.65E-01	-	-
1389231_at	Sgip1	SH3-domain GRB2-like (endophilin) interacting protein 1	313413	Rn.19477	BI296728	2.36	2.35	2.37	2.36	2.37	2.35	1.00	down	9.02E-01	9.70E-01	-	-
1377106_at	---	---	---	Rn.147873	AW533050	2.54	2.53	2.57	2.53	2.59	2.51	1.00	down	9.71E-01	9.91E-01	-	-
1369301_at	Aplnr	apelin receptor	83518	Rn.7985	NM_031349	2.24	2.23	2.24	2.24	2.24	2.23	1.00	down	7.96E-01	9.34E-01	-	-
1377364_at	---	---	---	---	BF399586	2.39	2.39	2.39	2.39	2.39	2.38	1.00	down	6.39E-01	8.95E-01	-	-
1388944_at	---	---	---	Rn.165242	BE109016	2.40	2.38	2.40	2.38	2.40	2.39	1.00	down	9.12E-01	9.74E-01	-	-
1397461_at	Gtdc2	glycosyltransferase 8 domain containing 2	366859	Rn.137563	BF416400	2.28	2.27	2.28	2.27	2.29	2.27	1.00	down	8.96E-01	9.67E-01	-	-
1393305_at	---	---	---	---	BF399398	2.47	2.48	2.48	2.54	2.47	2.41	1.00	up	9.79E-01	9.94E-01	-	-
1396520_at	---	---	---	Rn.147091	BF403354	2.30	2.29	2.31	2.30	2.30	2.30	1.00	up	8.85E-01	9.64E-01	-	-
1380342_at	LOC680885	hypothetical protein LOC680885	680885	Rn.12573	BF420511	2.39	2.37	2.42	2.39	2.40	2.40	1.00	up	9.41E-01	9.83E-01	-	-
1380864_at	---	---	---	---	BE110065	2.34	2.34	2.36	2.34	2.37	2.33	1.00	up	9.31E-01	9.81E-01	-	-
1395619_at	Sorbs3	sorbin and SH3 domain containing 3	282843	Rn.63481	BF547002	2.28	2.27	2.28	2.28	2.28	2.27	1.00	down	8.16E-01	9.41E-01	-	-
1372975_at	Lor	loricrin	502541	Rn.162608	BI278083	2.26	2.25	2.27	2.26	2.27	2.26	1.00	up	8.75E-01	9.61E-01	-	-
1378850_at	---	---	---	Rn.205963	BF410203	2.30	2.29	2.30	2.30	2.30	2.29	1.00	down	7.90E-01	9.33E-01	-	-
1376477_at	---	---	---	Rn.209877	BF391517	2.34	2.33	2.35	2.34	2.36	2.33	1.00	down	9.30E-01	9.80E-01	-	-
1379178_at	LOC686378	hypothetical protein LOC686378	686378	---	BF410468	2.32	2.31	2.32	2.31	2.32	2.31	1.00	down	8.22E-01	9.43E-01	-	-
1392103_at	---	---	---	Rn.210330	BF397163	2.36	2.35	2.36	2.35	2.38	2.33	1.00	up	9.49E-01	9.85E-01	-	-
1391983_at	LOC500227	hypothetical gene supported by BC079424	500227	Rn.50288	BI281586	2.37	2.37	2.37	2.37	2.37	2.37	1.00	down	7.49E-01	9.19E-01	-	-
1370258_at	Bzw2	basic leucine zipper and W2 domains 2	171439	Rn.13196	BI303268	2.31	2.30	2.32	2.32	2.31	2.30	1.00	up	8.81E-01	9.64E-01	-	-
1389945_at	---	---	---	Rn.216670	AI236919	2.29	2.28	2.29	2.28	2.30	2.28	1.00	up	9.21E-01	9.77E-01	-	-
1379521_at	Alg3	asparagine-linked glycosylation 3, alpha-1,3- mannosyltransferase homolog (	287983	Rn.10814	AW525817	4.89	5.27	4.52	4.90	4.89	4.89	1.00	down	8.97E-01	9.98E-01	-	-
1374989_at	Asb12	ankyrin repeat and SOCS box-containing 12	503446	Rn.8275	BI290522	2.33	2.32	2.34	2.35	2.33	2.31	1.00	up	9.39E-01	9.83E-01	-	-
1393473_at	RGD1563866	RGD1563866	315652	Rn.20195	BM390382	2.37	2.36	2.38	2.37	2.39	2.36	1.00	up	9.36E-01	9.82E-01	-	-
1383010_at	---	---	---	Rn.203400	AW531880	2.46	2.44	2.48	2.45	2.51	2.43	1.00	up	9.73E-01	9.92E-01	-	-
1398304_at	Fzd2	frizzled homolog 2 (Drosophila)	64512	Rn.92324	L02530	2.35	2.34	2.37	2.35	2.36	2.35	1.00	down	9.16E-01	9.75E-01	-	-
1398443_at	Lrrc4b	Leucine rich repeat containing 4B	308571	Rn.22207	AI602719	2.19	2.19	2.19	2.19	2.19	2.19	1.00	down	6.90E-01	9.05E-01	-	-
1377046_at	Ankrd6	ankyrin repeat domain 6	500430	Rn.45844	AW524407	2.38	2.37	2.39	2.37	2.41	2.37	1.00	up	9.52E-01	9.86E-01	-	-
1388210_at	Acot2	acyl-CoA thioesterase 2	192272	Rn.37524	Y09333	6.47	4.80	4.07	4.83	4.77	5.74	1.00	down	9.99E-01	1.00E+00	-	-
1379383_at	---	---	---	Rn.169518	BF288259	2.28	2.27	2.28	2.27	2.28	2.27	1.00	down	8.20E-01	9.42E-01	-	-
1382315_at	Tsc22d4	TSC22 domain family, member 4	684980	Rn.21359	BF286388	2.31	2.30	2.32	2.31	2.32	2.31	1.00	up	8.65E-01	9.58E-01	-	-
1398379_at	---	---	---	Rn.170555	BM386296	2.33	2.32	2.34	2.33	2.33	2.32	1.00	down	8.47E-01	9.52E-01	-	-
1390627_a_at	Tbx3	T-box 3	353305	Rn.162144	BE113656	2.12	2.12	2.12	2.12	2.12	2.12	1.00	down	7.40E-01	9.16E-01	-	-
1390712_at	Fry	furry homolog (Drosophila)	304244	Rn.36184	AW253742	2.34	2.33	2.35	2.34	2.34	2.34	1.00	up	8.68E-01	9.59E-01	-	-
1380759_at	---	---	---	---	BF418105	2.32	2.31	2.32	2.31	2.34	2.30	1.00	down	9.34E-01	9.81E-01	-	-
1387559_at	Grin3b	glutamate receptor, ionotropic, N-methyl-D-aspartate 3B	170796	Rn.162906	NM_133308	2.38	2.37	2.38	2.37	2.39	2.36	1.00	down	9.15E-01	9.75E-01	-	-
1377859_s_at	Prdm2	PR domain containing 2, with ZNF domain	313678	Rn.202632	BE120443	2.69	2.89	2.73	2.77	2.87	2.67	1.00	up	9.91E-01	9.97E-01	-	-
1396332_at	---	---	---	Rn.206000	BE109907	2.39	2.38	2.39	2.38	2.40	2.38	1.00	up	8.90E-01	9.66E-01	-	-
1378769_at	---	---	---	Rn.171636	BE096509	2.33	2.32	2.34	2.33	2.34	2.33	1.00	down	8.94E-01	9.67E-01	-	-
1396814_at	---	---	---	Rn.154116	BE106907	2.35	2.35	2.36	2.36	2.36	2.33	1.00	down	9.19E-01	9.76E-01	-	-
1397142_at	---	---	---	Rn.51517	BE108541	2.28	2.28	2.28	2.28	2.28	2.28	1.00	down	7.49E-01	9.19E-01	-	-
1397292_at	---	---	---	Rn.112856	BF412804	2.34	2.32	2.34	2.36	2.33	2.31	1.00	up	9.49E-01	9.85E-01	-	-
1373747_at	Cnih2	cornichon homolog 2 (Drosophila)	361705	Rn.18785	BG381691	2.25	2.24	2.25	2.24	2.25	2.24	1.00	down	8.09E-01	9.38E-01	-	-
1386401_at	---	---	---	---	H33654	2.30	2.29	2.30	2.29	2.29	2.30	1.00	up	8.70E-01	9.60E-01	-	-
1393534_at	---	---	---	---	AI059500	2.57	2.63	2.55	2.55	2.57	2.63	1.00	down	9.79E-01	9.94E-01	-	-
1393489_at	Rab66	Rab-66 protein	296610	Rn.46431	AW527282	2.36	2.34	2.36	2.35	2.38	2.34	1.00	up	9.40E-01	9.83E-01	-	-
1379048_at	---	---	---	---	BI296505	2.22	2.22	2.22	2.22	2.22	2.22	1.00	down	7.36E-01	9.15E-01	-	-
1369614_at	Rap2b	RAP2B, member of RAS oncogene family	170923	Rn.217110	NM_133410	2.35	2.35	2.36	2.35	2.36	2.35	1.00	down	8.58E-01	9.55E-01	-	-
1385647_at	---	---	---	Rn.135161	AA875123	2.31	2.31	2.33	2.32	2.34	2.31	1.00	up	9.40E-01	9.83E-01	-	-
1381140_at	---	---	---	Rn.216972	BF398056	2.46	2.44	2.47	2.45	2.48	2.44	1.00	down	9.49E-01	9.85E-01	-	-
1387286_at	Grm1	glutamate receptor, metabotropic 1	24414	Rn.87787	NM_017011	2.31	2.30	2.31	2.30	2.32	2.29	1.00	down	9.11E-01	9.73E-01	-	-
1376726_at	---	---	---	---	AI101117	2.36	2.35	2.37	2.36	2.37	2.36	1.00	up	8.83E-01	9.64E-01	-	-
1372898_at	Heatr6	HEAT repeat containing 6	497972	Rn.27022	BI291248	2.33	2.32	2.34	2.35	2.33	2.31	1.00	up	9.47E-01	9.85E-01	-	-
1375305_at	RGD1563912	RGD1563912	362256	Rn.9944	BI282028	2.22	2.21	2.22	2.22	2.22	2.21	1.00	down	7.79E-01	9.28E-01	-	-
1382582_at	---	---	---	Rn.199482	BG381461	2.68	2.79	2.67	2.67	2.67	2.79	1.00	down	9.87E-01	9.96E-01	-	-
1373232_at	LOC302022	similar to nidogen 2 protein	302022	Rn.13869	AI008975	2.50	2.49	2.50	2.50	2.50	2.49	1.00	down	8.13E-01	9.39E-01	-	-
1397792_at	---	---	---	Rn.216988	BF411652	2.39	2.38	2.39	2.38	2.38	2.39	1.00	up	8.20E-01	9.42E-01	-	-
1369685_at	Twist2	twist homolog 2 (Drosophila)	59327	Rn.218018	NM_021691	2.30	2.29	2.30	2.29	2.30	2.29	1.00	down	8.87E-01	9.65E-01	-	-
1394946_at	42077 /// RGD130	hypothetical LOC292199 /// similar to intracellular protein transport like (XM452292199 /// 308053		Rn.38655	BI289481	2.35	2.34	2.36	2.36	2.36	2.34	1.00	up	9.09E-01	9.73E-01	-	-
1397883_at	---	---	---	Rn.153398	---	2.79	---	2.79	---	2.79	---	1.00	up	9.94E-01	9.98E-01	-	-
1391180_at	---	---	---	Rn.172819	BF396097	2.42	2.39	2.41	2.41	2.41	2.40	1.00	down	9.33E-01	9.81E-01	-	-
1386295_at	---	---	---	Rn.206001	AI639051	2.41	2.39	2.41	2.40	2.41	2.39	1.00	down	9.18E-01	9.76E-01	-	-
1392029_at	RGD1306410	similar to CG14980-PB	360768	Rn.137253	BF403812	2.48	2.47	2.48	2.49	2.48	2.46	1.00	down	9.22E-01	9.77E-01	-	-
1380109_at	Cbx1	chromobox homolog 1 (HP1 beta homolog Drosophila)	360609	Rn.32816	BI290295	2.48	2.45	2.48	2.46	2.48	2.46	1.00	up	9.33E-01	9.81E-01	-	-
1393036_at	Psrc1	proline/serine-rich coiled-coil 1	691380	Rn.137457	AI044340	2.31	2.30	2.32	2.31	2.31	2.30	1.00	down	8.83E-01	9.64E-01	-	-
1377366_at	---	---	---	Rn.15176	BF389753	2.38	2.37	2.38	2.37	2.38	2.37	1.00	down	8.47E-01	9.52E-01	-	-
1392600_a_at	---	---	---	Rn.13751	AI176989	4.12	4.70	3.28	2.75	4.66	4.70	1.00	up	9.99E-01	1.00E+00	-	-
1393717_at	---	---	---	Rn.220491	BF397889	2.35	2.34	2.36	2.34	2.36	2.34	1.00	up	9.26E-01	9.79E-01	-	-
1397016_at	---	---	---	Rn.58180	BF393983	2.35	2.35	2.36	2.35	2.36	2.36	1.00	up	8.65E-01	9.58E-01	-	-
1394762_at	---	---	---	---	BF286921	2.37	2.37	2.39	2.37	2.39	2.36	1.00	down	9.35E-01	9.82E-01	-	-
1396718_at	---	---	---	---	---	---	---	---	---	---	---	1.00	up	9.34E-01	9.81E-01	-	-
1390105_at	B4galt2	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 2	313536	Rn.219217	BG381632	2.21	2.21	2.22	2.21	2.22	2.21	1.00	down	7.49E-01	9.19E-01	-	-
1367821_a_at	Cacna1a	calcium channel, voltage-dependent, P/Q type, alpha 1A subunit	25398	Rn.87769	BF400631	2.35	2.34	2.35	2.34	2.35	2.34	1.00	down	7.87E-01	9.31E-01	-	-
1380708_at	---	---	---	Rn.152720	BF396522	2.35	2.34	2.35	2.34	2.36	2.34	1.00	up	8.93E-01	9.67E-01	-	-
1397645_at	Krt17	keratin 17	287702	Rn.106755	BI286389	2.50	2.50	2.51	2.50	2.51	2.50	1.00	down	8.19E-01	9.42E-01	-	-
1373163_at	Usp28	ubiquitin specific peptidase 28	315639	Rn.6599	BI287702	2.39	2.38	2.41	2.39	2.40	2.39	1.00	up	9.23E-01	9.77E-01	-	-
1383446_at	RGD1305685	similar to hypothetical protein FLJ13089	360811	Rn.202650	BF553979	2.51	2.51	2.50	2.54	2.39	2.58	1.00	down	9.88E-01	9.96E-01	-	-
