

Translational profiling of mouse dopaminoceptive neurons reveals region-specific gene expression, exon usage, and striatal PGE2 modulatory effects

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LIST OF SUPPLEMENTARY TABLES

Supplementary Table 1: All_data

- 1a- Sample description incl. sex of mice
- 1b- Library description
- 1c- Count Table
- 1d- Cell type markers
- 1e- References for Table 1d

Supplementary Table 2: Complete-DESeq-results

Supplementary Table 3: DE-genes_PFC-vs-striatum

Analytical comparisons of differentially expressed genes between PFC and STR (i.e. DS + NAc), all in D1 samples (data from Supplementary Table 2).

- 3a- DE genes PFC>Str
- 3b- DE genes Str>PFC
- 3c- DE genes PFC>Str best (padj<0.001, L2FC≥1, baseMean≥10)
- 3d- DE genes Str>PFC best (padj<0.001, L2FC≥1, baseMean≥10)
- 3e- All PFC samples > all Str samples
- 3f- All Str samples > all PFC samples
- 3g- GO analysis mRNAs PFC>Str
- 3h- GO analysis mRNAs Str>PFC
- 3i- IUPHAR-identified mRNAs PFC>Str
- 3j- IUPHAR-identified mRNAs Str>PFC

Supplementary Table 4: DEXSeq_PFC-vs-Str_in-D1

Differentially expressed exons (DEXSeq) in PFC vs Str in D1 samples.

Exon usage analysis by the DEXseq package. DEXseq breaks down open reading frames into exon fragments (which do not necessarily correspond to full exons), and tests if there is a significant change in the relative usage of each of these fragments, i.e. in the ratio of sequencing reads mapping to this fragment, over the reads mapping to any other fragment of the same gene. FeatureID corresponds to the arbitrary numbering of the exonic fragment by DEXseq, and the genomic coordinates for each fragment are given in the genomicData.seqnames, genomicData.start and genomicData.end columns. padj is the multiple testing correction adjusted p-value for the differential usage of a given fragment, and log2fold corresponds to the fold-change of usage for that fragment.

Supplementary Table 5: DEXSeq_PFC-vs-Str_in-D1_Analyses

Analyses of results in Supplementary Table 4 (*see legend to Supplementary Table 4*).

5a- Exons PFC>Str padj<0.05

5b- Exons Str>PFC padj<0.05

5c- Gene counts

5d- Genes with at least one exon PFC>Str (Table 5a) with increased total mRNA (Table 3a)

5e- Genes with at least one exon Str>PFC (Table 5b) with increased total mRNA (Table 3b)

5f- *Arpp21* exon usage PFC vs Str

Supplementary Table 6: DE-genes_D1-vs-D2_in-Str

Analytical comparisons of differentially expressed genes between D1 and D2 in DS and NAc samples (data from Supplementary Table 2).

6a- DE genes D1>D2 in both DS and NAc

6b- DE genes D1>D2 only in DS

6c- DE genes D1>D2 only in NAc

6d- DE genes D2>D1 in both DS and NAc

6e- DE genes D2>D1 only in DS

6f- DE genes D2>D1 only in NAc

6g- DE genes with opposite variation in DS and NAc

6h- Best DE genes D1>D2 in DS (padj<0.001, L2FC≥1, baseMean≥10)

6i- Best DE genes D1>D2 in NAc (padj<0.001, L2FC≥1, baseMean≥10)

6j- Best DE genes D1>D2 common between DS and NAc (padj<0.01, L2FC≥1, baseMean≥10)

6k- Best DE genes D2>D1 in DS (padj<0.001, L2FC≥1, baseMean≥10)

6l- Best DE genes D2>D1 in NAc (padj<0.001, L2FC≥1, baseMean≥10)

6m- Best DE genes D2>D1 common between DS and NAc (padj<0.01, L2FC≥1, baseMean≥10)

6n- All D1 samples > all D2 samples in DS

6o- All D1 samples > all D2 samples in NAc

6p- All D1 samples > all D2 samples in DS and NAc (common to tables 6n and 6o)

6q- All D2 samples > all D1 samples in DS

6r- All D2 samples > all D1 samples in NAc

6s- All D2 samples > all D1 samples in DS and NAc (common to tables 6q and 6r)

6t- Summary

Supplementary Table 7: DE-genes_D1-vs-D2_in-STR_GO-IUPHAR

Analyses of mRNAs differentially expressed in D1 vs D2 samples (Supplementary Tables 6a-g) using gene ontology and IUPHAR classification.

7a- GO analysis mRNAs D1>D2 in both DS and NAc

7b- GO analysis mRNAs D1>D2 only in DS

7c- GO analysis mRNAs D1>D2 only in NAc

7d- GO analysis mRNAs D2>D1 in both DS and NAc

7e- GO analysis mRNAs D2>D1 only in DS

7f- GO analysis mRNAs D2>D1 only in NAc

7g- IUPHAR-identified mRNAs D1>D2

7h- IUPHAR-identified mRNAs D2>D1

Supplementary Table 8: DEXSeq_D1-vs-D2_in-DS

Differentially expressed exons (DEXSeq) between D1 and D2 in DS samples (*see legend to Supplementary Table 4*).

Supplementary Table 9: DEXSeq_D1-vs-D2_in-NAc

Differentially expressed exons (DEXSeq) between D1 and D2 in NAc samples (*see legend to Supplementary Table 4*).

Supplementary Table 10: DEXSeq_D1-vs-D2_in-DS-and-NAc_Analyses

Analyses of DEXSeq results in DS (Supplementary Table 8) and NAc (Supplementary Table 9), *and see legend to Supplementary Table 4*.

