



HAL
open science

A functional m⁶A-RNA methylation pathway in the oyster *Crassostrea gigas* assumes epitranscriptomic regulation of lophotrochozoan development

Lorane Le Franc, Benoit Bernay, Bruno Petton, Marc Since, Pascal Favrel, Guillaume Rivière

► To cite this version:

Lorane Le Franc, Benoit Bernay, Bruno Petton, Marc Since, Pascal Favrel, et al.. A functional m⁶A-RNA methylation pathway in the oyster *Crassostrea gigas* assumes epitranscriptomic regulation of lophotrochozoan development. *FEBS Journal*, In press, 10.1111/febs.15500 . hal-02952460

HAL Id: hal-02952460

<https://hal.sorbonne-universite.fr/hal-02952460>

Submitted on 29 Sep 2020

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.

**A functional m⁶A-RNA methylation pathway in the oyster
 Crassostrea gigas assumes epitranscriptomic regulation of
 lophotrochozoan development**

Journal:	<i>The FEBS Journal</i>
Manuscript ID	FJ-20-0151.R1
Manuscript Type:	Regular Paper
Date Submitted by the Author:	n/a
Complete List of Authors:	<p>Le Franc, Lorane; University of Caen Normandy, FRE 2030 BOREA MNHN SU UNICAEN UA CNRS IRD Bernay, Benoit; University of Caen Normandy, SF ICORE Proteogen Petton, Bruno; Ifremer, UMR 6539 LEMAR Since, Marc; University of Caen Normandy, SF ICORE PRISMM Comprehensive Cancer Center F Baclesse Favrel, Pascal; University of Caen Normandy, FRE 2030 BOREA MNHN SU UNICAEN UA CNRS IRD Rivière, Guillaume; University of Caen Normandy, FRE 2030 BOREA MNHN SU UNICAEN UA CNRS IRD</p>
Key Words:	

1
2
3 1 **A functional m⁶A-RNA methylation pathway in the oyster *Crassostrea gigas***
4
5
6 2 **assumes epitranscriptomic regulation of lophotrochozoan development**
7
8
9 3

10
11 4 **Authors**
12
13

14 5 Lorane LE FRANC¹, Benoit BERNAY², Bruno PETTON³, Marc SINCE⁴, Pascal FAVREL¹ and
15
16 6 Guillaume RIVIERE¹
17
18
19 7

20
21
22 8 **Addresses**
23
24

25 9 ¹Normandie Univ, UNICAEN, CNRS, BOREA, 14000 Caen, France.

26
27 10 Laboratoire Biologie des organismes et Ecosystèmes aquatiques (BOREA), Muséum
28
29 11 d'Histoire naturelle, Sorbonne Université, Université de Caen Normandie, Université des
30
31 12 Antilles, CNRS, IRD, Esplanade de la paix, 14032 Caen, France.
32
33

34
35 13 ²Normandie Univ, UNICAEN, SF ICORE, PROTEOGEN core facility, 14000 Caen, France
36
37

38 14 ³Ifremer, Laboratoire des Sciences de l'Environnement Marin, UMR 6539
39
40 15 CNRS/UBO/IRD/Ifremer, Centre Bretagne, 29280, Plouzané, France
41
42

43 16 ⁴ Normandie Univ, UNICAEN, Comprehensive Cancer Center F. Baclesse, SF ICORE,
44
45 17 PRISMM core facility, 14000 Caen, France.
46
47

48
49 18

50
51 19 **Corresponding author**
52

53 20 Guillaume Rivière (0033231565113 ; guillaume.riviere@unicaen.fr) , Normandie Univ,
54
55 21 UNICAEN, CNRS, BOREA, 14000 Caen, France (<https://borea.mnhn.fr/>). Tel :
56
57
58
59 22
60

1
2
3 **23 Running title**
4

5
6 **24** m⁶A-RNA methylation pathway in oyster development
7
8
9

10
11 **26 Abbreviations**
12

13
14 **27** N⁶-methyladenosine (m⁶A), Methyltransferase like (METTL), Wilms' tumor 1-associated
15
16 **28** protein (WTAP), RNA-binding motif 15 (RBM15), Ring finger E3 ubiquitin ligase (HAKAI), Zinc
17
18
19 **29** finger CCCH-type containing 13 (ZC3H13), AlkB homologue 5 (ALKBH5), Fat mass and
20
21 **30** obesity associated protein (FTO), YTH domain family protein (YTHDF), YTH domain
22
23
24 **31** containing protein (YTHDC), Heterogeneous nuclear ribonucleoproteins A2 B1
25
26
27 **32** (HNRNPA2B1), Proline rich coiled-coil 2a (Prrc2a), Eukaryotic initiation factor 3 (eIF3), Sterile
28
29 **33** sea water (SSW), Oocytes (E), Fertilized oocytes (F E), Two to eight cell embryos (2/8 C),
30
31
32 **34** Hours post fertilization (hpf), Morula (M), Blastula (B), Gastrula (G), D larvae (D), solid-phase
33
34
35 **35** reversible immobilization (SPRI), TPM (Transcripts Per Million), Gene ontology (GO), oyster
36
37 **36** m⁶A-interacting protein (Cg-m⁶A-BPs), S-adenosyl-methionine (SAM), maternal-to-zygotic
38
39
40 **37** transition (MZT), acetonitrile (ACN)
41
42
43

44
45 **39 Keywords**
46

47
48 **40** RNA, methylation, epitranscriptomics, oyster, development.
49
50

51
52
53
54 **42 Conflicts of interest**
55

56
57
58 **43** The authors declare they have no competing conflict of interest
59
60

Abstract

N^6 -methyladenosine (m^6A) is a prevalent epitranscriptomic mark in eukaryotic RNA, with crucial roles for mammalian and ecdysozoan development. Indeed, m^6A -RNA and the related protein machinery are important for splicing, translation, maternal-to-zygotic transition and cell differentiation. However, to date, the presence of an m^6A -RNA pathway remains unknown in more distant animals, questioning the evolution and significance of the epitranscriptomic regulation. Therefore, we investigated the m^6A -RNA pathway in the oyster *Crassostrea gigas*, a lophotrochozoan model whose development was demonstrated under strong epigenetic influence.

Using mass spectrometry and dot blot assays, we demonstrated that m^6A -RNA is actually present in the oyster and displays variations throughout early oyster development, with the lowest levels at the end of cleavage. In parallel, by *in silico* analyses, we were able to characterize at the molecular level a complete and conserved putative m^6A -machinery. The expression levels of the identified putative m^6A writers, erasers and readers were strongly regulated across oyster development. Finally, RNA pull-down coupled to LC-MS/MS allowed us to prove the actual presence of readers able to bind m^6A -RNA and exhibiting specific developmental patterns.

Altogether, our results demonstrate the conservation of a complete m^6A -RNA pathway in the oyster and strongly suggest its implication in early developmental processes including MZT.

This first demonstration and characterization of an epitranscriptomic regulation in a lophotrochozoan model, potentially involved in the embryogenesis, brings new insights into our understanding of developmental epigenetic processes and their evolution.

66 Introduction

67
68 The *N*⁶-methyladenosine (m⁶A) is the prevalent chemical RNA modification in all eukaryotic
69 coding and non-coding RNAs [1]. Messenger RNAs are the most heavily m⁶A methylated
70 RNAs, with m⁶A bases lying mostly in their 3' UTRs, at the vicinity of their stop codon [2–4]
71 and also in 5' UTRs and long internal exons [4,5]. *N*⁶-methylation of RNA adenosines is
72 responsible for RNA processing and, like DNA methylation or histone modifications,
73 contributes to the regulation of gene expression without changing the DNA or mRNA
74 sequence. Therefore m⁶A constitutes a new layer of post-transcriptional gene regulation, which
75 is emerging or has been proven critical in various biological processes, and referred to as
76 epitranscriptomic [2].

77
78 The dynamics and biological outcomes of m⁶A levels are the results of the activity of a complex
79 protein machinery comprising writers, erasers and readers. The addition of a methyl group to
80 the 6th nitrogen of RNA adenosines is catalysed by m⁶A writers with distinct properties.
81 Methyltransferase like 16 (METTL16) is a 'stand-alone' class I methyltransferase that
82 recognizes the UACA*GAGAA consensus sequence (with * indicating the target adenosine)
83 [6]. By contrast, METTL3 transfers methyl groups to adenosines within the RRA*CH motif
84 [2,3,7]. METTL3 is only active within a tripartite 'core complex' [8] comprising METTL3,
85 METTL14 which enhances the methyltransferase activity supported by the MTA-70 domain of
86 METTL3 [9,10] and the regulator protein Wilms' tumor 1-associated protein (WTAP) [4,9,11].
87 This core complex can interact with Virilizer-like (or KIAA1429) [12], ring finger E3 ubiquitin

1
2
3 88 ligase (HAKAI) [12,13], zinc finger CCCH-type containing 13 (ZC3H13) [12,14], RNA-binding
4
5
6 89 motif 15 (RBM15) and RBM15B [7,15] which are suspected to intervene in the core complex
7
8
9 90 activity and target specificity. The demethylation of adenosines has been demonstrated to be
10
11 91 an active process catalysed by eraser enzymes belonging to the Fe(II)/2-oxoglutarate
12
13 92 dioxygenase family: AlkB homologue 5 (ALKBH5) [16,17] and the fat mass and obesity
14
15 93 associated protein (FTO) [17,18].

16
17
18
19 94 A growing number of reader proteins which recognize the m⁶A-RNA mark is being described.
20
21 95 They may be divided into two classes depending on the presence of a YTH domain
22
23 96 (YTH) domain in their primary sequence. The YTH protein family includes YTH domain family
24
25 97 protein 1-3 (YTHDF1-3) and YTH domain containing protein 2 (YTHDC2), which are cytosolic
26
27 98 m⁶A readers involved in m⁶A-RNA stability and translation [19–22]. The fifth YTH member is
28
29
30
31
32 99 YTHDC1, which is present in the nucleus and controls splicing [23] and nuclear export [24] of
33
34
35 100 m⁶A-RNA. The second class of readers comprises proteins without YTH domain which are
36
37 101 involved in several molecular mechanisms. For example, the heterogeneous nuclear
38
39
40 102 ribonucleoprotein A2 B1 (HNRNPA2B1) is important for miRNA processing [25]. Insulin-like
41
42
43 103 growth factor 2 mRNA binding protein 1-3 (IGF2BP 1-3) [26] and proline-rich coiled-coil 2a
44
45 104 (Prcc2a) [27] participate in RNA stability while eukaryotic initiation factor 3 (eIF3) guides cap-
46
47
48 105 independent translation [5].

49
50 106
51
52
53 107 The m⁶A epitranscriptomes underlie important biological functions, most of which being related
54
55
56 108 to developmental processes, including the control of cell differentiation [27–32], maternal to
57
58 109 zygotic transition (MZT) [33], sex determination [7,34] and gametogenesis [16,21,35,36]. Such
59
60

1
2
3 110 critical epitranscriptomic outcomes are conserved in the animal evolution and were
4
5
6 111 characterized in both vertebrates and ecdysozoans, i.e. mammals and drosophila.

7
8 112 However, such conserved biological significance originates in diverse epitranscriptomic
9
10
11 113 mechanisms. Indeed, not all ecdysozoans bear a complete m⁶A-RNA machinery, such as *C.*
12
13 114 *elegans* whose genome is devoid of the related protein machinery with the exception of a
14
15
16 115 putative orthologue of METTL16 [37,38]. In addition, no m⁶A eraser has been described to
17
18
19 116 date in non-vertebrate models, and especially ecdysozoans such as the drosophila or *C.*
20
21 117 *elegans* [38–40], where it cannot be excluded that m⁶A-RNA methylation could be removed by
22
23
24 118 the activity of characterised 6mA-DNA demethylases [41,42]. This situation may illustrate a
25
26
27 119 growing complexity of epitranscriptomic mechanisms during the animal phylogeny and raises
28
29
30 120 fundamental questions about its evolution and its presence in organisms distant from
31
32 121 mammals and ecdysozoans. However, to date, no data about a possible epitranscriptomic
33
34
35 122 regulation is available to our knowledge in lophotrochozoans, the understudied sister group of
36
37 123 ecdysozoans within protostomes, although representing an important range of metazoan
38
39
40 124 biodiversity.

41
42
43 125 The Pacific oyster *Crassostrea gigas* (i.e. *Magallana gigas*) is a bivalve mollusc whose great
44
45 126 ecological and economical significance allowed its emergence as a model species within
46
47
48 127 lophotrochozoan organisms. As such, an important amount of genetic, transcriptomic and
49
50
51 128 epigenetic data have been generated in this model. Interestingly, the embryolarval
52
53 129 development of *C. gigas* is described to be under the strong epigenetic influence of DNA
54
55
56 130 methylation [43–47] and histone marks [48–50]. Besides, oyster development occurs exposed
57
58
59 131 to external environmental conditions, and in other models the m⁶A methylation of RNA and/or
60

1
2
3 132 the expression of its machinery can be induced by heat stress, UV exposure or endocrine
4
5
6 133 disruptors [5,51–54], questioning the presence of an m⁶A pathway in *C. gigas* and its
7
8 134 significance in oyster early development.

9
10
11 135 To investigate this, we measured m⁶A levels in RNA across the entire embryolarval life of the
12
13 136 oyster using mass spectrometry and dot-blot. We also searched the available *in silico*
14
15 137 resources for putative conserved m⁶A-related proteins in *C. gigas* genomic data as well as
16
17 138 their cognate expression kinetics using RNAseq assembly analyses. We also performed RNA-
18
19 139 pulldown with a synthetic m⁶A-RNA oligonucleotide coupled to liquid chromatography and
20
21 140 mass spectrometry (LC-MS/MS) to characterize potential oyster m⁶A-binding proteins. To our
22
23 141 knowledge, this study is the first report unravelling epitranscriptomic mechanisms outside
24
25 142 vertebrate and ecdysozoan animal models.
26
27
28
29
30
31

32 143

33 34 35 144 **Results:**

36
37
38 145

39
40
41 146 **m⁶A is present in oyster RNA, differentially affects distinct RNA populations and**
42
43 147 **displays variations during embryonic life.**

44
45
46 148 Mass spectrometry measurements revealed that m⁶A is present in oyster RNA, with global
47
48 149 m⁶A/A levels of ca. 0.3%, a value comparable to what has been found in the human and the
49
50 150 fruit fly (Figure 1A). Immunoblot assays indicate that total and polyA+ RNA present variable
51
52 151 amounts of m⁶A during oyster development and that these variations display distinct profiles
53
54 152 suggesting specific methylation patterns between RNA populations. Indeed, N⁶A-methylation
55
56 153 in total RNA is the highest in the early stages (oocytes and fertilized oocytes) then gradually
57
58
59
60

1
2
3 154 decreases until the morula stage before gradually increasing again up to the trochophore stage
4
5
6 155 when it recovers its maximum (Figure 1B). In contrast, m⁶A levels in polyA⁺ RNA are hardly
7
8 156 detected in early stages but display a peak in the gastrula and trochophore stages (Figure 1C).
9

10
11 157

12
13
14 158 **m⁶A machinery is conserved at the molecular level in the oyster.**

15
16 159 *In silico* analyses led to the identification of oyster sequences encoding putative orthologues
17
18
19 160 of m⁶A writers, erasers and readers that are present in the human and/or in the human and
20
21 161 the fruit fly.

22
23
24 162 All the eight m⁶A-RNA writers characterized in the human and/or drosophila at the time of the
25
26
27 163 study, namely METTL3, METTL14, WTAP, Virilizer-like, HAKAI, ZC3H13, RBM15/15B and
28
29
30 164 METTL16, were present in the oyster at the gene level. The encoded protein primary
31
32 165 sequences all display the specific domains required for enzymatic activity and/or binding. They
33
34
35 166 include MT-A70 and AdoMetMtases SF domains for METTL3, METTL14 and METTL16,
36
37 167 respectively, that bear the methyltransferase activity. Oyster WTAP and Virilizer-like
38
39
40 168 orthologues exhibit WTAP and VIR_N domains, respectively, that are required in their human
41
42
43 169 counterparts to bind and activate the catalytic subunit of the m⁶A-RNA methyltransferase
44
45
46 170 complex. Oyster Hakai and RBM15/15B present RHHL, RHF-Zn-BS and specific RRM
47
48 171 domains, respectively, similar to human and fruit fly orthologues. Besides, the oyster ZC3H13
49
50
51 172 bears the Rho SF domain present in the human, but not in the fruit fly orthologue (Figure 2A).
52
53 173 *C. gigas* also presents a putative m⁶A-RNA eraser, ALKBH5, which is present in the human
54
55
56 174 but has not been characterized in drosophila. The oyster ALKBH5 exhibits a 2OG-FeII_Oxy
57
58
59 175 domain suggestive of a presumably conserved catalytic functionality through fe²⁺-dependent
60

1
2
3 176 oxoglutarate oxidation. Of note, no orthologue of the human FTO eraser could be identified in
4
5
6 177 the oyster genomic or transcriptomic databases available to date (Figure 2B).

7
8 178 Many m⁶A reader orthologues have also been found in the oyster, including proteins containing
9
10
11 179 a YTH domain, such as YTHDF, YTHDC1 and YTHDC2. An oyster Prrc2a-like protein
12
13
14 180 produces homology with the human Prrc2a, especially within the m⁶A-binding GRE-rich
15
16
17 181 domain. Oyster readers also include a heterogeneous nuclear ribonucleoprotein-coding gene,
18
19 182 hnRNPA2B1 with greater sequence similarity with the drosophila counterpart than with the
20
21
22 183 human orthologue. Similarly, the IGF2BP-coding sequence has also been found in *C. gigas*
23
24 184 (Figure 2C). Five oyster sequences display homologies with eIF3a which is able to bind m⁶A-
25
26
27 185 RNA [5] but it was not possible to discriminate whether a unique oyster predicted protein was
28
29
30 186 an eIF3a orthologue.

31
32 187 Overall, these results indicate the conservation of a complete m⁶A-RNA machinery in the
33
34
35 188 oyster. The complete list of the identified genes encoding the conserved m⁶A machinery actors
36
37
38 189 and their isoforms, as well as the related information is given in the supplementary data (Data
39
40 190 S1).

41
42
43 191

44 45 192 **Oyster putative m⁶A actors display expression level variations across development.**

46
47
48 193 RNAseq data analyses showed that all the oyster m⁶A-related genes were expressed during
49
50
51 194 the early life (Figure 3). Their expression level displayed gene-specific profiles, most of them
52
53
54 195 being variable throughout oyster development.

55
56 196 The expression of writers belonging to the core methylation complex is weak overall. METTL3
57
58
59 197 and WTAP share similar profiles with little expression increasing up to the gastrulation and
60

1
2
3 198 remaining stable afterwards. In contrast METTL14 displays a weak expression level across
4
5
6 199 the embryo larval life. The expression profile of Virilizer-like resembles WTAP, while HAKAI,
7
8 200 RBM15/15B and METTL16 seem to have mRNA levels which decrease after cleavage,
9
10
11 201 whereas those of ZC3H13 transcript variants seem to drop at the D larva stage. Interestingly,
12
13
14 202 METTL16 mRNA levels display an opposite developmental profile when compared to METTL3
15
16 203 expression; with the highest values during cleavage which decrease later on (Figure 3A).
17
18
19 204 ALKBH5 transcripts are weakly represented within oyster early embryos and the higher TPM
20
21 205 values are found in gastrulas. However, maximum levels are observed after metamorphosis in
22
23
24 206 juveniles (Figure 3B).
25
26
27 207 Regarding m⁶A putative readers, the expression of YTH family genes during development
28
29 208 showed different patterns. In fact, YTHDF is the most represented YTH-domain bearing actor
30
31 209 and YTHDF TPM values are ca. 5-fold higher than all the other oyster YTH readers. YTHDF is
32
33
34 210 strongly expressed at the beginning of development until a peak at the morula stage. Prrc2a
35
36
37 211 is the most represented reader at the mRNA level in oyster embryos, and the sum of the TPM
38
39
40 212 of the two Prrc2a oyster isoforms are at most ca. 20-fold higher than those of YTH family.
41
42
43 213 However, Prrc2a and YTHDF transcript content profiles are similar across oyster development,
44
45
46 214 and also remind of the IGF2BP mRNA levels.
47
48
49 215 By contrast, the two isoforms of YTHDC1 identified by *in silico* analysis, YTHDC1.1 and
50
51 216 YTHDC1.2, display similar patterns together with YTHDC2, with a maximum representation in
52
53
54 217 gastrulas. The expression of hnRNPA2B1 isoforms has likewise patterns except for a marked
55
56 218 drop at the D larvae stage (Figure 3 C).
57
58
59 219
60

1
2
3 **220 Oyster orthologues of m⁶A-RNA interacting proteins bind m⁶A RNA *in vitro*.**
4

5
6 221 To determine whether oyster proteins can bind m⁶A-RNA, we performed RNA-pulldown of
7
8 222 cytoplasmic and nuclear embryonic cell extracts using a methylated versus a non-methylated
9
10
11 223 oligonucleotide, followed by LC/MS-MS characterisation and identification of the captured
12
13
14 224 proteins with the Mascot software.
15

16 225 In nuclear extracts, we detected 591 proteins able to bind both the methylated and
17
18 226 unmethylated oligos. We identified 43 proteins specific to unmethylated RNA while 131
19
20
21 227 proteins specifically bind the m⁶A-methylated oligo. In cytosolic extracts, there were
22
23
24 228 respectively 646, 436 and 36 of such proteins, respectively. Regardless of the methylation
25
26
27 229 status, more proteins in the cytoplasmic extracts can bind to the RNA oligonucleotides than in
28
29
30 230 the nuclear extracts (1118 proteins vs. 765, respectively). However, more nuclear proteins are
31
32 231 found exclusively bound to the m⁶A-containing oligo than cytoplasmic proteins (131 vs. 36, i.e.
33
34
35 232 17 % vs. 3 %, respectively). In addition, many nuclear and cytoplasmic proteins can bind both
36
37
38 233 the methylated and the non-methylated oligo (591 vs. 646, i.e. 77 % vs. 58 %). An important
39
40
41 234 number of proteins in the cytoplasmic extract were found exclusively bound to the non-
42
43
44 235 methylated oligo, whereas only a limited number of nuclear proteins display such a specificity
45
46
47 236 (436 vs. 43, i.e. 39 % vs. 6 %). Among the 167 m⁶A-specific proteins in oyster extracts, only 5
48
49
50 237 were found in both the nuclear and cytoplasmic extracts. These results show that oyster
51
52
53 238 proteins can directly or indirectly bind m⁶A-RNA, and suggest an important
54
55
56 239 compartmentalization of m⁶A-related processes.

57
58 240 Among the identified proteins in this assay, four of the putative oyster m⁶A readers are found,
59
60 241 YTHDC1, hnRNPA2B1, IGF2BP and eIF3. In the nuclear extracts YTHDC1 is uncovered as

1
2
3 242 m⁶A-specific whereas hnRNPA2B1 and IGF2BP were present complexed with both the m⁶A-
4
5
6 243 and A-oligos. In the cytoplasmic extracts, YTHDC1 and eIF3a are m⁶A-specific while
7
8 244 hnRNPA2B1, IGF2BP were pulled down by both methylated and unmethylated oligos (Figure
9
10
11 245 4A).

12
13 246 These results demonstrate that some proteins in the oyster can specifically bind m⁶A-RNA and
14
15
16 247 that the putative m⁶A reader orthologues in the oyster are conserved at the protein level and
17
18
19 248 are able to interact with m⁶A-RNA.

20
21
22 249

23
24 250 **The m⁶A-interacting protein-coding genes display clustered expression regulation and**
25
26
27 251 **functional annotation during oyster development.**

28
29 252 The mRNA expression level of the genes encoding the 162 oyster m⁶A-interacting protein (Cg-
30
31
32 253 m⁶A-BPs) was examined using RNAseq databases. Most of them display a specific and
33
34
35 254 regulated expression level across oyster developmental stages. However, three main
36
37
38 255 expression clusters could be distinguished according to their developmental mRNA expression
39
40
41 256 level profile. Cluster 1 includes genes that show high expression at the beginning of the embryo
42
43
44 257 life (i.e. cleavage) and strongly decrease after gastrulation; the second cluster contains weakly
45
46
47 258 expressed genes except in the latest examined larval phases, after gastrulation (i.e.
48
49
50 259 Trochophore and D Larvae); cluster 3 groups genes that show an expression peak during
51
52
53 260 gastrulation (Figure 4B).

54
55
56 261 The Gene Ontology annotation of the Cg-m⁶A-BP genes reveal that the distinct clusters are
57
58
59 262 related to distinct functional pathways as indicated by the little - if any - common GO terms
60
263 between them (Figure 4C). However, the functional pathways of all three gene clusters point

1
2
3 264 out to their implication in translation and its regulation, although the terms enriched in each
4
5
6 265 cluster illustrate different aspects of translation, such as translation initiation (cluster 1), splicing
7
8 266 and nuclear export (cluster 2) and ribosomal and mitochondrial processes (cluster 3)
9
10
11 267 respectively (Figure 4D).
12

13
14 268

16 269 **Discussion**

17
18
19
20 270 This work demonstrates that m⁶A-RNA is present and variable during the embryo-larval life of
21
22
23 271 the oyster, and that *C. gigas* exhibits putative conserved and functional m⁶A-RNA writers,
24
25
26 272 eraser and readers. The dynamics of such mark and of its actors strongly suggest a biological
27
28 273 significance of the epitranscriptomic pathway in the control of development of a
29
30
31 274 lophotrochozoan species, which has, to date, never been demonstrated to our knowledge.
32

33 275 m⁶A-RNA levels vary across oyster development.

34
35
36 276 Using mass spectrometry and immunological measurements, we showed that oyster RNA is
37
38
39 277 m⁶A-methylated. The global proportion of N⁶-methyladenosine in RNA in the developing oyster
40
41
42 278 (0.28 %) is similar to those observed elsewhere in the animal kingdom, such as in the fruit fly
43
44 279 (0.24 %) [34] or the human (0.11- 0.23 %) [55] (Figure 1A), despite those values are difficult
45
46
47 280 to compare because they were not measured within the same developmental phase (adult flies
48
49 281 and human cell lines vs. oyster embryos). However, the comparable magnitude of m⁶A-RNA
50
51
52 282 amounts between taxa, in contrast to DNA methylation [46], may indicate conserved biological
53
54
55 283 significance of epitranscriptomic processes between groups. The amount of m⁶A in total RNA
56
57 284 displays a striking decrease during cleavage and then recovers its maximum levels at the end
58
59
60 285 of the gastrulation (Figure 1B). Therefore, the m⁶A decrease in total RNA during cleavage, i.e.

1
2
3 286 before the transcription of the zygotic genome starts, reflects a degradation of maternal m⁶A-
4
5
6 287 RNAs or their demethylation. However, all RNA populations do not exhibit the same pattern,
7
8
9 288 indeed polyA⁺ RNAs are m⁶A methylated only after cleavage. The extent of polyadenylation
10
11 289 of oyster maternal messenger RNAs accumulating during vitellogenesis is unknown.
12
13
14 290 Therefore, which maternal RNA population(s) is methylated in oyster oocytes is unclear.
15
16 291 Nevertheless, the observation that m⁶A-RNA levels are variable and affecting distinct RNA
17
18
19 292 populations across embryonic stages strongly favours an important biological significance of
20
21
22 293 m⁶A-RNA in oyster development. We hypothesize that oyster maternal messenger RNAs are
23
24 294 poorly polyadenylated, and that m⁶A, aside polyadenylation, might play a role in the stability of
25
26
27 295 quiescent maternal mRNAs. Alternatively, other maternal RNA populations such as snRNA,
28
29
30 296 miRNA, rRNA or lncRNA might be methylated [6,15,25,56], which become demethylated or
31
32 297 degraded up to the morula stage. The later increase in m⁶A RNA after cleavage could therefore
33
34
35 298 be the result of the methylation of the increasingly transcribed RNAs from the blastula stage,
36
37 299 including polyadenylated mRNAs.