1394827_at	RGD1305680	similar to KIAA0240	301235	Rn.55468	AI012667	2.38	2.38	2.39	2.38	2.39	2.37	1.00	down	8.75E-01	9.61E-01	-	-
1393768_at	Lingo1	leucine rich repeat and Ig domain containing 1	316591	Rn.20269	AA818405	2.30	2.29	2.31	2.30	2.29	2.30	1.00	down	8.76E-01	9.61E-01	-	-
1396895_at	Isl1	ISL LIM homeobox 1	64444	Rn.202645	AW533821	2.31	2.30	2.31	2.30	2.32	2.29	1.00	down	9.19E-01	9.76E-01	-	-
1396835_at	---	---	---	Rn.163392	BE095505	2.34	2.32	2.36	2.33	2.35	2.33	1.00	down	9.44E-01	9.84E-01	-	-
1387066_a_at	Rgs12	regulator of G-protein signaling 12	54292	Rn.9796	NM_019339	2.27	2.26	2.27	2.27	2.27	2.26	1.00	down	8.44E-01	9.52E-01	-	-
1393715_s_at	T2	brachyury 2	681288	Rn.198111	BG376382	2.56	2.55	2.60	2.53	2.64	2.54	1.00	up	9.82E-01	9.95E-01	-	-
1373153_at	---	---	---	Rn.204974	AI230720	2.33	2.32	2.34	2.32	2.34	2.32	1.00	down	9.22E-01	9.77E-01	-	-
1384768_at	Zfp94	zinc finger protein 94	499095	Rn.58046	BF393575	2.31	2.28	2.29	2.28	2.33	2.28	1.00	up	9.65E-01	9.90E-01	-	-
1397831_at	---	---	---	Rn.46497	AW527319	2.34	2.32	2.33	2.35	2.33	2.32	1.00	down	9.31E-01	9.81E-01	-	-
1393929_at	Ccr6	chemokine (C-C motif) receptor 6	308163	Rn.161767	AI045155	2.30	2.29	2.30	2.30	2.30	2.29	1.00	up	8.97E-01	9.68E-01	-	-
1393359_at	Ap3b2	adaptor-related protein complex 3, beta 2 subunit	308777	Rn.217954	AW534487	2.25	2.25	2.26	2.25	2.25	2.25	1.00	down	8.08E-01	9.38E-01	-	-
1395843_at	---	---	---	---	AW143625	2.47	2.45	2.49	2.46	2.50	2.45	1.00	up	9.66E-01	9.90E-01	-	-
1391291_at	---	---	---	Rn.61576	BF410101	2.44	2.44	2.45	2.44	2.47	2.42	1.00	up	9.53E-01	9.86E-01	-	-
1396579_at	---	---	---	Rn.46727	AW527978	2.30	2.29	2.30	2.29	2.29	2.30	1.00	down	8.92E-01	9.66E-01	-	-
1368827_at	Gata6	GATA binding protein 6	29300	Rn.8701	AA955182	2.33	2.32	2.34	2.32	2.36	2.31	1.00	up	9.58E-01	9.88E-01	-	-
1379991_at	---	---	---	Rn.89999	AI176896	2.37	2.36	2.37	2.37	2.37	2.35	1.00	down	9.13E-01	9.74E-01	-	-
1386422_at	Dchs1	dachsous 1 (Drosophila)	308912	Rn.15768	H31750	2.31	2.31	2.32	2.31	2.32	2.31	1.00	down	8.64E-01	9.58E-01	-	-
1385223_at	---	---	---	Rn.63441	BF418672	2.51	2.50	2.51	2.51	2.52	2.49	1.00	down	9.20E-01	9.76E-01	-	-
1397966_at	---	---	---	Rn.60266	BF403413	2.35	2.35	2.36	2.35	2.36	2.35	1.00	down	7.84E-01	9.30E-01	-	-
1381367_at	---	---	---	Rn.209193	BF386721	2.25	2.25	2.26	2.25	2.26	2.24	1.00	down	9.11E-01	9.73E-01	-	-
1391429_at	Hfe2	hemochromatosis type 2 (juvenile) (human homolog)	310681	Rn.22490	AW434961	2.32	2.31	2.32	2.31	2.30	2.30	1.00	up	8.50E-01	9.85E-01	-	-
1368376_at	Nr0b2	nuclear receptor subfamily 0, group B, member 2	117274	Rn.10712	NM_057133	2.40	2.38	2.41	2.40	2.41	2.39	1.00	up	9.28E-01	9.80E-01	-	-
1381291_at	Ash1l	Ash1 (absent, small, or homeotic)-like (Drosophila)	310638	Rn.206058	BE106586	2.52	2.50	2.53	2.51	2.53	2.50	1.00	down	9.45E-01	9.84E-01	-	-
1395637_at	Asphd2	aspartate beta-hydroxylase domain containing 2	364948	Rn.51374	BF412025	2.23	2.22	2.23	2.23	2.22	2.22	1.00	down	8.03E-01	9.37E-01	-	-
1398445_at	---	---	---	Rn.170107	BF420311	2.34	2.30	2.38	2.34	2.35	2.33	1.00	up	9.71E-01	9.91E-01	-	-
1397980_at	---	---	---	Rn.210779	BF401691	2.43	2.42	2.44	2.43	2.46	2.42	1.00	up	9.51E-01	9.86E-01	-	-
1387625_at	Igfbp6	insulin-like growth factor binding protein 6	25641	Rn.6431	NM_013104	2.47	2.46	2.47	2.47	2.47	2.45	1.00	down	9.19E-01	9.76E-01	-	-
1384842_s_at	Fas	Fas (TNF receptor superfamily, member 6)	246097	Rn.162521	AI231631	2.34	2.33	2.36	2.33	2.35	2.34	1.00	up	9.35E-01	9.82E-01	-	-
1369170_at	Khsrp	KH-type splicing regulatory protein	171137	Rn.92643	NM_133602	2.62	2.60	2.63	2.64	2.61	2.59	1.00	up	9.65E-01	9.90E-01	-	-
1379698_at	---	---	---	Rn.22530	AI178631	2.30	2.30	2.31	2.32	2.31	2.29	1.00	up	9.27E-01	9.79E-01	-	-
1375632_at	/// Rpl38-ps1 /// R	similar to 60S ribosomal protein L38 /// ribosomal protein L38 /// ribosomal pro	83 /// 689284 /// 68	Rn.198996	H35210	12.18	11.47	11.26	11.74	11.47	11.70	1.00	down	9.98E-01	9.99E-01	-	-
1380467_at	Slc16a1	solute carrier family 16, member 1 (monocarboxylic acid transporter 1)	25027	Rn.6085	AI556510	2.28	2.27	2.28	2.28	2.28	2.27	1.00	down	8.43E-01	9.51E-01	-	-
1391133_at	Il17rc	interleukin 17 receptor C	297520	Rn.139872	BI282622	2.26	2.26	2.26	2.26	2.27	2.26	1.00	up	8.29E-01	9.46E-01	-	-
1380112_at	---	---	---	Rn.206866	AW531114	2.26	2.25	2.26	2.25	2.26	2.25	1.00	down	8.21E-01	9.43E-01	-	-
1379880_at	---	---	---	---	AI102926	2.36	2.36	2.37	2.36	2.39	2.35	1.00	down	9.46E-01	9.85E-01	-	-
1398022_at	---	---	---	Rn.210829	AF404957	2.43	2.42	2.45	2.43	2.46	2.41	1.00	down	9.60E-01	9.89E-01	-	-
1380501_x_at	Fkbp2	FK506 binding protein 2	293702	Rn.65866	BF561706	2.19	2.35	2.19	2.22	2.19	2.32	1.00	up	9.91E-01	9.97E-01	-	-
1371040_at	Slc1a5	solute carrier family 1 (neutral amino acid transporter), member 5	292657	Rn.28965	BG372334	2.32	2.31	2.33	2.32	2.34	2.31	1.00	down	9.36E-01	9.82E-01	-	-
1397625_at	---	---	---	Rn.204779	BE107694	2.50	2.49	2.51	2.49	2.50	2.50	1.00	down	9.14E-01	9.74E-01	-	-
1389706_at	---	---	---	Rn.165556	AI007639	2.36	2.34	2.37	2.35	2.37	2.34	1.00	down	9.36E-01	9.82E-01	-	-
1377014_at	RGD1308116	similar to hypothetical protein MGC42105	310376	Rn.19745	BG375383	2.39	2.37	2.39	2.38	2.39	2.36	1.00	down	9.45E-01	9.84E-01	-	-
1396374_at	---	---	---	---	BF394299	2.27	2.26	2.27	2.27	2.27	2.26	1.00	down	8.54E-01	9.55E-01	-	-
1380595_at	---	---	---	Rn.128483	AI071495	2.71	2.71	2.72	2.71	2.68	2.75	1.00	up	9.72E-01	9.92E-01	-	-
1382542_at	---	---	---	Rn.203970	BG668273	2.41	2.37	2.43	2.40	2.42	2.39	1.00	up	9.65E-01	9.90E-01	-	-
1396157_at	---	---	---	Rn.203071	BF548958	2.35	2.35	2.36	2.35	2.37	2.34	1.00	up	9.17E-01	9.75E-01	-	-
1395015_at	F8	coagulation factor VIII, procoagulant component	302470	Rn.95452	BE116550	2.32	2.29	2.31	2.31	2.35	2.27	1.00	down	9.74E-01	9.92E-01	-	-
1398166_at	---	---	---	Rn.160515	BF401600	2.38	2.38	2.40	2.40	2.39	2.37	1.00	down	9.51E-01	9.86E-01	-	-
1377882_at	Ttl3	tms-related tyrosine kinase 3	140635	Rn.6774	AA996414	2.31	2.30	2.31	2.30	2.32	2.29	1.00	down	9.37E-01	9.82E-01	-	-
1370797_at	Foxe3	forkhead box E3	171302	Rn.92407	L13207	2.17	2.17	2.18	2.17	2.18	2.17	1.00	down	8.20E-01	9.42E-01	-	-
1384708_at	---	---	---	Rn.172649	BF400

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1389694_at	Ky	kyphoscoliosis peptidase	315962	Rn.24084	BE111310	2.37	2.35	2.37	2.36	2.38	2.35	1.00	down	9.39E-01	9.83E-01	-	-
1375825_at	---	---	---	Rn.216939	BM382867	2.52	2.51	2.54	2.51	2.55	2.51	1.00	up	9.66E-01	9.90E-01	-	-
1378714_at	RGD1309873	similar to hypothetical protein BC010003	363112	Rn.45933	BI283367	2.35	2.35	2.38	2.37	2.38	2.36	1.00	up	9.49E-01	9.85E-01	-	-
1396173_at	Nrip3	nuclear receptor interacting protein 3	361625	Rn.48099	AW533345	2.34	2.34	2.35	2.34	2.35	2.34	1.00	down	8.69E-01	9.59E-01	-	-
1396629_at	Ormdl3	ORM1-like 3 (S. cerevisiae)	360618	Rn.202345	BF418824	2.27	2.27	2.28	2.29	2.28	2.26	1.00	up	9.19E-01	9.76E-01	-	-
1378871_at	Bai2	brain-specific angiogenesis inhibitor 2	313058	Rn.15364	AA924656	2.52	2.50	2.52	2.51	2.53	2.49	1.00	up	9.56E-01	9.88E-01	-	-
1389278_at	Tspy2	TSPY-like 2	302612	Rn.210101	BI282934	2.29	2.30	2.30	2.30	2.30	2.29	1.00	up	7.43E-01	9.17E-01	-	-
1389715_at	Ypel4	yippee-like 4 (Drosophila)	502643	Rn.23361	BG381499	2.38	2.36	2.39	2.37	2.40	2.36	1.00	down	9.63E-01	9.89E-01	-	-
1392585_at	---	---	---	Rn.203414	AI072302	2.30	2.29	2.30	2.29	2.30	2.29	1.00	down	8.70E-01	9.60E-01	-	-
1381157_at	---	---	---	---	BE110853	2.27	2.26	2.28	2.27	2.28	2.26	1.00	up	9.22E-01	9.77E-01	-	-
1370211_at	Nrgn	neurogranin	64356	Rn.11236	BE106940	2.23	2.23	2.24	2.23	2.24	2.23	1.00	down	7.70E-01	9.25E-01	-	-
1393385_at	RGD1560273	RGD1560273	498405	Rn.19392	AI060208	2.22	2.22	2.23	2.22	2.23	2.22	1.00	down	8.34E-01	9.48E-01	-	-
1380067_at	Myo5c	myosin VC	315820	Rn.2304	BI296036	2.34	2.33	2.36	2.34	2.36	2.32	1.00	down	9.60E-01	9.89E-01	-	-
1374867_at	---	---	---	Rn.176359	BI296536	2.33	2.32	2.33	2.32	2.33	2.32	1.00	up	8.81E-01	9.63E-01	-	-
1384322_at	---	---	---	Rn.51244	BE107680	2.39	2.38	2.40	2.38	2.39	2.39	1.00	down	9.03E-01	9.70E-01	-	-
1380951_at	---	---	---	Rn.155330	BE096680	2.27	2.27	2.28	2.27	2.28	2.27	1.00	down	8.67E-01	9.58E-01	-	-
1395398_at	---	---	---	Rn.207184	AI579828	2.41	2.40	2.41	2.41	2.42	2.40	1.00	down	8.91E-01	9.66E-01	-	-
1380083_at	Klk10	kallikrein related-peptidase 10	292850	Rn.78372	BI283346	2.34	2.33	2.34	2.33	2.35	2.32	1.00	down	9.36E-01	9.82E-01	-	-
1380653_at	---	---	---	Rn.208098	BE110230	2.35	2.34	2.36	2.35	2.37	2.33	1.00	down	9.53E-01	9.86E-01	-	-
1392231_at	Slk4	serine/threonine kinase 4	311622	Rn.166761	BE102758	4.70	4.80	4.69	4.75	4.76	4.69	1.00	down	9.86E-01	9.96E-01	-	-
1385910_at	---	---	---	Rn.219428	AA955157	2.36	2.36	2.37	2.36	2.37	2.36	1.00	down	8.69E-01	9.59E-01	-	-
1375800_at	---	---	---	Rn.171523	BE117206	2.23	2.23	2.23	2.23	2.23	2.22	1.00	down	8.50E-01	9.53E-01	-	-
1375222_at	LOC689154	Hypothetical protein LOC689154	689154	Rn.198590	AI575699	2.23	2.23	2.24	2.23	2.24	2.23	1.00	up	8.25E-01	9.45E-01	-	-