- 10a- Exons D1>D2 in DS padj<0.05
- 10b- Exons D2>D1 in DS padj<0.05
- 10c- Exons D1>D2 in NAc padj<0.05
- 10d- Exons D2>D1 in NAc padj<0.05
- 10e- Gene counts
- 10f- Genes with at least one exon D1>D2 in DS (Table 10a) with increased total mRNA (Tables 7a,b)
- 10g- Genes with at least one exon D2>D1 in DS (Table 10b) with increased total mRNA (Tables 7d,e)
- 10h- Genes with at least one exon D1>D2 in NAc (Table 10c) with increased total mRNA (Tables 7a,c)
- 10i- Genes with at least one exon D2>D1 in NAc (Table 10d) with increased total mRNA (Tables 7d,f)

Supplementary Table 11: DE-genes_DS-vs-NAc

Analytical comparisons of differentially expressed genes between DS and NAc in D1 and D2 samples (data from Supplementary Table 2).

- 11a- DE genes DS>NAc in both D1 and D2
- 11b- DE genes DS>NAc only in D1
- 11c- DE genes DS>NAc only in D2
- 11d- DE genes NAc>DS in both D1 and D2
- 11e- DE genes NAc>DS only in D1
- 11f- DE genes NAc>DS only in D2
- 11g- DE genes opposite variation in D1 and D2
- 11h- Best DE genes DS>NAc in D1 (padj<0.001, L2FC≥1, baseMean≥10)
- 11i- Best DE genes DS>NAc in D2 (padj<0.001, L2FC≥1, baseMean≥10)
- 11j- Best DE genes DS>NAc common between D1 and D2 (padj<0.001, L2FC≥1, baseMean≥10)
- 11k- Best DE genes NAc>DS in D1 (padj<0.001, L2FC≥1, baseMean≥10)
- 11l- Best DE genes NAc>DS in D2 (padj<0.001, L2FC≥1, baseMean≥10)
- 11m- Best DE genes NAc>DS common between D1 and D2 (padj<0.001, L2FC≥1, baseMean≥10)
- 11n- All DS samples > all NAc samples in D1
- 11o- All DS samples > all NAc samples in D2
- 11p- All DS samples > all NAc samples in D1 and D2 (common to tables 11n and 11o)
- 11q- All NAc samples > all DS samples in D1
- 11r- All NAc samples > all DS samples in D2
- 11s- All NAc samples > all DS samples in D1 and D2 (common to tables 11q and 11r)
- 11t- Summary

Supplementary Table 12: DE-genes_DS-vs-NAc_GO-IUPHAR

Analyses of mRNAs differentially expressed in DS vs NAc (Supplementary Tables 11a-g) using gene ontology and IUPHAR classification.

- 12a- GO analysis mRNAs DS>NAc in both D1 and D2
- 12b- GO analysis mRNAs DS>NAc only in D1
- 12c- GO analysis mRNAs DS>NAc only in D2
- 12d- GO analysis mRNAs NAc>DS in both D1 and D2
- 12e- GO analysis mRNAs NAc>DS only in D1
- 12f- GO analysis mRNAs NAc>DS only in D2
- 12g- IUPHAR-identified mRNAs DS>NAc

12h- IUPHAR-identified mRNAs NAc>DS

Supplementary Table 13: DEXSeq_DS-vs-NAc_in-D1

Differentially expressed exons (DEXSeq) between DS and NAc in D1 samples (*see legend to Supplementary Table 4*).

Supplementary Table 14: DEXSeq_DS-vs-NAc_in-D2

Differentially expressed exons (DEXSeq) between DS and NAc in D2 samples (*see legend to Supplementary Table 4*).

Supplementary Table 15: DEXSeq_DS-vs-NAc_in-D1-and-D2_Analyses

Analyses of DEXSeq results DS vs NAc, in D1 (Supplementary Table 13) and NAc (Supplementary Table 14) samples (*see legend to Supplementary Table 4*).

15a- Exons DS>NAc in D1 padj<0.05

15b- Exons NAc>DS in D1 padj<0.05

15c- Exons DS>NAc in D2 padj<0.05

15d- Exons NAc>DS in D2 padj<0.05

15e- Gene counts

15f- Genes with at least one exon DS>NAc in D1 (Table 15a) with increased total mRNA (Table 12a,d)

15g- Genes with at least one exon NAc>DS in D1 (Table 15b) with increased total mRNA (Table 12b,e)

15h- Genes with at least one exon DS>NAc in D2 (Table 15c) with increased total mRNA (Table 12a,f)

15i- Genes with at least one exon NAc>DS in D2 (Table 15d) with increased total mRNA (Table 15b,g)

Supplementary Table 16: DE-Transcription-factors_STR

Differentially expressed transcription factors (TF) in the striatum (data from Supplementary Tables 6 and 11).

16a- DE TFs D1 vs D2 common to DS and NAc

16b- DE TFs D1 vs D2 DS-specific

16c- DE TFs D1 vs D2 NAc-specific

16d- DE TFs DS vs NAc common to D1 and D2

16e- DE TFs DS vs NAc D1-specific

16f- DE TFs DS vs NAc D2-specific

Supplementary Table 17: IPA-upstream-analysis_DS-vs-NAc

Ingenuity pathway analysis (IPA-Partek) of DS vs NAc differences combining D1 and D2 neurons (limited to potentially endogenous factors).

Supplementary Table 18: Prostaglandin-related-gene-products

Expression of prostaglandin-related genes in striatal samples (data from Supplementary Table 2).

Supplementary Table 19: Statistical analyses

Complete results of statistical analyses for Figs. 3, 4, 5, and Supplementary Figs. 1, 2, 3, 8, 9, 10, and 11.