38
39
40 300 **The m⁶A-RNA machinery is conserved in the oyster and regulated during development.**

41
42 301 The important regulation of m⁶A levels during oyster development assumes the presence of a
43
44
45 302 related protein machinery. We identified *in silico* cDNA sequences encoding conserved
46
47
48 303 putatively functional orthologues of m⁶A-RNA writers, eraser and readers in the oyster, with
49
50
51 304 great confidence (homologies ranging from ca. 30 to 65 % with their human counterpart, see
52
53
54 305 Data S1). The writers include all the members of the methylation complex (METTL3, METTL14,
55
56 306 WTAP, Virilizer-like, Hakai, ZC3H13, RBM15/15B) identified to date in the human and the fruit
57
58 307 fly [7,11,12,14,15,57]. We also identified an orthologue of the stand-alone METTL16 m⁶A
59
60

1
2
3 308 methyltransferase. Each orthologue bears the conserved domain(s) demonstrated to be
4
5
6 309 implicated in the catalytic and/or binding activity of their cognate counterpart in other species,
7
8
9 310 such as the MT-A70 domain which transfers methyl groups from the S-adenosyl-methionine
10
11 311 (SAM) to the N^6 nitrogen of RNA adenines [57]. Of the two proteins that can erase RNA
12
13
14 312 methylation, only ALKBH5, which is important for mouse spermatogenesis [16], was identified
15
16 313 at the cDNA level in the oyster. Indeed, no *C. gigas* sequence displayed significant homology
17
18
19 314 with the mammalian FTO protein, whose functional significance remains controversial [17].
20
21
22 315 Most the characterized m⁶A-RNA readers are also present at the molecular level in the oyster
23
24 316 and are putatively able to bind m⁶A regarding their primary sequence, such as the YTHDC and
25
26
27 317 YTHDF family members [19,21,23,58], Prrc2A [27], HnRNPA2B1 [25] and IGF2BP [26]. Of
28
29
30 318 note, some of these readers have not been characterized to date in *D. melanogaster* but
31
32 319 display strong homologies between humans and oysters. In mammals, eIF3a has important
33
34
35 320 functional outcomes in cap-independent translational stress response [5]. However, it was not
36
37
38 321 possible to ascribe a single oyster sequence as a unique eIF3a orthologue (Data S1), although
39
40 322 its presence was demonstrated by RNA pull down (see below) (see Data S2). Altogether, *in*
41
42
43 323 *silico* results show the conservation of a complete m⁶A-RNA machinery in the oyster. To date
44
45 324 to our knowledge, this is the first demonstration in a lophotrochozoan organism of an
46
47
48 325 epitranscriptomic pathway. Its presence suggests its ancestral origin, and questions its
49
50
51 326 biological significance in oyster development.
52
53 327 To investigate this, we analysed the expression level of the m⁶A machinery genes using RNA-
54
55
56 328 seq data. Our results indicate that the core methylation complex (METTL3, METTL14 and
57
58
59 329 WTAP) would not be active during cleavage because of the absence of METTL3 and little
60

1
2
3 330 WTAP expression. METTL16 catalyses the downregulation of SAM methyl donor availability
4
5
6 331 in mammals [59]. If METTL16 function is conserved in the oyster as suggested by the high
7
8 332 sequence homology, the peak in METTL16 expression, together with the weak expression of
9
10
11 333 the core complex in 2/8 cell embryos is consistent with an absence of m⁶A-RNA up to the
12
13
14 334 blastula stage. Then, the core complex would likely be active as soon as the end of cleavage
15
16 335 (i.e. since the blastula stage), in line with the increase in m⁶A levels observed at the same time.
17
18
19 336 The correlation between the increasing METTL3 expression and m⁶A-RNA levels after
20
21 337 cleavage strongly favours the conservation of the methyltransferase activity of the oyster MT-
22
23
24 338 A70 domain. Interpreting the regulation of the m⁶A activity by the other methyltransferase
25
26 339 complex members (i.e. Virilizer-like, HAKAI, ZC3H13 and RBM15/15B) is difficult because how
27
28 340 - or even if - oyster orthologues act within the complex is not known. Nevertheless, their specific
29
30
31 341 expression profiles may reflect their implication in the regulation of distinct biological contexts.
32
33
34 342 There might be little functional significance of active m⁶A-RNA erasure during oyster
35
36 343 development, consistent with the normal embryonic phenotype of ALKBH5 knockdown mice
37
38
39 344 [16]. Overall, the m⁶A readers display distinct developmental expression patterns. While
40
41
42 345 YTHDF and Prrc2a peak during cleavage, YTHDC1, YTHDC2, IGF2BP and hnRNPA2B1
43
44
45 346 mRNA levels gradually increase up to the gastrulation and remain mostly highly expressed
46
47
48 347 afterwards (except for hnRNPA2B1 and IGF2BP). These profiles evoke the mediation of
49
50
51 348 distinct biological functions depending on the reader and the developmental phases.
52
53 349 Therefore, we hypothesized that YTHDF and Prrc2a might participate in the blastulean
54
55
56 350 transition in the oyster. Indeed, in the zebrafish, a YTHDF reader triggers the maternal-to-
57
58
59 351 zygotic transition through the decay of the maternal m⁶A RNAs during cleavage [33]. The role
60

1
2
3 352 in the axon myelination and specification of mouse oligodendrocytes [27] is unlikely conserved
4
5
6 353 for *Prrc2a* because the oyster orthologue is expressed before the neurogenesis is detected in
7
8 354 trochophore stages [60]. Alternatively, the early expression of *Prrc2a* suggests that it might
9
10
11 355 rather compete with YTHDF for m⁶A-RNA targets [27], thereby possibly acting in oyster MZT,
12
13
14 356 bringing new perspectives into this process which remains poorly understood in
15
16 357 lophotrochozoans. In mammals m⁶A is implicated in the embryonic cell fate [30,31] notably via
17
18
19 358 the regulation of cell differentiation by YTHDC2 [32] or hnRNPA2B1 [29]. In the oyster,
20
21
22 359 YTHDC1, YTHDC2, IGF2BP and hnRNPA2B1 have their maximum expression during
23
24 360 gastrulation correlated to the second m⁶A peak, suggesting similar implications.

25
26
27 361 **Putative oyster m⁶A readers actually bind m⁶A-RNA *in vitro*.**

28
29 362 To better approach the developmental processes involving m⁶A in the oyster, we characterized
30
31
32 363 the proteins that can interact with m⁶A-RNA using a methylated-RNA-pulldown / mass
33
34
35 364 spectrometry assay. We identified 162 proteins able to specifically bind the m⁶A-RNA oligo in
36
37
38 365 embryonic cell extracts, demonstrating the actual presence of genuine m⁶A-readers in the
39
40
41 366 oyster. Most (ca. 75 %) of these proteins were found in nuclear extracts and only 5 were found
42
43
44 367 in both the cytoplasmic and nuclear fractions, showing an important compartmentalization of
45
46
47 368 the epitranscriptomic pathway. Regarding the little number of m⁶A readers in other animals,
48
49
50 369 and because the assay conditions do not discriminate between direct and indirect interactions,
51
52
53 370 we hypothesize that most these proteins indirectly bind m⁶A via a limited number of 'scaffold'
54
55
56 371 m⁶A readers. Such authentic readers that only bind the m⁶A-RNA oligo in our assay likely
57
58
59 372 include YTHDC1 and eIF3a, which have been demonstrated to directly bind m⁶A in other
60
373 species, demonstrating the conservation of the m⁶A-binding capacity and specificity of the YTH

1
2
3 374 domain in the oyster. Besides, YTHDC1 is found in both cell fractions, suggesting its
4
5
6 375 implication in the trafficking of m⁶A-RNA across the nuclear envelope [24], and reinforcing the
7
8 376 hypothesis that YTH proteins could participate in oyster MZT and cell differentiation. The
9
10
11 377 presence of the oyster eIF3a in the cytoplasm is consistent with a conserved role in m⁶A-
12
13
14 378 mediated translation processes, such as cap-independent translation [5].

15
16 379 **Possible functions of m⁶A-RNA in oyster development.**

17
18
19 380 We investigated the expression level and the functional annotation of the 162 genes encoding
20
21 381 the m⁶A-interacting proteins across oyster early life. These genes can be clustered into three
22
23
24 382 successive expression phases corresponding to three distinct functional pathways, which are
25
26
27 383 independent albeit all mostly related to translation regulation. The cluster 1 is mostly expressed
28
29 384 during the cleavage and the associated GO terms are related to the initiation of translation,
30
31
32 385 consistent with maternal RNA consumption before MZT is complete and the zygotic genome
33
34
35 386 becomes fully activated. The genes within cluster 3 show an expression peak during
36
37 387 gastrulation. Their ontology terms evoke ribosomal and mitochondrial processes, the latter
38
39
40 388 being required for energy supply and signalling integration during gastrulation [61–64]. The
41
42
43 389 cluster 2 contains genes that peak after gastrulation and which are related to splicing and
44
45
46 390 nuclear export. Such functional annotations are in line with a fine regulation of transcript variant
47
48 391 translation within the distinct cell lineages in the three cell layers of the late embryos.

49
50 392

51
52
53 393 Taken together, our findings bring to light a possible implication of m⁶A in oyster development.

54
55
56 394 First, during cleavage the decrease of m⁶A-RNA, the weak expression of methyltransferase
57
58 395 complex genes, the maximum of YTHDF gene expression and the expression of Cg-m⁶A-BPs
59
60

1
2
3 396 related to the initiation of the translation strongly suggest the implication of m⁶A in MZT in *C.*
4
5
6 397 *gigas*. Second, the increasing m⁶A level during gastrula stage is correlated to the increase of
7
8 398 methyltransferase complex gene expression. In addition, the increased RNA level of readers
9
10
11 399 putatively related to cell differentiation and the peak of gene expression of Cg-m⁶A-BPs
12
13 400 associated to ribosomal and mitochondrial processes, support the hypothesize of a m⁶A
14
15
16 401 implication in gastrulation. Finally, the highest m⁶A level at the trochophore stage, the gene
17
18
19 402 expression of the methyltransferase complex and of readers associated to cell differentiation,
20
21
22 403 as well as high RNA level of Cg-m⁶A-BPs related to splicing and nuclear export is correlated
23
24 404 with the fine cell differentiation taking place at this stage. However, inferring the biological
25
26
27 405 significance of m⁶A in development from the indirect and incomplete functional annotation of
28
29
30 406 the oyster genome is only limited. Characterization of the precise targets of m⁶A and how their
31
32
33 407 individual methylation is regulated across development, for example using high throughput
34
35
36 408 sequencing of precipitated m⁶A-RNA (MeRIP-seq), could be extremely relevant to better
37
38 409 understand this issue. In addition, despite sequence conservation and binding ability of oyster
39
40 410 actor orthologues strongly suggest functional conservation, future dedicated studies such as
41
42
43 411 biochemical inhibition or gene inactivation could help demonstrate their genuine biological
44
45
46 412 function. Besides, there seems to be an inverse correlation between m⁶A-RNA and 5mC-DNA
47
48
49 413 levels during the considered oyster developmental window [46]. This may suggest an interplay
50
51
52 414 between epigenetic and epitranscriptomic marks, possibly reflecting competition for methyl-
53
54
55 415 donor availability [59] or a link by histone epigenetic pathways [65,66].
56
57
58 416 Regarding the potential influence of the environment on m⁶A and the accumulation of RNA in
59
60 417 oocytes, we are at present investigating our hypothesis that m⁶A may convey intergenerational

1
2
3 418 epitranscriptomic inheritance of maternal life traits in the oyster. On an evolutionary
4
5
6 419 perspective, the presence of a putatively fully conserved epitranscriptomic pathway in the
7
8 420 oyster suggests that it was already present in the bilaterian common ancestor thereby in favour
9
10
11 421 of an important biological significance. Why *Drosophila* and *Caenorhabditis* seem to have lost
12
13 422 specific m⁶A-RNA erasers could be related to a sub-functionalization of the DMAD [41] and
14
15
16 423 NMAD-1 [42] N⁶-methyladenine DNA demethylase activity broadened towards RNA. However,
17
18
19 424 more work is required to better understand the evo-devo implications of our results.
20
21
22 425

23
24 426 To conclude, in this work we report the discovery and characterisation of a putatively complete
25
26 427 epitranscriptomic pathway in a lophotrochozoan organism, the oyster *Crassostrea gigas*. This
27
28 428 pathway includes the m⁶A mark in RNA and the actors of all the aspects of its regulation
29
30 429 (writers, eraser, readers) which are conserved at the molecular level and putatively functional.
31
32 430 We show that m⁶A levels are variable across oyster development and that m⁶A differentially
33
34 431 affects distinct RNA populations. Expression levels of the related enzymatic machinery is
35
36 432 consistent with the observed m⁶A level variations. We demonstrate the m⁶A binding capacity
37
38 433 and specificity of putative oyster m⁶A readers in the cytoplasm and nucleus of embryolarval
39
40 434 cells. These readers mediate distinct putative biological outcomes depending on the
41
42 435 development stage considered. From these results we hypothesize that early decay of
43
44 436 maternal m⁶A RNA participates in maternal-to-zygotic transition during cleavage and that later
45
46 437 *de novo* zygotic m⁶A methylation contributes to gastrulation and cell differentiation. This first
47
48 438 characterisation of an m⁶A-epitranscriptomic pathway in a lophotrochozoan organism, together
49
50 439 with its potential implication in development, opens new perspectives on the evolution of
51
52
53
54
55
56
57
58
59
60

1
2
3 440 epigenetic mechanisms and on the potential epitranscriptomic inheritance of environmentally-
4
5
6 441 induced life traits.
7
8
9 442

10
11
12 443 **Methods:**
13
14
15
16 444

17
18 445 **Animals:**
19

20
21 446 Broodstock oysters [67] and oyster embryos [46] were obtained at the IFREMER marine
22
23 447 facilities (Argenton, France) as previously described. Briefly, gametes of mature broodstock
24
25 448 oysters were obtained by stripping the gonads and filtering the recovered material on a 60 µm
26
27 449 mesh to remove large debris. Oocytes were collected as the remaining fraction on a 20 µm
28
29 450 mesh and spermatozoa as the passing fraction on a 20 µm mesh. Oocytes were pre-incubated
30
31 451 in 5 L of UV-treated and 1 µm filtered sterile sea water (SSW) at 21 °C until germinal vesicle
32
33 452 breakdown. Fertilization was triggered by the addition of ca. 10 spermatozooids per oocyte. After
34
35 453 the expulsion of the second polar body was assessed by light microscopy, embryos were
36
37 454 transferred in 150 L tanks of oxygenated SSW at 21 °C. The development stages were
38
39 455 determined by light microscopy observation. The stages collected were oocytes (E,
40
41 456 immediately before sperm addition), fertilized oocytes (F E, immediately before transfer to
42
43 457 150L tanks), two to eight cell embryos (2/8 C, ca. 1.5 hours post fertilization (hpf)), morula (M,
44
45 458 ca. 4 hpf), blastula (B, ca. 6 hpf), gastrula (G, ca. 10 hpf), trochophore (T, ca 16 hpf) and D
46
47 459 larvae (D, ca. 24 hpf). For each development stage, 3 million embryos were collected as the
48
49 460 remaining fraction on a 20 µm mesh and centrifuged at 123 g for 5min at room temperature.
50
51
52
53
54
55
56
57
58
59
60

1
2
3 461 Supernatant was discarded and samples of 1 million embryos were then snap-frozen in liquid
4
5
6 462 nitrogen directly of after resuspension in Tri-Reagent (Sigma-Aldrich, St Louis, MO, USA) (1
7
8 463 mL/10⁶ embryos) and stored at -80 °C. Three distinct experiments were realized (February to
9
10
11 464 May 2019) using the gametes of 126 to 140 broodstock animals, respectively.
12

13
14 465

15
16 466 **RNA extraction:**

- 17
18
19 467
 - total RNA extraction

20
21 468 RNA was extracted using phenol-chloroform followed by affinity chromatography as previously
22
23
24 469 described [68]. Briefly, embryos were ground in Tri-Reagent (Sigma-Aldrich) and RNA was
25
26
27 470 purified using affinity chromatography (Nucleospin RNA II kit, Macherey-Nagel, Duren,
28
29
30 471 Germany). Potential contaminating DNA was removed by digestion with rDNase (Macherey-
31
32 472 Nagel) according to the manufacturer's instructions for 15 min at 37 °C then RNA was purified
33
34
35 473 using Beckman Coulter's solid-phase reversible immobilization (SPRI) paramagnetic beads
36
37
38 474 (AgencourtAMPure XP, Beckman Coulter, Brea, CA, USA) according to the manufacturer's
39
40 475 instructions. Briefly, paramagnetic beads and RNAs were mixed slowly and incubated 5 min
41
42
43 476 at room temperature followed by 2 min on a magnetic rack. Cleared supernatant was removed,
44
45
46 477 and beads were washed three times with 70 % ethanol. After 4 min of drying at room
47
48 478 temperature, RNAs were mixed slowly with RNase free water and incubated for 1 min at room
49
50
51 479 temperature on the magnetic rack. Eluted total RNA was stored at -80 °C.
52

- 53
54 480
 - PolyA RNA enrichment

55
56
57 481 Poly-A RNA was extracted from total RNA by oligo-dT affinity chromatography (NucleoTrap
58
59 482 mRNA kit, Macherey-Nagel) according to the manufacturer's instructions. Briefly, up to 130 µg
60

1
2
3 483 of total RNAs were mixed with oligo-dT latex beads and incubated for 5 min at 68 °C then 10
4
5
6 484 min at room temperature. After centrifugation (2,000 g then 11,000 g), the pellets were washed
7
8 485 three times on the microfilter and dried by centrifugation at 11,000 g for 1 min. Finally, polyA+
9
10
11 486 RNA was incubated with RNase-free water for 7 min at 68 °C then centrifuged at 11,000 g for
12
13
14 487 1 min. Eluted polyA+ RNA was stored at -80 °C until needed.

15
16 488 Total and polyA-enriched RNA purity and concentrations were assayed by spectrophotometry
17
18
19 489 (Nanodrop, Thermo Scientific, Waltham, MA, USA).

20
21
22 490

23
24 491 **m⁶A quantification by LC-MS/MS:**

- 25
26
27 492 • RNA hydrolysis

28
29 493 To generate nucleosides for quantification against standard curves, 5 µg of total RNA were
30
31
32 494 denatured for 10 min at 70 °C followed by 10 min on ice, and hydrolyzed with 100 U Nuclease
33
34
35 495 S1 (50 U/µL, Promega, Madison, WI, USA) in Nuclease S1 buffer (Promega) in a final reaction
36
37 496 volume of 25 µL for 2 h at 37 °C under gentle shaking. Samples were then incubated with
38
39
40 497 alkaline phosphatase buffer (Promega) for 5 min at room temperature, before 10 U alkaline
41
42
43 498 phosphatase (Promega) were added and incubated further for 2 h at 37 °C under gentle
44
45 499 shaking. Ten extra units of alkaline phosphatase were added after 1 hour of incubation to
46
47
48 500 complete the reaction. Finally, samples were centrifuged at 13,000 rpm for 10 min at 4 °C and
49
50
51 501 the supernatant containing digested total RNA was collected and kept at -20 °C before
52
53 502 quantification.

- 54
55
56
57 503 • m⁶A quantification:

58
59
60

1
2
3 504 The apparatus was composed of a NexeraX² UHPLC system coupled with LCMS8030 Plus
4
5 505 (Shimadzu, Kyoto, Japan) mass spectrometer using an electrospray interface in positive mode.

6
7
8 506 The column (1.7 μm , 100x3 mm) was a HILIC Aquity[®] Amide (Waters, Millford, MA, USA)
9
10
11 507 maintained at 35 °C. The injection volume and run-to-run time were 3 μL and 10 min,
12
13
14 508 respectively. The flow rate was set to 1 mL/min. Mobile phase was initially composed of a
15
16 509 mixture of ammonium formate solution (10 mM) containing 0.2 % (v/v) formic acid and 95 %
17
18
19 510 acetonitrile (ACN) and it was maintained for 1 min. Then, a linear gradient was applied to reach
20
21
22 511 83 % ACN for 6 min. The composition returned to the initial conditions and the column was
23
24 512 equilibrated for 3 min.

25
26
27 513 The mass spectrometer was running in the Multiple Reaction Monitoring (MRM) acquisition
28
29 514 mode. LabSolutions 5.86 SP1 software was used to process the data. The desolvation
30
31
32 515 temperature was 230 °C, source temperature was 400 °C and nitrogen flows were 2.5 L/min
33
34
35 516 for the cone and 15 L/min for the desolvation. The capillary voltage was +4.5 kV. For each
36
37 517 compound, two transitions were monitored from the fragmentation of the $[\text{M}+\text{H}]^+$ ion. The first
38
39
40 518 transition (A in Table S1) was used for quantification and the second one (B in Table S1) for
41
42
43 519 confirmation of the compound according to European Commission Decision 2002/657/EC
44
45 520 (Table S1).

46
47
48 521 Blank plasma samples were analysed to check specificity. Calibrators were prepared using
49
50 522 diluted solutions of A (Toronto Research Chemical, Toronto, Canada) and m⁶A (Carbosynth,
51
52
53 523 Berkshire, UK) in water at 1, 2, 5, 10, 20 50, 100 ng/mL. The calibration curves were drawn by
54
55
56 524 plotting the ratio of the peak area of A and m⁶A. For both nucleosides, a quadratic regression
57
58
59 525 with 1/C weighting resulted in standard curves with $R^2 > 0.998$ and more than 75% of standards
60

1
2
3 526 with back-calculated concentrations within 15% of their nominal values as recommended for
4
5
6 527 by the European medicines agency for bioanalytical methods [69]. The limits of quantifications
7
8 528 for both compounds were considered as the lowest concentrations of the calibration curve.
9
10
11 529 m⁶A/A ratios were calculated for each single sample using the determined concentrations.
12
13
14 530 Final results are the average of three technical replicates.
15

16 531

17
18
19 532 **m⁶A quantification by immunoblotting:**

20
21 533 Immunological quantification of m⁶A was performed by dot-blot using total and polyA+ RNAs.
22
23
24 534 Dogfish total RNA (Dr. A. Gautier, personal communication) and a synthetic unmethylated
25
26
27 535 RNA oligo (Eurogentec, Liege, Belgium) were used as positive and negative controls,
28
29
30 536 respectively. RNA samples were denatured for 15 min at 55 °C with gentle shaking in
31
32
33 537 denaturing solution (2.2 M formaldehyde, 50 % formamide, 0.5X MOPS, DEPC water) followed
34
35
36 538 by 2 min on ice. Blotting was performed on a vacuum manifold as follows: a nylon membrane
37
38
39 539 (Amersham Hybond-N+, GE Healthcare life Sciences, Chicago, IL, USA) was pre-hydrated in
40
41
42 540 DEPC water for 5 min, then each well was washed twice with 10X SSC (Sigma-Aldrich) before
43
44
45 541 RNA was spotted onto the membrane and incubated for 15 min at room temperature. Then,
46
47
48 542 vacuum aspiration was applied and each well was washed twice with 10X SSC. After heat
49
50
51 543 crosslinking for 2 h at 70 °C, the membrane was rehydrated with DEPC water for 5 min, washed
52
53
54 544 with PBS then PBST (PBS, 0.1 % Tween-20) for 5 min each and blocked with two 5 min
55
56
57 545 incubations with blocking buffer (PBS, 0.1 % Tween-20, 10 % dry milk, 1 % BSA) at room
58
59
60 546 temperature. The blocked membrane was incubated overnight at 4 °C under gentle shaking
with the anti-m⁶A primary antibody (Total RNA: Millipore (Burlington, MA, USA) ABE572, 1 :

1
2
3 548 1,000 dilution in blocking buffer; polyA+ RNA: Diagenode (Liege, Belgium) C15200082, 1 : 500
4
5
6 549 dilution in blocking buffer) followed by four washes of PBST for 5 min. The secondary antibody
7
8 550 (Total RNA: Dako (Santa Clara, CA, USA) P0447 goat anti-mouse HRP antibody, 1 : 10,000
9
10
11 551 dilution; polyA+ RNA: Invitrogen (Carlsbad, CA, USA) A21202 donkey anti-mouse Alexa 488,
12
13 552 1 : 250 dilution) was diluted in PBST supplemented with 5 % dry milk and added onto the
14
15
16 553 membrane for 1 h 30 (total RNA) or 1 h (polyA+ RNA) at room temperature under gentle
17
18
19 554 shaking. Membranes were extensively washed in PBST (at least 4 washes of 5 min for total
20
21
22 555 RNA and 5 min then 1 h for polyA+ RNA) then total and polyA+ RNA immunoblots were
23
24 556 visualized using chemiluminescence (ECL kit, Promega) or fluorescence scanning at 480-530
25
26
27 557 nm (Pro Xpress, Perkin-Elmer, Waltham, MA, USA), respectively. The amount of m⁶A was
28
29
30 558 inferred from dot intensity measurements using ImageJ (v.1.49). Signal intensities were
31
32 559 determined as 'integrated densities as a percentage of the total' which corresponds to the area
33
34 560 under the curve of the signal of each dot after membrane background and negative control
35
36
37 561 signal subtraction.
38
39
40 562

41 42 563 ***In silico* analyses:**

43
44
45 564 All protein and RNA sequences of the m⁶A machinery of *Homo sapiens* and *Drosophila*
46
47
48 565 *melanogaster* (Data S1) were recovered by their published designation (i.e., 'METTL3' or
49
50 566 'YTHDF' etc.) and their identified protein sequence (ie. RefSeq accession number NP...)
51
52
53 567 collected from NCBI and used as query sequences to search for putative homologue
54
55
56 568 sequences in *Crassostrea gigas* databases. The presence of oyster orthologue RNA and
57
58
59 569 protein sequences were investigated by reciprocal
60

1
2
3 570 BLAST(<https://blast.ncbi.nlm.nih.gov/Blast.cgi>) on the *Crassostrea gigas* GigaTON [70] and
4
5
6 571 NCBI databases and results were compared between the two oyster databases. Domain
7
8 572 prediction was performed with CD-search software
9
10
11 573 (<https://www.ncbi.nlm.nih.gov/Structure/cdd/wrpsb.cgi>) with default settings on protein
12
13
14 574 sequences of *Homo sapiens*, *Drosophila melanogaster* and *Crassostrea gigas*. The GRE-rich
15
16 575 domain identified in vertebrate Prrc2a sequence [27] was performed with ProtParam
17
18
19 576 (<https://web.expasy.org/cgi-bin/protparam/protparam>).

20
21
22 577

23 24 578 **Protein machinery mRNA expression analyses:**

25
26
27 579 The transcriptome data of the different development stages are available on the GigaTON
28
29
30 580 database [70,71]. The correspondence between development stages in our study, and the
31
32
33 581 GigaTON database were assessed using light microscopy based on the morphological
34
35
36 582 description by Zhang et al., 2012 [71] (Table S2). Expression data was expressed in TPM
37
38
39 583 (Transcripts Per Million) [72] to provide a normalized comparison of gene expression between
40
41
42 584 all samples. The actual presence of some transcripts that display unclear or chimeric
43
44
45 585 sequences within available oyster databases was assessed using RT-PCR (Data S1).

46
47
48 586

49 587 **Protein m⁶A RNA pull down:**

- 50
51 588
 - Protein extraction and RNA affinity chromatography

52
53 589 Protein extraction and RNA affinity chromatography were performed as described previously
54
55
56 590 [27] with some modifications as follows. Equal amounts (1 million individuals) of each
57
58
59 591 developmental stage (oocyte to D larvae) were pooled together then homogenized in 3.5
60

1
2
3 592 volumes of buffer A (10 mM KCl, 1.5 mM MgCl₂, 10 mM HEPES, pH 7.9, DEPC water, 1X
4
5
6 593 Protease inhibitor cocktail, DTT 0.5 mM) by extensive pipetting (ca. 30 times) and incubated
7
8 594 10 min at 4 °C. Embryos were ground with 10 slow 23G-needle syringe strokes and centrifuged
9
10
11 595 at 2,000 rpm for 10 min at 4 °C. The supernatant was diluted in 0.11 volume of buffer B (1.4 M
12
13 596 KCl, 0.03 M MgCl₂, HEPES 0.3 M, pH 7.9, DEPC water), centrifuged at 10,000 g for 1 h at 4
14
15
16 597 °C and the supernatant containing cytosolic proteins was stored at -80 °C. The pellet of the
17
18
19 598 first centrifugation, containing nuclei, was re-suspended in two volumes of buffer C (0.42 M
20
21 599 NaCl, 1.5 mM MgCl₂, 0.2 mM EDTA, 25 % glycerol, 20 mM HEPES, pH 7.9, 0.5 mM PMSF,
22
23
24 600 0.5 mM DTT, water DEPC). Nuclei were then lysed with a 23 G needle (10 vigorous syringe
25
26
27 601 strokes) followed by centrifugation at 30,000 rpm for 30 min at 4 °C and the supernatant
28
29
30 602 containing nuclear proteins was stored at -80 °C.