1382314_at	G1p2	interferon, alpha-inducible protein (clone IFI-15K)	298693	Rn.198318	BE096523	2.63	2.62	2.66	2.66	2.63	2.62	1.00	down	9.97E-01	9.98E-01	-	-
1375154_at	---	---	---	Rn.212091	BI291268	2.31	2.30	2.32	2.31	2.30	2.31	1.00	down	9.49E-01	9.85E-01	-	-
1379017_at	---	---	---	Rn.26612	AI111697	2.38	2.37	2.39	2.38	2.40	2.36	1.00	down	9.60E-01	9.89E-01	-	-
1384004_at	Gpr158	G protein-coupled receptor 158	291352	---	AI030360	2.30	2.29	2.31	2.30	2.31	2.29	1.00	down	9.24E-01	9.78E-01	-	-
1378693_at	Shc2	SHC (Src homology 2 domain containing) transforming protein 2	314612	Rn.120041	BF394159	2.45	2.43	2.48	2.44	2.47	2.44	1.00	down	9.67E-01	9.90E-01	-	-
1369649_at	Cacna2d1	calcium channel, voltage-dependent, alpha2/delta subunit 1	25399	Rn.11276	AF400662	2.30	2.29	2.30	2.30	2.30	2.29	1.00	down	8.89E-01	9.65E-01	-	-
1395515_at	Bhlhb9	basic helix-loop-helix domain containing, class B, 9	317407	Rn.154656	BG668905	2.34	2.33	2.35	2.34	2.35	2.34	1.00	down	9.17E-01	9.75E-01	-	-
1368772_at	Slc4a3	solute carrier family 4 (anion exchanger), member 3	24781	Rn.87739	NM_017049	2.30	2.30	2.31	2.31	2.31	2.29	1.00	up	9.15E-01	9.75E-01	-	-
1395356_at	OC683953 /// Prrt	similar to NG5 protein /// proline-rich transmembrane protein 1	406167 /// 683953	Rn.144293	BF562588	2.13	2.13	2.14	2.13	2.14	2.13	1.00	down	8.04E-01	9.37E-01	-	-
1390909_at	---	---	---	Rn.17796	AI171480	2.46	2.44	2.47	2.45	2.47	2.44	1.00	down	9.55E-01	9.87E-01	-	-
1378225_at	Mmp14	Matrix metalloepitdase 14 (membrane-inserted)	81707	Rn.10371	AI176440	2.29	2.29	2.29	2.29	2.30	2.29	1.00	up	8.60E-01	9.57E-01	-	-
1392368_at	---	---	---	---	BE117273	2.55	2.55	2.56	2.55	2.58	2.53	1.00	up	9.57E-01	9.88E-01	-	-
1369765_at	Ascl1	achaete-scute complex homolog 1 (Drosophila)	64186	Rn.32936	NM_022384	2.41	2.40	2.43	2.43	2.41	2.39	1.00	up	9.62E-01	9.89E-01	-	-
1390017_at	Hapln2	Hyaluronan and proteoglycan link protein 2	64057	Rn.76545	BF393931	2.45	2.44	2.45	2.44	2.45	2.44	1.00	down	8.43E-01	9.51E-01	-	-
1380206_at	---	---	---	Rn.206659	BE096005	2.51	2.43	2.58	2.50	2.61	2.41	1.00	up	9.92E-01	9.98E-01	-	-
1373154_at	RGD1563583	similar to mKIAA0998 protein	299208	Rn.2885	BI278842	2.29	2.29	2.30	2.29	2.30	2.29	1.00	up	9.02E-01	9.70E-01	-	-
1380618_at	---	---	---	---	AI178792	2.45	2.43	2.44	2.43	2.46	2.42	1.00	down	9.51E-01	9.86E-01	-	-
1391953_at	Msx2	msh homeobox 2	25483	Rn.10414	BI284209	2.38	2.37	2.40	2.38	2.41	2.36	1.00	up	9.70E-01	9.91E-01	-	-
1377038_at	Tbx19	T-box 19	304935	Rn.25358	BF403923	2.37	2.36	2.38	2.36	2.39	2.36	1.00	up	9.53E-01	9.86E-01	-	-
1397636_at	RGD1311249	similar to RIKEN cDNA B230312A22	298201	Rn.63818	BF389573	2.30	2.30	2.31	2.30	2.30	2.30	1.00	up	8.17E-01	9.41E-01	-	-
1379093_at	---	---	---	Rn.206013	BF404377	2.43	2.43	2.45	2.43	2.46	2.42	1.00	up	9.60E-01	9.89E-01	-	-
1396931_at	---	---	---	Rn.204556	AI137091	2.50	2.48	2.55	2.49	2.58	2.46	1.00	down	9.87E-01	9.96E-01	-	-
1395047_at	Tnks2	tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase 2	309512	Rn.75288	BF397243	2.39	2.38	2.39	2.39	2.38	2.38	1.00	down	8.76E-01	9.62E-01	-	-
1393799_at	Unc5b	Unc-5 homolog B (C. elegans)	60630	Rn.34617	BI303989	2.31	2.31	2.32	2.31	2.32	2.31	1.00	down	8.99E-01	9.69E-01	-	-
1375878_at	RGD1308049	similar to RIKEN cDNA 2410004C24	293690	Rn.12740	AI177929	2.32	2.31	2.32	2.32	2.32	2.31	1.00	up	8.83E-01	9.58E-01	-	-
1370753_at	Olr1078	olfactory receptor 1078	299593	Rn.120045	M64376	2.26	2.25	2.26	2.25	2.26	2.25	1.00	down	8.66E-01	9.58E-01	-	-
1398238_at	---	---	---	Rn.173138	BE107786	2.36	2.34	2.36	2.36	2.36	2.35	1.00	up	9.19E-01	9.76E-01	-	-
1391644_at	LOC689601	similar to density-regulated protein	689601	Rn.101864	AW920336	2.41	2.39	2.41	2.40	2.42	2.40	1.00	up	9.47E-01	9.85E-01	-	-
1368713_at	Mmp10	matrix metalloepeptidase 10	117061	Rn.9946	NM_133514	2.46	2.45	2.47	2.45	2.48	2.44	1.00	down	9.61E-01	9.89E-01	-	-
1388235_at	Smr3a	submaxillary gland androgen regulated protein 3A	498341	Rn.113967	X77816	2.42	2.40	2.43	2.41	2.45	2.39	1.00	up	9.74E-01	9.92E-01	-	-
1394813_at	---	---	---	Rn.169133	AI547996	2.37	2.36	2.37	2.36	2.37	2.36	1.00	down	9.24E-01	9.78E-01	-	-
1388001_at	Lrit1	leucine-rich repeat, immunoglobulin-like and transmembrane domains 1	246214	Rn.20309	AB028461	2.40	2.38	2.41	2.39	2.42	2.39	1.00	up	8.54E-01	9.86E-01	-	-
1394557_at	---	---	---	Rn.206836	AW535242	2.44	2.43	2.45	2.44	2.45	2.44	1.00	down	8.96E-01	9.67E-01	-	-
1373741_at	Pus1	pseudouridylate synthase 1	304567	Rn.11475	BM386451	5.57	6.14	6.83	6.46	5.61	6.45	1.00	down	9.99E-01	1.00E+00	-	-
1375679_at	RGD1307235	similar to RIKEN cDNA 2310035C23	309053	Rn.38202	AI460592	2.42	2.41	2.42	2.41	2.43	2.41	1.00	up	9.15E-01	9.75E-01	-	-
1387500_at	Mid1	midline 1	54252	Rn.15169	NM_022927	2.37	2.36	2.38	2.39	2.38	2.36	1.00	up	9.47E-01	9.85E-01	-	-
1385593_at	---	---	---	---	AI060012	2.27	2.26	2.27	2.27	2.28	2.26	1.00	down	9.23E-01	9.77E-01	-	-
1390251_at	Hhipl1	HHIP-like 1	362781	Rn.13263	BF418998	2.37	2.36	2.38	2.37	2.38	2.36	1.00	down	9.45E-01	9.84E-01	-	-
1390069_at	---	---	---	Rn.152076	BI299977	2.53	2.49	2.56	2.55	2.55	2.47	1.00	down	9.84E-01	9.95E-01	-	-
1380355_s_at	Slc6a17	solute carrier family 6 (neurotransmitter transporter), member 17	613226	Rn.186904	AW527869	2.35	2.34	2.36	2.35	2.36	2.35	1.00	down	9.22E-01	9.77E-01	-	-
1390472_at	Naaa	N-acylethanolamine acid amidase	497009	Rn.101943	AI412627	2.34	2.33	2.34	2.33	2.33	2.34	1.00	up	9.00E-01	9.69E-01	-	-
1386395_at	---	---	---	Rn.134526	H31724	2.35	2.34	2.35	2.35	2.36	2.34	1.00	down	9.22E-01	9.77E-01	-	-
1373799_at	---	---	---	---	BF415845	2.15	2.14	2.15	2.15	2.15	2.14	1.00	down	7.80E-01	9.28E-01	-	-
1386679_at	---	---	---	Rn.199608	BF562962	2.52	2.48	2.55	2.51	2.52	2.51	1.00	up	9.75E-01	9.93E-01	-	-
1377709_at	---	---	---	Rn.164831	AI072532	2.25	2.24	2.25	2.24	2.25	2.24	1.00	down	9.01E-01	9.69E-01	-	-
1394782_at	LOC362464	similar to aryl hydrocarbon receptor nuclear translocator-like 2	362464	---	AI547795	2.52	2.47	2.48	2.48	2.57	2.42	1.00	down	9.86E-01	9.96E-01	-	-
1396453_at	---	---	---	---	BM386772	2.47	2.44	2.51	2.45	2.53	2.43	1.00	up	9.86E-01	9.96E-01	-	-
1377805_at	---	---	---	Rn.201797	AW433937	2.48	2.47	2.50	2.48	2.49	2.48	1.00	down	9.53E-01	9.86E-01	-	-
1377506_at	Gdf1 /// Lass1	growth differentiation factor 1 /// LAG1 homolog, ceramide synthase 1	290658 /// 306351	Rn.202347	BI289525	2.42	2.42	2.42	2.42	2.42	2.42	1.00	up	7.29E-01	9.14E-01	-	-
1389824_at	Camk2a	calcium/calmodulin-dependent protein kinase II alpha	25400	Rn.107499	BF404381	2.32	2.31	2.32	2.31	2.33	2.31	1.00	down	9.08E-01	9.72E-01	-	-
1378857_at	LOC680282	hypothetical protein LOC680282	680282	Rn.181498	AI716196	2.35	2.34	2.36	2.34	2.36	2.34	1.00	down	9.36E-01	9.82E-01	-	-
1374873_at	---	---	---	Rn.168174	AW251378	2.33	2.33	2.34	2.33	2.34	2.33	1.00	down	7.99E-01	9.35E-01	-	-
1391233_at	---	---	---	Rn.41807	BG377517	2.52	2.51	2.53	2.52	2.54	2.51	1.00	up	9.43E-01	9.84E-01	-	-
1384748_at	Mmel1	membrane metallo-endopeptidase-like 1	313755	Rn.50873	BE106100	2.43	2.43	2.44	2.43	2.45	2.43	1.00	up	9.34E-01	9.81E-01	-	-
1376461_at	LOC686198	hypothetical protein LOC686198	686198	---	BF400223	2.32	2.31	2.32	2.31	2.32	2.31	1.00	down	8.51E-01	9.53E-01	-	-
1389925_at	---	---	---	---	BE100162	2.27	2.26	2.27	2.27	2.27	2.26	1.00	down	8.50E-01	9.53E-01	-	-
1396210_at	---	---	---	Rn.156797	BF387033	2.49	2.48	2.50	2.49	2.54	2.44	1.00	down	9.84E-01	9.95E-01	-	-
1385292_at	Sc65	Synaptonemal complex protein SC65	59101	Rn.90100	BI303187	2.37	2.36	2.38	2.36	2.38	2.36	1.00	down	9.32E-01	9.81E-01	-	-
1379213_at	---	---	---	Rn.146212	BF400921	2.36	2.35	2.37	2.36	2.37	2.36	1.00	up	9.01E-01	9.69E-01	-	-
1387865_at	Dut	deoxyuridine triphosphatase	497778	Rn.6102	AI411157	9.20	10.13	10.24	9.87	9.88	9.82	1.00	up	9.98E-01	1.00E+00	-	-
1389183_at	Pms2	PMS2 postmeiotic segregation increased 2 (S. cerevisiae)	288479	Rn.102072	BI281709	2.55	2.55	3.52	2.74	2.56	3.33	1.00	down	9.99E-01	1.00E+00	-	-
1381574_at	Tmem195	transmembrane protein 195	362732	Rn.152690	BF403907	2.33	2.32	2.33	2.33	2.34	2.31	1.00	down	9.37E-01	9.82E-01	-	-
1370996_at	Rasgrf1	RAS protein-specific guanine nucleotide-releasing factor 1	192213	Rn.135776	AI577569	2.22	2.22	2.23	2.22	2.23	2.22	1.00	down	9.10E-01	9.73E-01	-	-
1396727_at	---	---	---	Rn.59182	BF403436	2.27	2.27	2.27	2.27	2.28	2.27	1.00	down	8.79E-01	9.63E-01	-	-
1395452_at	---	---	---	---	AW535316	2.36	2.35	2.36	2.35	2.37	2.34	1.00	up	9.48E-01	9.85E-01	-	-
1379489_at	---	---	---	Rn.169573	BI286796	2.29	2.28	2.30	2.29	2.30	2.29	1.00	up	9.17E-01	9.75E-01	-	-
1369111_at	Fabp1	fatty acid binding protein 1, liver	24360	Rn.36412	NM_012556	2.46	2.45	2.48	2.45	2.49	2.45	1.00	up	9.70E-01	9.91E-01	-	-
1370924_at	LOC362350 /// Tcrb	similar to T-cell receptor beta-2 chain C region /// T-cell receptor beta chain	24820 /// 362350	Rn.34871	BG378607	2.33	2.32	2.33	2.32	2.34	2.31	1.00	down	9.48E-01	9.85E-01	-	-
1368324_at	Brca2	breast cancer 2	360254	Rn.103225	NM_031542	2.35	2.33	2.35	2.34	2.35	2.33	1.00	down	9.39E-01	9.83E-01	-	-
1398009_at	RGD1308775	similar to RIKEN cDNA 4921536K21	305476	Rn.163259	AW528388	2.36	2.35	2.38	2.36	2.37	2.36	1.00	up	9.31E-01	9.81E-01	-	-