31
32 603 To identify putative proteins able to bind m⁶A-RNA, the cytosolic and nuclear fractions were
33
34
35 604 submitted to affinity chromatography using 5'-biotin-labelled RNA oligonucleotides either
36
37
38 605 bearing N⁶-methylated adenosines or not. The methylated adenosines were designed to lie
39
40
41 606 within RRACH motifs, according to the conserved methylated consensus sequence in other
42
43 607 organisms [2,3,7,33,73] (oligo-m⁶A: 5'Biotin-AGAAAAGACAACCAACGAGRR-m⁶A-
44
45 608 CWCAUCAU-3', oligo-A: 5'Biotin-AGAAAAGACAACCAACGAGRRACWCAUCAU-3', R = A or
46
47
48 609 G, W = A or U, Eurogentec).

49
50 610 For RNA pull down, streptavidin-conjugated magnetic beads (Dynabeads Myone Streptavidin,
51
52
53 611 Invitrogen) were pre-blocked with 0.2 mg/mL tRNA (Sigma-Aldrich) and 0.2 mg/mL BSA for 1
54
55
56 612 h at 4 °C under gentle rotation followed by three washes with 0.1 M NaCl. To avoid the
57
58
59 613 identification of non-target proteins, cytosolic and nuclear protein extracts were cleared with
60

1
2
3 614 pre-blocked magnetic beads in binding buffer (50 mM Tris-HCl, 250 mM NaCl, 0.4 mM EDTA,
4
5
6 615 0.1 % NP-40, DEPC water, 1 mM DTT, 0.4 U/ μ L RNAsin) for 1 h at 4 °C under gentle rotation.
7
8 616 After incubation on magnetic rack, the supernatants containing putative target proteins were
9
10
11 617 collected and mixed with pre-blocked magnetic beads and oligo-m⁶A or oligo-A for 2 h at 4 °C
12
13
14 618 under gentle rotation. The beads binding putative target proteins were washed three times with
15
16 619 binding buffer and diluted in 50 mM ammonium bicarbonate.

17
18
19
20 620 • Identification of m⁶A-binding proteins by LC-MS/MS:

21
22 621 Protein samples were first reduced, alkylated and digested with trypsin then desalted and
23
24
25 622 concentrated onto a μ C18 Omix (Agilent, Santa Clara, CA, USA) before analysis.

26
27
28 623 The chromatography step was performed on a NanoElute (Bruker Daltonics, Billerica, MA,
29
30 624 USA) ultra-high pressure nano flow chromatography system. Peptides were concentrated onto
31
32
33 625 a C18 pepmap 100 (5 mm x 300 μ m i.d.) precolumn (Thermo Scientific) and separated at 50
34
35
36 626 °C onto a reversed phase Reprosil column (25 cm x 75 μ m i.d.) packed with 1.6 μ m C18 coated
37
38 627 porous silica beads (Ionopticks, Parkville, Victoria, Australia). Mobile phases consisted of 0.1
39
40
41 628 % formic acid, 99.9 % water (v/v) (A) and 0.1 % formic acid in 99.9 % ACN (v/v) (B). The
42
43
44 629 nanoflow rate was set at 400 nL/min, and the gradient profile was as follows: from 2 to 15 % B
45
46 630 within 60 min, followed by an increase to 25 % B within 30 min and further to 37 % within 10
47
48
49 631 min, followed by a washing step at 95 % B and re-equilibration.

50
51 632 MS experiments were carried out on an TIMS-TOF pro mass spectrometer (Bruker Daltonics)
52
53
54 633 with a modified nano-electrospray ion source (CaptiveSpray, Bruker Daltonics). The system
55
56
57 634 was calibrated each week and mass precision was better than 1 ppm. A 1600 spray voltage
58
59 635 with a capillary temperature of 180 °C was typically employed for ionizing. MS spectra were
60

1
2
3 636 acquired in the positive mode in the mass range from 100 to 1700 m/z. In the experiments
4
5
6 637 described here, the mass spectrometer was operated in PASEF mode with exclusion of single
7
8 638 charged peptides. A number of 10 PASEF MS/MS scans was performed during 1.16 seconds
9
10
11 639 from charge range 2-5.

12
13 640 The fragmentation pattern was used to determine the sequence of the peptide. Database
14
15
16 641 searching was performed using the Mascot 2.6.1 program (Matrix Science) with a *Crassostrea*
17
18 642 *gigas* Uniprot database (including 25,982 entries). The variable modifications allowed were as
19
20
21 643 follows: C-Carbamidomethyl, K-acetylation, methionine oxidation, and Deamidation (NQ). The
22
23
24 644 'Trypsin' parameter was set to 'Semispecific'. Mass accuracy was set to 30 ppm and 0.05 Da
25
26
27 645 for MS and MS/MS mode respectively. Mascot data were then transferred to Proline validation
28
29
30 646 software (<http://www.profi-proteomics.fr/proline/>) for data filtering according to a significance
31
32 647 threshold of <0.05 and the elimination of protein redundancy on the basis of proteins being
33
34
35 648 evidenced by the same set or a subset of peptides (Data S2).

36
37
38 649 • Gene ontology analysis:

39
40
41 650 The mRNA sequences of the characterized m⁶A-binding proteins were identified using tBlastn
42
43 651 [74–76] against the GigaTON database [70] with default settings. Gene ontology (GO)
44
45
46 652 analyses were carried out with the GO annotations obtained from GigaTON database gene
47
48
49 653 universe [70]. GO term-enrichment tests were performed using the goseq (V1.22.0) R package
50
51 654 [77] with p-values calculated by the Wallenius method and filtered using REVIGO [78]. GO
52
53
54 655 terms with a p-value < 0.05 were considered significantly enriched (Data S3).

55
56 656

57
58
59 657 **Statistical analyses and graph production:**
60

1
2
3 658 Results are given as the mean \pm SD of three independent experiments unless otherwise stated.
4
5
6 659 They were analysed using one-way ANOVA or Kruskal-wallis tests when required, depending
7
8 660 on the normality of result distribution. The normality was tested using the Shapiro-Wilk's test
9
10
11 661 and homoscedasticity of variances with Bartlett's tests. Statistics and graphics were computed
12
13
14 662 with Prism v.6 (Graphpad), R (v.3.6.1) and RStudio (v.1.0.153) softwares. The R packages
15
16 663 *eulerr* [79] and *Complexheatmap* [80] were used for production of specific figures.
17
18
19 664
20
21
22 665
23
24

25 666 **Author contribution**

26
27
28 667 Experiment design: GR, LLF.

29
30 668 Benchwork and bioinformatics: LLF, GR, BB, BP, MS.

31
32
33 669 Data analysis: LLF, GR, BB, MS.

34
35
36 670 Manuscript writing and editing: LLF, GR, PF, BB, MS, BP.

37
38
39 671

40 41 672 **Acknowledgements**

42
43
44 673 The authors would like to acknowledge PRISMM core facility collaborators R. Delepée and S.

45
46 674 Lagadu for their expertise in m⁶A/A UHPLC-MS/MS quantification. We also thank J. Pontin for

47
48
49 675 technical assistance and J. Le Grand for help with sampling.
50

51
52 676

53 54 677 **Funding sources and disclosure of conflicts of interest** 55 56 57 58 59 60

1
2
3 678 This work was supported by the French National program CNRS EC2CO (Ecosphère
4
5
6 679 Continentale et Côtière 'HERITAGE' to G. Rivière) and the council of the Normandy Region
7
8 680 (RIN ECUME to P. Favrel). The authors declare they have no conflict of interest.
9

10
11 681
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

For Review Only

682 **References:**

- 683 1 Saletore Y, Meyer K, Korlach J, Vilfan ID, Jaffrey S & Mason CE (2012) The birth of the
684 Epitranscriptome: deciphering the function of RNA modifications. *Genome Biol.* **13**, 175.
- 685 2 Meyer KD, Saletore Y, Zumbo P, Elemento O, Mason CE & Jaffrey SR (2012)
686 Comprehensive analysis of mRNA methylation reveals enrichment in 3' UTRs and near
687 stop codons. *Cell* **149**, 1635–1646.
- 688 3 Dominissini D, Moshitch-moshkovitz S, Schwartz S, Salmon-Divon M, Ungar L, Osenberg
689 S, Cesarkas K, Jacob-hirsch J, Amariglio N, Kupiee M, Sorek R & Rechavi G (2012)
690 Topology of the human and mouse m⁶A RNAmethylomes revealed by m⁶A-seq.
691 *Nature* **485**, 201–206.
- 692 4 Ke S, Alemu EA, Mertens C, Gantman EC, Fak JJ, Mele A, Haripal B, Zucker-Scharff I,
693 Moore MJ, Park CY, Vågbø CB, Kusnierczyk A, Klungland A, Darnell JE, Darnell RB,
694 Kuśnierczyk A, Klungland A, Darnell JE, Darnell RB, Kusnierczyk A, Klungland A,
695 Darnell JE & Darnell RB (2015) A majority of m⁶A residues are in the last exons,
696 allowing the potential for 3' UTR regulation. *Genes Dev.* **29**, 2037–2053.
- 697 5 Meyer KD, Patil DP, Zhou J, Zinoviev A, Skabkin MA, Elemento O, Pestova T V., Qian SB
698 & Jaffrey SR (2015) 5' UTR m⁶A Promotes Cap-Independent Translation. *Cell* **163**,
699 999–1010.
- 700 6 Pendleton KE, Chen B, Liu K, Hunter O V., Xie Y, Tu BP & Conrad NK (2017) The U6
701 snRNA m⁶A Methyltransferase METTL16 Regulates SAM Synthetase Intron Retention.
702 *Cell* **169**, 824-835.e14.
- 703 7 Lence T, Akhtar J, Bayer M, Schmid K, Spindler L, Ho CH, Kreim N, Andrade-Navarro MA,
704 Poeck B, Helm M & Roignant JY (2016) M⁶A modulates neuronal functions and sex
705 determination in *Drosophila*. *Nature* **540**, 242–247.
- 706 8 Bokar JA, Shambaugh ME, Polayes D, Matera AG & Rottman FM (1997) Purification and
707 cDNA cloning of the AdoMet-binding subunit of the human mRNA (N⁶-adenosine)-
708 methyltransferase. *RNA* **3**, 1233–47.
- 709 9 Liu J, Yue Y, Han D, Wang X, Fu YY, Zhang L, Jia G, Yu M, Lu Z, Deng X, Dai Q, Chen W
710 & He C (2013) A METTL3–METTL14 complex mediates mammalian nuclear RNA N⁶-
711 adenosine methylation. *Nat. Chem. Biol.* **10**, 93–95.
- 712 10 Wang X, Feng J, Xue Y, Guan Z, Zhang D, Liu Z, Gong Z, Wang Q, Huang J, Tang C,
713 Zou T & Yin P (2016) Structural basis of N⁶-adenosine methylation by the METTL3-
714 METTL14 complex. *Nature* **534**, 575–578.
- 715 11 Ping X-LL, Sun B-FF, Wang L, Xiao W, Yang X, Wang W-JJ, Adhikari S, Shi Y, Lv Y,
716 Chen Y-SS, Zhao X, Li A, Yang YGYY-G, Dahal U, Lou X-MM, Liu X, Huang J, Yuan W-
717 PP, Zhu X-FF, Cheng T, Zhao Y-LL, Wang X, Danielsen JMRR, Liu F & Yang YGYY-G
718 (2014) Mammalian WTAP is a regulatory subunit of the RNA N⁶-methyladenosine
719 methyltransferase. *Cell Res.* **24**, 177–189.
- 720 12 Yue Y, Liu J, Cui X, Cao J, Luo G, Zhang Z, Cheng T, Gao M, Shu X, Ma H, Wang F,
721 Wang X, Shen B, Wang Y, Feng X, He C & Liu J (2018) VIRMA mediates preferential
722 m⁶A mRNA methylation in 3'UTR and near stop codon and associates with alternative
723 polyadenylation. *Cell Discov.* **4**, 10.
- 724 13 Růžička K, Zhang M, Campilho A, Bodi Z, Kashif M, Saleh M, Eeckhout D, El-Showk S, Li
725 H, Zhong S, Jaeger G De, Mongan NP, Hejátko J, Helariutta Y & Fray RG (2017)
726 Identification of factors required for m⁶A mRNA methylation in *Arabidopsis* reveals a

- 1
2
3 727 role for the conserved E3 ubiquitin ligase HAKAI. *New Phytol.* **215**, 157–172.
4
- 5 728 14 Knuckles P, Lence T, Haussmann IU, Jacob D, Kreim N, Carl SH, Masiello I, Hares T,
6 729 Villaseñor R, Hess D, Andrade-Navarro MA, Biggiogera M, Helm M, Soller M, Bühler M
7 730 & Roignant J-YY (2018) Zc3h13/Flacc is required for adenosine methylation by bridging
8 731 the mRNA-binding factor Rbm15/Spenito to the m⁶A machinery component
9 732 Wtap/Fl(2)d. *Genes Dev.* **32**, 1–15.
10
- 11 733 15 Patil DP, Chen CK, Pickering BF, Chow A, Jackson C, Guttman M & Jaffrey SR (2016)
12 734 m⁶A RNA methylation promotes XIST-mediated transcriptional repression. *Nature* **537**,
13 735 369–373.
14
- 15 736 16 Zheng G, Dahl JA, Niu Y, Fedorcsak P, Huang CM, Li CJ, Vågbo CB, Shi Y, Wang WL,
16 737 Song SH, Lu Z, Bosmans RPG, Dai Q, Hao YJ, Yang X, Zhao WM, Tong WM, Wang
17 738 XJ, Bogdan F, Furu K, Fu Y, Jia G, Zhao X, Liu J, Krokan HE, Klungland A, Yang YG &
18 739 He C (2013) ALKBH5 Is a Mammalian RNA Demethylase that Impacts RNA Metabolism
19 740 and Mouse Fertility. *Mol. Cell* **49**, 18–29.
20
- 21 741 17 Mauer J, Luo X, Blanjoie A, Jiao X, Grozhik A V, Patil DP, Linder B, Pickering BF,
22 742 Vasseur J-J, Chen Q, Gross SS, Elemento O, Debart F, Kiledjian M & Jaffrey SR (2017)
23 743 Reversible methylation of m⁶Am in the 5' cap controls mRNA stability. *Nature* **541**, 371–
24 744 375.
25
- 26 745 18 Jia G, Fu Y, Zhao X, Dai Q, Zheng G, Yang YGYG-GGYG-G, Yi C, Lindahl T, Pan T,
27 746 Yang YGYG-GGYG-G & He C (2011) N⁶-Methyladenosine in nuclear RNA is a major
28 747 substrate of the obesity-associated FTO. *Nat. Chem. Biol.* **7**, 885–887.
29
- 30 748 19 Wang X, Lu Z, Gomez A, Hon GC, Yue Y, Han D, Fu Y, Parisien M, Dai Q, Jia G, Ren B,
31 749 Pan T, He C, Zhike L, Gomez A, Hon GC, Yue Y, Han D, Fu Y, Årisien M, Dai Q, Jia G,
32 750 Ren B, Pan T & He C (2014) N⁶-methyladenosine-dependent regulation of messenger
33 751 RNA stability. *Nature* **505**, 117–120.
34
- 35 752 20 Wang X, Zhao BS, Roundtree IA, Lu Z, Han D, Ma H, Weng X, Chen K, Shi H & He C
36 753 (2015) N⁶-methyladenosine modulates messenger RNA translation efficiency. *Cell* **161**,
37 754 1388–1399.
38
- 39 755 21 Hsu PJ, Zhu Y, Ma H, Guo Y, Shi X, Liu Y, Qi M, Lu Z, Shi H, Wang J, Cheng Y, Luo G,
40 756 Dai Q, Liu M, Guo X, Sha J, Shen B & He C (2017) Ythdc2 is an N⁶-methyladenosine
41 757 binding protein that regulates mammalian spermatogenesis. *Cell Res.* **27**, 1115–1127.
42
- 43 758 22 Shi H, Wang X, Lu Z, Zhao BS, Ma H, Hsu PJ, Liu C & He C (2017) YTHDF3 facilitates
44 759 translation and decay of N⁶-methyladenosine-modified RNA. *Cell Res.* **27**, 315–328.
45
- 46 760 23 Xiao W, Adhikari S, Dahal U, Chen Y-S, Hao Y-J, Sun B-F, Sun H-Y, Li A, Ping X-L, Lai
47 761 W-Y, Wang XX-J, Ma H-L, Huang C-M, Yang YY-G, Huang N, Jiang G-B, Wang H-L,
48 762 Zhou Q, Wang XX-J, Zhao Y-L & Yang YY-G (2016) Nuclear m⁶A Reader YTHDC1
49 763 Regulates mRNA Splicing. *Mol. Cell* **61**, 507–519.
50
- 51 764 24 Roundtree IA, Luo G-ZZ, Zhang Z, Wang X, Zhou T, Cui Y, Sha J, Huang X, Guerrero L,
52 765 Xie P, He E, Shen B & He C (2017) YTHDC1 mediates nuclear export of N⁶-
53 766 methyladenosine methylated mRNAs. *Elife* **6**, 1–28.
54
- 55 767 25 Alarcón CR, Goodarzi H, Lee H, Liu X, Tavazoie SFSSF & Tavazoie SFSSF (2015)
56 768 HNRNPA2B1 Is a Mediator of m⁶A-Dependent Nuclear RNA Processing Events. *Cell*
57 769 **162**, 1299–1308.
58
- 59 770 26 Huang H, Weng H, Sun W, Qin X, Shi H, Wu H, Zhao BS, Mesquita A, Liu C, Yuan CL,
60 771 Hu YC, Hüttelmaier S, Skibbe JR, Su R, Deng X, Dong L, Sun M, Li C, Nachtergaele S,

- 1
2
3 772 Wang Y, Hu C, Ferchen K, Greis KD, Jiang X, Wei M, Qu L, Guan JL, He C, Yang J &
4 773 Chen J (2018) Recognition of RNA N6-methyladenosine by IGF2BP proteins enhances
5 774 mRNA stability and translation. *Nat. Cell Biol.* **20**, 285–295.
- 6
7 775 27 Wu R, Li A, Sun B, Sun J-GG, Zhang J, Zhang T, Chen Y, Xiao Y, Gao Y, Zhang Q, Ma J,
8 776 Yang X, Liao Y, Lai W-YY, Qi X, Wang S, Shu Y, Wang H-LL, Wang F, Yang Y-GG &
9 777 Yuan Z (2018) A novel m6A reader Prrc2a controls oligodendroglial specification and
10 778 myelination. *Cell Res.* **29**, 23–41.
- 11
12 779 28 Bertero A, Brown S, Madrigal P, Osnato A, Ortmann D, Yiangou L, Kadiwala J, Hubner
13 780 NC, De Los Mozos IR, Sadee C, Lenaerts A-SS, Nakanoh S, Grandy R, Farnell E, Ule
14 781 J, Stunnenberg HG, Mendjan S, Vallier L, Sadée C, Lenaerts A-SS, Nakanoh S, Grandy
15 782 R, Farnell E, Ule J, Stunnenberg HG, Mendjan S & Vallier L (2018) The SMAD2/3
16 783 interactome reveals that TGF β controls m 6 A mRNA methylation in pluripotency.
17 784 *Nature* **555**, 256–259.
- 18
19 785 29 Kwon J, Jo YJ, Namgoong S & Kim NH (2019) Functional roles of hnRNPA2/B1 regulated
20 786 by METTL3 in mammalian embryonic development. *Sci. Rep.* **9**, 8640.
- 21
22 787 30 Geula S, Moshitch-Moshkovitz S, Dominissini D, Mansour AAF, Kol N, Salmon-Divon M,
23 788 Hershkovitz V, Peer E, Mor N, Manor YS, Ben-Haim MS, Eyal E, Yunger S, Pinto Y,
24 789 Jaitin DA, Viukov S, Rais Y, Krupalnik V, Chomsky E, Zerbib M, Maza I, Rechavi Y,
25 790 Massarwa R, Hanna S, Amit I, Levanon EY, Amariglio N, Stern-Ginossar N,
26 791 Novershtern N, Rechavi G & Hanna JH (2015) m6A mRNA methylation facilitates
27 792 resolution of naïve pluripotency toward differentiation. *Science (80-.)*. **347**, 1002–1006.
- 28
29 793 31 Batista PJ, Molinie B, Wang J, Qu K, Zhang J, Li L, Bouley DM, Lujan E, Haddad B,
30 794 Daneshvar K, Carter AC, Flynn RA, Zhou C, Lim KS, Dedon P, Wernig M, Mullen AC,
31 795 Xing Y, Giallourakis CC, Chang HY, Howard Y, Batista PJ, Molinie B, Wang J, Qu K,
32 796 Zhang J, Li L, Bouley DM, Dedon P, Wernig M, Mullen AC, Xing Y, Giallourakis CC &
33 797 Chang HY (2014) M⁶A RNA modification controls cell fate transition in mammalian
34 798 embryonic stem cells. *Cell Stem Cell* **15**, 707–719.
- 35
36 799 32 Wojtas MN, Pandey RR, Mendel M, Homolka D, Sachidanandam R & Pillai RS (2017)
37 800 Regulation of m6A Transcripts by the 3'→5' RNA Helicase YTHDC2 Is Essential for a
38 801 Successful Meiotic Program in the Mammalian Germline. *Mol. Cell* **68**, 374-387.e12.
- 39
40 802 33 Zhao BS, Wang X, Beadell A V., Lu Z, Shi H, Kuuspalu A, Ho RK & He C (2017) M6A-
41 803 dependent maternal mRNA clearance facilitates zebrafish maternal-to-zygotic transition.
42 804 *Nature* **542**, 475–478.
- 43
44 805 34 Kan L, Grozhik A V., Vedanayagam J, Patil DP, Pang N, Lim K-S, Huang Y-C, Joseph B,
45 806 Lin C-J, Despic V, Guo J, Yan D, Kondo S, Deng W-M, Dedon PC, Jaffrey SR & Lai EC
46 807 (2017) The m6A pathway facilitates sex determination in *Drosophila*. *Nat. Commun.* **8**,
47 808 15737.
- 48
49 809 35 Kasowitz SD, Ma J, Anderson SJ, Leu NA, Xu Y, Gregory BD, Schultz RM & Wang PJ
50 810 (2018) Nuclear m 6 A reader YTHDC1 regulates alternative polyadenylation and splicing
51 811 during mouse oocyte development. *PLoS Genet.* **14**, 1–28.
- 52
53 812 36 Ivanova I, Much C, Di Giacomo M, Azzi C, Morgan M, Moreira PN, Monahan J, Carrieri C,
54 813 Enright AJ, O'Carroll D, Giacomo M Di, Azzi C, Morgan M, Moreira PN, Monahan J,
55 814 Carrieri C, Enright AJ, O'carroll D, Di Giacomo M, Azzi C, Morgan M, Moreira PN,
56 815 Monahan J, Carrieri C, Enright AJ & O'carroll D (2017) The RNA m 6 A Reader
57 816 YTHDF2 Is Essential for the Post-transcriptional Regulation of the Maternal
58 817 Transcriptome and Oocyte Competence. *Mol. Cell* **67**, 1059-1067.e4.
- 59
60

- 1
2
3 818 37 Lence T, Paolantoni C, Worpenberg L & Roignant JY (2019) Mechanistic insights into m⁶A
4 819 A RNA enzymes. *Biochim. Biophys. Acta - Gene Regul. Mech.* **1862**, 222–229.
5
6 820 38 Balacco DL & Soller M (2018) The m⁶A writer: Rise of a machine for growing tasks.
7 821 *Biochemistry* **58**, acs.biochem.8b01166.
8
9 822 39 Lence T, Soller M & Roignant JY (2017) A fly view on the roles and mechanisms of the
10 823 m⁶A mRNA modification and its players. *RNA Biol.* **14**, 1232–1240.
11
12 824 40 Robbens S, Rouzé P, Cock JM, Spring J, Worden AZ & Van De Peer Y (2008) The FTO
13 825 gene, implicated in human obesity, is found only in vertebrates and marine algae. *J.*
14 826 *Mol. Evol.* **66**, 80–84.
15
16 827 41 Zhang G, Huang H, Liu D, Cheng Y, Liu X, Zhang W, Yin R, Zhang D, Zhang P, Liu J, Li
17 828 C, Liu B, Luo Y, Zhu Y, Zhang N, He S, He C, Wang H & Chen D (2015) N⁶-
18 829 methyladenine DNA modification in *Drosophila*. *Cell* **161**, 893–906.
19
20 830 42 Greer EL, Blanco MA, Gu L, Sendinc E, Liu J, Aristizábal-Corrales D, Hsu CH, Aravind L,
21 831 He C & Shi Y (2015) DNA methylation on N⁶-adenine in *C. elegans*. *Cell* **161**, 868–878.
22
23 832 43 Riviere G, He Y, Tecchio S, Crowell E, Sourdain P, Guo X & Favrel P (2017) Dynamics
24 833 of DNA methylomes underlie oyster development. *PLOS Genet.* **13**, 1–16.
25
26 834 44 Sussarellu R, Lebreton M, Rouxel J, Akcha F, Riviere G & Rivière G (2018) Copper
27 835 induces expression and methylation changes of early development genes in
28 836 *Crassostrea gigas* embryos. *Aquat. Toxicol.* **196**, submitted.
29
30 837 45 Rondon R, Grunau C, Fallet M, Charlemagne N, Sussarellu R, Chaparro C, Montagnani
31 838 C, Mitta G, Bachère E, Akcha F & Cosseau C (2017) Effects of a parental exposure to
32 839 diuron on Pacific oyster spat methylome. *Environ. Epigenetics* **3**, 1–13.
33
34 840 46 Riviere G, Wu G-CC, Fellous A, Goux D, Sourdain P & Favrel P (2013) DNA Methylation
35 841 Is Crucial for the Early Development in the Oyster *C. gigas*. *Mar. Biotechnol.* **15**, 1–15.
36
37 842 47 Saint-Carlier E & Riviere G (2015) Regulation of Hox orthologues in the oyster
38 843 *Crassostrea gigas* evidences a functional role for promoter DNA methylation in an
39 844 invertebrate. *FEBS Lett.* **589**, 1459–1466.
40
41 845 48 Fellous A, Favrel P & Riviere G (2015) Temperature influences histone methylation and
42 846 mRNA expression of the Jmj-C histone-demethylase orthologues during the early
43 847 development of the oyster *Crassostrea gigas*. *Mar. Genomics* **19**, 23–30.
44
45 848 49 Fellous A, Favrel P, Guo X & Riviere G (2014) The Jumonji gene family in *Crassostrea*
46 849 *gigas* suggests evolutionary conservation of Jmj-C histone demethylases orthologues in
47 850 the oyster gametogenesis and development. *Gene* **538**, 164–175.
48
49 851 50 Fellous A, Le Franc L, Jouaux A, Goux D, Favrel P & Rivière G (2019) Histone
50 852 Methylation Participates in Gene Expression Control during the Early Development of
51 853 the Pacific Oyster *Crassostrea gigas*. *Genes (Basel)*. **10**, 695.
52
53 854 51 Zhou J, Wan J, Gao X, Zhang X, Jaffrey SR & Qian S-B (2015) Dynamic m⁶A mRNA
54 855 methylation directs translational control of heat shock response. *Nature* **526**, 591–594.
55
56 856 52 Lu Z, Ma Y, Li Q, Liu E, Jin M, Zhang L & Wei C (2019) The role of N⁶-methyladenosine
57 857 RNA methylation in the heat stress response of sheep (*Ovis aries*). *Cell Stress*
58 858 *Chaperones* **24**, 333–342.
59
60 859 53 Xiang Y, Laurent B, Hsu C, Nachtergaele S, Lu Z, Sheng W, Xu C, Chen H, Ouyang J,