1382539_at	---	---	---	---	AI171022	4.49	5.45	5.24	4.28	5.26	5.64	1.00	down	9.99E-01	1.00E+00	-	-
1381698_at	---	---	---	Rn.150733	AA943098	2.14	2.14	2.14	2.14	2.14	2.14	1.00	down	8.41E-01	9.50E-01	-	-
1377437_at	AD1565158 /// Veg	similar to VEPH isoform A /// ventricular zone expressed PH domain homolog	361954 /// 502705	Rn.158250	AI013299	2.52	2.50	2.53	2.51	2.52	2.50	1.00	down	9.56E-01	9.88E-01	-	-
1370328_at	Dkk3	dickkopf homolog 3 (Xenopus laevis)	171548	Rn.12516	AF245040	2.36	2.36	2.37	2.36	2.37	2.36	1.00	down	7.99E-01	9.35E-01	-	-
1387594_at	Qtrt1	queuine tRNA-ribosyltransferase 1	64016	Rn.53858	NM_022250	2.34	2.33	2.35	2.34	2.35	2.32	1.00	down	9.48E-01	9.85E-01	-	-
1368401_at	Gria2	glutamate receptor, ionotropic, AMPA 2	29627	Rn.91361	NM_017261	2.29	2.27	2.29	2.28	2.29	2.27	1.00	down	9.31E-01	9.81E-01	-	-
1387331_at	Atp4b	ATPase, H+/K+ exchanging, beta polypeptide	24217	Rn.10033	NM_012510	2.27	2.26	2.27	2.26	2.28	2.26	1.00	down	8.69E-01	9.81E-01	-	-
1380195_at	---	---	---	Rn.203902	AI145357	2.30	2.30	2.30	2.30	2.29	2.29	1.00	down	8.44E-01	9.52E-01	-	-
1384622_at	RGD1309482	Similar to chromosome 10 open reading frame 4; similar to putative acid phos	365458	Rn.23684	AI136557	2.31	2.31	2.32	2.31	2.33	2.31	1.00	up	9.43E-01	9.84E-01	-	-
1379460_at	Sgip1	SH3-domain GRB2-like (endophilin) interacting protein 1	313413	Rn.19477	BF387898	2.49	2.49	2.50	2.49	2.51	2.48	1.00	up	9.61E-01	9.89E-01	-	-
1376603_at	Wdr21	WD repeat domain 21	362762	Rn.24961	AI169243	2.49	2.50	2.49	2.49	2.51	2.49	1.00	up	9.38E-01	9.82E-01	-	-
1392435_at	Hspb7	heat shock protein family, member 7 (cardiovascular)	50565	Rn.21809	AI072744	2.15	2.15	2.16	2.15	2.16	2.15	1.00	down	8.62E-01	9.57E-01	-	-
1377803_at	Ccdc153	coiled-coil domain containing 153	300663	Rn.15323	BF555990	2.32	2.31	2.32	2.31	2.33	2.31	1.00	up	9.42E-01	9.84E-01	-	-
1372992_at	---	---	---	Rn.154182	BI298809	2.36	2.35	2.40	2.40	2.37	2.34	1.00	down	9.79E-01	9.94E-01	-	-
1379370_at	Sspn	sarcospan	500364	Rn.22364	AA818657	2.34	2.34	2.36	2.36	2.35	2.33	1.00	down	9.59E-01	9.89E-01	-	-
1370419_a_at	Sh3kbp1	SH3-domain kinase binding protein 1	84357	Rn.107226	AF230520	2.36	2.35	2.37	2.35	2.38	2.34	1.00	down	9.60E-01	9.89E-01	-	-
1395612_at	Peli3	pellino 3	309157	Rn.212107	BI297603	2.28	2.27	2.29	2.28	2.29	2.27	1.00	down	9.13E-01	9.74E-01	-	-
1381002_at	Asb1	ankyrin repeat and SOCS box-containing 1	316628	Rn.220453	AI711108	2.29	2.28	2.29	2.28	2.29	2.28	1.00	down	8.90E-01	9.66E-01	-	-
1377200_at	---	---	---	Rn.207729	BF400865	2.43	2.42	2.44	2.44	2.42	2.42	1.00	down	9.33E-01	9.81E-01	-	-
1376423_at	Actb	actin-like 7b	313183	Rn.63585	BF396984	2.44	2.43	2.44	2.43	2.44	2.44	1.00	down	8.83E-01	9.64E-01	-	-
1385013_at	Wnt1	wingless-type MMTV integration site family, member 1	24881	Rn.138108	AW534197	2.33	2.32	2.33	2.33	2.34	2.31	1.00	up	9.45E-01	9.84E-01	-	-
1368090_at	Prx	periaxin	78960	Rn.10395	NM_023976	2.41	2.40	2.43	2.41	2.42	2.42	1.00	up	9.39E-01	9.83E-01	-	-
1384604_at	---	---	---	---	BF390790	2.58	2.52	2.59	2.56	2.64	2.50	1.00	up	9.90E-01	9.97E-01	-	-
1396485_at	Btbd10	BTB (POZ) domain containing 10	308890	Rn.2717	AI705403	2.02	2.02	2.03	2.03	2.02	2.02	1.00	up	8.23E-01	9.43E-01	-	-
1378615_at	Brwd1	bromodomain and WD repeat domain containing 1	304061	Rn.205787	BE112424	2.36	2.36	2.37	2.36	2.37	2.36	1.00	up	8.57E-01	9.55E-01	-	-
1369951_at	Ctrb1	chymotrypsinogen B1	24291	Rn.105845	NM_012536	2.46	2.45	2.47	2.46	2.48	2.43	1.00	down	9.74E-01	9.92E-01	-	-
1368300_at	Adora2a	adenosine A2a receptor	25369	Rn.11180	AF228694	2.31	2.31	2.31	2.31	2.31	2.30	1.00	down	8.74E-01	9.61E-01	-	-
1370458_at	Hdgfrp3	hepatoma-derived growth factor, related protein 3	252941	Rn.17383	AF389347	2.38	2.37	2.38	2.38	2.38	2.38	1.00	up	8.56E-01	9.55E-01	-	-
1396670_at	---	---	---	Rn.169801	BE097242	2.32	2.31	2.33	2.32	2.33	2.31	1.00	down	9.24E-01	9.78E-01	-	-
1392239_at	---	---	---	---	BF386993	2.33	2.32	2.34	2.33	2.34	2.33	1.00	up	9.01E-01	9.69E-01	-	-
1387209_at	Olig1	oligodendrocyte transcription factor 1	60394	Rn.45339	NM_021770	2.36	2.36	2.37	2.35	2.37	2.35	1.00	down	9.15E-01	9.75E-01	-	-
1384459_at	---	---	---	Rn.20111	AI072270	2.34	2.34	2.35	2.34	2.35	2.33	1.00	down	9.31E-01	9.81E-01	-	-
1381722_at	LOC501283	similar to lipid droplet associated protein	501283	Rn.54204	BE112898	2.32	2.31	2.33	2.32	2.32	2.32	1.00	up	8.97E-01	9.68E-01	-	-
1389740_at	---	---	---	Rn.168223	BI296432	2.34	2.32	2.34	2.34	2.33	2.33	1.00	up	9.35E-01	9.82E-01	-	-
1393353_at	RGD1304810	similar to 6430573F11Rik protein	306504	Rn.150783	AI044301	2.54	2.57	2.55	2.54	2.55	2.58	1.00	up	9.70E-01	9.91E-01	-	-
1389007_at	RGD1307524	similar to Friedreich ataxia region gene X123	309415	Rn.8399	AI231799	2.34	2.33	2.34	2.33	2.34	2.34	1.00	up	9.18E-01	9.76E-01	-	-
1397649_at	---	---	---	---	BI298462	2.43	2.42	2.44	2.42	2.46	2.40	1.00	up	9.75E-01	9.92E-01	-	-
1390066_at	OC888367 /// Nr2f	similar to Orphan nuclear receptor EAR-2 (V-erbA-related protein EAR-2) /// n	245980 /// 688367	Rn.25840	AI102726	2.42	2.41	2.44	2.42	2.46	2.38	1.00	down	9.82E-01	9.95E-01	-	-
1382751_at	Wfdc10	WAP four-disulfide core domain 10	685216	Rn.106551	BF549536	2.38	2.37	2.38	2.37	2.39	2.36	1.00	down	9.63E-01	9.90E-01	-	-
1384776_x_at	RGD1564722	similar to C19orf36 protein	362832	Rn.11739	AI716186	2.35	2.34	2.36	2.34	2.37	2.34	1.00	down	9.60E-01	9.89E-01	-	-
1377531_at	---	---	---	Rn.209143	BF405592	2.28	2.27	2.28	2.28	2.27	2.27	1.00	down	9.28E-01	9.80E-01	-	-
1380649_at	---	---	---	---	AI236606	2.34	2.33	2.34	2.34	2.35	2.33	1.00	up	9.44E-01	9.84E-01	-	-
1383304_at	---	---	---	Rn.203727	AA996870	2.35	2.34	2.36	2.35	2.36	2.34	1.00	down	9.43E-01	9.84E-01	-	-
1390812_a_at	Rerg	RAS-like, estrogen-regulated, growth-inhibitor	502916	Rn.19093	AI170076	2.32	2.30	2.31	2.31	2.31	2.30	1.00	down	9.41E-01	9.83E-01	-	-
1389058_at	Trim29	tripartite motif-containing 29	300656	Rn.9452	BI279694	2.26	2.25	2.26	2.25	2.27	2.25	1.00	down	9.41E-01	9.83E-01	-	-
1398387_at	MGC72614	hypothetical LOC310540	310540	Rn.20514	AI009530	2.41	2.40	2.41	2.41	2.41	2.40	1.00	down	8.80E-01	9.63E-01	-	-
1397044_at	---	---	---	Rn.209287	BF387373	2.22	2.22	2.23	2.22	2.24	2.22	1.00	up	9.43E-01	9.84E-01	-	-
1379584_at	---	---	---	Rn.164418	AA848944	2.53	2.49	2.57	2.52	2.60	2.47	1.00	up	9.91E-01	9.97E-01	-	-
1389766_at	RGD1309036	hypothetical LOC292874	292874	Rn.23075	AA925385	2.37	2.36	2.37	2.36	2.37	2.36	1.00	down	8.42E-01	9.51E

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1396156_at	---	---	---	Rn.55081	BE120371	2.32	2.31	2.32	2.32	2.32	2.32	1.00	down	9.03E-01	9.70E-01	-	-
1372929_at	Kcnma1	potassium large conductance calcium-activated channel, subfamily M, alpha	83731	Rn.30616	AI010839	2.38	2.37	2.40	2.40	2.39	2.36	1.00	up	9.73E-01	9.92E-01	-	-
1396333_at	---	---	---	Rn.148372	AW520959	2.36	2.34	2.36	2.35	2.36	2.34	1.00	down	9.57E-01	9.88E-01	-	-
1371161_at	Ppp1r3b	protein phosphatase 1, regulatory (inhibitor) subunit 3B	192280	Rn.30046	Y18208	2.32	2.31	2.33	2.32	2.34	2.31	1.00	up	9.63E-01	9.90E-01	-	-
1375250_at	B4galt1	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 1	24390	Rn.17157	BF549771	2.07	2.07	2.07	2.07	2.07	2.07	1.00	down	8.05E-01	9.37E-01	-	-
1395302_at	---	---	---	Rn.148842	BE104435	2.37	2.36	2.38	2.37	2.37	2.36	1.00	down	9.48E-01	9.85E-01	-	-
1369857_a_at	Slc14a1	solute carrier family 14 (urea transporter), member 1	54301	Rn.10654	U81518	2.40	2.33	2.41	2.35	2.47	2.33	1.00	up	9.92E-01	9.98E-01	-	-
1391865_at	Rnf151	ring finger protein 151	302977	Rn.89276	BF282921	2.35	2.34	2.35	2.35	2.36	2.35	1.00	up	9.27E-01	9.79E-01	-	-
1373279_at	Ctnnbip1	catenin, beta-interacting protein 1	503000	Rn.36076	BI275726	2.43	2.49	2.36	2.40	2.36	2.51	1.00	down	9.93E-01	9.98E-01	-	-
1379400_at	---	---	---	Rn.17900	AI044556	2.31	2.32	2.32	2.31	2.32	2.32	1.00	up	9.09E-01	9.72E-01	-	-
1375243_at	---	---	---	---	BE113157	2.10	2.10	2.11	2.10	2.11	2.10	1.00	down	8.41E-01	9.50E-01	-	-
1385526_at	Atg5	ATG5 autophagy related 5 homolog (S. cerevisiae)	365601	Rn.98385	AA956721	6.39	6.97	7.75	6.96	6.97	7.17	1.00	up	9.99E-01	1.00E+00	-	-
1379119_at	---	---	---	---	BF393042	2.39	2.38	2.41	2.38	2.42	2.37	1.00	down	9.81E-01	9.94E-01	-	-
1369730_a_at	Gfra4	GDNF family receptor alpha 4	66023	Rn.64500	AJ294475	2.27	2.27	2.28	2.27	2.28	2.27	1.00	down	9.27E-01	9.79E-01	-	-
1397501_at	Wnt11	wingless-type MMTV integration site family, member 11	140584	Rn.55941	AA945807	2.25	2.25	2.26	2.25	2.26	2.25	1.00	up	8.40E-01	9.50E-01	-	-
1376475_at	---	---	---	Rn.172640	BF413090	2.32	2.30	2.32	2.31	2.33	2.30	1.00	up	9.68E-01	9.91E-01	-	-
1369287_at	Syt9	synaptotagmin IX	60564	Rn.10194	NM_053324	2.26	2.25	2.26	2.25	2.27	2.25	1.00	down	9.41E-01	9.83E-01	-	-
1368337_at	Glycam1	glycosylation dependent cell adhesion molecule 1	25258	Rn.10939	NM_012794	2.38	2.37	2.40	2.38	2.39	2.39	1.00	up	9.58E-01	9.88E-01	-	-
1391804_at	---	---	---	---	AW533795	2.62	4.24	2.47	3.01	3.02	3.30	1.00	up	9.99E-01	1.00E+00	-	-
1387444_at	Ptprh	protein tyrosine phosphatase, receptor type, H	171125	Rn.10285	NM_133592	2.32	2.31	2.32	2.32	2.33	2.31	1.00	down	9.49E-01	9.85E-01	-	-
1380658_at	---	---	---	Rn.209213	BF402406	2.33	2.32	2.34	2.33	2.34	2.32	1.00	up	9.54E-01	9.86E-01	-	-
1384697_at	---	---	---	---	AA944400	2.39	2.37	2.40	2.39	2.39	2.38	1.00	up	9.62E-01	9.89E-01	-	-
1396656_at	---	---	---	Rn.210007	BF410595	2.36	2.35	2.37	2.36	2.37	2.35	1.00	up	9.40E-01	9.83E-01	-	-
1392298_at	Acap3	ArfGAP with coiled-coil, ankyrin repeat and PH domains 3	313772	Rn.144386	AI549151	2.28	2.28	2.29	2.28	2.29	2.28	1.00	down	9.17E-01	9.75E-01	-	-
1376736_at	LOC688990	hypothetical protein LOC688990	688990	Rn.37063	BG375419	2.39	2.38	2.40	2.38	2.41	2.37	1.00	down	9.73E-01	9.92E-01	-	-
1381087_at	---	---	---	---	AW253893	2.18	2.18	2.19	2.18	2.19	2.18	1.00	down	8.81E-01	9.64E-01	-	-
1387132_at	Lipe	lipase, hormone sensitive	25330	Rn.10566	NM_012859	2.41	2.40	2.42	2.41	2.42	2.40	1.00	down	9.53E-01	9.86E-01	-	-
1385354_at	RGD1564327	similar to integrin alpha 8	364786	Rn.69726	BE120766	2.47	2.46	2.47	2.46	2.47	2.46	1.00	down	9.40E-01	9.83E-01	-	-
1379870_at	Chrnb1	Cholinergic receptor, nicotinic, beta 1 (muscle)	24261	Rn.44611	BF403312	2.47	2.46	2.47	2.46	2.48	2.46	1.00	down	9.53E-01	9.86E-01	-	-
1373421_at	Tgif1	TGFB-induced factor homeobox 1	316742	Rn.154349	BM392224	5.04	4.75	5.19	4.55	5.42	5.01	1.00	up	9.99E-01	1.00E+00	-	-
1379893_at	---	---	---	---	AI044998	2.48	2.48	2.48	2.48	2.47	2.47	1.00	down	9.03E-01	9.70E-01	-	-
1385821_at	---	---	---	Rn.57713	BF392004	2.57	2.53	2.61	2.55	2.62	2.53	1.00	up	9.90E-01	9.97E-01	-	-
1382638_at	---	---	---	Rn.163720	AI058645	2.43	2.42	2.43	2.42	2.45	2.40	1.00	down	9.77E-01	9.93E-01	-	-
1372418_at	RGD1560859	similar to 2300003P22Rik protein	500243	Rn.199287	BI285443	2.27	2.27	2.28	2.27	2.28	2.27	1.00	up	9.09E-01	9.72E-01	-	-
1378158_at	Brms1	breast cancer metastasis-suppressor 1	293668	Rn.2839	BF408114	2.79	3.03	2.80	2.87	2.92	2.84	1.00	down	9.96E-01	9.98E-01	-	-
1380570_at	---	---	---	---	AI145593	2.39	2.37	2.40	2.38	2.39	2.39	1.00	up	9.60E-01	9.89E-01	-	-
1393852_at	Vps37b	vacuolar protein sorting 37 homolog B (S. cerevisiae)	288659	Rn.144032	BE115334	4.93	4.11	4.50	4.47	4.92	4.15	1.00	up	9.99E-01	1.00E+00	-	-
1396498_at	---	---	---	Rn.57880	BF393477	2.22	2.22	2.22	2.22	2.22	2.22	1.00	down	8.88E-01	9.65E-01	-	-
1385201_at	Tmem182	transmembrane protein 182	501129	Rn.147922	BE098235	2.39	2.37	2.42	2.38	2.42	2.38	1.00	down	9.83E-01	9.95E-01	-	-
1391567_at	Notch1	Notch homolog 1, translocation-associated (Drosophila)	25496	Rn.25046	AI502150	2.32	2.31	2.32	2.31	2.33	2.30	1.00	down	9.60E-01	9.89E-01	-	-
1375770_at	---	---	---	Rn.153652	BF404963	2.36	2.35	2.36	2.35	2.38	2.34	1.00	up	9.70E-01	9.91E-01	-	-
1390016_at	---	---	---	Rn.200088	BF415854	2.41	2.40	2.42	2.41	2.42	2.40	1.00	down	9.63E-01	9.89E-01	-	-
1391034_at	---	---	---	---	BE110994	2.27	2.27	2.28	2.27	2.29	2.26	1.00	up	9.55E-01	9.87E-01	-	-
1387501_at	Sympo	synaptopodin	60324	Rn.42910	NM_021695	2.36	2.35	2.37	2.37	2.36	2.35	1.00	up	9.42E-01	9.83E-01	-	-
1371174_a_at	Satr2	somatostatin receptor 2	54305	Rn.9929	X98234	2.30	2.29	2.32	2.30	2.31	2.30	1.00	down	9.60E-01	9.89E-01	-	-
1392448_at	---	---	---	Rn.14542	AA955519	2.42	2.40	2.42	2.41	2.43	2.39	1.00	down	9.76E-01	9.93E-01	-	-
1369832_at	Adam3a	ADAM metallopeptidase domain 3A (cyritestin 1)	57021	Rn.42918	NM_020302	2.29	2.28	2.30	2.29	2.30	2.29	1.00	down	9.35E-01	9.82E-01	-	-
1375982_at	---	---	---	Rn.17340	BI296037	2.32	2.32	2.33	2.32	2.34	2.31	1.00	up	9.68E-01	9.91E-01	-	-
1378447_at	---	---	---	Rn.203272	AA849989	2.58	2.62	2.65	2.62	2.61	2.62	1.00	down	9.85E-01	9.96E-01	-	-
1368458_at	Cyp7a1	cytochrome P450, family 7, subfamily a, polypeptide 1	25428	Rn.10737	NM_012942	2.24	2.23	2.24	2.23	2.24	2.23	1.00	down	9.30E-01	9.81E-01	-	-
1391521_at	---	---	---	Rn.16889	AA858748	2.36	2.35	2.36	2.35	2.37	2.35	1.00	down	9.42E-01	9.84E-01	-	-
1382803_at	Map4k1	mitogen activated protein kinase kinase kinase kinase 1	292763	Rn.137063	AI237423	2.45	2.44	2.46	2.44	2.47	2.43	1.00	down	9.76E-01	9.93E-01	-	-
1397231_at	Sprn	Shadow of prion protein homolog (zebrafish)	541462	Rn.23342	AW530092	2.34	2.34	2.34	2.34	2.33	2.33	1.00	down	9.29E-01	9.80E-01	-	-
1380886_at	---	---	---	Rn.58553	AI145907	2.59	2.55	2.59	2.56	2.64	2.52	1.00	up	9.92E-01	9.97E-01	-	-
1377980_at	RGD1305725	similar to chromosome 20 open reading frame 102	362255	Rn.38631	AI549077	2.40	2.39	2.40	2.39	2.41	2.40	1.00	up	9.58E-01	9.89E-01	-	-
1379790_at	Dll4	delta-like 4 (Drosophila)	311332	Rn.147393	BI288729	2.52	2.51	2.52	2.52	2.52	2.51	1.00	down	8.38E-01	9.49E-01	-	-
1391760_at	---	---	---	Rn.16892	BI293190	2.31	2.31	2.32	2.31	2.32	2.31	1.00	down	9.40E-01	9.83E-01	-	-
1392721_at	---	---	---	Rn.147841	AI113185	2.36	2.35	2.37	2.35	2.36	2.36	1.00	down	9.48E-01	9.85E-01	-	-
1394970_at	Cars	cysteinyl-tRNA synthetase	293638	Rn.14865	BI279660	2.40	2.39	2.40	2.39	2.40	2.39	1.00	down	9.45E-01	9.84E-01	-	-
1387591_at	Il2ra	interleukin 2 receptor, alpha	25704	Rn.9872	NM_013163	2.39	2.39	2.40	2.39	2.39	2.39	1.00	down	9.08E-01	9.72E-01	-	-
1369807_at	Bdkrb1	bradykinin receptor B1	81509	Rn.10762	NM_030851	2.30	2.29	2.31	2.30	2.32	2.29	1.00	down	9.67E-01	9.90E-01	-	-
1397974_at	---	---	---	---	BE110207	2.28	2.27	2.29	2.28	2.29	2.28	1.00	up	9.47E-01	9.85E-01	-	-
1396370_at	---	---	---	Rn.171001	BF412463	2.43	2.43	2.44	2.43	2.46	2.41	1.00	up	9.81E-01	9.94E-01	-	-
1396867_at	Rln3	Relaxin 3	266997	Rn.45123	AW521175	2.41	2.41	2.43	2.41	2.43	2.40	1.00	up	9.72E-01	9.92E-01	-	-
1372065_at	Art3	ADP-ribosyltransferase 3	305235	Rn.4077	AI104393	2.28	2.27	2.29	2.27	2.29	2.27	1.00	down	9.68E-01	9.91E-01	-	-
1392740_at	Dbt	dihydrolipoamide branched chain transacylase E2	29611	Rn.198610	AI070435	2.34	2.34	2.34	2.34	2.35	2.34	1.00	up	9.11E-01	9.73E-01	-	-
1389872_at	Rnf123	ring finger protein 123	100190936	Rn.203837	AI008996	2.62	2.62	2.62	2.62	2.62	2.62	1.00	down	9.12E-01	9.74E-01	-	-
1377284_at	---	---	---	Rn.51197	BE112795	2.35	2.34	2.36	2.34	2.37	2.33	1.00	down	9.77E-01	9.93E-01	-	-
1393509_at	---	---	---	---	AI175807	2.87	2.38	2.39	2.81	2.45	2.37	1.00	down	9.99E-01	1.00E+00	-	-
1382709_at	Slamf6	SLAM family member 6	498287	Rn.145463	AI178618	2.23	2.22	2.23	2.23	2.23	2.22	1.00	down	9.04E-01	9.71E-01	-	-
1377355_at	RGD1306750	LOC362451	362451	Rn.209024	BI279326	2.68	2.65	2.68	2.67	2.68	2.66	1.00	up	9.76E-01	9.93E-01	-	-
1387633_at	Prg2	proteoglycan 2, bone marrow	58826	Rn.10674	NM_031619	2.38	2.37	2.39	2.38	2.41	2.36	1.00	up	9.81E-01	9.94E-01	-	-
1369716_s_at	Lgals5 /// Lgals9	lectin, galactose binding, soluble 5 /// lectin, galactoside-binding, soluble, 9	25475 /// 25476	Rn.64588	NM_012976	2.41	2.37	2.40	2.39	2.40	2.39	1.00	down	9.77E-01	9.93E-01	-	-
1385944_at	---	---	---	Rn.211828	AA875348	2.45	2.45	2.46	2.44	2.48	2.45	1.00	up	9.77E-01	9.93E-01	-	-
1394949_at	---	---	---	Rn.93326	BF399419	2.32	2.31	2.33	2.32	2.34	2.31	1.00	down	9.89E-01	9.91E-01	-	-
1396923_at	Ophn1	oligophrenin 1	312108	Rn.51010	BF400678	2.31	2.30	2.32	2.31	2.32	2.30	1.00	up	9.63E-01	9.89E-01	-	-
1379744_at	Saa4	serum amyloid A4, constitutive	365245	Rn.25066	AI137930	2.37	2.37	2.38	2.37	2.38	2.36	1.00	down	9.62E-01	9.89E-01	-	-
1372410_at	C1qtnf6	C1q and tumor necrosis factor related protein 6	315114	Rn.17708	AW251360	2.37	2.36	2.37	2.37	2.36	2.36	1.00	down	9.49E-01	9.85E-01	-	-
1387403_at	Rgs8	regulator of G-protein signaling 8	54297	Rn.89634	NM_019344	2.30	2.29	2.30	2.30	2.30	2.30	1.00	down	9.37E-01	9.82E-01	-	-
1380026_at	---	---	---	---	BF405898	2.30	2.30	2.31	2.30	2.31	2.30	1.00	down	9.32E-01	9.81E-01	-	-
1397301_at	---	---	---	Rn.43453	BM386743	2.37	2.36	2.38	2.36	2.39	2.35	1.00	up	9.77E-01	9.93E-01	-	-
1374166_at	---	---	---	Rn.140754	AW252076	2.38	2.37	2.39	2.38	2.39	2.37	1.00	down	9.71E-01	9.91E-01	-	-
1386316_at	---	---	---	---	AI639328	2.38	2.38	2.40	2.38	2.40	2.38	1.00	up	9.75E-01	9.92E-01	-	-
1380005_at	---	---	---	---	AI045312	2.34	2.34	2.35	2.34	2.35	2.34	1.00	up	9.45E-01	9.84E-01	-	-
1378794_at	---	---	---	Rn.209616	BF389754	2.31	2.29	2.32	2.30	2.32	2.29	1.00	up	9.75E-01	9.92E-01	-	-
1379852_at	Znf512b	Zinc finger protein 512B	311721	Rn.160649	AW527227	2.25	2.25	2.26	2.26	2.25	2.25	1.00	up	9.38E-01	9.82E-01	-	-
1373889_at	RGD1559482	similar to immunoglobulin superfamily, member 7	498022	---	BF387360	2.37	2.37	2.39	2.37	2.39	2.37	1.00	up	9.69E-01	9.91E-01	-	-
1398113_at	Synm	Synemin, intermediate filament protein	308709	Rn.46362	AW533329	2.19	2.19	2.19	2.18	2.19	2.19	1.00	down	8.51E-01	9.53E-01	-	-
1385032_at	---	---	---	Rn.171373	BE114028	2.43	2.43	2.44	2.43	2.44	2.43	1.00	down	9.31E-01	9.81E-01	-	-
1375840_at	---	---	---	Rn.173312	BF404611	2.34	2.32	2.34	2.33	2.35	2.32	1.00	down	9.78E-01	9.93E-01	-	-
1375735_at	---	---	---	Rn.41745	BF391294	2.35	2.35	2.36	2.35	2.36	2.35	1.00	down	9.46E-01	9.84E-01	-	-
1384761_at	---	---	---	Rn.165904	AI501676	2.64	2.64	2.64	2.64	2.65	2.64	1.00	down	9.13E-01	9.74E-01	-	-
1380925_at	---	---	---	Rn.207594	BF420093	2.39	2.37	2.40	2.40	2.39	2.37	1.00	up	9.79E-01	9.94E-01	-	-
1381861_x_at	Actc1	actin, alpha, cardiac muscle 1	29275	---	AI703739	2.38	2.37	2.40	2.37	2.42	2.35	1.00	down	9.88E-01	9.96E-01	-	-
1388826_at	Atxn2l	ataxin 2-like	361649	Rn.220440	BE349657	3.10	3.17	3.11	3.19	3.11	3.08	1.00	down	9.93E-01	9.98E-01	-	-