- 1
2
3 860 Wang S, Ling D, Hsu P, Zou L, Jambhekar A & He C (2017) m6A RNA methylation
4 861 regulates the UV-induced DNA damage response. *Nature* **543**, 573–576.
5
6 862 54 Cayir A, Barrow TM, Guo L & Byun HM (2019) Exposure to environmental toxicants
7 863 reduces global N6-methyladenosine RNA methylation and alters expression of RNA
8 864 methylation modulator genes. *Environ. Res.* **175**, 228–234.
9
10 865 55 Liu J, Li K, Cai J, Zhang M, Zhang X, Xiong X, Meng H, Xu X, Huang Z, Fan J & Yi C
11 866 (2019) Landscape and Regulation of M⁶A and M⁶Am Methylome Across Human and
12 867 Mouse Tissues. *SSRN Electron. J.*, 1–56.
13
14 868 56 Ren W, Lu J, Huang M, Gao L, Li D, Greg Wang G & Song J (2019) Structure and
15 869 regulation of ZCCHC4 in m6A-methylation of 28S rRNA. *Nat. Commun.* **10**, 5042.
16
17 870 57 Bokar JA, Shambaugh ME, Polayes D, Matera AG & Rottman FM (1997) Purification and
18 871 cDNA cloning of the AdoMet-binding subunit of the human mRNA (N6-adenosine)-
19 872 methyltransferase. *RNA* **3**, 1233–1247.
20
21 873 58 Theler D, Dominguez C, Blatter M, Boudet J & Allain FHT (2014) Solution structure of the
22 874 YTH domain in complex with N6-methyladenosine RNA: A reader of methylated RNA.
23 875 *Nucleic Acids Res.* **42**, 13911–13919.
24
25 876 59 Shima H, Matsumoto M, Ishigami Y, Ebina M, Muto A, Sato Y, Kumagai S, Ochiai K,
26 877 Suzuki T & Igarashi K (2017) S-Adenosylmethionine Synthesis Is Regulated by
27 878 Selective N6-Adenosine Methylation and mRNA Degradation Involving METTL16 and
28 879 YTHDC1. *Cell Rep.* **21**, 3354–3363.
29
30 880 60 Yurchenko O V., Skiteva OI, Voronezhskaya EE & Dyachuk VA (2018) Nervous system
31 881 development in the Pacific oyster, *Crassostrea gigas* (Mollusca: Bivalvia). *Front. Zool.*
32 882 **15**, 1–21.
33
34 883 61 Ratnaparkhi A (2013) Signaling by folded gastrulation is modulated by mitochondrial
35 884 fusion and fission. *J. Cell Sci.* **126**, 5369–5376.
36
37 885 62 Ren L, Zhang C, Tao L, Hao J, Tan K, Miao K, Yu Y, Sui L, Wu Z, Tian J & An L (2017)
38 886 High-resolution profiles of gene expression and DNA methylation highlight mitochondrial
39 887 modifications during early embryonic development. *J. Reprod. Dev.* **63**, 247–261.
40
41 888 63 Prudent J, Popgeorgiev N, Bonneau B, Thibaut J, Gadet R, Lopez J, Gonzalo P, Rimokh
42 889 R, Manon S, Houart C, Herbomel P, Aouacheria A & Gillet G (2013) Bcl-wav and the
43 890 mitochondrial calcium uniporter drive gastrula morphogenesis in zebrafish. *Nat.*
44 891 *Commun.* **4**.
45
46 892 64 Dumollard R, Duchon M & Carroll J (2007) The Role of Mitochondrial Function in the
47 893 Oocyte and Embryo. *Curr. Top. Dev. Biol.* **77**, 21–49.
48
49 894 65 Huang H, Weng H, Zhou K, Wu T, Zhao BS, Sun MM, Chen Z, Deng X, Xiao G, Auer F,
50 895 Klemm L, Wu H, Zuo Z, Qin X, Dong Y, Zhou Y, Qin H, Tao S, Du J, Liu J, Lu Z, Yin H,
51 896 Mesquita A, Yuan CL, Hu Y-CC, Sun W, Su R, Dong L, Shen C, Li C, Qing Y, Jiang X,
52 897 Wu X, Sun MM, Guan J-LL, Qu L, Wei M, Müschen M, Huang G, He C, Yang J & Chen
53 898 J (2019) Histone H3 trimethylation at lysine 36 guides m6A RNA modification co-
54 899 transcriptionally. *Nature* **567**, 414–419.
55
56 900 66 Wang Y, Li Y, Yue M, Wang J, Kumar S, Wechsler-Reya RJ, Zhang Z, Ogawa Y, Kellis M,
57 901 Duyster G & Zhao JC (2018) N6-methyladenosine RNA modification regulates
58 902 embryonic neural stem cell self-renewal through histone modifications. *Nat. Neurosci.*
59 903 **21**, 195–206.
60

- 1
2
3 904 67 Petton B, Pernet F, Robert R & Boudry P (2013) Temperature influence on pathogen
4 905 transmission and subsequent mortalities in juvenile pacific oysters *Crassostrea gigas*.
5 906 *Aquac. Environ. Interact.* **3**, 257–273.
6
7 907 68 Riviere G, Fellous A, Franco A, Bernay B & Favrel P (2011) A crucial role in fertility for the
8 908 oyster angiotensin-converting enzyme orthologue CgACE. *PLoS One* **6**.
9
10 909 69 EMA (2011) *Guideline on bioanalytical method validation*.
11 910 *EMA/CHMP/EWP/192217/2009*.
12
13 911 70 Riviere G, Klopp C, Ibouniyamine N, Huvet A, Boudry P & Favrel P (2015) GigaTON: An
14 912 extensive publicly searchable database providing a new reference transcriptome in the
15 913 pacific oyster *Crassostrea gigas*. *BMC Bioinformatics* **16**, 1–12.
16
17 914 71 Zhang G, Fang X, Guo X, Li L, Luo R, Xu F, Yang P, Zhang L, Wu F, Chen Y, Wang J,
18 915 Peng C, Meng J, Yang L, Liu J, Wen B, Zhang N & Huang Z (2012) The oyster genome
19 916 reveals stress adaptation and complexity of shell formation. *Nature* **490**, 49–54.
20
21 917 72 Li B, Ruotti V, Stewart RM, Thomson JA & Dewey CN (2010) RNA-Seq gene expression
22 918 estimation with read mapping uncertainty. *Bioinformatics* **26**, 493–500.
23
24 919 73 Qi ST, Ma JY, Wang ZB, Guo L, Hou Y & Sun QY (2016) N6 -methyladenosine
25 920 sequencing highlights the involvement of mRNA methylation in oocyte meiotic
26 921 maturation and embryo development by regulating translation in *xenopus laevis*. *J. Biol.*
27 922 *Chem.* **291**, 23020–23026.
28
29 923 74 Altschul SF, Madden TL, Schäffer AA, Zhang J, Zhang Z, Miller W & Lipman DJ (1997)
30 924 Gapped BLAST and PSI-BLAST: a new generation of protein database search
31 925 programs. *Nucleic Acids Res.* **25**, 3389–3402.
32
33 926 75 Cock PJA, Chilton JM, Grüning B, Johnson JE & Soranzo N (2015) NCBI BLAST+
34 927 integrated into Galaxy. *Gigascience* **4**, 0–6.
35
36 928 76 Camacho C, Coulouris G, Avagyan V, Ma N, Papadopoulos J, Bealer K & Madden TL
37 929 (2009) BLAST+: Architecture and applications. *BMC Bioinformatics* **10**, 1–9.
38
39 930 77 Young MD, Wakefield MJ, Smyth GK & Oshlack A (2010) Gene ontology analysis for
40 931 RNA-seq: accounting for selection bias. *Genome Biol.* **11**, R14.
41
42 932 78 Supek F, Bošnjak M, Škunca N & Šmuc T (2011) Revigo summarizes and visualizes long
43 933 lists of gene ontology terms. *PLoS One* **6**.
44
45 934 79 Larsson J (2019) eulerr: Area-Proportional Euler and Venn Diagrams with Ellipses. .
46
47 935 80 Gu Z, Eils R & Schlesner M (2016) Complex heatmaps reveal patterns and correlations in
48 936 multidimensional genomic data. *Bioinformatics* **32**, 2847–2849.
49
50 937
51
52 938
53
54
55
56
57
58
59
60

1
2
3 939 **Figure legends**
4
5

6 940 Figure 1: m⁶A levels across oyster development.
7
8
9

10 941 **A.** m⁶A level quantified by LC-MS/MS in *Crassostrea gigas* embryo-larval stages pooled from
11
12 942 oocytes to D-larvae (n= 3) is compared to the m⁶A level in *Homo sapiens* and *Drosophila*
13
14 943 *melanogaster*; **B.** Dot blot quantification of m⁶A in total RNA throughout oyster development
15
16 944 (n=3); **C.** Dot blot quantification of m⁶A in polyA+ RNAs throughout oyster development (n=3)
17
18 945 Kruskal-Wallis test, $\alpha < 0,05$. E: Egg, F E: fertilized egg, 2/8C: two to eight cell embryos, M:
19
20 946 Morula, B: Blastula, G: Gastrula, T: Trochophore, D: D larvae. Chemiluminescence (B) and
21
22 947 fluorescence (C) are measured as a ratio between dot intensity of development stages and
23
24 948 their respective controls for each amount of RNA (120ng, 60ng and 30ng).
25
26
27
28
29
30
31
32
33
34
35

36 950 Figure 2: The putative conserved m⁶A machinery in *Crassostrea gigas*.
37
38
39

40 951 Domain architecture of actors of the m⁶A machinery identified by *in silico* analyses in the oyster
41
42 952 compared to the fruit fly and human, **A.** Writer proteins; **B.** Eraser protein; **C.** Reader proteins.
43
44 953 Putative domains involved in m⁶A processes are coloured (writers, green; eraser, red; readers,
45
46 954 blue). Other domains identified but not involved in m⁶A processes are indicated in grey. Only
47
48 955 one isoform is represented for each protein and each species for clarity (see supplementary
49
50 956 figure S2 for other isoforms).
51
52
53
54
55
56

57 958 Figure 3: Gene expression of the putative m⁶A machinery throughout oyster development
58
59
60

1
2
3 959 Expression levels of writers (**A**), eraser (**B**) and readers (**C**) identified by *in silico* analysis at
4
5
6 960 each development stage were inferred from the GigaTON database. Expression levels are
7
8 961 given in Transcripts Per kilobases per Million Reads (TPM) as the mean of the GigaTON values
9
10
11 962 according to the table S2. E: Egg, 2/8C: two to eight cell, M: Morula, B: Blastula, G: Gastrula,
12
13
14 963 T: Trochophore, D: D larvae, S: Spat, J: Juvenile.

15
16 964

17
18
19 965 Figure 4: Characterization of m⁶A-RNA binding proteins in oyster development.

20
21 966 **A.** Venn diagrams representation of proteins bound to the A- and/or m⁶A- oligos in nuclear and
22
23
24 967 cytosolic fractions of oyster embryo-larval stages. The number of proteins identified is
25
26
27 968 indicated. Some actors characterized in this study are highlighted: eIF3, YTHC1, hnRNPA2B1
28
29 969 and IGF2BP. **B.** Heatmap of gene expression levels of the proteins that bind specifically to the
30
31
32 970 m⁶A-oligo throughout oyster development. The expression level is normalized regarding the
33
34
35 971 maximum value for each gene according to the GigaTON database. **C.** GO term distribution
36
37 972 among the three expression clusters in B. **D.** Examples of GO term enrichment within the
38
39
40 973 expression clusters of the m⁶A-bound proteins. The $-\log_{10}(\text{p-value})$ associated to each term
41
42
43 974 is given. E: Egg, 2/8C: two to eight cells, M: Morula, B: Blastula, G: Gastrula, T: Trochophore,
44
45 975 D: D larvae, S: Spat, J: Juvenile.

46
47
48 976
49
50
51
52
53
54
55
56
57
58
59
60

1
2
3 977 **Supporting information:**

4
5 978 Data S1: Complete list of *in silico* identified putative m⁶A machinery proteins and their
6
7
8 979 respective BLAST results

9
10 980 Data S2: Identified proteins by RNA pull down coupled with mass spectrometry with m⁶A or
11
12
13 981 A-oligo, in nuclear or cytosolic protein extracts

14
15 982 Data S3: Complete list of GO terms of clustered genes of m⁶A interacting proteins (p-
16
17
18 983 value<0,05)

19
20 984 Table S1: Transitions used for each compound. A: first transition, B: second transition

21
22
23 985 Table S2: Table of correspondence between development stages in our study, and the
24
25
26 986 GigaTON database.

27
28
29 987
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

1
2
3 1 **A functional m⁶A-RNA methylation pathway in the oyster *Crassostrea gigas***
4
5
6 2 **assumes epitranscriptomic regulation of lophotrochozoan development**
7
8
9 3

10
11 4 **Authors**
12

13
14 5 Lorane LE FRANC¹, Benoit BERNAY², Bruno PETTON³, Marc SINCE⁴, Pascal FAVREL¹ and
15
16 6 Guillaume RIVIERE¹
17
18
19 7

20
21
22 8 **Addresses**
23

24
25 9 ¹Normandie Univ, UNICAEN, CNRS, BOREA, 14000 Caen, France.
26

27 10 Laboratoire Biologie des organismes et Ecosystèmes aquatiques (BOREA), Muséum
28
29 11 d'Histoire naturelle, Sorbonne Université, Université de Caen Normandie, Université des
30
31 12 Antilles, CNRS, IRD, Esplanade de la paix, 14032 Caen, France.
32
33

34
35 13 ²Normandie Univ, UNICAEN, SF ICORE, PROTEOGEN core facility, 14000 Caen, France
36

37
38 14 ³Ifremer, Laboratoire des Sciences de l'Environnement Marin, UMR 6539
39
40 15 CNRS/UBO/IRD/Ifremer, Centre Bretagne, 29280, Plouzané, France
41
42

43 16 ⁴ Normandie Univ, UNICAEN, Comprehensive Cancer Center F. Baclesse, SF ICORE,
44
45 17 PRISMM core facility, 14000 Caen, France.
46
47

48
49
50
51 19 **Corresponding author**
52

53 20 Guillaume Rivière (0033231565113 ; guillaume.riviere@unicaen.fr) , Normandie Univ,
54
55 21 UNICAEN, CNRS, BOREA, 14000 Caen, France (<https://borea.mnhn.fr/>). Tel :
56
57
58
59 22
60

1
2
3 **23 Running title**

4
5
6 **24 m⁶A-RNA methylation pathway in oyster development**

7
8 **25**

9
10
11 **26 Abbreviations**

12
13 **27 N⁶-methyladenosine (m⁶A), Methyltransferase like (METTL), Wilms' tumor 1-associated**
14
15
16 **28 protein (WTAP), RNA-binding motif 15 (RBM15), Ring finger E3 ubiquitin ligase (HAKAI), Zinc**
17
18
19 **29 finger CCCH-type containing 13 (ZC3H13), AlkB homologue 5 (ALKBH5), Fat mass and**
20
21
22 **30 obesity associated protein (FTO), YTH domain family protein (YTHDF), YTH domain**
23
24 **31 containing protein (YTHDC), Heterogeneous nuclear ribonucleoproteins A2 B1**
25
26
27 **32 (HNRNPA2B1), Proline rich coiled-coil 2a (Prcc2a), Eukaryotic initiation factor 3 (eIF3), Sterile**
28
29
30 **33 sea water (SSW), Oocytes (E), Fertilized oocytes (F E), Two to eight cell embryos (2/8 C),**
31
32
33 **34 Hours post fertilization (hpf), Morula (M), Blastula (B), Gastrula (G), D larvae (D), solid-phase**
34
35
36 **35 reversible immobilization (SPRI), TPM (Transcripts Per Million), Gene ontology (GO), oyster**
37
38
39 **36 m⁶A-interacting protein (Cg-m⁶A-BPs), S-adenosyl-methionine (SAM), maternal-to-zygotic**
40
41
42 **37 transition (MZT), acetonitrile (ACN)**

43
44 **38**

45 **39 Keywords**

46
47
48 **40 RNA, methylation, epitranscriptomics, oyster, development.**

49
50
51 **41**

52
53
54 **42 Conflicts of interest**

55
56
57
58 **43 The authors declare they have no competing conflict of interest**
59
60

Abstract

N^6 -methyladenosine (m^6A) is a prevalent epitranscriptomic mark in eukaryotic RNA, with crucial roles for mammalian and ecdysozoan development. Indeed, m^6A -RNA and the related protein machinery are important for splicing, translation, maternal-to-zygotic transition and cell differentiation. However, to date, the presence of an m^6A -RNA pathway remains unknown in more distant animals, questioning the evolution and significance of the epitranscriptomic regulation. Therefore, we investigated the m^6A -RNA pathway in the oyster *Crassostrea gigas*, a lophotrochozoan model whose development was demonstrated under strong epigenetic influence.

Using mass spectrometry and dot blot assays, we demonstrated that m^6A -RNA is actually present in the oyster and displays variations throughout early oyster development, with the lowest levels at the end of cleavage. In parallel, by *in silico* analyses, we were able to characterize at the molecular level a complete and conserved putative m^6A -machinery. The expression levels of the identified putative m^6A writers, erasers and readers were strongly regulated across oyster development. Finally, RNA pull-down coupled to LC-MS/MS allowed us to prove the actual presence of readers able to bind m^6A -RNA and exhibiting specific developmental patterns.

Altogether, our results demonstrate the conservation of a complete m^6A -RNA pathway in the oyster and strongly suggest its implication in early developmental processes including MZT.

This first demonstration and characterization of an epitranscriptomic regulation in a lophotrochozoan model, potentially involved in the embryogenesis, brings new insights into our understanding of developmental epigenetic processes and their evolution.

66 Introduction

67
68 The *N*⁶-methyladenosine (m⁶A) is the prevalent chemical RNA modification in all eukaryotic
69 coding and non-coding RNAs [1]. Messenger RNAs are the most heavily m⁶A methylated
70 RNAs, with m⁶A bases lying mostly in their 3' UTRs, at the vicinity of their stop codon [2–4]
71 and also in 5' UTRs and long internal exons [4,5]. *N*⁶-methylation of RNA adenosines is
72 responsible for RNA processing and, like DNA methylation or histone modifications,
73 contributes to the regulation of gene expression without changing the DNA or mRNA
74 sequence. Therefore m⁶A constitutes a new layer of post-transcriptional gene regulation, which
75 is emerging or has been proven critical in various biological processes, and referred to as
76 epitranscriptomic [2].

77
78 The dynamics and biological outcomes of m⁶A levels are the results of the activity of a complex
79 protein machinery comprising writers, erasers and readers. The addition of a methyl group to
80 the 6th nitrogen of RNA adenosines is catalysed by m⁶A writers with distinct properties.
81 Methyltransferase like 16 (METTL16) is a 'stand-alone' class I methyltransferase that
82 recognizes the UACA*GAGAA consensus sequence (with * indicating the target adenosine)
83 [6]. By contrast, METTL3 transfers methyl groups to adenosines within the RRA*CH motif
84 [2,3,7]. METTL3 is only active within a tripartite 'core complex' [8] comprising METTL3,
85 METTL14 which enhances the methyltransferase activity supported by the MTA-70 domain of
86 METTL3 [9,10] and the regulator protein Wilms' tumor 1-associated protein (WTAP) [4,9,11].
87 This core complex can interact with Virilizer-like (or KIAA1429) [12], ring finger E3 ubiquitin

1
2
3 88 ligase (HAKAI) [12,13], zinc finger CCCH-type containing 13 (ZC3H13) [12,14], RNA-binding
4
5
6 89 motif 15 (RBM15) and RBM15B [7,15] which are suspected to intervene in the core complex
7
8
9 90 activity and target specificity. The demethylation of adenosines has been demonstrated to be
10
11 91 an active process catalysed by eraser enzymes belonging to the Fe(II)/2-oxoglutarate
12
13 92 dioxygenase family: AlkB homologue 5 (ALKBH5) [16,17] and the fat mass and obesity
14
15 93 associated protein (FTO) [17,18].

16
17
18
19 94 A growing number of reader proteins which recognize the m⁶A-RNA mark is being described.
20
21 95 They may be divided into two classes depending on the presence of a YTH domain
22
23 96 (YTH) domain in their primary sequence. The YTH protein family includes YTH domain family
24
25 97 protein 1-3 (YTHDF1-3) and YTH domain containing protein 2 (YTHDC2), which are cytosolic
26
27 98 m⁶A readers involved in m⁶A-RNA stability and translation [19–22]. The fifth YTH member is
28
29 99 YTHDC1, which is present in the nucleus and controls splicing [23] and nuclear export [24] of
30
31
32 100 m⁶A-RNA. The second class of readers comprises proteins without YTH domain which are
33
34
35 101 involved in several molecular mechanisms. For example, the heterogeneous nuclear
36
37 102 ribonucleoprotein A2 B1 (HNRNPA2B1) is important for miRNA processing [25]. Insulin-like
38
39 103 growth factor 2 mRNA binding protein 1-3 (IGF2BP 1-3) [26] and proline-rich coiled-coil 2a
40
41 104 (Prrc2a) [27] participate in RNA stability while eukaryotic initiation factor 3 (eIF3) guides cap-
42
43 105 independent translation [5].
44
45
46
47
48
49
50
51
52

53 106
54
55 107 The m⁶A epitranscriptomes underlie important biological functions, most of which being related
56
57 108 to developmental processes, including the control of cell differentiation [27–32], maternal to
58
59 109 zygotic transition (MZT) [33], sex determination [7,34] and gametogenesis [16,21,35,36]. Such
60

1
2
3 110 critical epitranscriptomic outcomes are conserved in the animal evolution and were
4
5
6 111 characterized in both vertebrates and ecdysozoans, i.e. mammals and drosophila.

7
8 112 However, such conserved biological significance originates in diverse epitranscriptomic
9
10
11 113 mechanisms. Indeed, not all ecdysozoans bear a complete m⁶A-RNA machinery, such as *C.*
12
13 114 *elegans* whose genome is devoid of the related protein machinery with the exception of a
14
15
16 115 putative orthologue of METTL16 [37,38]. In addition, no m⁶A eraser has been described to
17
18
19 116 date in non-vertebrate models, and especially ecdysozoans such as the drosophila or *C.*
20
21 117 *elegans* [38–40], where it cannot be excluded that m⁶A-RNA methylation could be removed by
22
23
24 118 the activity of characterised 6mA-DNA demethylases [41,42]. This situation may illustrate a
25
26
27 119 growing complexity of epitranscriptomic mechanisms during the animal phylogeny and raises
28
29
30 120 fundamental questions about its evolution and its presence in organisms distant from
31
32 121 mammals and ecdysozoans. However, to date, no data about a possible epitranscriptomic
33
34
35 122 regulation is available to our knowledge in lophotrochozoans, the understudied sister group of
36
37 123 ecdysozoans within protostomes, although representing an important range of metazoan
38
39
40 124 biodiversity.

41
42 125 The Pacific oyster *Crassostrea gigas* (i.e. *Magallana gigas*) is a bivalve mollusc whose great
43
44
45 126 ecological and economical significance allowed its emergence as a model species within
46
47
48 127 lophotrochozoan organisms. As such, an important amount of genetic, transcriptomic and
49
50
51 128 epigenetic data have been generated in this model. Interestingly, the embryolarval
52
53 129 development of *C. gigas* is described to be under the strong epigenetic influence of DNA
54
55
56 130 methylation [43–47] and histone marks [48–50]. Besides, oyster development occurs exposed
57
58
59 131 to external environmental conditions, and in other models the m⁶A methylation of RNA and/or
60

1
2
3 132 the expression of its machinery can be induced by heat stress, UV exposure or endocrine
4
5
6 133 disruptors [5,51–54], questioning the presence of an m⁶A pathway in *C. gigas* and its
7
8 134 significance in oyster early development.

9
10
11 135 To investigate this, we measured m⁶A levels in RNA across the entire embryolarval life of the
12
13
14 136 oyster using mass spectrometry and dot-blot. We also searched the available *in silico*
15
16 137 resources for putative conserved m⁶A-related proteins in *C. gigas* genomic data as well as
17
18
19 138 their cognate expression kinetics using RNAseq assembly analyses. We also performed RNA-
20
21 139 pulldown with a synthetic m⁶A-RNA oligonucleotide coupled to liquid chromatography and
22
23
24 140 mass spectrometry (LC-MS/MS) to characterize potential oyster m⁶A-binding proteins. To our
25
26
27 141 knowledge, this study is the first report unravelling epitranscriptomic mechanisms outside
28
29 142 vertebrate and ecdysozoan animal models.

30
31
32 143

33 34 35 144 **Results:**

36
37
38 145

39
40
41 146 **m⁶A is present in oyster RNA, differentially affects distinct RNA populations and**
42
43 147 **displays variations during embryonic life.**

44
45
46 148 Mass spectrometry measurements revealed that m⁶A is present in oyster RNA, with global
47
48 149 m⁶A/A levels of ca. 0.3%, a value comparable to what has been found in the human and the
49
50
51 150 fruit fly (Figure 1A). Immunoblot assays indicate that total and polyA⁺ RNA present variable
52
53
54 151 amounts of m⁶A during oyster development and that these variations display distinct profiles
55
56 152 suggesting specific methylation patterns between RNA populations. Indeed, N⁶A-methylation
57
58
59 153 in total RNA is the highest in the early stages (oocytes and fertilized oocytes) then gradually
60

1
2
3 154 decreases until the morula stage before gradually increasing again up to the trochophore stage
4
5
6 155 when it recovers its maximum (Figure 1B). In contrast, m⁶A levels in polyA⁺ RNA are hardly
7
8 156 detected in early stages but display a peak in the gastrula and trochophore stages (Figure 1C).
9

10
11 157

12
13
14 158 **m⁶A machinery is conserved at the molecular level in the oyster.**

15
16 159 *In silico* analyses led to the identification of oyster sequences encoding putative orthologues
17
18
19 160 of m⁶A writers, erasers and readers that are present in the human and/or in the human and
20
21 161 the fruit fly.

22
23
24 162 All the eight m⁶A-RNA writers characterized in the human and/or drosophila at the time of the
25
26
27 163 study, namely METTL3, METTL14, WTAP, Virilizer-like, HAKAI, ZC3H13, RBM15/15B and
28
29
30 164 METTL16, were present in the oyster at the gene level. The encoded protein primary
31
32 165 sequences all display the specific domains required for enzymatic activity and/or binding. They
33
34
35 166 include MT-A70 and AdoMetMtases SF domains for METTL3, METTL14 and METTL16,
36
37 167 respectively, that bear the methyltransferase activity. Oyster WTAP and Virilizer-like
38
39
40 168 orthologues exhibit WTAP and VIR_N domains, respectively, that are required in their human
41
42
43 169 counterparts to bind and activate the catalytic subunit of the m⁶A-RNA methyltransferase
44
45
46 170 complex. Oyster Hakai and RBM15/15B present RHHL, RHF-Zn-BS and specific RRM
47
48 171 domains, respectively, similar to human and fruit fly orthologues. Besides, the oyster ZC3H13
49
50
51 172 bears the Rho SF domain present in the human, but not in the fruit fly orthologue (Figure 2A).
52
53 173 *C. gigas* also presents a putative m⁶A-RNA eraser, ALKBH5, which is present in the human
54
55
56 174 but has not been characterized in drosophila. The oyster ALKBH5 exhibits a 2OG-FeII_Oxy
57
58
59 175 domain suggestive of a presumably conserved catalytic functionality through fe²⁺-dependent
60

1
2
3 176 oxoglutarate oxidation. Of note, no orthologue of the human FTO eraser could be identified in
4
5
6 177 the oyster genomic or transcriptomic databases available to date (Figure 2B).

7
8 178 Many m⁶A reader orthologues have also been found in the oyster, including proteins containing
9
10
11 179 a YTH domain, such as YTHDF, YTHDC1 and YTHDC2. An oyster Prrc2a-like protein
12
13
14 180 produces homology with the human Prrc2a, especially within the m⁶A-binding GRE-rich
15
16
17 181 domain. Oyster readers also include a heterogeneous nuclear ribonucleoprotein-coding gene,
18
19 182 hnRNPA2B1 with greater sequence similarity with the drosophila counterpart than with the
20
21
22 183 human orthologue. Similarly, the IGF2BP-coding sequence has also been found in *C. gigas*
23
24 184 (Figure 2C). Five oyster sequences display homologies with eIF3a which is able to bind m⁶A-
25
26
27 185 RNA [5] but it was not possible to discriminate whether a unique oyster predicted protein was
28
29
30 186 an eIF3a orthologue.

31
32 187 Overall, these results indicate the conservation of a complete m⁶A-RNA machinery in the
33
34
35 188 oyster. The complete list of the identified genes encoding the conserved m⁶A machinery actors
36
37
38 189 and their isoforms, as well as the related information is given in the supplementary data (Data
39
40 190 S1).

41
42
43 191

44 45 192 **Oyster putative m⁶A actors display expression level variations across development.**

46
47
48 193 RNAseq data analyses showed that all the oyster m⁶A-related genes were expressed during
49
50
51 194 the early life (Figure 3). Their expression level displayed gene-specific profiles, most of them
52
53
54 195 being variable throughout oyster development.