1375748_at	---	---	---	---	BE101954	2.23	2.22	2.23	2.22	2.24	2.23	1.00	up	9.81E-01	9.89E-01	-	-
1370701_at	Gabrq	gamma-aminobutyric acid (GABA) receptor, theta	65187	Rn.81067	AF419333	2.35	2.34	2.36	2.35	2.36	2.34	1.00	down	9.53E-01	9.86E-01	-	-
1384077_at	---	---	---	Rn.24128	BF282029	2.32	2.31	2.32	2.32	2.33	2.31	1.00	down	9.50E-01	9.85E-01	-	-
1387536_at	Scn5a	sodium channel, voltage-gated, type V, alpha subunit	25665	Rn.32074	NM_013125	2.58	2.58	2.58	2.58	2.58	2.58	1.00	down	9.00E-01	9.69E-01	-	-
1378878_at	RGD1306811	similar to hypothetical protein FLJ25530	300517	Rn.24384	AI145106	2.39	2.38	2.40	2.40	2.39	2.39	1.00	down	9.62E-01	9.89E-01	-	-
1380591_at	---	---	---	---	AW528430	2.34	2.33	2.35	2.33	2.36	2.32	1.00	up	9.78E-01	9.93E-01	-	-
1392904_at	Pwwp2a	PWWP domain containing 2A	303060	Rn.28786	BF544602	2.57	2.56	2.59	2.57	2.60	2.56	1.00	down	9.80E-01	9.94E-01	-	-
1377984_at	Itpkb	inositol 1,4,5-trisphosphate 3-kinase B	54260	Rn.22498	AI102896	2.37	2.37	2.38	2.37	2.38	2.37	1.00	up	9.50E-01	9.85E-01	-	-
1397748_at	Mrm1	Mitochondrial rRNA methyltransferase 1 homolog (S. cerevisiae)	363661	Rn.43486	AW521583	6.18	5.76	7.99	7.32	5.87	6.73	1.00	down	1.00E+00	1.00E+00	-	-
1387845_at	Kcng3	potassium voltage-gated channel, subfamily G, member 3	171011	Rn.82689	NM_133426	2.29	2.28	2.30	2.29	2.30	2.29	1.00	up	9.59E-01	9.89E-01	-	-
1393623_at	---	---	---	Rn.167930	AI502247	2.34	2.33	2.34	2.33	2.34	2.33	1.00	down	9.53E-01	9.86E-01	-	-
1376118_at	Otub2	OTU domain, ubiquitin aldehyde binding 2	314405	Rn.18862	BE109604	2.31	2.30	2.31	2.31	2.31	2.30	1.00	up	9.52E-01	9.86E-01	-	-
1378251_at	Treml1	triggering receptor expressed on myeloid cells-like 1	501096	Rn.198829	BF415104	2.36	2.36	2.37	2.36	2.36	2.36	1.00	up	9.37E-01	9.82E-01	-	-
1390680_at	---	---	---	Rn.2136	AI059409	2.38	2.38	2.39	2.38	2.39	2.38	1.00	down	9.07E-01	9.72E-01	-	-
1396212_at	---	---	---	Rn.162950	BE114358	2.45	2.43	2.47	2.43	2.51	2.41	1.00	up	9.93E-01	9.98E-01	-	-
1397433_at	---	---	---	Rn.171578	BF417146	2.36	2.35	2.36	2.35	2.36	2.35	1.00	down	9.61E-01	9.89E-01	-	-
1375588_at	Fgd6	FYVE, RhoGEF and PH domain containing 6	500824	Rn.162933	BF405893	2.27	2.27	2.28	2.27	2.28	2.27	1.00	up	9.40E-01	9.83E-01	-	-
1385591_at	---	---	---	Rn.160274	BI300437	2.53	2.51	2.56	2.52	2.60	2.48	1.00	down	9.94E-01	9.98E-01	-	-
1384057_at	Ankrd6	ankyrin repeat domain 6	500430	Rn.45844	BF390984	2.41	2.40	2.41	2.41	2.42	2.40	1.00	down	9.71E-01	9.92E-01	-	-
1368408_at	Grk5	G protein-coupled receptor kinase 5	59075	Rn.6500	NM_030829	2.42	2.37	2.41	2.39	2.43	2.38	1.00	up	9.89E-01	9.96E-01	-	-
1395718_at	---	---	---	Rn.160126	BE102746	2.24	2.24	2.25	2.24	2.25	2.24	1.00	up	9.32E-01	9.81E-01	-	-
1396011_at	---	---	---	---	BF392919	2.27	2.26	2.27	2.26	2.28	2.26	1.00	up	9.75E-01	9.92E-01	-	-
1379123_at	Sez6l2	seizure related 6 homolog (mouse)-like 2	308988	Rn.30285	BF388562	2.28	2.29	2.30	2.29	2.29	2.28	1.00	up	9.65E-01	9.90E-01	-	-
1390886_at	Ccdc39	Coiled-coil domain containing 39	310315	Rn.219691	BE111565	2.52	2.50	2.53	2.52	2.53	2.50	1.00	down	9.80E-01	9.94E-01	-	-
1387767_a_at	Col2a1	collagen, type II, alpha 1	25412	Rn.10124	AF305418	2.42	2.41	2.44	2.42	2.44	2.41	1.00	down	9.81E-01	9.94E-01	-	-
1378561_at	---	---	---	Rn.47770	BE106215	2.43	2.41	2.44	2.41	2.46	2.41	1.00	down	9.87E-01	9.96E-01	-	-
1391275_at	---	---	---	Rn.38652	AI575658	2.43	2.41	2.43	2.44	2.43	2.40	1.00	up	9.84E-01	9.95E-01	-	-
1387442_at	Egr4	early growth response 4	25129	Rn.31998	NM_019137	2.44	2.42	2.46	2.44	2.44	2.44	1.00	up	9.82E-01	9.95E-01	-	-
1395307_at	Anks1b	ankyrin repeat and sterile alpha motif domain containing 1B	314721	---	AI409823	2.34	2.33	2.34	2.34	2.35	2.32	1.00	up	9.76E-01	9.93E-01	-	-
1395478_at	Eef1a2	eukaryotic translation elongation factor 1 alpha 2	24799	Rn.9764	BF411920	2.25	2.25	2.25	2.25	2.25	2.25	1.00	down	9.11E-01	9.73E-01	-	-
1394785_at	---	---	---	Rn.147969	BE329290	3.08	2.60	3.23	2.58	3.40	2.94	1.00	down	9.99E-01	1.00E+00	-	-
1395168_at	---	---	---	---	AI045103	2.45	2.44	2.45	2.43	2.47	2.43	1.00	down	9.82E-01	9.94E-01	-	-
1391939_at	---	---	---	Rn.137157	BI294978	2.71	2.68	2.63	2.63	2.62	2.77	1.00	up	9.96E-01	9.98E-01	-	-
1369850_at	Ugt2a1	UDP glucuronosyltransferase 2 family, polypeptide A1	63867	Rn.138121	NM_022228	2.33	2.32	2.33	2.32	2.33	2.32	1.00	down	9.60E-01	9.89E-01	-	-
1390740_at	---	---	---	---	BF401709	2.38	2.37	2.39	2.37	2.40	2.36	1.00	up	9.79E-01	9.94E-01	-	-
1385086_at	Bub1	budding uninhibited by benzimidazoles 1 homolog (S. cerevisiae)	296137	Rn.56816	BF388785	2.41	2.40	2.42	2.41	2.44	2.39	1.00	up	9.85E-01	9.95E-01	-	-
1396668_at	---	---	---	Rn.173532	BF410178	2.44	2.42	2.45	2.43	2.47	2.41	1.00	up	9.87E-01	9.96E-01	-	-
1398492_at	---	---	---	Rn.62726	BF395819	2.36	2.36	2.37	2.36	2.37	2.35	1.00	down	9.69E-01	9.91E-01	-	-
1398333_at	---	---	---	Rn.163791	AI598434	8.48	9.21	8.97	8.95	9.31	8.41	1.00	up	9.99E-01	1.00E+00	-	-
1379749_at	---	---	---	---	AI230509	2.50	2.51	2.52	2.50	2.52	2.50	1.00	down	9.76E-01	9.93E-01	-	-
1391789_at	Txnl1	thioredoxin-like 1	140922	Rn.40430	BF555110	2.85	2.85	2.92	2.89	2.91	2.82	1.00	up	9.94E-01	9.98E-01	-	-
1369839_at	Amph	amphiphysin	60668	Rn.44463	AI502247	2.58	2.58	2.60	2.59	2.59	2.58	1.00	down	9.80E-01	9.89E-01	-	-
1397103_at	---	---	---	Rn.171621	BF393095	2.43	2.42	2.46	2.45	2.45	2.41	1.00	up	9.88E-01	9.96E-01	-	-
1394718_at	---	---	---	Rn.202804	BF396080	2.44	2.44	2.44	2.44	2.44	2.44	1.00	up	9.33E-01	9.81E-01	-	-
1390663_at	---	---	---	Rn.212191	BG373109	2.31	2.29	2.31	2.30	2.31	2.30	1.00	down	9.73E-01	9.92E-01	-	-
1393754_at	Tbc1d1	TBC1 domain family, member 1	360937	Rn.24535	BM383480	2.41	2.41	2.42	2.42	2.42	2.39	1.00	down	9.78E-01	9.93E-01	-	-
1381546_at	---	---	---	---	BI290770	2.30	2.28	2.30	2.29	2.31	2.28	1.00	down	9.80E-01	9.94E-01	-	-
1387897_at	Cnp	2',3'-cyclic nucleotide 3' phosphodiesterase	25275	Rn.31762	L16532	2.28	2.28	2.29	2.28	2.29	2.28	1.00	up	9.35E-01	9.82E-01	-	-
1390560_at	Hel308	DNA helicase HEL308	360912	Rn.104354	AW434242	2.33	2.32	2.33	2.32	2.33	2.32	1.00	up	9.61E-01	9.89E-01	-	-
1380832_at	---	---	---	Rn.155195	BF403913	2.44	2.41	2.44	2.43	2.44	2.42	1.00	down	9.85E-01	9.96E-01	-

ProbeSetID	Gene Symbol	Gene Title	Gene ID	UniGene ID	Public ID	GCRMA Intensities (log2)						Unpaired t-test Csa vs Ctrl (triplicates)					
						SEP3 (Ctrl)	SEP4 (Ctrl)	S6 (Ctrl)	SEP7 (Csa)	SEP8 (Csa)	SEP9 (Csa)	FCAbsolute	Regulation	p-value	adj-pval	REG	MTC
1369333_a_at	Rims2	regulating synaptic membrane exocytosis 2	116839	Rn.161948	NM_053945	2.75	2.76	2.82	2.77	2.82	2.74	1.00	down	9.95E-01	9.98E-01	-	-
1397772_at	---	---	---	Rn.17067	BF390195	2.38	2.38	2.39	2.39	2.39	2.38	1.00	down	9.65E-01	9.90E-01	-	-
1382243_at	---	---	---	Rn.21747	BE120628	2.34	2.33	2.35	2.34	2.34	2.33	1.00	up	9.72E-01	9.92E-01	-	-
1397459_at	---	---	---	Rn.171633	BE119278	2.48	2.48	2.49	2.48	2.49	2.48	1.00	down	9.69E-01	9.91E-01	-	-
1398030_at	---	---	---	Rn.171212	BE109892	2.56	2.59	2.57	2.57	2.60	2.55	1.00	down	9.90E-01	9.97E-01	-	-
1394340_at	Inpp1	inositol polyphosphate-1-phosphatase	316376	Rn.20288	BF523172	2.45	2.44	2.45	2.44	2.46	2.45	1.00	up	9.72E-01	9.92E-01	-	-
1390540_at	---	---	---	Rn.50326	BF400717	2.24	2.23	2.25	2.24	2.25	2.23	1.00	up	9.76E-01	9.93E-01	-	-
1392290_at	---	---	---	Rn.147671	BE095472	2.36	2.35	2.37	2.35	2.37	2.36	1.00	up	9.76E-01	9.93E-01	-	-
1387552_at	Dlgap2	discs, large (Drosophila) homolog-associated protein 2	116681	Rn.10705	NM_053901	2.35	2.33	2.37	2.35	2.36	2.34	1.00	up	9.87E-01	9.96E-01	-	-
1396955_at	---	---	---	Rn.146888	BF405025	2.37	2.36	2.38	2.37	2.38	2.36	1.00	up	9.70E-01	9.91E-01	-	-
1368484_at	Abcb9	ATP-binding cassette, sub-family B (MDR/TAP), member 9	63886	Rn.44870	NM_022238	2.42	2.40	2.43	2.42	2.44	2.40	1.00	up	9.90E-01	9.97E-01	-	-
1375980_at	Nxn	nucleoredoxin	360577	Rn.105982	BI285437	2.49	2.49	2.50	2.39	2.50	2.60	1.00	down	9.97E-01	9.99E-01	-	-
1397347_at	---	---	---	Rn.173150	BF394194	2.27	2.27	2.27	2.27	2.28	2.27	1.00	down	9.62E-01	9.89E-01	-	-
1386716_at	---	---	---	Rn.17067	BF562934	2.41	2.40	2.43	2.40	2.43	2.40	1.00	down	9.88E-01	9.96E-01	-	-
1387608_at	Ido1	indoleamine 2,3-dioxygenase 1	66029	Rn.64513	NM_023973	2.26	2.26	2.27	2.26	2.27	2.25	1.00	down	9.76E-01	9.93E-01	-	-
1370475_at	Cyp2b3	cytochrome P450IIB3	286953	Rn.4845	M20406	2.40	2.39	2.41	2.40	2.40	2.40	1.00	down	9.67E-01	9.90E-01	-	-
1381718_at	---	---	---	---	BE109530	2.16	2.16	2.16	2.16	2.17	2.15	1.00	down	9.61E-01	9.89E-01	-	-
1379142_at	---	---	---	Rn.173148	BF393107	2.34	2.33	2.35	2.34	2.35	2.32	1.00	down	9.85E-01	9.96E-01	-	-
1370741_at	Olr1696	olfactory receptor 1696	294158	Rn.222102	AF034896	2.27	2.26	2.27	2.27	2.27	2.26	1.00	down	9.73E-01	9.92E-01	-	-
1398181_at	---	---	---	Rn.58166	BF394267	2.28	2.27	2.28	2.27	2.29	2.27	1.00	up	9.76E-01	9.93E-01	-	-
1381622_at	---	---	---	Rn.161742	BF416192	2.56	2.55	2.58	2.55	2.59	2.54	1.00	up	9.90E-01	9.97E-01	-	-
1380913_at	---	---	---	---	BG374053	2.47	2.46	2.48	2.47	2.49	2.46	1.00	down	9.87E-01	9.96E-01	-	-
1371001_at	---	---	---	Rn.105613	AI237038	2.29	2.28	2.30	2.30	2.29	2.28	1.00	down	9.73E-01	9.92E-01	-	-