55
56 196 The expression of writers belonging to the core methylation complex is weak overall. METTL3
57
58
59 197 and WTAP share similar profiles with little expression increasing up to the gastrulation and
60

1
2
3 198 remaining stable afterwards. In contrast METTL14 displays a weak expression level across
4
5
6 199 the embryo larval life. The expression profile of Virilizer-like resembles WTAP, while HAKAI,
7
8 200 RBM15/15B and METTL16 seem to have mRNA levels which decrease after cleavage,
9
10
11 201 whereas those of ZC3H13 transcript variants seem to drop at the D larva stage. Interestingly,
12
13
14 202 METTL16 mRNA levels display an opposite developmental profile when compared to METTL3
15
16 203 expression; with the highest values during cleavage which decrease later on (Figure 3A).
17
18
19 204 ALKBH5 transcripts are weakly represented within oyster early embryos and the higher TPM
20
21 205 values are found in gastrulas. However, maximum levels are observed after metamorphosis in
22
23
24 206 juveniles (Figure 3B).
25
26
27 207 Regarding m⁶A putative readers, the expression of YTH family genes during development
28
29 208 showed different patterns. In fact, YTHDF is the most represented YTH-domain bearing actor
30
31 209 and YTHDF TPM values are ca. 5-fold higher than all the other oyster YTH readers. YTHDF is
32
33
34 210 strongly expressed at the beginning of development until a peak at the morula stage. Prrc2a
35
36
37 211 is the most represented reader at the mRNA level in oyster embryos, and the sum of the TPM
38
39
40 212 of the two Prrc2a oyster isoforms are at most ca. 20-fold higher than those of YTH family.
41
42
43 213 However, Prrc2a and YTHDF transcript content profiles are similar across oyster development,
44
45 214 and also remind of the IGF2BP mRNA levels.
46
47
48 215 By contrast, the two isoforms of YTHDC1 identified by *in silico* analysis, YTHDC1.1 and
49
50 216 YTHDC1.2, display similar patterns together with YTHDC2, with a maximum representation in
51
52
53 217 gastrulas. The expression of hnRNPA2B1 isoforms has likewise patterns except for a marked
54
55
56 218 drop at the D larvae stage (Figure 3 C).
57
58
59 219
60

1
2
3 **220 Oyster orthologues of m⁶A-RNA interacting proteins bind m⁶A RNA *in vitro*.**
4

5
6 221 To determine whether oyster proteins can bind m⁶A-RNA, we performed RNA-pulldown of
7
8 222 cytoplasmic and nuclear embryonic cell extracts using a methylated versus a non-methylated
9
10
11 223 oligonucleotide, followed by LC/MS-MS characterisation and identification of the captured
12
13
14 224 proteins with the Mascot software.

15
16 225 In nuclear extracts, we detected 591 proteins able to bind both the methylated and
17
18
19 226 unmethylated oligos. We identified 43 proteins specific to unmethylated RNA while 131
20
21 227 proteins specifically bind the m⁶A-methylated oligo. In cytosolic extracts, there were
22
23
24 228 respectively 646, 436 and 36 of such proteins, respectively. Regardless of the methylation
25
26
27 229 status, more proteins in the cytoplasmic extracts can bind to the RNA oligonucleotides than in
28
29
30 230 the nuclear extracts (1118 proteins vs. 765, respectively). However, more nuclear proteins are
31
32 231 found exclusively bound to the m⁶A-containing oligo than cytoplasmic proteins (131 vs. 36, i.e.
33
34 232 17 % vs. 3 %, respectively). In addition, many nuclear and cytoplasmic proteins can bind both
35
36
37 233 the methylated and the non-methylated oligo (591 vs. 646, i.e. 77 % vs. 58 %). An important
38
39
40 234 number of proteins in the cytoplasmic extract were found exclusively bound to the non-
41
42
43 235 methylated oligo, whereas only a limited number of nuclear proteins display such a specificity
44
45 236 (436 vs. 43, i.e. 39 % vs. 6 %). Among the 167 m⁶A-specific proteins in oyster extracts, only 5
46
47
48 237 were found in both the nuclear and cytoplasmic extracts. These results show that oyster
49
50
51 238 proteins can directly or indirectly bind m⁶A-RNA, and suggest an important
52
53 239 compartmentalization of m⁶A-related processes.

54
55
56 240 Among the identified proteins in this assay, four of the putative oyster m⁶A readers are found,
57
58 241 YTHDC1, hnRNPA2B1, IGF2BP and eIF3. In the nuclear extracts YTHDC1 is uncovered as
59
60

1
2
3 242 m⁶A-specific whereas hnRNPA2B1 and IGF2BP were present complexed with both the m⁶A-
4
5
6 243 and A-oligos. In the cytoplasmic extracts, YTHDC1 and eIF3a are m⁶A-specific while
7
8 244 hnRNPA2B1, IGF2BP were pulled down by both methylated and unmethylated oligos (Figure
9
10
11 245 4A).

12
13 246 These results demonstrate that some proteins in the oyster can specifically bind m⁶A-RNA and
14
15
16 247 that the putative m⁶A reader orthologues in the oyster are conserved at the protein level and
17
18
19 248 are able to interact with m⁶A-RNA.

20
21
22 249

23
24 250 **The m⁶A-interacting protein-coding genes display clustered expression regulation and**
25
26
27 251 **functional annotation during oyster development.**

28
29 252 The mRNA expression level of the genes encoding the 162 oyster m⁶A-interacting protein (Cg-
30
31
32 253 m⁶A-BPs) was examined using RNAseq databases. Most of them display a specific and
33
34
35 254 regulated expression level across oyster developmental stages. However, three main
36
37
38 255 expression clusters could be distinguished according to their developmental mRNA expression
39
40
41 256 level profile. Cluster 1 includes genes that show high expression at the beginning of the embryo
42
43
44 257 life (i.e. cleavage) and strongly decrease after gastrulation; the second cluster contains weakly
45
46
47 258 expressed genes except in the latest examined larval phases, after gastrulation (i.e.
48
49
50 259 Trochophore and D Larvae); cluster 3 groups genes that show an expression peak during
51
52
53 260 gastrulation (Figure 4B).

54
55
56 261 The Gene Ontology annotation of the Cg-m⁶A-BP genes reveal that the distinct clusters are
57
58
59 262 related to distinct functional pathways as indicated by the little - if any - common GO terms
60
263 between them (Figure 4C). However, the functional pathways of all three gene clusters point

1
2
3 264 out to their implication in translation and its regulation, although the terms enriched in each
4
5
6 265 cluster illustrate different aspects of translation, such as translation initiation (cluster 1), splicing
7
8 266 and nuclear export (cluster 2) and ribosomal and mitochondrial processes (cluster 3)
9
10
11 267 respectively (Figure 4D).
12

13
14 268

16 269 **Discussion**

17
18
19
20 270 This work demonstrates that m⁶A-RNA is present and variable during the embryo-larval life of
21
22
23 271 the oyster, and that *C. gigas* exhibits putative conserved and functional m⁶A-RNA writers,
24
25
26 272 eraser and readers. The dynamics of such mark and of its actors strongly suggest a biological
27
28 273 significance of the epitranscriptomic pathway in the control of development of a
29
30
31 274 lophotrochozoan species, which has, to date, never been demonstrated to our knowledge.
32

33 275 **m⁶A-RNA levels vary across oyster development.**

34
35
36 276 Using mass spectrometry and immunological measurements, we showed that oyster RNA is
37
38
39 277 m⁶A-methylated. The global proportion of N⁶-methyladenosine in RNA in the developing oyster
40
41
42 278 (0.28 %) is similar to those observed elsewhere in the animal kingdom, such as in the fruit fly
43
44 279 (0.24 %) [34] or the human (0.11- 0.23 %) [55] (Figure 1A), despite those values are difficult
45
46
47 280 to compare because they were not measured within the same developmental phase (adult flies
48
49 281 and human cell lines vs. oyster embryos). However, the comparable magnitude of m⁶A-RNA
50
51
52 282 amounts between taxa, in contrast to DNA methylation [46], may indicate conserved biological
53
54
55 283 significance of epitranscriptomic processes between groups. The amount of m⁶A in total RNA
56
57 284 displays a striking decrease during cleavage and then recovers its maximum levels at the end
58
59
60 285 of the gastrulation (Figure 1B). Therefore, the m⁶A decrease in total RNA during cleavage, i.e.

1
2
3 286 before the transcription of the zygotic genome starts, reflects a degradation of maternal m⁶A-
4
5
6 287 RNAs or their demethylation. However, all RNA populations do not exhibit the same pattern,
7
8 288 indeed polyA⁺ RNAs are m⁶A methylated only after cleavage. The extent of polyadenylation
9
10
11 289 of oyster maternal messenger RNAs accumulating during vitellogenesis is unknown.
12
13
14 290 Therefore, which maternal RNA population(s) is methylated in oyster oocytes is unclear.
15
16 291 Nevertheless, the observation that m⁶A-RNA levels are variable and affecting distinct RNA
17
18
19 292 populations across embryonic stages strongly favours an important biological significance of
20
21
22 293 m⁶A-RNA in oyster development. We hypothesize that oyster maternal messenger RNAs are
23
24 294 poorly polyadenylated, and that m⁶A, aside polyadenylation, might play a role in the stability of
25
26
27 295 quiescent maternal mRNAs. Alternatively, other maternal RNA populations such as snRNA,
28
29
30 296 miRNA, rRNA or lncRNA might be methylated [6,15,25,56], which become demethylated or
31
32 297 degraded up to the morula stage. The later increase in m⁶A RNA after cleavage could therefore
33
34
35 298 be the result of the methylation of the increasingly transcribed RNAs from the blastula stage,
36
37
38 299 including polyadenylated mRNAs.

300 **The m⁶A-RNA machinery is conserved in the oyster and regulated during development.**

301 The important regulation of m⁶A levels during oyster development assumes the presence of a
302 related protein machinery. We identified *in silico* cDNA sequences encoding conserved
303 putatively functional orthologues of m⁶A-RNA writers, eraser and readers in the oyster, with
304 great confidence (homologies ranging from ca. 30 to 65 % with their human counterpart, see
305 Data S1). The writers include all the members of the methylation complex (METTL3, METTL14,
306 WTAP, Virilizer-like, Hakai, ZC3H13, RBM15/15B) identified to date in the human and the fruit
307 fly [7,11,12,14,15,57]. We also identified an orthologue of the stand-alone METTL16 m⁶A
308

1
2
3 308 methyltransferase. Each orthologue bears the conserved domain(s) demonstrated to be
4
5
6 309 implicated in the catalytic and/or binding activity of their cognate counterpart in other species,
7
8
9 310 such as the MT-A70 domain which transfers methyl groups from the S-adenosyl-methionine
10
11 311 (SAM) to the N^6 nitrogen of RNA adenines [57]. Of the two proteins that can erase RNA
12
13
14 312 methylation, only ALKBH5, which is important for mouse spermatogenesis [16], was identified
15
16 313 at the cDNA level in the oyster. Indeed, no *C. gigas* sequence displayed significant homology
17
18
19 314 with the mammalian FTO protein, whose functional significance remains controversial [17].
20
21
22 315 Most the characterized m⁶A-RNA readers are also present at the molecular level in the oyster
23
24 316 and are putatively able to bind m⁶A regarding their primary sequence, such as the YTHDC and
25
26
27 317 YTHDF family members [19,21,23,58], Prrc2A [27], HnRNPA2B1 [25] and IGF2BP [26]. Of
28
29
30 318 note, some of these readers have not been characterized to date in *D. melanogaster* but
31
32 319 display strong homologies between humans and oysters. In mammals, eIF3a has important
33
34
35 320 functional outcomes in cap-independent translational stress response [5]. However, it was not
36
37
38 321 possible to ascribe a single oyster sequence as a unique eIF3a orthologue (Data S1), although
39
40 322 its presence was demonstrated by RNA pull down (see below) (see Data S2). Altogether, *in*
41
42
43 323 *silico* results show the conservation of a complete m⁶A-RNA machinery in the oyster. To date
44
45 324 to our knowledge, this is the first demonstration in a lophotrochozoan organism of an
46
47
48 325 epitranscriptomic pathway. Its presence suggests its ancestral origin, and questions its
49
50
51 326 biological significance in oyster development.

52
53 327 To investigate this, we analysed the expression level of the m⁶A machinery genes using RNA-
54
55
56 328 seq data. Our results indicate that the core methylation complex (METTL3, METTL14 and
57
58
59 329 WTAP) would not be active during cleavage because of the absence of METTL3 and little
60

1
2
3 330 WTAP expression. METTL16 catalyses the downregulation of SAM methyl donor availability
4
5
6 331 in mammals [59]. If METTL16 function is conserved in the oyster as suggested by the high
7
8 332 sequence homology, the peak in METTL16 expression, together with the weak expression of
9
10
11 333 the core complex in 2/8 cell embryos is consistent with an absence of m⁶A-RNA up to the
12
13
14 334 blastula stage. Then, the core complex would likely be active as soon as the end of cleavage
15
16 335 (i.e. since the blastula stage), in line with the increase in m⁶A levels observed at the same time.
17
18
19 336 The correlation between the increasing METTL3 expression and m⁶A-RNA levels after
20
21 337 cleavage strongly favours the conservation of the methyltransferase activity of the oyster MT-
22
23
24 338 A70 domain. Interpreting the regulation of the m⁶A activity by the other methyltransferase
25
26 339 complex members (i.e. Virilizer-like, HAKAI, ZC3H13 and RBM15/15B) is difficult because how
27
28 340 - or even if - oyster orthologues act within the complex is not known. Nevertheless, their specific
29
30
31 341 expression profiles may reflect their implication in the regulation of distinct biological contexts.
32
33
34 342 There might be little functional significance of active m⁶A-RNA erasure during oyster
35
36 343 development, consistent with the normal embryonic phenotype of ALKBH5 knockdown mice
37
38
39 344 [16]. Overall, the m⁶A readers display distinct developmental expression patterns. While
40
41
42 345 YTHDF and Prrc2a peak during cleavage, YTHDC1, YTHDC2, IGF2BP and hnRNPA2B1
43
44
45 346 mRNA levels gradually increase up to the gastrulation and remain mostly highly expressed
46
47
48 347 afterwards (except for hnRNPA2B1 and IGF2BP). These profiles evoke the mediation of
49
50
51 348 distinct biological functions depending on the reader and the developmental phases.
52
53 349 Therefore, we hypothesized that YTHDF and Prrc2a might participate in the blastulean
54
55
56 350 transition in the oyster. Indeed, in the zebrafish, a YTHDF reader triggers the maternal-to-
57
58 351 zygotic transition through the decay of the maternal m⁶A RNAs during cleavage [33]. The role
59
60

1
2
3 352 in the axon myelination and specification of mouse oligodendrocytes [27] is unlikely conserved
4
5
6 353 for *Prrc2a* because the oyster orthologue is expressed before the neurogenesis is detected in
7
8 354 trochophore stages [60]. Alternatively, the early expression of *Prrc2a* suggests that it might
9
10
11 355 rather compete with YTHDF for m⁶A-RNA targets [27], thereby possibly acting in oyster MZT,
12
13
14 356 bringing new perspectives into this process which remains poorly understood in
15
16 357 lophotrochozoans. In mammals m⁶A is implicated in the embryonic cell fate [30,31] notably via
17
18
19 358 the regulation of cell differentiation by YTHDC2 [32] or hnRNPA2B1 [29]. In the oyster,
20
21
22 359 YTHDC1, YTHDC2, IGF2BP and hnRNPA2B1 have their maximum expression during
23
24 360 gastrulation correlated to the second m⁶A peak, suggesting similar implications.
25

26
27 361 **Putative oyster m⁶A readers actually bind m⁶A-RNA *in vitro*.**

28
29 362 To better approach the developmental processes involving m⁶A in the oyster, we characterized
30
31
32 363 the proteins that can interact with m⁶A-RNA using a methylated-RNA-pulldown / mass
33
34
35 364 spectrometry assay. We identified 162 proteins able to specifically bind the m⁶A-RNA oligo in
36
37
38 365 embryonic cell extracts, demonstrating the actual presence of genuine m⁶A-readers in the
39
40
41 366 oyster. Most (ca. 75 %) of these proteins were found in nuclear extracts and only 5 were found
42
43
44 367 in both the cytoplasmic and nuclear fractions, showing an important compartmentalization of
45
46
47 368 the epitranscriptomic pathway. Regarding the little number of m⁶A readers in other animals,
48
49
50 369 and because the assay conditions do not discriminate between direct and indirect interactions,
51
52
53 370 we hypothesize that most these proteins indirectly bind m⁶A via a limited number of 'scaffold'
54
55
56 371 m⁶A readers. Such authentic readers that only bind the m⁶A-RNA oligo in our assay likely
57
58
59 372 include YTHDC1 and eIF3a, which have been demonstrated to directly bind m⁶A in other
60
373 species, demonstrating the conservation of the m⁶A-binding capacity and specificity of the YTH

1
2
3 374 domain in the oyster. Besides, YTHDC1 is found in both cell fractions, suggesting its
4
5
6 375 implication in the trafficking of m⁶A-RNA across the nuclear envelope [24], and reinforcing the
7
8
9 376 hypothesis that YTH proteins could participate in oyster MZT and cell differentiation. The
10
11 377 presence of the oyster eIF3a in the cytoplasm is consistent with a conserved role in m⁶A-
12
13
14 378 mediated translation processes, such as cap-independent translation [5].

16 379 **Possible functions of m⁶A-RNA in oyster development.**

18
19 380 We investigated the expression level and the functional annotation of the 162 genes encoding
20
21 381 the m⁶A-interacting proteins across oyster early life. These genes can be clustered into three
22
23
24 382 successive expression phases corresponding to three distinct functional pathways, which are
25
26
27 383 independent albeit all mostly related to translation regulation. The cluster 1 is mostly expressed
28
29 384 during the cleavage and the associated GO terms are related to the initiation of translation,
30
31
32 385 consistent with maternal RNA consumption before MZT is complete and the zygotic genome
33
34
35 386 becomes fully activated. The genes within cluster 3 show an expression peak during
36
37 387 gastrulation. Their ontology terms evoke ribosomal and mitochondrial processes, the latter
38
39
40 388 being required for energy supply and signalling integration during gastrulation [61–64]. The
41
42
43 389 cluster 2 contains genes that peak after gastrulation and which are related to splicing and
44
45
46 390 nuclear export. Such functional annotations are in line with a fine regulation of transcript variant
47
48 391 translation within the distinct cell lineages in the three cell layers of the late embryos.

49
50 392
51
52
53 393 Taken together, our findings bring to light a possible implication of m⁶A in oyster development.
54
55
56 394 First, during cleavage the decrease of m⁶A-RNA, the weak expression of methyltransferase
57
58 395 complex genes, the maximum of YTHDF gene expression and the expression of Cg-m⁶A-BPs
59
60

1
2
3 396 related to the initiation of the translation strongly suggest the implication of m⁶A in MZT in *C.*
4
5
6 397 *gigas*. Second, the increasing m⁶A level during gastrula stage is correlated to the increase of
7
8 398 methyltransferase complex gene expression. In addition, the increased RNA level of readers
9
10
11 399 putatively related to cell differentiation and the peak of gene expression of *Cg*-m⁶A-BPs
12
13 400 associated to ribosomal and mitochondrial processes, support the hypothesize of a m⁶A
14
15
16 401 implication in gastrulation. Finally, the highest m⁶A level at the trochophore stage, the gene
17
18
19 402 expression of the methyltransferase complex and of readers associated to cell differentiation,
20
21
22 403 as well as high RNA level of *Cg*-m⁶A-BPs related to splicing and nuclear export is correlated
23
24 404 with the fine cell differentiation taking place at this stage. However, inferring the biological
25
26
27 405 significance of m⁶A in development from the indirect and incomplete functional annotation of
28
29
30 406 the oyster genome is only limited. Characterization of the precise targets of m⁶A and how their
31
32
33 407 individual methylation is regulated across development, for example using high throughput
34
35
36 408 sequencing of precipitated m⁶A-RNA (MeRIP-seq), could be extremely relevant to better
37
38
39 409 understand this issue. In addition, despite sequence conservation and binding ability of oyster
40
41
42 410 actor orthologues strongly suggest functional conservation, future dedicated studies such as
43
44
45 411 biochemical inhibition or gene inactivation could help demonstrate their genuine biological
46
47
48 412 function. Besides, there seems to be an inverse correlation between m⁶A-RNA and 5mC-DNA
49
50
51 413 levels during the considered oyster developmental window [46]. This may suggest an interplay
52
53
54 414 between epigenetic and epitranscriptomic marks, possibly reflecting competition for methyl-
55
56
57 415 donor availability [59] or a link by histone epigenetic pathways [65,66].
58
59
60 416 Regarding the potential influence of the environment on m⁶A and the accumulation of RNA in
61
62
63 417 oocytes, we are at present investigating our hypothesis that m⁶A may convey intergenerational

1
2
3 418 epitranscriptomic inheritance of maternal life traits in the oyster. On an evolutionary
4
5
6 419 perspective, the presence of a putatively fully conserved epitranscriptomic pathway in the
7
8
9 420 oyster suggests that it was already present in the bilaterian common ancestor thereby in favour
10
11 421 of an important biological significance. Why *Drosophila* and *Caenorhabditis* seem to have lost
12
13 422 specific m⁶A-RNA erasers could be related to a sub-functionalization of the DMAD [41] and
14
15
16 423 NMAD-1 [42] N⁶-methyladenine DNA demethylase activity broadened towards RNA. However,
17
18
19 424 more work is required to better understand the evo-devo implications of our results.
20

21 425
22
23
24 426 To conclude, in this work we report the discovery and characterisation of a putatively complete
25
26
27 427 epitranscriptomic pathway in a lophotrochozoan organism, the oyster *Crassostrea gigas*. This
28
29
30 428 pathway includes the m⁶A mark in RNA and the actors of all the aspects of its regulation
31
32 429 (writers, eraser, readers) which are conserved at the molecular level and putatively functional.
33

34
35 430 We show that m⁶A levels are variable across oyster development and that m⁶A differentially
36
37
38 431 affects distinct RNA populations. Expression levels of the related enzymatic machinery is
39
40 432 consistent with the observed m⁶A level variations. We demonstrate the m⁶A binding capacity
41
42
43 433 and specificity of putative oyster m⁶A readers in the cytoplasm and nucleus of embryolarval
44
45 434 cells. These readers mediate distinct putative biological outcomes depending on the
46
47
48 435 development stage considered. From these results we hypothesize that early decay of
49
50
51 436 maternal m⁶A RNA participates in maternal-to-zygotic transition during cleavage and that later
52
53 437 *de novo* zygotic m⁶A methylation contributes to gastrulation and cell differentiation. This first
54
55
56 438 characterisation of an m⁶A-epitranscriptomic pathway in a lophotrochozoan organism, together
57
58
59 439 with its potential implication in development, opens new perspectives on the evolution of
60

1
2
3 440 epigenetic mechanisms and on the potential epitranscriptomic inheritance of environmentally-
4
5
6 441 induced life traits.

7
8 442

9
10
11
12 443 **Methods:**

13
14
15 444

16
17
18 445 **Animals:**

19
20
21 446 Broodstock oysters [67] and oyster embryos [46] were obtained at the IFREMER marine
22
23 447 facilities (Argenton, France) as previously described. Briefly, gametes of mature broodstock
24
25 448 oysters were obtained by stripping the gonads and filtering the recovered material on a 60 µm
26
27 449 mesh to remove large debris. Oocytes were collected as the remaining fraction on a 20 µm
28
29 450 mesh and spermatozoa as the passing fraction on a 20 µm mesh. Oocytes were pre-incubated
30
31 451 in 5 L of UV-treated and 1 µm filtered sterile sea water (SSW) at 21 °C until germinal vesicle
32
33 452 breakdown. Fertilization was triggered by the addition of ca. 10 spermatozooids per oocyte. After
34
35 453 the expulsion of the second polar body was assessed by light microscopy, embryos were
36
37 454 transferred in 150 L tanks of oxygenated SSW at 21 °C. The development stages were
38
39 455 determined by light microscopy observation. The stages collected were oocytes (E,
40
41 456 immediately before sperm addition), fertilized oocytes (F E, immediately before transfer to
42
43 457 150L tanks), two to eight cell embryos (2/8 C, ca. 1.5 hours post fertilization (hpf)), morula (M,
44
45 458 ca. 4 hpf), blastula (B, ca. 6 hpf), gastrula (G, ca. 10 hpf), trochophore (T, ca 16 hpf) and D
46
47 459 larvae (D, ca. 24 hpf). For each development stage, 3 million embryos were collected as the
48
49 460 remaining fraction on a 20 µm mesh and centrifuged at 123 g for 5min at room temperature.
50
51
52
53
54
55
56
57
58
59
60

1
2
3 461 Supernatant was discarded and samples of 1 million embryos were then snap-frozen in liquid
4
5
6 462 nitrogen directly of after resuspension in Tri-Reagent (Sigma-Aldrich, St Louis, MO, USA) (1
7
8 463 mL/10⁶ embryos) and stored at -80 °C. Three distinct experiments were realized (February to
9
10
11 464 May 2019) using the gametes of 126 to 140 broodstock animals, respectively.
12

13
14 46515
16 466 **RNA extraction:**

- 17
-
- 18
-
- 19 467
- total RNA extraction

20
21 468 RNA was extracted using phenol-chloroform followed by affinity chromatography as previously
22
23
24 469 described [68]. Briefly, embryos were ground in Tri-Reagent (Sigma-Aldrich) and RNA was
25
26
27 470 purified using affinity chromatography (Nucleospin RNA II kit, Macherey-Nagel, Duren,
28
29
30 471 Germany). Potential contaminating DNA was removed by digestion with rDNase (Macherey-
31
32 472 Nagel) according to the manufacturer's instructions for 15 min at 37 °C then RNA was purified
33
34
35 473 using Beckman Coulter's solid-phase reversible immobilization (SPRI) paramagnetic beads
36
37
38 474 (AgencourtAMPure XP, Beckman Coulter, Brea, CA, USA) according to the manufacturer's
39
40 475 instructions. Briefly, paramagnetic beads and RNAs were mixed slowly and incubated 5 min
41
42
43 476 at room temperature followed by 2 min on a magnetic rack. Cleared supernatant was removed,
44
45
46 477 and beads were washed three times with 70 % ethanol. After 4 min of drying at room
47
48 478 temperature, RNAs were mixed slowly with RNase free water and incubated for 1 min at room
49
50
51 479 temperature on the magnetic rack. Eluted total RNA was stored at -80 °C.
52

- 53
-
- 54 480
- PolyA RNA enrichment

55
56
57 481 Poly-A RNA was extracted from total RNA by oligo-dT affinity chromatography (NucleoTrap
58
59 482 mRNA kit, Macherey-Nagel) according to the manufacturer's instructions. Briefly, up to 130 µg
60

1
2
3 483 of total RNAs were mixed with oligo-dT latex beads and incubated for 5 min at 68 °C then 10
4
5
6 484 min at room temperature. After centrifugation (2,000 g then 11,000 g), the pellets were washed
7
8 485 three times on the microfilter and dried by centrifugation at 11,000 g for 1 min. Finally, polyA+
9
10
11 486 RNA was incubated with RNase-free water for 7 min at 68 °C then centrifuged at 11,000 g for
12
13
14 487 1 min. Eluted polyA+ RNA was stored at -80 °C until needed.

15
16 488 Total and polyA-enriched RNA purity and concentrations were assayed by spectrophotometry
17
18
19 489 (Nanodrop, Thermo Scientific, Waltham, MA, USA).

20
21
22 490

23
24 491 **m⁶A quantification by LC-MS/MS:**

- 25
26
27 492
 - RNA hydrolysis

28
29 493 To generate nucleosides for quantification against standard curves, 5 µg of total RNA were
30
31
32 494 denatured for 10 min at 70 °C followed by 10 min on ice, and hydrolyzed with 100 U Nuclease
33
34
35 495 S1 (50 U/µL, Promega, Madison, WI, USA) in Nuclease S1 buffer (Promega) in a final reaction
36
37 496 volume of 25 µL for 2 h at 37 °C under gentle shaking. Samples were then incubated with
38
39
40 497 alkaline phosphatase buffer (Promega) for 5 min at room temperature, before 10 U alkaline
41
42
43 498 phosphatase (Promega) were added and incubated further for 2 h at 37 °C under gentle
44
45 499 shaking. Ten extra units of alkaline phosphatase were added after 1 hour of incubation to
46
47
48 500 complete the reaction. Finally, samples were centrifuged at 13,000 rpm for 10 min at 4 °C and
49
50
51 501 the supernatant containing digested total RNA was collected and kept at -20 °C before
52
53 502 quantification.

- 54
55
56
57 503
 - m⁶A quantification:
- 58
59
60

1
2
3 504 The apparatus was composed of a NexeraX² UHPLC system coupled with LCMS8030 Plus
4
5
6 505 (Shimadzu, Kyoto, Japan) mass spectrometer using an electrospray interface in positive mode.