1383329_at	Pdcd4	programmed cell death 4	64031	Rn.206228	BI303892	2.29	2.28	2.29	2.29	2.29	2.28	1.00	down	9.57E-01	9.88E-01	-	-
1373567_at	RGD1561530	similar to Tle6 protein	299637	Rn.71420	BF418590	2.36	2.35	2.38	2.38	2.36	2.34	1.00	up	9.91E-01	9.97E-01	-	-
1394525_at	---	---	---	---	BM385125	2.63	2.57	2.73	2.59	2.79	2.56	1.00	up	9.98E-01	9.99E-01	-	-
1387428_at	Cacnb1	calcium channel, voltage-dependent, beta 1 subunit	50688	Rn.9417	NM_017346	2.34	2.33	2.34	2.34	2.34	2.33	1.00	up	9.68E-01	9.91E-01	-	-
1379414_at	LOC679949	similar to CG4502-PA, isoform A	679949	Rn.222110	AA997596	2.23	2.23	2.24	2.23	2.24	2.22	1.00	down	9.75E-01	9.92E-01	-	-
1385275_at	Wnt16	wingless-type MMTV integration site family, member 16	500047	Rn.209854	BF391286	2.39	2.37	2.39	2.38	2.39	2.38	1.00	up	9.76E-01	9.93E-01	-	-
1377247_at	---	---	---	Rn.176528	BI296714	2.48	2.45	2.49	2.47	2.48	2.47	1.00	down	9.89E-01	9.96E-01	-	-
1381382_at	Atp6ap1l	ATPase, H+ transporting, lysosomal accessory protein 1-like	361875	Rn.73792	AW433978	2.25	2.24	2.25	2.24	2.26	2.23	1.00	up	9.85E-01	9.96E-01	-	-
1385631_at	---	---	---	Rn.133452	AA925529	2.49	2.46	2.51	2.48	2.54	2.44	1.00	down	9.96E-01	9.98E-01	-	-
1372374_at	Car1	carbonic anhydrase 1	310218	Rn.6854	BM383006	2.31	2.29	2.32	2.30	2.33	2.29	1.00	up	9.91E-01	9.97E-01	-	-
1394592_at	---	---	---	Rn.172046	BF287078	2.39	2.38	2.40	2.38	2.42	2.37	1.00	up	9.91E-01	9.97E-01	-	-
1398008_at	Zfhx2	zinc finger homeobox 2	305888	Rn.161359	BE120093	2.38	2.37	2.38	2.39	2.38	2.35	1.00	up	9.90E-01	9.97E-01	-	-
1375124_at	Pan3	PAN3 polyA specific ribonuclease subunit homolog (S. cerevisiae)	360760	Rn.163191	AW533917	2.31	2.30	2.32	2.31	2.33	2.30	1.00	down	9.87E-01	9.96E-01	-	-
1369803_at	Pitx	pancreas specific transcription factor, 1a	117034	Rn.10536	NM_053984	2.57	2.55	2.62	2.61	2.57	2.56	1.00	up	9.95E-01	9.98E-01	-	-
1389086_at	---	---	---	Rn.19527	BF408444	2.29	2.28	2.30	2.29	2.30	2.29	1.00	up	9.77E-01	9.93E-01	-	-
1394897_at	Dos	downstream of Stk11	314622	Rn.91597	AW528942	2.36	2.35	2.37	2.35	2.37	2.35	1.00	down	9.86E-01	9.96E-01	-	-
1373513_at	---	---	---	Rn.163737	AI012419	2.38	2.36	2.39	2.37	2.38	2.37	1.00	down	9.84E-01	9.95E-01	-	-
1387573_a_at	Nr5a2	nuclear receptor subfamily 5, group A, member 2	60349	Rn.42941	NM_021742	2.38	2.37	2.39	2.37	2.39	2.37	1.00	up	9.88E-01	9.96E-01	-	-
1394270_at	Mks1	Meckel syndrome, type 1	287612	Rn.198890	AW920330	2.31	2.31	2.32	2.31	2.32	2.31	1.00	down	9.76E-01	9.93E-01	-	-
1377443_at	---	---	---	Rn.173133	BF401187	2.41	2.36	2.41	2.43	2.42	2.32	1.00	down	9.97E-01	9.99E-01	-	-
1394924_at	Mpp7	membrane protein, palmitoylated 7 (MAGUK p55 subfamily member 7)	307035	Rn.34512	AW530852	2.34	2.34	2.36	2.34	2.36	2.33	1.00	up	9.89E-01	9.96E-01	-	-
1378336_at	---	---	---	---	AI144907	2.33	2.33	2.34	2.33	2.34	2.33	1.00	down	9.54E-01	9.88E-01	-	-
1391752_at	---	---	---	Rn.62732	BF394182	2.50	2.46	2.49	2.48	2.52	2.46	1.00	down	9.94E-01	9.98E-01	-	-
1378151_at	---	---	---	Rn.81217	BE114019	2.47	2.44	2.50	2.46	2.51	2.44	1.00	down	9.96E-01	9.98E-01	-	-
1393472_at	---	---	---	Rn.147796	AI072025	2.51	2.51	2.52	2.50	2.53	2.50	1.00	down	9.87E-01	9.96E-01	-	-
1392335_at	---	---	---	Rn.211376	BF404176	2.25	2.24	2.25	2.25	2.25	2.24	1.00	down	9.76E-01	9.93E-01	-	-
1383522_at	Utx	ubiquitously transcribed tetratricopeptide repeat, X chromosome	317178	Rn.105636	AI045086	2.43	2.42	2.43	2.42	2.43	2.43	1.00	up	9.51E-01	9.86E-01	-	-
1388670_at	Kif1a	Kinesin family member 1A	363288	Rn.1723	BI286880	2.35	2.35	2.36	2.35	2.36	2.35	1.00	up	9.82E-01	9.95E-01	-	-
1397394_at	---	---	---	Rn.204656	BF412275	2.49	2.48	2.50	2.49	2.50	2.48	1.00	up	9.85E-01	9.96E-01	-	-
1378424_at	Trim46	tripartite motif-containing 46	310641	Rn.34764	BI288748	2.18	2.18	2.19	2.18	2.19	2.18	1.00	up	9.65E-01	9.90E-01	-	-
1368351_at	Scn10a	sodium channel, voltage-gated, type X, alpha subunit	29571	Rn.10246	NM_017247	2.33	2.32	2.34	2.33	2.34	2.33	1.00	down	9.82E-01	9.94E-01	-	-
1392110_at	---	---	---	Rn.136399	AA818585	2.42	2.41	2.43	2.42	2.44	2.40	1.00	down	9.91E-01	9.97E-01	-	-
1375139_at	---	---	---	Rn.208682	BF406295	2.38	2.37	2.39	2.39	2.39	2.36	1.00	down	9.91E-01	9.97E-01	-	-
1377566_at	---	---	---	Rn.50211	BE102845	2.28	2.27	2.28	2.27	2.28	2.27	1.00	up	9.71E-01	9.92E-01	-	-
1368802_at	---	---	---	Rn.37400	NM_016989	2.27	2.26	2.27	2.26	2.27	2.26	1.00	up	9.74E-01	9.92E-01	-	-
1391002_at	---	---	---	Rn.1842	AA801280	2.26	2.26	2.27	2.26	2.27	2.25	1.00	down	9.86E-01	9.96E-01	-	-
1390899_at	LRRTM1	leucine rich repeat transmembrane neuronal 1	679668	Rn.171424	BE115269	2.33	2.31	2.34	2.32	2.33	2.32	1.00	down	9.87E-01	9.96E-01	-	-
1386535_at	Ddx3x	DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, X-linked	317335	Rn.95841	BG667163	8.39	8.48	8.70	8.35	8.52	8.70	1.00	down	9.99E-01	1.00E+00	-	-
1369058_a_at	Hap1	huntingtin-associated protein 1	29430	Rn.37430	AI412750	2.21	2.21	2.22	2.21	2.22	2.21	1.00	down	9.67E-01	9.90E-01	-	-
1377159_at	Tsc22d4	TSC22 domain family, member 4	684980	Rn.21359	BE120729	2.38	2.36	2.39	2.38	2.39	2.36	1.00	down	9.93E-01	9.98E-01	-	-
1388450_at	---	---	---	---	BI279570	8.22	8.26	8.33	8.13	8.31	8.37	1.00	up	9.99E-01	1.00E+00	-	-
1383575_at	Ctnnd2	catenin (cadherin-associated protein), delta 2 (neural plakophilin-related arm-	114028	Rn.15163	BG376561	2.26	2.25	2.26	2.26	2.27	2.25	1.00	up	9.82E-01	9.95E-01	-	-
1369736_at	Emp1	epithelial membrane protein 1	25314	Rn.19723	NM_012843	2.39	2.38	2.39	2.38	2.40	2.37	1.00	down	9.90E-01	9.97E-01	-	-
1381714_at	---	---	---	Rn.170953	BE105488	2.45	2.44	2.49	2.44	2.50	2.43	1.00	up	9.97E-01	9.98E-01	-	-
1394505_at	---	---	---	---	AI228568	2.33	2.33	2.34	2.33	2.35	2.31	1.00	up	9.93E-01	9.98E-01	-	-
1395649_at	Lhfpl4	lipoma HMGIC fusion partner-like 4	353230	Rn.145133	BF542654	2.29	2.28	2.29	2.28	2.29	2.28	1.00	up	9.74E-01	9.92E-01	-	-
1392131_at	---	---	---	---	AI012870	2.44	2.45	2.47	2.45	2.46	2.45	1.00	up	9.90E-01	9.97E-01	-	-
1373751_at	---	---	---	Rn.20626	BF396319	2.27	2.26	2.27	2.27	2.27	2.26	1.00	down	9.79E-01	9.94E-01	-	-
1391955_at	Rab19	RAB19, member RAS oncogene family	500088	Rn.53184	BI291339	2.36	2.35	2.37	2.36	2.37	2.36	1.00	up	9.87E-01	9.96E-01	-	-
1378532_at	---	---	---	Rn.205367	AI407172	2.45	2.45	2.46	2.45	2.46	2.45	1.00	up	9.87E-01	9.96E-01	-	-
1397785_at	---	---	---	Rn.50191	BE102056	2.32	2.31	2.32	2.32	2.32	2.31	1.00	up	9.80E-01	9.94E-01	-	-
1398889_at	RGD1311117	similar to KIAA1409 protein	314401	Rn.43444	BE113846	2.30	2.29	2.31	2.30	2.31	2.28	1.00	up	9.92E-01	9.97E-01	-	-
1370926_at	Muc4	mucin 4, cell surface associated	303887	Rn.24930	BM391100	2.39	2.38	2.40	2.40	2.39	2.37	1.00	up	9.93E-01	9.98E-01	-	-
1390956_at	Apol11a	apolipoprotein L 11a	300060	Rn.35355	BI294909	2.35	2.34	2.36	2.35	2.35	2.34	1.00	down	9.84E-01	9.95E-01	-	-
1393624_at	---	---	---	Rn.164893	AA925062	2.29	2.28	2.29	2.28	2.29	2.29	1.00	down	9.85E-01	9.96E-01	-	-
1395971_at	---	---	---	Rn.177344	BI291276	2.45	2.45	2.44	2.45	2.46	2.44	1.00	up	9.91E-01	9.97E-01	-	-
1388461_at	Shd	src homology 2 domain-containing transforming protein D	316507	Rn.222032	BG380732	2.33	2.32	2.34	2.33	2.33	2.32	1.00	up	9.86E-01	9.96E-01	-	-
1381587_at	---	---	---	Rn.49928	AI231910	2.26	2.25	2.26	2.25	2.26	2.25	1.00	down	9.88E-01	9.96E-01	-	-
1379892_at	Cd22	CD22 molecule	308501	Rn.25921	AI408289	2.21	2.20	2.21	2.21	2.20	2.20	1.00	up	9.85E-01	9.96E-01	-	-
1378786_at	---	---	---	Rn.24326	AI228437	2.35	2.35	2.36	2.35	2.36	2.35	1.00	up	9.89E-01	9.97E-01	-	-
1376848_at	---	---	---	Rn.199361	AI137988	9.32	9.27	9.76	9.47	9.45	9.44	1.00	down	1.00E+00	1.00E+00	-	-
1382359_at	---	---	---	Rn.166084	AI045029	2.47	2.46	2.49	2.46	2.50	2.45	1.00	down	9.96E-01	9.98E-01	-	-
1389467_at	Tmem100	transmembrane protein 100	497979	Rn.18850	BM391248	2.43	2.41	2.43	2.42	2.45	2.41	1.00	down	9.95E-01	9.98E-01	-	-
1377115_at	---	---	---	---	AW254275	2.32	2.31	2.32	2.32	2.32	2.32	1.00	up	9.78E-01	9.93E-01	-	-
1377215_at	---	---	---	---	BF403845	2.38	2.36	2.37	2.36	2.39	2.36	1.00	up	9.94E-01	9.98E-01	-	-
1398153_at	---	---	---	Rn.210713	BF400866	2.34	2.32	2.33	2.33	2.35	2.31	1.00	down	9.95E-01	9.98E-01	-	-
1382415_at	LOC360807	LOC360807	360807	Rn.79033	BI289373	3.10	2.80	2.80	2.86	2.88	2.96	1.00	down	9.99E-01	1.00E+00	-	-
1390824_at	RGD1304963	Similar to hypothetical protein MGC38716	313891	Rn.39102	BG374233	2.24	2.23	2.24	2.24	2.25	2.23	1.00	down	9.89E-01	9.96E-01	-	-
1391177_at	Txlna	taxilin alpha	682457	Rn.217158	BE119696	2.25	2.25	2.26	2.26	2.25	2.24	1.00	down	9.87E-01	9.96E-01	-	-
1378253_at	---	---	---	Rn.204972	AI555294	2.74	2.73	2.76	2.76	2.75	2.72	1.00	up	9.96E-01	9.98E-01	-	-
1384683_at	---	---	---	Rn.147192	AW524562	2.31	2.29	2.32	2.29	2.35	2.28	1.00	up	9.97E-01	9.99E-01	-	-
1368161_a_at	Ahsg	alpha-2-HS-glycoprotein	25373	Rn.32083	NM_012898	2.51	2.50	2.52	2.50	2.52	2.50	1.00	down	9.94E-01	9.98E-01	-	-
1389675_at	Ier5l	immediate early response 5-like	499772	Rn.162656	AW532282	2.32	2.31	2.33	2.32	2.33	2.32	1.00	up	9.90E-01	9.97E-01	-	-
1388054_a_at	Vcan	versican	114122	Rn.35666	AF072892	2.38	2.36	2.39	2.37	2.40	2.36	1.00	up	9.96E-01	9.98E-01	-	-