7
8 506 The column (1.7 μ m, 100x3 mm) was a HILIC Aquity[®] Amide (Waters, Millford, MA, USA)
9
10
11 507 maintained at 35 °C. The injection volume and run-to-run time were 3 μ L and 10 min,
12
13
14 508 respectively. The flow rate was set to 1 mL/min. Mobile phase was initially composed of a
15
16
17 509 mixture of ammonium formate solution (10 mM) containing 0.2 % (v/v) formic acid and 95 %
18
19
20 510 acetonitrile (ACN) and it was maintained for 1 min. Then, a linear gradient was applied to reach
21
22
23 511 83 % ACN for 6 min. The composition returned to the initial conditions and the column was
24
25
26 512 equilibrated for 3 min.

27 513 The mass spectrometer was running in the Multiple Reaction Monitoring (MRM) acquisition
28
29
30 514 mode. LabSolutions 5.86 SP1 software was used to process the data. The desolvation
31
32
33 515 temperature was 230 °C, source temperature was 400 °C and nitrogen flows were 2.5 L/min
34
35
36 516 for the cone and 15 L/min for the desolvation. The capillary voltage was +4.5 kV. For each
37
38
39 517 compound, two transitions were monitored from the fragmentation of the [M+H]⁺ ion. The first
40
41
42 518 transition (A in Table S1) was used for quantification and the second one (B in Table S1) for
43
44
45 519 confirmation of the compound according to European Commission Decision 2002/657/EC
46
47
48 520 (Table S1).

49
50
51 521 Blank plasma samples were analysed to check specificity. Calibrators were prepared using
52
53
54 522 diluted solutions of A (Toronto Research Chemical, Toronto, Canada) and m⁶A (Carbosynth,
55
56
57 523 Berkshire, UK) in water at 1, 2, 5, 10, 20 50, 100 ng/mL. The calibration curves were drawn by
58
59
60 524 plotting the ratio of the peak area of A and m⁶A. For both nucleosides, a quadratic regression
525 with 1/C weighting resulted in standard curves with R²>0.998 and more than 75% of standards

1
2
3 526 with back-calculated concentrations within 15% of their nominal values as recommended for
4
5
6 527 by the European medicines agency for bioanalytical methods [69]. The limits of quantifications
7
8 528 for both compounds were considered as the lowest concentrations of the calibration curve.
9
10
11 529 m⁶A/A ratios were calculated for each single sample using the determined concentrations.
12
13
14 530 Final results are the average of three technical replicates.
15

16 531

17
18
19 532 **m⁶A quantification by immunoblotting:**

20
21 533 Immunological quantification of m⁶A was performed by dot-blot using total and polyA+ RNAs.
22
23
24 534 Dogfish total RNA (Dr. A. Gautier, personal communication) and a synthetic unmethylated
25
26
27 535 RNA oligo (Eurogentec, Liege, Belgium) were used as positive and negative controls,
28
29
30 536 respectively. RNA samples were denatured for 15 min at 55 °C with gentle shaking in
31
32
33 537 denaturing solution (2.2 M formaldehyde, 50 % formamide, 0.5X MOPS, DEPC water) followed
34
35
36 538 by 2 min on ice. Blotting was performed on a vacuum manifold as follows: a nylon membrane
37
38
39 539 (Amersham Hybond-N+, GE Healthcare life Sciences, Chicago, IL, USA) was pre-hydrated in
40
41
42 540 DEPC water for 5 min, then each well was washed twice with 10X SSC (Sigma-Aldrich) before
43
44
45 541 RNA was spotted onto the membrane and incubated for 15 min at room temperature. Then,
46
47
48 542 vacuum aspiration was applied and each well was washed twice with 10X SSC. After heat
49
50
51 543 crosslinking for 2 h at 70 °C, the membrane was rehydrated with DEPC water for 5 min, washed
52
53
54 544 with PBS then PBST (PBS, 0.1 % Tween-20) for 5 min each and blocked with two 5 min
55
56
57 545 incubations with blocking buffer (PBS, 0.1 % Tween-20, 10 % dry milk, 1 % BSA) at room
58
59
60 546 temperature. The blocked membrane was incubated overnight at 4 °C under gentle shaking
547 with the anti-m⁶A primary antibody (Total RNA: Millipore (Burlington, MA, USA) ABE572, 1 :

1
2
3 548 1,000 dilution in blocking buffer; polyA+ RNA: Diagenode (Liege, Belgium) C15200082, 1 : 500
4
5
6 549 dilution in blocking buffer) followed by four washes of PBST for 5 min. The secondary antibody
7
8 550 (Total RNA: Dako (Santa Clara, CA, USA) P0447 goat anti-mouse HRP antibody, 1 : 10,000
9
10
11 551 dilution; polyA+ RNA: Invitrogen (Carlsbad, CA, USA) A21202 donkey anti-mouse Alexa 488,
12
13
14 552 1 : 250 dilution) was diluted in PBST supplemented with 5 % dry milk and added onto the
15
16 553 membrane for 1 h 30 (total RNA) or 1 h (polyA+ RNA) at room temperature under gentle
17
18
19 554 shaking. Membranes were extensively washed in PBST (at least 4 washes of 5 min for total
20
21
22 555 RNA and 5 min then 1 h for polyA+ RNA) then total and polyA+ RNA immunoblots were
23
24 556 visualized using chemiluminescence (ECL kit, Promega) or fluorescence scanning at 480-530
25
26
27 557 nm (Pro Xpress, Perkin-Elmer, Waltham, MA, USA), respectively. The amount of m⁶A was
28
29
30 558 inferred from dot intensity measurements using ImageJ (v.1.49). Signal intensities were
31
32
33 559 determined as 'integrated densities as a percentage of the total' which corresponds to the area
34
35 560 under the curve of the signal of each dot after membrane background and negative control
36
37 561 signal subtraction.
38
39
40 562

41 42 563 ***In silico* analyses:**

43
44
45 564 All protein and RNA sequences of the m⁶A machinery of *Homo sapiens* and *Drosophila*
46
47
48 565 *melanogaster* (Data S1) were recovered by their published designation (i.e., 'METTL3' or
49
50
51 566 'YTHDF' etc.) and their identified protein sequence (ie. RefSeq accession number NP...)
52
53
54 567 collected from NCBI and used as query sequences to search for putative homologue
55
56
57 568 sequences in *Crassostrea gigas* databases. The presence of oyster orthologue RNA and
58
59 569 protein sequences were investigated by reciprocal
60

1
2
3 570 BLAST(<https://blast.ncbi.nlm.nih.gov/Blast.cgi>) on the *Crassostrea gigas* GigaTON [70] and
4
5
6 571 NCBI databases and results were compared between the two oyster databases. Domain
7
8 572 prediction was performed with CD-search software
9
10
11 573 (<https://www.ncbi.nlm.nih.gov/Structure/cdd/wrpsb.cgi>) with default settings on protein
12
13
14 574 sequences of *Homo sapiens*, *Drosophila melanogaster* and *Crassostrea gigas*. The GRE-rich
15
16 575 domain identified in vertebrate Prrc2a sequence [27] was performed with ProtParam
17
18
19 576 (<https://web.expasy.org/cgi-bin/protparam/protparam>).

20
21
22 577

23 24 578 **Protein machinery mRNA expression analyses:**

25
26
27 579 The transcriptome data of the different development stages are available on the GigaTON
28
29
30 580 database [70,71]. The correspondence between development stages in our study, and the
31
32
33 581 GigaTON database were assessed using light microscopy based on the morphological
34
35
36 582 description by Zhang et al., 2012 [71] (Table S2). Expression data was expressed in TPM
37
38
39 583 (Transcripts Per Million) [72] to provide a normalized comparison of gene expression between
40
41
42 584 all samples. The actual presence of some transcripts that display unclear or chimeric
43
44
45 585 sequences within available oyster databases was assessed using RT-PCR (Data S1).

46
47
48 586

49 50 587 **Protein m⁶A RNA pull down:**

- 51 588 • Protein extraction and RNA affinity chromatography

52
53 589 Protein extraction and RNA affinity chromatography were performed as described previously
54
55
56 590 [27] with some modifications as follows. Equal amounts (1 million individuals) of each
57
58
59 591 developmental stage (oocyte to D larvae) were pooled together then homogenized in 3.5
60

1
2
3 592 volumes of buffer A (10 mM KCl, 1.5 mM MgCl₂, 10 mM HEPES, pH 7.9, DEPC water, 1X
4
5
6 593 Protease inhibitor cocktail, DTT 0.5 mM) by extensive pipetting (ca. 30 times) and incubated
7
8 594 10 min at 4 °C. Embryos were ground with 10 slow 23G-needle syringe strokes and centrifuged
9
10
11 595 at 2,000 rpm for 10 min at 4 °C. The supernatant was diluted in 0.11 volume of buffer B (1.4 M
12
13 596 KCl, 0.03 M MgCl₂, HEPES 0.3 M, pH 7.9, DEPC water), centrifuged at 10,000 g for 1 h at 4
14
15
16 597 °C and the supernatant containing cytosolic proteins was stored at -80 °C. The pellet of the
17
18
19 598 first centrifugation, containing nuclei, was re-suspended in two volumes of buffer C (0.42 M
20
21 599 NaCl, 1.5 mM MgCl₂, 0.2 mM EDTA, 25 % glycerol, 20 mM HEPES, pH 7.9, 0.5 mM PMSF,
22
23
24 600 0.5 mM DTT, water DEPC). Nuclei were then lysed with a 23 G needle (10 vigorous syringe
25
26
27 601 strokes) followed by centrifugation at 30,000 rpm for 30 min at 4 °C and the supernatant
28
29
30 602 containing nuclear proteins was stored at -80 °C.

31
32 603 To identify putative proteins able to bind m⁶A-RNA, the cytosolic and nuclear fractions were
33
34
35 604 submitted to affinity chromatography using 5'-biotin-labelled RNA oligonucleotides either
36
37
38 605 bearing N⁶-methylated adenosines or not. The methylated adenosines were designed to lie
39
40
41 606 within RRACH motifs, according to the conserved methylated consensus sequence in other
42
43 607 organisms [2,3,7,33,73] (oligo-m⁶A: 5'Biotin-AGAAAAGACAACCAACGAGRR-m⁶A-
44
45 608 CWCAUCAU-3', oligo-A: 5'Biotin-AGAAAAGACAACCAACGAGRRACWCAUCAU-3', R = A or
46
47
48 609 G, W = A or U, Eurogentec).

49
50 610 For RNA pull down, streptavidin-conjugated magnetic beads (Dynabeads Myone Streptavidin,
51
52
53 611 Invitrogen) were pre-blocked with 0.2 mg/mL tRNA (Sigma-Aldrich) and 0.2 mg/mL BSA for 1
54
55
56 612 h at 4 °C under gentle rotation followed by three washes with 0.1 M NaCl. To avoid the
57
58
59 613 identification of non-target proteins, cytosolic and nuclear protein extracts were cleared with
60

1
2
3 614 pre-blocked magnetic beads in binding buffer (50 mM Tris-HCl, 250 mM NaCl, 0.4 mM EDTA,
4
5 615 0.1 % NP-40, DEPC water, 1 mM DTT, 0.4 U/ μ L RNasin) for 1 h at 4 °C under gentle rotation.
6
7
8 616 After incubation on magnetic rack, the supernatants containing putative target proteins were
9
10
11 617 collected and mixed with pre-blocked magnetic beads and oligo-m⁶A or oligo-A for 2 h at 4 °C
12
13
14 618 under gentle rotation. The beads binding putative target proteins were washed three times with
15
16 619 binding buffer and diluted in 50 mM ammonium bicarbonate.

17
18
19
20 620 • Identification of m⁶A-binding proteins by LC-MS/MS:

21
22 621 Protein samples were first reduced, alkylated and digested with trypsin then desalted and
23
24
25 622 concentrated onto a μ C18 Omix (Agilent, Santa Clara, CA, USA) before analysis.

26
27
28 623 The chromatography step was performed on a NanoElute (Bruker Daltonics, Billerica, MA,
29
30 624 USA) ultra-high pressure nano flow chromatography system. Peptides were concentrated onto
31
32
33 625 a C18 pepmap 100 (5 mm x 300 μ m i.d.) precolumn (Thermo Scientific) and separated at 50
34
35
36 626 °C onto a reversed phase Reprosil column (25 cm x 75 μ m i.d.) packed with 1.6 μ m C18 coated
37
38 627 porous silica beads (Ionopticks, Parkville, Victoria, Australia). Mobile phases consisted of 0.1
39
40
41 628 % formic acid, 99.9 % water (v/v) (A) and 0.1 % formic acid in 99.9 % ACN (v/v) (B). The
42
43
44 629 nanoflow rate was set at 400 nL/min, and the gradient profile was as follows: from 2 to 15 % B
45
46 630 within 60 min, followed by an increase to 25 % B within 30 min and further to 37 % within 10
47
48
49 631 min, followed by a washing step at 95 % B and re-equilibration.

50
51 632 MS experiments were carried out on an TIMS-TOF pro mass spectrometer (Bruker Daltonics)
52
53
54 633 with a modified nano-electrospray ion source (CaptiveSpray, Bruker Daltonics). The system
55
56
57 634 was calibrated each week and mass precision was better than 1 ppm. A 1600 spray voltage
58
59 635 with a capillary temperature of 180 °C was typically employed for ionizing. MS spectra were
60

1
2
3 636 acquired in the positive mode in the mass range from 100 to 1700 m/z. In the experiments
4
5
6 637 described here, the mass spectrometer was operated in PASEF mode with exclusion of single
7
8 638 charged peptides. A number of 10 PASEF MS/MS scans was performed during 1.16 seconds
9
10
11 639 from charge range 2-5.

12
13 640 The fragmentation pattern was used to determine the sequence of the peptide. Database
14
15
16 641 searching was performed using the Mascot 2.6.1 program (Matrix Science) with a *Crassostrea*
17
18 642 *gigas* Uniprot database (including 25,982 entries). The variable modifications allowed were as
19
20
21 643 follows: C-Carbamidomethyl, K-acetylation, methionine oxidation, and Deamidation (NQ). The
22
23
24 644 'Trypsin' parameter was set to 'Semispecific'. Mass accuracy was set to 30 ppm and 0.05 Da
25
26
27 645 for MS and MS/MS mode respectively. Mascot data were then transferred to Proline validation
28
29
30 646 software (<http://www.profiroteomics.fr/proline/>) for data filtering according to a significance
31
32 647 threshold of <0.05 and the elimination of protein redundancy on the basis of proteins being
33
34
35 648 evidenced by the same set or a subset of peptides (Data S2).

36
37
38 649 • Gene ontology analysis:

39
40
41 650 The mRNA sequences of the characterized m⁶A-binding proteins were identified using tBlastn
42
43 651 [74–76] against the GigaTON database [70] with default settings. Gene ontology (GO)
44
45
46 652 analyses were carried out with the GO annotations obtained from GigaTON database gene
47
48
49 653 universe [70]. GO term-enrichment tests were performed using the goseq (V1.22.0) R package
50
51 654 [77] with p-values calculated by the Wallenius method and filtered using REVIGO [78]. GO
52
53
54 655 terms with a p-value < 0.05 were considered significantly enriched (Data S3).

55
56 656

57
58
59 657 **Statistical analyses and graph production:**
60

1
2
3 658 Results are given as the mean \pm SD of three independent experiments unless otherwise stated.
4
5
6 659 They were analysed using one-way ANOVA or Kruskal-wallis tests when required, depending
7
8 660 on the normality of result distribution. The normality was tested using the Shapiro-Wilk's test
9
10
11 661 and homoscedasticity of variances with Bartlett's tests. Statistics and graphics were computed
12
13
14 662 with Prism v.6 (Graphpad), R (v.3.6.1) and RStudio (v.1.0.153) softwares. The R packages
15
16 663 *eulerr* [79] and *Complexheatmap* [80] were used for production of specific figures.
17
18
19 664
20
21
22 665
23
24

25 666 **Author contribution**

26
27
28 667 Experiment design: GR, LLF.

29
30 668 Benchwork and bioinformatics: LLF, GR, BB, BP, MS.

31
32
33 669 Data analysis: LLF, GR, BB, MS.

34
35
36 670 Manuscript writing and editing: LLF, GR, PF, BB, MS, BP.

37
38
39 671

40 41 672 **Acknowledgements**

42
43
44 673 The authors would like to acknowledge PRISMM core facility collaborators R. Delepée and S.
45
46 674 Lagadu for their expertise in m⁶A/A UHPLC-MS/MS quantification. We also thank J. Pontin for
47
48
49 675 technical assistance and J. Le Grand for help with sampling.
50
51
52 676

53 54 677 **Funding sources and disclosure of conflicts of interest**

55
56
57
58
59
60

1
2
3 678 This work was supported by the French National program CNRS EC2CO (Ecosphère
4
5
6 679 Continentale et Côtière 'HERITAGe' to G. Rivière) and the council of the Normandy Region
7
8 680 (RIN ECUME to P. Favrel). The authors declare they have no conflict of interest.
9

10
11 681
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

For Review Only

682 **References:**

- 683 1 Saletore Y, Meyer K, Korlach J, Vilfan ID, Jaffrey S & Mason CE (2012) The birth of the
684 Epitranscriptome: deciphering the function of RNA modifications. *Genome Biol.* **13**, 175.
- 685 2 Meyer KD, Saletore Y, Zumbo P, Elemento O, Mason CE & Jaffrey SR (2012)
686 Comprehensive analysis of mRNA methylation reveals enrichment in 3' UTRs and near
687 stop codons. *Cell* **149**, 1635–1646.
- 688 3 Dominissini D, Moshitch-moshkovitz S, Schwartz S, Salmon-Divon M, Ungar L, Osenberg
689 S, Cesarkas K, Jacob-hirsch J, Amariglio N, Kupiee M, Sorek R & Rechavi G (2012)
690 Topology of the human and mouse m6A RNAmethylomes revealed by m6A-seq.
691 *Nature* **485**, 201–206.
- 692 4 Ke S, Alemu EA, Mertens C, Gantman EC, Fak JJ, Mele A, Haripal B, Zucker-Scharff I,
693 Moore MJ, Park CY, Vågbø CB, Kusnierczyk A, Klungland A, Darnell JE, Darnell RB,
694 Kuśnierczyk A, Klungland A, Darnell JE, Darnell RB, Kusnierczyk A, Klungland A,
695 Darnell JE & Darnell RB (2015) A majority of m6A residues are in the last exons,
696 allowing the potential for 3' UTR regulation. *Genes Dev.* **29**, 2037–2053.
- 697 5 Meyer KD, Patil DP, Zhou J, Zinoviev A, Skabkin MA, Elemento O, Pestova T V., Qian SB
698 & Jaffrey SR (2015) 5' UTR m6A Promotes Cap-Independent Translation. *Cell* **163**,
699 999–1010.
- 700 6 Pendleton KE, Chen B, Liu K, Hunter O V., Xie Y, Tu BP & Conrad NK (2017) The U6
701 snRNA m6A Methyltransferase METTL16 Regulates SAM Synthetase Intron Retention.
702 *Cell* **169**, 824-835.e14.
- 703 7 Lence T, Akhtar J, Bayer M, Schmid K, Spindler L, Ho CH, Kreim N, Andrade-Navarro MA,
704 Poeck B, Helm M & Roignant JY (2016) M6A modulates neuronal functions and sex
705 determination in *Drosophila*. *Nature* **540**, 242–247.
- 706 8 Bokar JA, Shambaugh ME, Polayes D, Matera AG & Rottman FM (1997) Purification and
707 cDNA cloning of the AdoMet-binding subunit of the human mRNA (N6-adenosine)-
708 methyltransferase. *RNA* **3**, 1233–47.
- 709 9 Liu J, Yue Y, Han D, Wang X, Fu YY, Zhang L, Jia G, Yu M, Lu Z, Deng X, Dai Q, Chen W
710 & He C (2013) A METTL3–METTL14 complex mediates mammalian nuclear RNA N6-
711 adenosine methylation. *Nat. Chem. Biol.* **10**, 93–95.
- 712 10 Wang X, Feng J, Xue Y, Guan Z, Zhang D, Liu Z, Gong Z, Wang Q, Huang J, Tang C,
713 Zou T & Yin P (2016) Structural basis of N6-adenosine methylation by the METTL3-
714 METTL14 complex. *Nature* **534**, 575–578.
- 715 11 Ping X-LL, Sun B-FF, Wang L, Xiao W, Yang X, Wang W-JJ, Adhikari S, Shi Y, Lv Y,
716 Chen Y-SS, Zhao X, Li A, Yang YGYY-G, Dahal U, Lou X-MM, Liu X, Huang J, Yuan W-
717 PP, Zhu X-FF, Cheng T, Zhao Y-LL, Wang X, Danielsen JMRR, Liu F & Yang YGYY-G
718 (2014) Mammalian WTAP is a regulatory subunit of the RNA N6-methyladenosine
719 methyltransferase. *Cell Res.* **24**, 177–189.
- 720 12 Yue Y, Liu J, Cui X, Cao J, Luo G, Zhang Z, Cheng T, Gao M, Shu X, Ma H, Wang F,
721 Wang X, Shen B, Wang Y, Feng X, He C & Liu J (2018) VIRMA mediates preferential
722 m6A mRNA methylation in 3'UTR and near stop codon and associates with alternative
723 polyadenylation. *Cell Discov.* **4**, 10.
- 724 13 Růžička K, Zhang M, Campilho A, Bodi Z, Kashif M, Saleh M, Eeckhout D, El-Showk S, Li
725 H, Zhong S, Jaeger G De, Mongan NP, Hejátko J, Helariutta Y & Fray RG (2017)
726 Identification of factors required for m6A mRNA methylation in *Arabidopsis* reveals a

- 1
2
3 727 role for the conserved E3 ubiquitin ligase HAKAI. *New Phytol.* **215**, 157–172.
4
- 5 728 14 Knuckles P, Lence T, Haussmann IU, Jacob D, Kreim N, Carl SH, Masiello I, Hares T,
6 729 Villaseñor R, Hess D, Andrade-Navarro MA, Biggiogera M, Helm M, Soller M, Bühler M
7 730 & Roignant J-YY (2018) Zc3h13/Flacc is required for adenosine methylation by bridging
8 731 the mRNA-binding factor Rbm15/Spenito to the m⁶A machinery component
9 732 Wtap/Fl(2)d. *Genes Dev.* **32**, 1–15.
- 10
11 733 15 Patil DP, Chen CK, Pickering BF, Chow A, Jackson C, Guttman M & Jaffrey SR (2016)
12 734 m⁶A RNA methylation promotes XIST-mediated transcriptional repression. *Nature* **537**,
13 735 369–373.
- 14
15 736 16 Zheng G, Dahl JA, Niu Y, Fedorcsak P, Huang CM, Li CJ, Vågbo CB, Shi Y, Wang WL,
16 737 Song SH, Lu Z, Bosmans RPG, Dai Q, Hao YJ, Yang X, Zhao WM, Tong WM, Wang
17 738 XJ, Bogdan F, Furu K, Fu Y, Jia G, Zhao X, Liu J, Krokan HE, Klungland A, Yang YG &
18 739 He C (2013) ALKBH5 Is a Mammalian RNA Demethylase that Impacts RNA Metabolism
19 740 and Mouse Fertility. *Mol. Cell* **49**, 18–29.
- 20
21 741 17 Mauer J, Luo X, Blanjoie A, Jiao X, Grozhik A V, Patil DP, Linder B, Pickering BF,
22 742 Vasseur J-J, Chen Q, Gross SS, Elemento O, Debart F, Kiledjian M & Jaffrey SR (2017)
23 743 Reversible methylation of m⁶Am in the 5' cap controls mRNA stability. *Nature* **541**, 371–
24 744 375.
- 25
26 745 18 Jia G, Fu Y, Zhao X, Dai Q, Zheng G, Yang YGYG-GGYG-G, Yi C, Lindahl T, Pan T,
27 746 Yang YGYG-GGYG-G & He C (2011) N⁶-Methyladenosine in nuclear RNA is a major
28 747 substrate of the obesity-associated FTO. *Nat. Chem. Biol.* **7**, 885–887.
- 29
30 748 19 Wang X, Lu Z, Gomez A, Hon GC, Yue Y, Han D, Fu Y, Parisien M, Dai Q, Jia G, Ren B,
31 749 Pan T, He C, Zhike L, Gomez A, Hon GC, Yue Y, Han D, Fu Y, Årisien M, Dai Q, Jia G,
32 750 Ren B, Pan T & He C (2014) N⁶-methyladenosine-dependent regulation of messenger
33 751 RNA stability. *Nature* **505**, 117–120.
- 34
35 752 20 Wang X, Zhao BS, Roundtree IA, Lu Z, Han D, Ma H, Weng X, Chen K, Shi H & He C
36 753 (2015) N⁶-methyladenosine modulates messenger RNA translation efficiency. *Cell* **161**,
37 754 1388–1399.
- 38
39 755 21 Hsu PJ, Zhu Y, Ma H, Guo Y, Shi X, Liu Y, Qi M, Lu Z, Shi H, Wang J, Cheng Y, Luo G,
40 756 Dai Q, Liu M, Guo X, Sha J, Shen B & He C (2017) Ythdc2 is an N⁶-methyladenosine
41 757 binding protein that regulates mammalian spermatogenesis. *Cell Res.* **27**, 1115–1127.
- 42
43 758 22 Shi H, Wang X, Lu Z, Zhao BS, Ma H, Hsu PJ, Liu C & He C (2017) YTHDF3 facilitates
44 759 translation and decay of N⁶-methyladenosine-modified RNA. *Cell Res.* **27**, 315–328.
- 45
46 760 23 Xiao W, Adhikari S, Dahal U, Chen Y-S, Hao Y-J, Sun B-F, Sun H-Y, Li A, Ping X-L, Lai
47 761 W-Y, Wang XX-J, Ma H-L, Huang C-M, Yang YY-G, Huang N, Jiang G-B, Wang H-L,
48 762 Zhou Q, Wang XX-J, Zhao Y-L & Yang YY-G (2016) Nuclear m⁶A Reader YTHDC1
49 763 Regulates mRNA Splicing. *Mol. Cell* **61**, 507–519.
- 50
51 764 24 Roundtree IA, Luo G-ZZ, Zhang Z, Wang X, Zhou T, Cui Y, Sha J, Huang X, Guerrero L,
52 765 Xie P, He E, Shen B & He C (2017) YTHDC1 mediates nuclear export of N⁶-
53 766 methyladenosine methylated mRNAs. *Elife* **6**, 1–28.
- 54
55 767 25 Alarcón CR, Goodarzi H, Lee H, Liu X, Tavazoie SFSSF & Tavazoie SFSSF (2015)
56 768 HNRNPA2B1 Is a Mediator of m⁶A-Dependent Nuclear RNA Processing Events. *Cell*
57 769 **162**, 1299–1308.
- 58
59 770 26 Huang H, Weng H, Sun W, Qin X, Shi H, Wu H, Zhao BS, Mesquita A, Liu C, Yuan CL,
60 771 Hu YC, Hüttelmaier S, Skibbe JR, Su R, Deng X, Dong L, Sun M, Li C, Nachtergaele S,

- 1
2
3 772 Wang Y, Hu C, Ferchen K, Greis KD, Jiang X, Wei M, Qu L, Guan JL, He C, Yang J &
4 773 Chen J (2018) Recognition of RNA N6-methyladenosine by IGF2BP proteins enhances
5 774 mRNA stability and translation. *Nat. Cell Biol.* **20**, 285–295.
6
7 775 27 Wu R, Li A, Sun B, Sun J-GG, Zhang J, Zhang T, Chen Y, Xiao Y, Gao Y, Zhang Q, Ma J,
8 776 Yang X, Liao Y, Lai W-YY, Qi X, Wang S, Shu Y, Wang H-LL, Wang F, Yang Y-GG &
9 777 Yuan Z (2018) A novel m6A reader Prrc2a controls oligodendroglial specification and
10 778 myelination. *Cell Res.* **29**, 23–41.
11
12 779 28 Bertero A, Brown S, Madrigal P, Osnato A, Ortmann D, Yiangou L, Kadiwala J, Hubner
13 780 NC, De Los Mozos IR, Sadee C, Lenaerts A-SS, Nakanoh S, Grandy R, Farnell E, Ule
14 781 J, Stunnenberg HG, Mendjan S, Vallier L, Sadée C, Lenaerts A-SS, Nakanoh S, Grandy
15 782 R, Farnell E, Ule J, Stunnenberg HG, Mendjan S & Vallier L (2018) The SMAD2/3
16 783 interactome reveals that TGF β controls m 6 A mRNA methylation in pluripotency.
17 784 *Nature* **555**, 256–259.
18
19 785 29 Kwon J, Jo YJ, Namgoong S & Kim NH (2019) Functional roles of hnRNPA2/B1 regulated
20 786 by METTL3 in mammalian embryonic development. *Sci. Rep.* **9**, 8640.
21
22 787 30 Geula S, Moshitch-Moshkovitz S, Dominissini D, Mansour AAF, Kol N, Salmon-Divon M,
23 788 Hershkovitz V, Peer E, Mor N, Manor YS, Ben-Haim MS, Eyal E, Yunger S, Pinto Y,
24 789 Jaitin DA, Viukov S, Rais Y, Krupalnik V, Chomsky E, Zerbib M, Maza I, Rechavi Y,
25 790 Massarwa R, Hanna S, Amit I, Levanon EY, Amariglio N, Stern-Ginossar N,
26 791 Novershtern N, Rechavi G & Hanna JH (2015) m6A mRNA methylation facilitates
27 792 resolution of naïve pluripotency toward differentiation. *Science (80-.)*. **347**, 1002–1006.
28
29 793 31 Batista PJ, Molinie B, Wang J, Qu K, Zhang J, Li L, Bouley DM, Lujan E, Haddad B,
30 794 Daneshvar K, Carter AC, Flynn RA, Zhou C, Lim KS, Dedon P, Wernig M, Mullen AC,
31 795 Xing Y, Giallourakis CC, Chang HY, Howard Y, Batista PJ, Molinie B, Wang J, Qu K,
32 796 Zhang J, Li L, Bouley DM, Dedon P, Wernig M, Mullen AC, Xing Y, Giallourakis CC &
33 797 Chang HY (2014) M⁶A RNA modification controls cell fate transition in mammalian
34 798 embryonic stem cells. *Cell Stem Cell* **15**, 707–719.
35
36 799 32 Wojtas MN, Pandey RR, Mendel M, Homolka D, Sachidanandam R & Pillai RS (2017)
37 800 Regulation of m6A Transcripts by the 3'→5' RNA Helicase YTHDC2 Is Essential for a
38 801 Successful Meiotic Program in the Mammalian Germline. *Mol. Cell* **68**, 374-387.e12.
39
40 802 33 Zhao BS, Wang X, Beadell A V., Lu Z, Shi H, Kuuspalu A, Ho RK & He C (2017) M6A-
41 803 dependent maternal mRNA clearance facilitates zebrafish maternal-to-zygotic transition.
42 804 *Nature* **542**, 475–478.
43
44 805 34 Kan L, Grozhik A V., Vedanayagam J, Patil DP, Pang N, Lim K-S, Huang Y-C, Joseph B,
45 806 Lin C-J, Despic V, Guo J, Yan D, Kondo S, Deng W-M, Dedon PC, Jaffrey SR & Lai EC
46 807 (2017) The m6A pathway facilitates sex determination in *Drosophila*. *Nat. Commun.* **8**,
47 808 15737.
48
49 809 35 Kasowitz SD, Ma J, Anderson SJ, Leu NA, Xu Y, Gregory BD, Schultz RM & Wang PJ
50 810 (2018) Nuclear m 6 A reader YTHDC1 regulates alternative polyadenylation and splicing
51 811 during mouse oocyte development. *PLoS Genet.* **14**, 1–28.
52
53 812 36 Ivanova I, Much C, Di Giacomo M, Azzi C, Morgan M, Moreira PN, Monahan J, Carrieri C,
54 813 Enright AJ, O'Carroll D, Giacomo M Di, Azzi C, Morgan M, Moreira PN, Monahan J,
55 814 Carrieri C, Enright AJ, O'carroll D, Di Giacomo M, Azzi C, Morgan M, Moreira PN,
56 815 Monahan J, Carrieri C, Enright AJ & O'carroll D (2017) The RNA m 6 A Reader
57 816 YTHDF2 Is Essential for the Post-transcriptional Regulation of the Maternal
58 817 Transcriptome and Oocyte Competence. *Mol. Cell* **67**, 1059-1067.e4.
59
60

- 1
2
3 818 37 Lence T, Paolantoni C, Worpenberg L & Roignant JY (2019) Mechanistic insights into m⁶A
4 819 RNA enzymes. *Biochim. Biophys. Acta - Gene Regul. Mech.* **1862**, 222–229.
5
6 820 38 Balacco DL & Soller M (2018) The m⁶A writer: Rise of a machine for growing tasks.
7 821 *Biochemistry* **58**, acs.biochem.8b01166.
8
9 822 39 Lence T, Soller M & Roignant JY (2017) A fly view on the roles and mechanisms of the
10 823 m⁶A mRNA modification and its players. *RNA Biol.* **14**, 1232–1240.
11
12 824 40 Robbens S, Rouzé P, Cock JM, Spring J, Worden AZ & Van De Peer Y (2008) The FTO
13 825 gene, implicated in human obesity, is found only in vertebrates and marine algae. *J.*
14 826 *Mol. Evol.* **66**, 80–84.
15
16 827 41 Zhang G, Huang H, Liu D, Cheng Y, Liu X, Zhang W, Yin R, Zhang D, Zhang P, Liu J, Li
17 828 C, Liu B, Luo Y, Zhu Y, Zhang N, He S, He C, Wang H & Chen D (2015) N⁶-
18 829 methyladenine DNA modification in *Drosophila*. *Cell* **161**, 893–906.
19
20 830 42 Greer EL, Blanco MA, Gu L, Sendinc E, Liu J, Aristizábal-Corrales D, Hsu CH, Aravind L,
21 831 He C & Shi Y (2015) DNA methylation on N⁶-adenine in *C. elegans*. *Cell* **161**, 868–878.
22
23 832 43 Riviere G, He Y, Tecchio S, Crowell E, Sourdain P, Guo X & Favrel P (2017) Dynamics
24 833 of DNA methylomes underlie oyster development. *PLOS Genet.* **13**, 1–16.
25
26 834 44 Sussarellu R, Lebreton M, Rouxel J, Akcha F, Riviere G & Rivière G (2018) Copper
27 835 induces expression and methylation changes of early development genes in
28 836 *Crassostrea gigas* embryos. *Aquat. Toxicol.* **196**, submitted.
29
30 837 45 Rondon R, Grunau C, Fallet M, Charlemagne N, Sussarellu R, Chaparro C, Montagnani
31 838 C, Mitta G, Bachère E, Akcha F & Cosseau C (2017) Effects of a parental exposure to
32 839 diuron on Pacific oyster spat methylome. *Environ. Epigenetics* **3**, 1–13.
33
34 840 46 Riviere G, Wu G-CC, Fellous A, Goux D, Sourdain P & Favrel P (2013) DNA Methylation
35 841 Is Crucial for the Early Development in the Oyster *C. gigas*. *Mar. Biotechnol.* **15**, 1–15.
36
37 842 47 Saint-Carlier E & Riviere G (2015) Regulation of Hox orthologues in the oyster
38 843 *Crassostrea gigas* evidences a functional role for promoter DNA methylation in an
39 844 invertebrate. *FEBS Lett.* **589**, 1459–1466.
40
41 845 48 Fellous A, Favrel P & Riviere G (2015) Temperature influences histone methylation and
42 846 mRNA expression of the Jmj-C histone-demethylase orthologues during the early
43 847 development of the oyster *Crassostrea gigas*. *Mar. Genomics* **19**, 23–30.
44
45 848 49 Fellous A, Favrel P, Guo X & Riviere G (2014) The Jumonji gene family in *Crassostrea*
46 849 *gigas* suggests evolutionary conservation of Jmj-C histone demethylases orthologues in
47 850 the oyster gametogenesis and development. *Gene* **538**, 164–175.
48
49 851 50 Fellous A, Le Franc L, Jouaux A, Goux D, Favrel P & Rivière G (2019) Histone
50 852 Methylation Participates in Gene Expression Control during the Early Development of
51 853 the Pacific Oyster *Crassostrea gigas*. *Genes (Basel)*. **10**, 695.
52
53 854 51 Zhou J, Wan J, Gao X, Zhang X, Jaffrey SR & Qian S-B (2015) Dynamic m⁶A mRNA
54 855 methylation directs translational control of heat shock response. *Nature* **526**, 591–594.
55
56 856 52 Lu Z, Ma Y, Li Q, Liu E, Jin M, Zhang L & Wei C (2019) The role of N⁶-methyladenosine
57 857 RNA methylation in the heat stress response of sheep (*Ovis aries*). *Cell Stress*
58 858 *Chaperones* **24**, 333–342.
59
60 859 53 Xiang Y, Laurent B, Hsu C, Nachtergaele S, Lu Z, Sheng W, Xu C, Chen H, Ouyang J,

- 1
2
3 860 Wang S, Ling D, Hsu P, Zou L, Jambhekar A & He C (2017) m6A RNA methylation
4 861 regulates the UV-induced DNA damage response. *Nature* **543**, 573–576.
5
6 862 54 Cayir A, Barrow TM, Guo L & Byun HM (2019) Exposure to environmental toxicants
7 863 reduces global N6-methyladenosine RNA methylation and alters expression of RNA
8 864 methylation modulator genes. *Environ. Res.* **175**, 228–234.
9
10 865 55 Liu J, Li K, Cai J, Zhang M, Zhang X, Xiong X, Meng H, Xu X, Huang Z, Fan J & Yi C
11 866 (2019) Landscape and Regulation of M⁶A and M⁶Am Methylome Across Human and
12 867 Mouse Tissues. *SSRN Electron. J.*, 1–56.
13
14 868 56 Ren W, Lu J, Huang M, Gao L, Li D, Greg Wang G & Song J (2019) Structure and
15 869 regulation of ZCCHC4 in m6A-methylation of 28S rRNA. *Nat. Commun.* **10**, 5042.
16
17 870 57 Bokar JA, Shambaugh ME, Polayes D, Matera AG & Rottman FM (1997) Purification and
18 871 cDNA cloning of the AdoMet-binding subunit of the human mRNA (N6-adenosine)-
19 872 methyltransferase. *RNA* **3**, 1233–1247.
20
21 873 58 Theler D, Dominguez C, Blatter M, Boudet J & Allain FHT (2014) Solution structure of the
22 874 YTH domain in complex with N6-methyladenosine RNA: A reader of methylated RNA.
23 875 *Nucleic Acids Res.* **42**, 13911–13919.
24
25 876 59 Shima H, Matsumoto M, Ishigami Y, Ebina M, Muto A, Sato Y, Kumagai S, Ochiai K,
26 877 Suzuki T & Igarashi K (2017) S-Adenosylmethionine Synthesis Is Regulated by
27 878 Selective N6-Adenosine Methylation and mRNA Degradation Involving METTL16 and
28 879 YTHDC1. *Cell Rep.* **21**, 3354–3363.
29
30 880 60 Yurchenko O V., Skiteva OI, Voronezhskaya EE & Dyachuk VA (2018) Nervous system
31 881 development in the Pacific oyster, *Crassostrea gigas* (Mollusca: Bivalvia). *Front. Zool.*
32 882 **15**, 1–21.
33
34 883 61 Ratnaparkhi A (2013) Signaling by folded gastrulation is modulated by mitochondrial
35 884 fusion and fission. *J. Cell Sci.* **126**, 5369–5376.
36
37 885 62 Ren L, Zhang C, Tao L, Hao J, Tan K, Miao K, Yu Y, Sui L, Wu Z, Tian J & An L (2017)
38 886 High-resolution profiles of gene expression and DNA methylation highlight mitochondrial
39 887 modifications during early embryonic development. *J. Reprod. Dev.* **63**, 247–261.
40
41 888 63 Prudent J, Popgeorgiev N, Bonneau B, Thibaut J, Gadet R, Lopez J, Gonzalo P, Rimokh
42 889 R, Manon S, Houart C, Herbomel P, Aouacheria A & Gillet G (2013) Bcl-wav and the
43 890 mitochondrial calcium uniporter drive gastrula morphogenesis in zebrafish. *Nat.*
44 891 *Commun.* **4**.
45
46 892 64 Dumollard R, Duchon M & Carroll J (2007) The Role of Mitochondrial Function in the
47 893 Oocyte and Embryo. *Curr. Top. Dev. Biol.* **77**, 21–49.
48
49 894 65 Huang H, Weng H, Zhou K, Wu T, Zhao BS, Sun MM, Chen Z, Deng X, Xiao G, Auer F,
50 895 Klemm L, Wu H, Zuo Z, Qin X, Dong Y, Zhou Y, Qin H, Tao S, Du J, Liu J, Lu Z, Yin H,
51 896 Mesquita A, Yuan CL, Hu Y-CC, Sun W, Su R, Dong L, Shen C, Li C, Qing Y, Jiang X,
52 897 Wu X, Sun MM, Guan J-LL, Qu L, Wei M, Müschen M, Huang G, He C, Yang J & Chen
53 898 J (2019) Histone H3 trimethylation at lysine 36 guides m6A RNA modification co-
54 899 transcriptionally. *Nature* **567**, 414–419.
55
56 900 66 Wang Y, Li Y, Yue M, Wang J, Kumar S, Wechsler-Reya RJ, Zhang Z, Ogawa Y, Kellis M,
57 901 Duyster G & Zhao JC (2018) N6-methyladenosine RNA modification regulates
58 902 embryonic neural stem cell self-renewal through histone modifications. *Nat. Neurosci.*
59 903 **21**, 195–206.

- 1
2
3 904 67 Petton B, Pernet F, Robert R & Boudry P (2013) Temperature influence on pathogen
4 905 transmission and subsequent mortalities in juvenile pacific oysters *Crassostrea gigas*.
5 906 *Aquac. Environ. Interact.* **3**, 257–273.
6
7 907 68 Riviere G, Fellous A, Franco A, Bernay B & Favrel P (2011) A crucial role in fertility for the
8 908 oyster angiotensin-converting enzyme orthologue CgACE. *PLoS One* **6**.
9
10 909 69 EMA (2011) *Guideline on bioanalytical method validation*.
11 910 *EMA/CHMP/EWP/192217/2009*.
12
13 911 70 Riviere G, Klopp C, Ibouniyamine N, Huvet A, Boudry P & Favrel P (2015) GigaTON: An
14 912 extensive publicly searchable database providing a new reference transcriptome in the
15 913 pacific oyster *Crassostrea gigas*. *BMC Bioinformatics* **16**, 1–12.
16
17 914 71 Zhang G, Fang X, Guo X, Li L, Luo R, Xu F, Yang P, Zhang L, Wu F, Chen Y, Wang J,
18 915 Peng C, Meng J, Yang L, Liu J, Wen B, Zhang N & Huang Z (2012) The oyster genome
19 916 reveals stress adaptation and complexity of shell formation. *Nature* **490**, 49–54.
20
21 917 72 Li B, Ruotti V, Stewart RM, Thomson JA & Dewey CN (2010) RNA-Seq gene expression
22 918 estimation with read mapping uncertainty. *Bioinformatics* **26**, 493–500.
23
24 919 73 Qi ST, Ma JY, Wang ZB, Guo L, Hou Y & Sun QY (2016) N6 -methyladenosine
25 920 sequencing highlights the involvement of mRNA methylation in oocyte meiotic
26 921 maturation and embryo development by regulating translation in *xenopus laevis*. *J. Biol.*
27 922 *Chem.* **291**, 23020–23026.
28
29 923 74 Altschul SF, Madden TL, Schäffer AA, Zhang J, Zhang Z, Miller W & Lipman DJ (1997)
30 924 Gapped BLAST and PSI-BLAST: a new generation of protein database search
31 925 programs. *Nucleic Acids Res.* **25**, 3389–3402.
32
33 926 75 Cock PJA, Chilton JM, Grüning B, Johnson JE & Soranzo N (2015) NCBI BLAST+
34 927 integrated into Galaxy. *Gigascience* **4**, 0–6.
35
36 928 76 Camacho C, Coulouris G, Avagyan V, Ma N, Papadopoulos J, Bealer K & Madden TL
37 929 (2009) BLAST+: Architecture and applications. *BMC Bioinformatics* **10**, 1–9.
38
39 930 77 Young MD, Wakefield MJ, Smyth GK & Oshlack A (2010) Gene ontology analysis for
40 931 RNA-seq: accounting for selection bias. *Genome Biol.* **11**, R14.
41
42 932 78 Supek F, Bošnjak M, Škunca N & Šmuc T (2011) Revigo summarizes and visualizes long
43 933 lists of gene ontology terms. *PLoS One* **6**.
44
45 934 79 Larsson J (2019) eulerr: Area-Proportional Euler and Venn Diagrams with Ellipses. .
46
47 935 80 Gu Z, Eils R & Schlesner M (2016) Complex heatmaps reveal patterns and correlations in
48 936 multidimensional genomic data. *Bioinformatics* **32**, 2847–2849.
49
50 937
51
52 938
53
54
55
56
57
58
59
60

1
2
3 939 **Figure legends**
4
5

6 940 Figure 1: m⁶A levels across oyster development.
7
8

9
10 941 **A.** m⁶A level quantified by LC-MS/MS in *Crassostrea gigas* embryo-larval stages pooled from
11
12 942 oocytes to D-larvae (n= 3) is compared to the m⁶A level in *Homo sapiens* and *Drosophila*
13
14 943 *melanogaster*; **B.** Dot blot quantification of m⁶A in total RNA throughout oyster development
15
16 944 (n=3); **C.** Dot blot quantification of m⁶A in polyA+ RNAs throughout oyster development (n=3)
17
18 945 Kruskal-Wallis test, $\alpha < 0,05$. E: Egg, F E: fertilized egg, 2/8C: two to eight cell embryos, M:
19
20 946 Morula, B: Blastula, G: Gastrula, T: Trochophore, D: D larvae. Chemiluminescence (B) and
21
22 947 fluorescence (C) are measured as a ratio between dot intensity of development stages and
23
24 948 their respective controls for each amount of RNA (120ng, 60ng and 30ng).
25
26
27
28
29
30

31
32 949

33
34 950 Figure 2: The putative conserved m⁶A machinery in *Crassostrea gigas*.
35

36
37 951 Domain architecture of actors of the m⁶A machinery identified by *in silico* analyses in the oyster
38
39 952 compared to the fruit fly and human, **A.** Writer proteins; **B.** Eraser protein; **C.** Reader proteins.
40
41 953 Putative domains involved in m⁶A processes are coloured (writers, green; eraser, red; readers,
42
43 954 blue). Other domains identified but not involved in m⁶A processes are indicated in grey. Only
44
45 955 one isoform is represented for each protein and each species for clarity (see supplementary
46
47 956 figure S2 for other isoforms).
48
49
50
51

52
53 957

54
55 958 Figure 3: Gene expression of the putative m⁶A machinery throughout oyster development
56
57
58
59
60

1
2
3 959 Expression levels of writers (**A**), eraser (**B**) and readers (**C**) identified by *in silico* analysis at
4
5
6 960 each development stage were inferred from the GigaTON database. Expression levels are
7
8 961 given in Transcripts Per kilobases per Million Reads (TPM) as the mean of the GigaTON values
9
10
11 962 according to the table S2. E: Egg, 2/8C: two to eight cell, M: Morula, B: Blastula, G: Gastrula,
12
13
14 963 T: Trochophore, D: D larvae, S: Spat, J: Juvenile.

15
16 964

17
18
19 965 Figure 4: Characterization of m⁶A-RNA binding proteins in oyster development.

20
21 966 **A.** Venn diagrams representation of proteins bound to the A- and/or m⁶A- oligos in nuclear and
22
23
24 967 cytosolic fractions of oyster embryo-larval stages. The number of proteins identified is
25
26
27 968 indicated. Some actors characterized in this study are highlighted: eIF3, YTHC1, hnRNPA2B1
28
29
30 969 and IGF2BP. **B.** Heatmap of gene expression levels of the proteins that bind specifically to the
31
32
33 970 m⁶A-oligo throughout oyster development. The expression level is normalized regarding the
34
35
36 971 maximum value for each gene according to the GigaTON database. **C.** GO term distribution
37
38
39 972 among the three expression clusters in B. **D.** Examples of GO term enrichment within the
40
41
42 973 expression clusters of the m⁶A-bound proteins. The $-\log_{10}(\text{p-value})$ associated to each term
43
44
45 974 is given. E: Egg, 2/8C: two to eight cells, M: Morula, B: Blastula, G: Gastrula, T: Trochophore,
46
47
48 975 D: D larvae, S: Spat, J: Juvenile.

49
50 976 **Supporting information:**

51
52 977 Data S1: Complete list of *in silico* identified putative m⁶A machinery proteins and their
53
54
55 978 respective BLAST results

56
57 979 Data S2: Identified proteins by RNA pull down coupled with mass spectrometry with m⁶A or
58
59
60 980 A-oligo, in nuclear or cytosolic protein extracts

1
2
3 981 Data S3: Complete list of GO terms of clustered genes of m⁶A interacting proteins (p-
4
5
6 982 value<0,05)
7

8 983 Table S1: Transitions used for each compound. A: first transition, B: second transition
9

10
11 984 Table S2: Table of correspondence between development stages in our study, and the
12
13
14 985 GigaTON database.
15

16 986
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

For Review Only

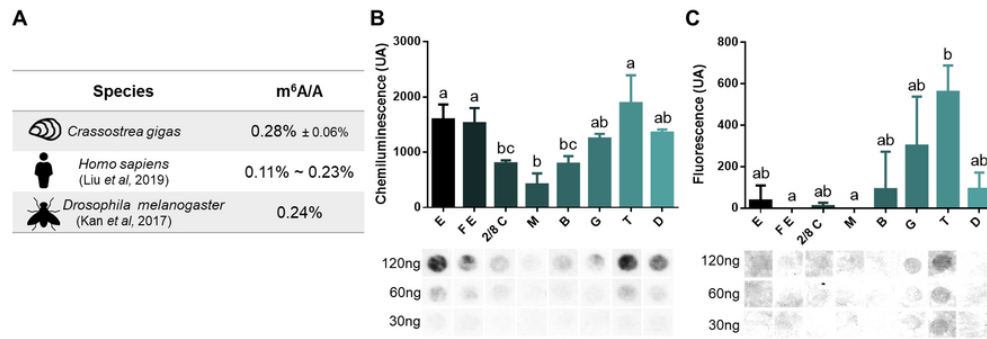


Figure 1: m⁶A levels across oyster development.

A. m⁶A level quantified by LC-MS/MS in *Crassostrea gigas* embryo-larval stages pooled from oocytes to D-larvae (n= 3) is compared to the m⁶A level in *Homo sapiens* and *Drosophila melanogaster*; B. Dot blot quantification of m⁶A in total RNA throughout oyster development (n=3); C. Dot blot quantification of m⁶A in polyA+ RNAs throughout oyster development (n=3) Kruskal-Wallis test, $\alpha < 0,05$. E: Egg, F E: fertilized egg, 2/8C: two to eight cell embryos, M: Morula, B: Blastula, G: Gastrula, T: Trochophore, D: D larvae. Chemiluminescence (B) and fluorescence (C) are measured as a ratio between dot intensity of development stages and their respective controls for each amount of RNA (120ng, 60ng and 30ng).

75x25mm (300 x 300 DPI)

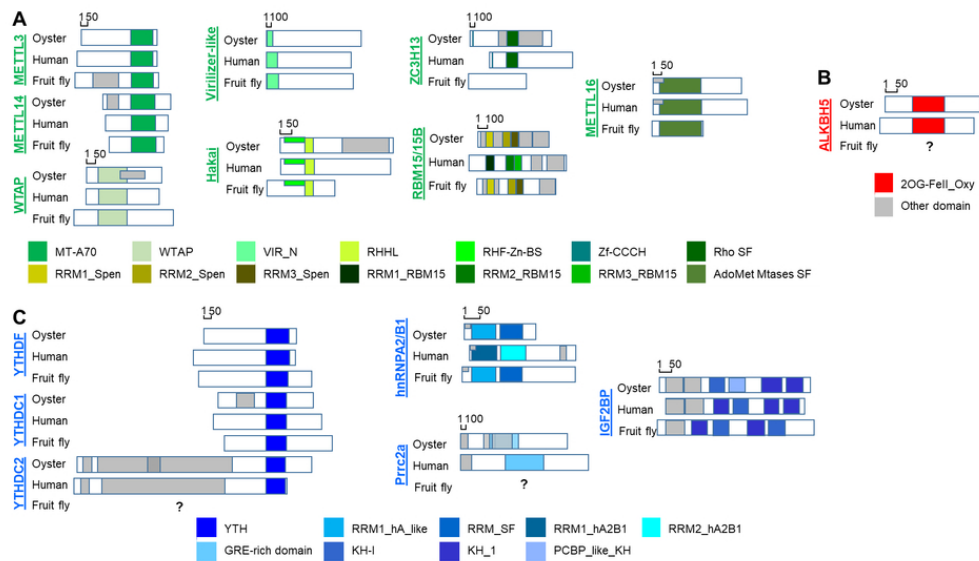


Figure 2: The putative conserved m6A machinery in *Crassostrea gigas*. Domain architecture of actors of the m6A machinery identified by in silico analyses in the oyster compared to the fruit fly and human, A. Writer proteins; B. Eraser protein; C. Reader proteins. Putative domains involved in m6A processes are coloured (writers, green; eraser, red; readers, blue). Other domains identified but not involved in m6A processes are indicated in grey. Only one isoform is represented for each protein and each species for clarity (see supplementary figure S2 for other isoforms).

80x47mm (300 x 300 DPI)

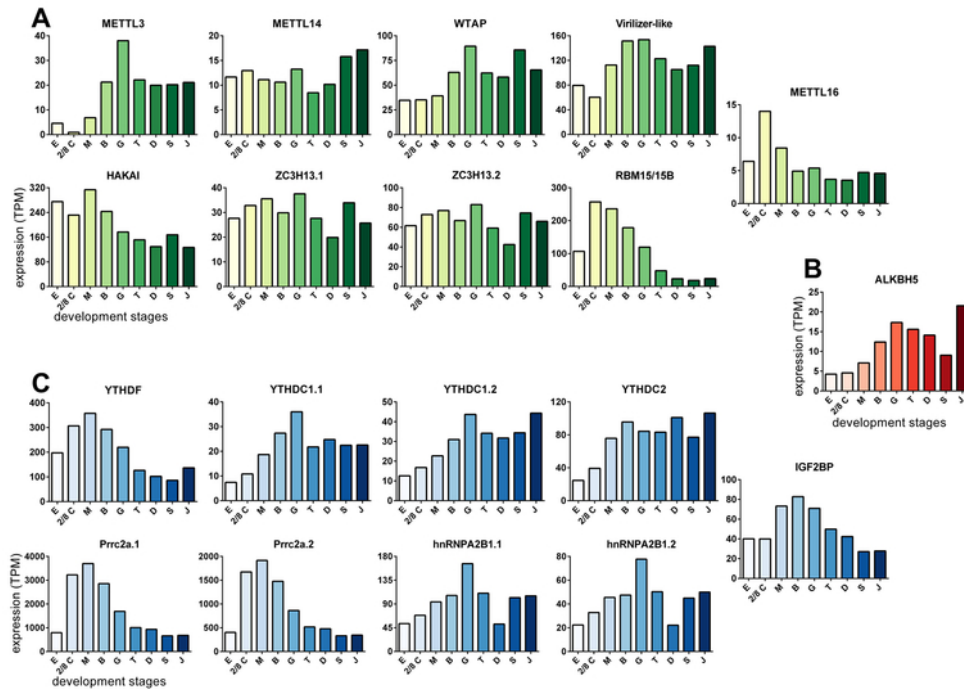


Figure 3: Gene expression of the putative m6A machinery throughout oyster development. Expression levels of writers (A), eraser (B) and readers (C) identified by in silico analysis at each development stage were inferred from the GigaTON database. Expression levels are given in Transcripts Per kilobases per Million Reads (TPM) as the mean of the GigaTON values according to the table S2. E: Egg, 2/8C: two to eight cell, M: Morula, B: Blastula, G: Gastrula, T: Trochophore, D: D larvae, S: Spat, J: Juvenile.