1381380_at	---	---	---	Rn.56351	BG376534	2.28	2.27	2.28	2.27	2.28	2.27	1.00	up	9.88E-01	9.96E-01	-	-
1371194_at	Tnfaip6	tumor necrosis factor alpha induced protein 6	84397	Rn.195358	AF195103	2.44	2.42	2.45	2.43	2.45	2.43	1.00	down	9.94E-01	9.98E-01	-	-
1384566_at	---	---	---	Rn.12632	AF127038	2.44	2.42	2.46	2.44	2.45	2.43	1.00	down	9.96E-01	9.98E-01	-	-
1390763_at	---	---	---	Rn.15175	BF555727	2.44	2.43	2.44	2.43	2.44	2.44	1.00	up	9.88E-01	9.96E-01	-	-
1368617_at	Serpina5	serine (or cysteine) peptidase inhibitor, clade A, member 5	65051	Rn.30006	NM_022957	2.37	2.36	2.39	2.37	2.40	2.36	1.00	up	9.96E-01	9.98E-01	-	-
1395429_at	Chrna7	Cholinergic receptor, nicotinic, alpha 7	25302	Rn.9698	BF281401	2.37	2.36	2.37	2.36	2.37	2.36	1.00	up	9.93E-01	9.98E-01	-	-
1390904_at	Ryr1	ryanodine receptor 1, skeletal muscle	114207	Rn.198152	AW530219	2.31	2.30	2.32	2.31	2.32	2.31	1.00	down	9.94E-01	9.98E-01	-	-
1368830_at	Src	v-src sarcoma (Schmidt-Ruppin A-2) viral oncogene homolog (avian)	83805	Rn.112600	AI175986	2.23	2.22	2.23	2.22	2.23	2.23	1.00	up	9.84E-01	9.95E-01	-	-
1378926_at	Znf710	Zinc finger protein 710	293044	Rn.124431	BF387639	2.21	2.20	2.21	2.21	2.21	2.21	1.00	up	9.84E-01	9.95E-01	-	-
1374898_at	RGD1311422	similar to CG8841-PA	287822	Rn.113761	AW527473	2.42	2.43	2.42	2.43	2.42	2.41	1.00	down	9.94E-01	9.98E-01	-	-
1368560_at	Kcnj5	potassium inwardly-rectifying channel, subfamily J, member 5	29713	Rn.10047	D50135	2.34	2.34	2.35	2.34	2.35	2.34	1.00	up	9.89E-01	9.97E-01	-	-
1397472_at	---	---	---	Rn.167815	AI454728	2.39	2.38	2.39	2.38	2.39	2.39	1.00	down	9.90E-01	9.97E-01	-	-
1398231_at	---	---	---	Rn.129584	BE107399	2.31	2.31	2.32	2.32	2.32	2.31	1.00	down	9.91E-01	9.97E-01	-	-
1375505_at	Tnfaip2	Tumor necrosis factor, alpha-induced protein 2	299339	Rn.34387	BF414914	2.28	2.28	2.28	2.28	2.28	2.28	1.00	down	9.85E-01	9.96E-01	-	-
1393031_at	Abo2	histo-blood group ABO system transferase 2	100301568	---	BI287075	2.40	2.41	2.40	2.39	2.40	2.41	1.00	up	9.93E-01	9.98E-01	-	-
1368621_at	Aqp9	aquaporin 9	65054	Rn.30018	NM_022960	2.29	2.28	2.29	2.29	2.30	2.28	1.00	up	9.92E-01	9.97E-01	-	-
1381571_at	---	---	---	Rn.98687	BE108395	2.17	2.17	2.17	2.17	2.17	2.17	1.00	up	9.87E-01	9.96E-01	-	-
1379552_s_at	Rap2ip	Rap2 interacting protein	303569	Rn.102473	AI535169	2.38	2.37	2.38	2.38	2.39	2.37	1.00	up	9.92E-01	9.97E-01	-	-
1372957_at	---	---	---	Rn.204562	BE101323	2.23	2.22	2.23	2.22	2.25	2.22	1.00	down	9.96E-01	9.98E-01	-	-
1390683_at	---	---	---	Rn.170971	BF418127	2.41	2.40	2.41	2.40	2.41	2.40	1.00	down	9.93E-01	9.98E-01	-	-
1377544_at	Gpr68	G protein-coupled receptor 68	314386	Rn.16653	BF416118	2.31	2.31	2.32	2.31	2.31	2.31	1.00	up	9.89E-01	9.96E-01	-	-
1367458_at	Lypla2	lysophospholipase 2	83510	Rn.8586	NM_031342	2.27	2.26	2.27	2.26	2.27	2.26	1.00	down	9.95E-01	9.98E-01	-	-
1369139_at	Pdc	phosducin	25343	Rn.9739	M33530	2.54	2.52	2.55	2.54	2.56	2.51	1.00	down	9.98E-01	9.99E-01	-	-
1387474_at	Tacr1	tachykinin receptor 1	24807	Rn.89609	J05097	2.25	2.23	2.26	2.24	2.25	2.24	1.00	down	9.96E-01	9.98E-01	-	-
1391173_at	---	---	---	Rn.147729	BF389308	9.47	9.33	9.58	9.10	9.61	9.67	1.00	up	1.00E+00	1.00E+00	-	-
1384221_at	Zfp469	zinc finger protein 469	304302	Rn.20495	AF409196	2.33	2.32	2.34	2.33	2.34	2.32	1.00	down	9.95E-01	9.98E-01	-	-
1395647_at	Tufm	Tu translation elongation factor, mitochondrial	293481	Rn.48850	AA684690	2.33	2.32	2.34	2.32	2.34	2.32	1.00	down	9.97E-01	9.99E-01	-	-
1369572_at	Mcpt1	mast cell protease 1	29265	Rn.202971	NM_017145	2.35	2.32	2.39	2.34	2.40	2.32	1.00	up	9.99E-01	1.00E+00	-	-
1375832_at	---	---	---	---	BF399764	2.13	2.13	2.13	2.13	2.13	2.13	1.00	up	9.89E-01	9.96E-01	-	-
1375157_at	Mll6	Myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila);	303504	Rn.25100	AA943117	2.28	2.28	2.29	2.29	2.29	2.27	1.00	down	9.96E-01	9.98E-01	-	-
1380985_at	---	---	---	Rn.151556	BG373668	2.35	2.35	2.35	2.35	2.36	2.34	1.00	up	9.96E-01	9.98E-01	-	-
1386861_at	Pthlh	parathyroid hormone-like hormone	24695	Rn.9750	NM_012636	2.43	2.43	2.44	2.45	2.44	2.41	1.00	down	9.98E-01	9.99E-01	-	-
1392376_at	---	---	---	---	BF405182	2.33	2.33	2.35	2.33	2.35	2.33	1.00	up	9.98E-01	9.99E-01	-	-
1385710_at	Tnfrsf17	tumor necrosis factor receptor superfamily, member 17	287034	Rn.17380	BF559673	2.23	2.25	2.24	2.23	2.27	2.22	1.00	up	9.99E-01	1.00E+00	-	-
1386100_at	---	---	---	Rn.209058	BF288469	2.38	2.37	2.39	2.37	2.41	2.36	1.00	down	9.98E-01	1.00E+00	-	-
1369837_at	Gulo	gulonolactone (L-) oxidase	60671	Rn.115212	NM_022220	2.33	2.32	2.34	2.33	2.34	2.32	1.00	up	9.97E-01	9.98E-01	-	-
1381480_at	Sarm1	sterile alpha and TIR motif containing 1	287545	Rn.67850	BE096539	2.20	2.20	2.21	2.20	2.21	2.20	1.00	up	9.95E-01	9.98E-01	-	-
1381740_at	---	---	---	---	BF409784	2.22	2.21	2.22	2.21	2.22	2.21	1.00	down	9.96E-01	9.98E-01	-	-
1390060_at	---	---	---	Rn.209853	BF404459	2.37	2.35	2.37	2.36	2.37	2.36	1.00	down	9.97E-01	9.99E-01	-	-
1384924_at	Pmd	prion protein 2 (dublet)	113910	Rn.94278	BF551984	2.38	2.38	2.38	2.37	2.40	2.36	1.00	down	9.98E-01	9.99E-01	-	-
1393903_at	---	---	---	Rn.216794	AW526742	2.41	2.39	2.42	2.40	2.42	2.40	1.00	up	9.99E-01	1.00E+00	-	-
1387245_at	Lipf	lipase, gastric	50682	Rn.11192	NM_017341	2.28	2.27	2.28	2.27	2.29	2.27	1.00	up	9.98E-01	9.99E-01	-	-
1397049_at	---	---	---	Rn.154363	BF403412	2.28	2.27	2.28	2.27	2.28	2.27	1.00	up	9.97E-01	9.99E-01	-	-
1395755_at	---	---	---	Rn.159965	BI294237	2.42	2.40	2.41	2.42	2.41	2.40	1.00	down	9.99E-01	1.00E+00	-	-
1371407_at	Nckap1	NCK-associated protein 1	58823	Rn.2611	AI178285	8.31	8.47	8.15	8.27	8.14	8.52	1.00	down	1.00E+00	1.00E+00	-	-
1390858_at	Vcpip1	valosin containing protein (p97)/p47 complex interacting protein 1	286761	Rn.204326	BM383657	7.79	6.86	7.13	6.96	7.45	7.36	1.00	down	1.00E+00	1.00E+00	-	-
1368510_at	Gata1	GATA binding protein 1	25172	Rn.10024	NM_012764	2.31	2.30	2.32	2.31	2.32	2.30	1.00	down	1.00E+00	1.00E+00	-	-
1397384_at	---	---	---	Rn.82598	BM391073	2.34	2.33	2.35	2.34	2.36	2.33	1.00	up	1.00E+00	1.00E+00	-	-
1384780_at	Cpne4	copine IV	367160	Rn.57966	BF402747	2.40	2.38	2.42	2.39	2.41	2.39	1.00	up	1.00E+00	1.00E+00

ENRICHED PATHWAYS

KEGG Pathway	#Genes	Coeff	Odd ratio	P-Value	FDR	Enriched	Genes	Gene symbols
Ribosome	66	0.618914585	46.8200529	6.97E-18	1.44E-15	enriched	28298, 29236, 29282, 29288, 29304, 64205, 81768, 94266, 140654, 140655, 140661, 287417, 290641, 291434, 293418, 296709, 297755	Rps6, Rpsa, Rpl17, Rps3a, Rps3, Rps16, Rpl26, Rpl22, Rps27, Rplp0, Rpl35, Rpl18a, Rpl23, Rpl7, Rpl32, Rplp1, Rpl27a
Protein processing in endoplasmic reticulum	140	0.374511813	10.25170616	2.86E-09	2.96E-07	enriched	24224, 24887, 25596, 79255, 81784, 85430, 192235, 286900, 287275, 287280, 288444, 289754, 297504, 298068, 299331, 361233, 362356, 500972, 689134	Bcl2, Bax, Hsp90aa1, Xbp1, Atf4, Hyou1, Rpn1, Herpud1, Vimp, Cul1, Skp1, Hsph1, Ssr3, Edem1, Sec61b, Stt3a, Sec61g, Ssr1, Sec24a
Protein export	21	0.616556251	46.13885661	7.29E-09	5.03E-07	enriched	293142, 298068, 498351, 689134, 691393	Oxa1l, Sec61b, Spcs2, Sec61g, Srp72, Srp72
Peroxisome	68	0.328236227	7.689528868	2.20E-04	0.009125253	enriched	25270, 25284, 79244, 85255, 94340, 113956, 114027, 305581, 310645	Amacr, Abcd3, Acsl5, Dao, Hsd17b4, Pecr, Pmvk, Hacl1, Pex13
Terpenoid backbone biosynthesis	12	0.524015975	25.95992294	4.12E-04	0.012196616	enriched	24450, 89784, 310645	Hmgcs2, Pmvk, Idi1

DIRECTIONAL ANALYSIS

KEGG Pathway	#Genes	Coeff	Odd ratio	P-Value	FDR	Direction	Genes	Gene symbol
Ribosome	62	0.774370575	123.0277138	8.79E-26	1.82E-23	up	140654, 140655, 140661, 287417, 290641, 291434, 29236, 29282, 29288, 29304, 293418, 296709, 297755, 64205, 81768, 94266	Rps6, Rpsa, Rpl17, Rps3a, Rps3, Rps16, Rpl26, Rpl22, Rps27, Rplp0, Rpl35, Rpl18a, Rpl23, Rpl7, Rplp1, Rpl27a
Protein export	19	0.723316768	89.57983565	7.28E-11	7.53E-09	up	293142, 498351, 689134, 691393	Oxa1l, Spcs2, Sec61g, Srp72, Srp72
Protein processing in endoplasmic reticulum	136	0.351071919	8.86201701	4.89E-10	3.38E-08	up	192235, 24224, 25596, 286900, 287275, 289754, 297504, 361233, 362356, 500972, 689134, 79255, 81784, 85430	Bcl2, Xbp1, Atf4, Hyou1, Rpn1, Herpud1, Vimp, Cul1, Ssr3, Edem1, Stt3a, Sec61g, Ssr1, Sec24a
Terpenoid backbone biosynthesis	12	-0.553522884	0.032067001	1.21E-04	0.004158625	down	24450, 310645, 89784	Hmgcs2, Pmvk, Idi1
Peroxisome	67	-0.304390515	0.150820068	3.27E-04	0.009666056	down	113956, 114027, 25270, 25284, 305581, 310645, 79244, 85255	Amacr, Abcd3, Dao, Hsd17b4, Pecr, Pmvk, Hacl1, Pex13

gene	species	sense sequence	antisense sequence	amplicon size	intron size
Gusb	mouse	CTCTGGTGGCCTTACCTGAT	CAGTTGTTGTCACCTTCACCTC	75	783
Hprt	mouse	GGAGCGGTAGCACCTCCT	CTGGTTCATCATCGCTAATCAC	116	10839
Nupr1	mouse	GAAGCTGCTGACCAAGTTCC	GTGTGGTGTCTGTGGTCTGG	91	1308
IL27	mouse	GATTGCCAGGAGTGAACCTG	CGAGGAAGCAGAGTCTCTCAG	114	1437
Bip	mouse	CTGAGGCGTATTTGGGAAAG	TCATGACATTCAGTCCAGCAA	120	509
Chop	mouse	GCGACAGAGCCAGAATAACA	GATGCACTTCCTTCTGGAACA	61	2818
Atf4	mouse	ATGATGGCTTGGCCAGTG	CCATTTTCTCCAACATCCAATC	88	111
Nupr1	human	ATAGCCTGGCCCATTCCTAC	GCCTCCACCTCCTGTAACC	89	584