65x46mm (300 x 300 DPI)

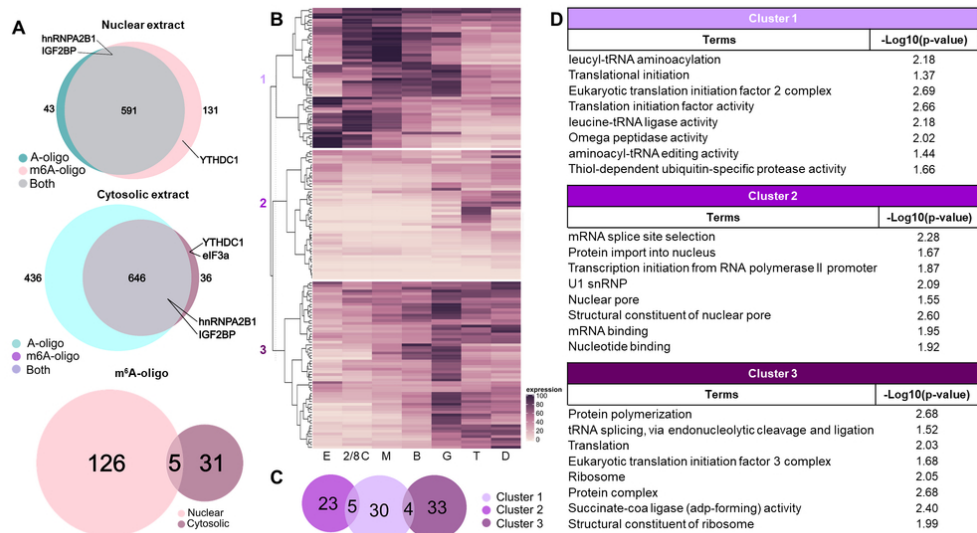


Figure 4: Characterization of m6A-RNA binding proteins in oyster development. A. Venn diagrams representation of proteins bound to the A- and/or m6A- oligos in nuclear and cytosolic fractions of oyster embryo-larval stages. The number of proteins identified is indicated. Some actors characterized in this study are highlighted: eIF3, YTHC1, hnRNPA2B1 and IGF2BP. B. Heatmap of gene expression levels of the proteins that bind specifically to the m6A-oligo throughout oyster development. The expression level is normalized regarding the maximum value for each gene according to the GigaTON database. C. GO term distribution among the three expression clusters in B. D. Examples of GO term enrichment within the expression clusters of the m6A-bound proteins. The $-\log_{10}(p\text{-value})$ associated to each term is given. E: Egg, 2/8C: two to eight cells, M: Morula, B: Blastula, G: Gastrula, T: Trochophore, D: D larvae, S: Spat, J: Juvenile.

85x49mm (300 x 300 DPI)

Data S1: Complete list of in silico identified putative m6A machinery proteins and their respective BLAST results

Probable assembly artefact highlighted in grey

Specie	database	sequence accession number	length	conserved domain
<u>METTL3</u>				
<i>Homo sapiens</i>	NCBI	gi 21361827 (NP_062826.2)	580	MT-A70
<i>Drosophila melanogaster</i> (IME4)	NCBI	gi 21355141 (NP_651204.1)	608	MT-A70 MDN1
<i>Crassostrea gigas</i>	GIGATON	CHOYP_PHUM_PHUM423190.1.1	554	MT-A70
	NCBI	gi 762092209 (XP_011428532.1)	555	MT-A70
<u>METTL14</u>				
<i>Homo sapiens</i>	NCBI	gi 24308265 (NP_066012.1)	456	MT-A70
<i>Drosophila melanogaster</i> (CG7818)	NCBI	gi 19920926 (NP_609205.1)	397	MT-A70
<i>Crassostrea gigas</i>	GIGATON	CHOYP_MET14.1.1	495	MT-A70 MttA_Hfc106
		CHOYP_LOC100743733.1.1	723	MT-A70 7tmA_NPR-like_invertebrate
	NCBI	gi 762082967 (XP_011424173.1)	470	MT-A70 MttA_Hfc106
<u>WTAP</u>				
<i>Homo sapiens</i>	NCBI	gi 395455090 (NP_001257460.1)	396	WTAP
		gi 23199974 (NP_690596.1)	151	WTAP
		gi 395455092 (NP_001257461.1)	170	WTAP
<i>Drosophila melanogaster</i> (FL(2)D)	NCBI	gi 24653459 (NP_523732.2)	536	WTAP
		gi 24653461 (NP_725327.1)	412	WTAP
<i>Crassostrea gigas</i>	GIGATON	CHOYP_FL2D.1.1	406	WTAP IncA
		CHOYP_SODM.1.2	252	WTAP IncA
		CHOYP_LOC100121674.1.1	290	WTAP IncA
	NCBI	gi 762078268 (XP_011453082.1)	406	WTAP IncA

VIRILIZER-LIKE

<i>Homo sapiens</i> (Virilizer-like, VIRMA)	NCBI	gi 33946282 (NP_056311.2)	1812	VIR_N	
		gi 33946280 (NP_892121.1)	1147	VIR_N	
<i>Drosophila melanogaster</i> (Virilizer)	NCBI	gi 17864576 (NP_524900.1)	1854	VIR_N	
<i>Crassostrea gigas</i>	GIGATON	CHOYP_VIR.1.1	2021	VIR_N	
	NCBI	gi 762120202 (XP_011443024.1)	2023	VIR_N	
		gi 762120200 (XP_011443023.1)	2023	VIR_N	
		gi 1139822239 (XP_019927346.1)	2022	VIR_N	
		gi 1139822241 (XP_019927347.1)	2021	VIR_N	
gi 1139822243 (XP_019927348.1)	1717	VIR_N	PTZ00249 super family		

HAKAI

<i>Homo sapiens</i>	NCBI	gi 209180481 (NP_079090.2)	491	RHF-Zn-BS	RHHL	
		gi 546230945 (NP_001271220.1)	490	RHF-Zn-BS	RHHL	
<i>Drosophila melanogaster</i>	NCBI	gi 19921556 (NP_609993.1)	302	RHF-Zn-BS	RHHL	
		gi 24585301 (NP_724217.1)	311	RHF-Zn-BS	RHHL	
		gi 442628448 (NP_788075.2)	464	RHF-Zn-BS	RHHL	
		gi 442628450 (NP_001260593.1)	473	RHF-Zn-BS	RHHL	
<i>Crassostrea gigas</i>	GIGATON	CHOYP_LOC100864501.1.1	504	RHF-Zn-BS	RHHL	PHA03247 super family
	NCBI	gi 762140345 (XP_011453340.1)	498	RHF-Zn-BS	RHHL	PHA03247 super family
		gi 762140347 (XP_011453341.1)	497	RHF-Zn-BS	RHHL	PHA03247 super family

ZC3H13

<i>Homo sapiens</i>	NCBI	gi 1060099240 (NP_001317493.1)	1669	Zf-CCCH	Rho SF	
		gi 1060099108 (NP_001317496.1)	1668	Zf-CCCH	Rho SF	

		gi 116008442 (NP_055885.3)	1564	Zf-CCCH	Rho SF		
<i>Drosophila melanogaster</i> (CG7358)	NCBI	gi 24643154 (NP_573339.1)	1150				
		gi 665392303 (NP_001285418.1)	1139				
		gi 665392305 (NP_001285419.1)	842				
<i>Crassostrea gigas</i>	GIGATON	CHOYP_BRAFLDRAFT_120702.1.1	1631	Zf-CCCH	Rho SF	dnaA super family	PTZ00121
		CHOYP_LOC100568158.1.1	1611	Zf-CCCH	Rho SF	dnaA super family	PTZ00121
	NCBI	gi 762096734 (XP_011430912.1)	1400	Rho SF		dnaA super family	PTZ00121
		gi 762096736 (XP_011430913.1)	1400	Rho SF		dnaA super family	PTZ00121
		gi 762096738 (XP_011430914.1)	1380	Rho SF		PHA03307	PTZ00121
		gi 762096740 (XP_011430915.1)	1329	Rho SF			PTZ00121

RBM15/15B

<i>Homo sapiens</i>	NCBI	gi 47933339 (NP_073605)	977	RRM1_RBM15	RRM2_RBM15	RRM3_RBM15	SF-CC1	SPOC	
		gi 319996623 (NP_001188474)	969	RRM1_RBM15	RRM2_RBM15	RRM3_RBM15	SF-CC1	SPOC	
		gi 54607124 (NP_037418)	890	RRM1_RBM15	RRM2_RBM15	RRM3_RBM15	U2AF_Ig SF	SPOC	
<i>Drosophila melanogaster</i> (SPENITO/NITO)	NCBI	gi 24586450 (NP_724633)	793	RRM1_Spen	RRM2_Spen	RRM3_Spen	RRM	SPOC	
		gi 19921778 (NP_610339)	793	RRM1_Spen	RRM2_Spen	RRM3_Spen	RRM	SPOC	
		gi 665399388 (NP_001286174)	793	RRM1_Spen	RRM2_Spen	RRM3_Spen	RRM	SPOC	
<i>Crassostrea gigas</i>	GIGATON	CHOYP_LOC663518.1.1	717	RRM1_Spen	RRM2_Spen	RRM3_Spen	RRM	SPOC	PTZ00449 SF
	NCBI	gi 762129377 (XP_011447812)	717	RRM1_Spen	RRM2_Spen	RRM3_Spen	RRM	SPOC	PTZ00449 SF

METTL16

<i>Homo sapiens</i>	NCBI	gi 122114654 (NP_076991.3)	562	AdoMet Mtases SF	S-adenosylmethionine binding site
<i>Drosophila melanogaster</i> (CG7544)	NCBI	gi 19922302 (NP_611015.1)	305	AdoMet Mtases SF	
	GIGATON	CHOYP_LOC100561572.1.1	527	AdoMet Mtases SF	S-adenosylmethionine binding site

<i>Crassostrea gigas</i>	NCBI	gi 762141911 (XP_011454156.1)	538	AdoMet Mtases SF	S-adenosylmethionine binding site
		gi 762141913 (XP_011454157.1)	527	AdoMet Mtases SF	S-adenosylmethionine binding site

ALKBH5

<i>Homo sapiens</i>	NCBI	gi 148539642 (NP_060228.3)	394	2OG-FelI_Oxy
<i>Drosophila melanogaster</i>				
<i>Crassostrea gigas</i>	GIGATON	CHOYP_BRAFLDRAFT_126925.1.1	403	2OG-FelI_Oxy
	NCBI	gi 762097205 (XP_011431161.1)	374	2OG-FelI_Oxy

YTHDC1

<i>Homo sapiens</i>	NCBI	gi 72534750 (NP_001026902.1)	727	YTH
		gi 94536805 (NP_588611.2)	709	YTH
		gi 1061213987 (NP_001317627.1)	735	YTH
<i>Drosophila melanogaster</i> (YT521)	NCBI	gi 24656811 (NP_647811.2)	721	YTH
		gi 24656816 (NP_728876.1)	710	YTH
<i>Crassostrea gigas</i>	GIGATON	CHOYP_YTDC1.2.2	636	YTH CDC27
		CHOYP_LOC586835.1.1	545	YTH CDC27
	NCBI	gi 762070401 (XP_011447601.1)	636	YTH CDC27

YTHDC2

<i>Homo sapiens</i>	NCBI	gi 269847874 (NP_073739.3)	1430	YTH HrpA R3H_DEXH_helicase DEXHc_YTHDC2 OB_NTP_bind
		gi 1066536696 (NP_001332904.1)	1268	YTH HrpA DEXHc_YTHDC2 OB_NTP_bind
		gi 1066546270 (NP_001332905.1)	1130	YTH HrpA DEAD-like_helicase_N SF ANKYR OB_NTP_bind
<i>Drosophila melanogaster</i>				
<i>Crassostrea gigas</i>	GIGATON	CHOYP_YTDC2.1.1	1572	YTH HrpA R3H super family Ank_2
	NCBI	gi 762086858 (XP_011425711.1)	1572	YTH HrpA R3H super family Ank_2

YTHDF

<i>Homo sapiens</i>	NCBI	gi 29791407 (AAH50284.1)	559	YTH	RPA_2b-aaRSs_OBF_like	PHA03247 super family
		gi 12803469 (AAH02559.1)	579	YTH		
		gi 31419299 (AAH52970.1)	585	YTH		
<i>Drosophila melanogaster</i> (CG6422)		gi 21356147 (NP_651322.1)	700	YTH		
		gi 24649883 (NP_733067.1)	699	YTH		
		gi 161078590 (NP_001097905.1)	694	YTH		
<i>Crassostrea gigas</i>	GIGATON	CHOYP_COX1.6.15	532	YTH		
		CHOYP_LOC100371022.1.1	531	YTH		
	NCBI	gi 762146089 (XP_011456337.1)	522	YTH		

hnRNPA2B1

<i>Homo sapiens</i>	NCBI	gi 4504447 (NP_002128.1)	341	RRM1_hA2B1	RRM2_hA2B1	Putative DNA binding site	hnRNPA1
		gi 14043072 (NP_112533.1)	353	RRM1_hA2B1	RRM2_hA2B1	Putative DNA binding site	hnRNPA1
<i>Drosophila melanogaster</i> (hrb98DE)	NCBI	gi 24650831 (NP_733249.1)	364	RRM1_hA_like	RRM_SF	Putative DNA binding site	
		gi 17738267 (NP_524543.1)	365	RRM1_hA_like	RRM_SF	Putative DNA binding site	
		gi 24650838 (NP_733252.1)	361	RRM1_hA_like	RRM_SF	Putative DNA binding site	
		gi 24650833 (NP_733250.1)	360	RRM1_hA_like	RRM_SF	Putative DNA binding site	
<i>Crassostrea gigas</i>	GIGATON	CHOYP_LOC100748395.1.7	229	RRM1_hA_like	RRM_SF	Putative DNA binding site	
		CHOYP_LOC100748395.2.7	394	RRM1_hA_like	RRM_SF	Putative DNA binding site	
		CHOYP_LOC100748395.3.7	315	RRM1_hA_like	RRM_SF	Putative DNA binding site	
		CHOYP_LOC100748395.4.7	372	RRM1_hA_like	RRM_SF	Putative DNA binding site	
		CHOYP_LOC100748395.6.7	315	RRM1_hA_like	RRM_SF	Putative DNA binding site	
		CHOYP_AGAP_AGAP002374.1.1	236	RRM_SF			

		CHOYP_LOC100748395.5.7	205	RRM_SF	
	NCBI	gi 762104361 (XP_011434715.1)	370	RRM1_hA_like	RRM_SF Putative DNA binding site
		gi 762104364 (XP_011434716.1)	369	RRM1_hA_like	RRM_SF Putative DNA binding site
		gi 762104366 (XP_011434717.1)	363	RRM1_hA_like	RRM_SF Putative DNA binding site
		gi 762104368 (XP_011434718.1)	353	RRM1_hA_like	RRM_SF Putative DNA binding site

Prrc2a

<i>Homo sapiens</i>	NCBI	gi 314122241 (NP_004629.3)	2157	GRE-rich domain	BAT2_N
<i>Drosophila melanogaster</i>					
<i>Crassostrea gigas</i>	GIGATON	CHOYP_LOC100559941.1.2	2578	GRE-rich domain	BAT2_N PTZ00121 PTZ00449
		CHOYP_LOC100559941.2.2	2554	GRE-rich domain	BAT2_N PTZ00121 PTZ00449
		gi 1139830093 (XP_019928978.1)	2922	GRE-rich domain	BAT2_N PTZ00121 PTZ00449

IGF2BP

<i>Homo sapiens</i>	NCBI	gi 56237027 (NP_006537.3)	577	KH-I	KH-1	RRM1_IGF2BP1	RRM2_IGF2BP1	
		gi 238624257 (NP_001153895.1)	438	KH-I	KH-1	RRM1_IGF2BP1	RRM_SF super family	
		gi 64085377 (NP_006539.3)	599	KH-I	KH-1	PCBP_like_KH	RRM1_IGF2BP2	RRM2_IGF2BP2
		gi 56118219 (NP_001007226.1)	556	KH-I	KH-1	PCBP_like_KH	RRM1_IGF2BP2	RRM2_IGF2BP2
		gi 631226390 (NP_001278798.1)	605	KH-I	KH-1	PCBP_like_KH	RRM1_IGF2BP2	RRM_SF super family
		gi 631226392 (NP_001278801.1)	542	KH-I	KH-1	PCBP_like_KH	RRM_SF super family	
		gi 631226396 (NP_001278802.1)	536	KH-I	KH-1	PCBP_like_KH	RRM2_IGF2BP2	
		gi 631226394 (NP_001278803.1)	493	KH-I	KH-1	PCBP_like_KH	RRM2_IGF2BP2	
		gi 631226398 (NP_001278804.1)	463	KH-I	KH-1	PCBP_like_KH	RRM_SF super family	
		gi 30795212 (NP_006538.2)	579	KH-I	KH-1	PCBP_like_KH	RRM1_IGF2BP3	RRM2_IGF2BP3
				gi 386764188 (NP_001036268.2)	631	KH-I	KH-1	RRM2_VICKZ

<i>Drosophila melanogaster</i> (IGF-II binding protein)	NCBI	gi 386764191 (NP_001245616.1)	638	KH-I	KH-1	RRM2_VICKZ
		gi 17530887 (NP_511111.1)	566	KH-I	KH-1	
		gi 24641097 (NP_727451.1)	573	KH-I	KH-1	
		gi 281360685 (NP_001162717.1)	580	KH-I	KH-1	
<i>Crassostrea gigas</i>	GIGATON	CHOYP_LOC100114171.1.1	607	KH-I	KH-1	PCBP_like_KH RRM1_VICKZ RRM_SF super family
	NCBI	gi 762079091 (XP_011412002.1)	611	KH-I	KH-1	PCBP_like_KH RRM1_VICKZ RRM_SF super family
		gi 762079093 (XP_011412008.1)	607	KH-I	KH-1	PCBP_like_KH RRM1_VICKZ RRM_SF super family
		gi 762079095 (XP_011412017.1)	590	KH-I	KH-1	PCBP_like_KH RRM1_VICKZ RRM_SF super family

eIF3a

<i>Homo sapiens</i>	NCBI	gi 4503509(NP_003741.1)	1382	PINT	Smc super family	U2AF_Ig super family	dnaA super family	Rho SF
<i>Drosophila melanogaster</i> (IGF-II binding protein)	NCBI	gi 665393171 (NP_730838.3)	1140	PINT	DUF5401	Rho SF		
		gi 24643988 (NP_649470.2)	1140	PINT	DUF5401	Rho SF		
<i>Crassostrea gigas</i>	GIGATON	CHOYP_BRAFLDRAFT_75590.1.1	155					
		CHOYP_UBP47.2.2	1253	PAM	DUF5401			
		CHOYP_MROH1.1.1	1046	PAM	DUF5401			
	NCBI	gi 762160635 (XP_011418535.1)	759	PAM	DUF5401			
		gi 762122193 (XP_011444042.1)	1252	PAM	DUF5401			

Data S1: Complete list of in silico identified putative m6A machinery proteins and their respective BLAST results

Crassostrea gigas		Homo sapiens				Drosophila melanogaster			
METTL3	CHOYP_PHUM_PHUM423190.1.1	gi 21361827 (NP_062826.2)				gi 21365141 (NP_651204.1)			
	gi 762092209 (XP_011428532.1)	52.3%	52.31%			73.26%	73.96%		
METTL14	CHOYP_MET14.1.1	gi 24306269 (NP_066012.1)				gi 19920926 (NP_609205.1)			
	CHOYP_LOC100743733.1.1	62.03%	60.88%			58.05%	57.76%		
WTAP	CHOYP_FLJD.1.1	gi 395455090 (NP_001257460.1)	gi 23199974 (NP_690596.1)	gi 395455092 (NP_001257461.1)		gi 24653459 (NP_523732.2)	gi 24653461 (NP_725327.1)		
	CHOYP_SODM1.2	52.68%	47.55%	47.55%	47.55%	56.16%	58.42%		
	CHOYP_LOC100121674.1.1	47.55%	47.52%	47.55%	47.55%	60.40%	60.40%		
	gi 762078268 (XP_011453082.1)	51.06%	47.55%	47.55%	47.55%	56.16%	58.42%		
VIRILIZER-like	CHOYP_VIR.1.1	gi 33946282 (NP_056311.2)	gi 33946282 (NP_092121.1)			gi 17864576 (NP_524900.1)			
	gi 762120202 (XP_011443024.1)	30.70%	29.59%			25.49%			
	gi 762120203 (XP_011443023.1)	30.85%	30.17%			25.49%			
	gi 1139822239 (XP_019927346.1)	30.85%	30.17%			25.49%			
	gi 1139822241 (XP_019927347.1)	30.95%	30.24%			25.49%			
HAKAI	CHOYP_LOC100864501.1.1	gi 209180481 (NP_079090.2)	gi 546230945 (NP_001271220.1)			gi 19921556 (NP_609993.1)	gi 24585301 (NP_724217.1)	gi 442628448 (NP_788075.2)	gi 442628450 (NP_001260593.1)
	gi 762140343 (XP_011453340.1)	43.27%	43.96%			60.45%	60.45%	60.45%	60.45%
ZC3H13	CHOYP_BRAFDRRAFT_120702.1.1	gi 1060099240 (NP_001317493.1)	gi 1060099108 (NP_001317496.1)	gi 116008442 (NP_055885.3)		gi 24643154 (NP_573339.1)	gi 665392303 (NP_001285418.1)	gi 665392305 (NP_001285419.1)	
	CHOYP_LOC100568158.1.1	37.11%	37.11%	37.11%		N/A	N/A	N/A	
	gi 762096734 (XP_011430912.1)	31.48%	31.48%	40.00%		N/A	N/A	N/A	
	gi 762096736 (XP_011430913.1)	31.48%	31.48%	40.00%		N/A	N/A	N/A	
	gi 762096738 (XP_011430914.1)	31.48%	31.48%	40.00%		N/A	N/A	N/A	
	gi 762096740 (XP_011430915.1)	31.65%	31.65%	40.58%		N/A	N/A	N/A	
RBM15/15B	CHOYP_LOC663518.1.1	gi 47933339 (NP_073605)	gi 319996623 (NP_001188474)	gi 54607124 (NP_037418)		gi 24586450 (NP_724633)	gi 19921778 (NP_610339)	gi 665399368 (NP_001286174)	
	gi 762129377 (XP_011447812)	56.73%	56.73%	61.59%		59.22%	59.22%	59.22%	
METTL16	CHOYP_LOC100561572.1.1	gi 122114654 (NP_076991.3)				gi 19922302 (NP_611015.1)			
	gi 762141911 (XP_011454156.1)	38.05%	37.68%			38.81%			
ALKBH5	CHOYP_BRAFDRRAFT_126925.1.1	gi 148539642 (NP_060228.3)							
	gi 762097205 (XP_011431161.1)	72.43%	72.43%						
YTHDC1	CHOYP_YTDC1.2.2	gi 72534750 (NP_001026902.1)	gi 94536805 (NP_588611.2)	gi 1061213987 (NP_001317627.1)		gi 24656811 (NP_647811.2)	gi 24656816 (NP_728876.1)		
	CHOYP_LOC358935.1.1	46.81%	45.30%			57.74%			
YTHDC2	CHOYP_YTDC2.1.1	gi 26984784 (NP_073739.3)	gi 106653696 (NP_001332904.1)	gi 1066546270 (NP_001332905.1)					
	gi 762086858 (XP_011425711.1)	53.86%	51.83%	52.05%		46.53%			
YTHDF	CHOYP_COX1.6.15	gi 29791407 (AAH0284.1)	gi 12803469 (AAH02559.1)	gi 31419289 (AAH02970.1)		gi 21356147 (NP_651322.1)	gi 24649883 (NP_733067.1)	gi 161078590 (NP_001097905.1)	
	CHOYP_LOC100371022.1.1	53.09%	53.77%	52.05%		71.51%	71.51%	71.51%	
hmRNP2B1	CHOYP_LOC100748395.1.7	gi 4504447 (NP_002128.1)	gi 14043072 (NP_112533.1)			gi 24650831 (NP_733249.1)	gi 17738267 (NP_524543.1)	gi 24650836 (NP_733252.1)	gi 24650833 (NP_733250.1)
	CHOYP_LOC100748395.2.7	55.37%	54.71%			58.14%	58.14%	58.14%	58.14%
	CHOYP_LOC100748395.3.7	55.37%	54.71%			58.14%	57.71%	58.14%	58.14%
	CHOYP_LOC100748395.4.7	55.37%	54.71%			58.14%	58.14%	58.14%	58.14%
	CHOYP_LOC100748395.5.7	55.37%	54.71%			58.14%	57.71%	58.14%	58.14%
	CHOYP_AGAP_AGAP002374.1.1	54.24%	53.53%			58.14%	58.23%	58.23%	58.23%
	CHOYP_LOC100748395.6.7	55.37%	54.71%			58.14%	58.14%	58.14%	58.14%
	gi 762104361 (XP_011434715.1)	55.37%	55.37%			58.14%	58.14%	58.14%	58.14%
Prrc2a	CHOYP_LOC100559941.1.2	gi 314122241 (NP_004629.3)							
	gi 1139830093 (XP_019928978.1)	46.02%	46.02%						
IGF2BP	CHOYP_LOC100114171.1.1	gi 56237027 (NP_006537.3)	gi 238624257 (NP_001153895.1)	gi 64085377 (NP_006539.3)	gi 56118219 (NP_001007226.1)	gi 631226390 (NP_001278798.1)	gi 631226392 (NP_001278801.1)	gi 631226396 (NP_001278802.1)	gi 631226394 (NP_001278803.1)
	gi 762079091 (XP_011412002.1)	34.87%	35.71%	35.86%	N/A	35.50%	34.93%	35.34%	35.85%
	gi 762079093 (XP_011412003.1)	34.80%	36.39%	35.96%	35.52%	35.61%	35.53%	35.93%	36.38%
	gi 762079095 (XP_011412017.1)	35.04%	36.39%	35.96%	36.24%	36.11%	35.83%	36.38%	36.38%
	gi 762079095 (XP_011412017.1)	34.80%	36.39%	35.96%	36.24%	36.11%	35.83%	36.38%	36.38%
eIF3a	CHOYP_BRAFDRRAFT_75690.1.1	gi 45035096 (NP_003741.1)				gi 665393171 (NP_730838.3)	gi 24643988 (NP_649470.2)		
	CHOYP_UBP47.2.2	40.86%	45.97%			45.97%	45.97%		
	CHOYP_MRCH1.1.1	63.83%	63.71%			50.89%	50.89%		
	gi 762160835 (XP_011418535.1)	54.20%	54.20%			44.89%	44.89%		
gi 762122193 (XP_011444042.1)	58.13%	58.13%			48.45%	48.45%			

For Review Only

Data S2: Identified proteins by RNA pull down coupled with mass spectrometry with m6A or A-oligo, in nuclear or cytosolic protein extracts

Proteins identified in nuclear extracts

Oligo	Accession	Description
m6A	K1PTY5_CRAGI	Protocadherin Fat 4
m6A	K1QNA2_CRAGI	Vitellogenin-6
m6A	K1QBR5_CRAGI	Uncharacterized protein
m6A	K1PFG1_CRAGI	Uncharacterized protein
m6A	K1P9A4_CRAGI	Beta-1,3-glucan-binding protein
m6A	K1QHI5_CRAGI	Pyruvate carboxylase, mitochondrial
m6A	K1QQ94_CRAGI	Uncharacterized protein
m6A	K1R5B4_CRAGI	Proteasome activator complex subunit 4
m6A	K1R164_CRAGI	Galectin-4
m6A	K1PNI6_CRAGI	Heterogeneous nuclear ribonucleoprotein A/B
m6A	K1QMX5_CRAGI	Uncharacterized protein
m6A	K1PQP2_CRAGI	Nucleolin
m6A	K1QXR4_CRAGI	Pancreatic lipase-related protein 2
m6A	K1R7V7_CRAGI	Tubulin beta chain
m6A	K1RGT5_CRAGI	Metalloendopeptidase
m6A	K1QSX8_CRAGI	ATPase family AAA domain-containing protein 2B
m6A	K1R9B6_CRAGI	H/ACA ribonucleoprotein complex subunit 4
m6A	K1RWS2_CRAGI	Transcriptional activator protein Pur-alpha
m6A	K1RLF8_CRAGI	Splicing factor 3B subunit 3
m6A	K1R3U2_CRAGI	Uncharacterized protein
m6A	K1QQ68_CRAGI	Tubulin alpha chain
m6A	K1QVJ8_CRAGI	Piwi-like protein 1
m6A	K1PVA1_CRAGI	Transitional endoplasmic reticulum ATPase
m6A	K1QKB5_CRAGI	Uncharacterized protein
m6A	K1QHM2_CRAGI	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2
m6A	K1QII6_CRAGI	Tubulin alpha chain
m6A	K1QSQ9_CRAGI	Putative ATP-dependent RNA helicase an3
m6A	K1QQ27_CRAGI	Pancreatic lipase-related protein 2
m6A	K1QMA4_CRAGI	RRP5-like protein
m6A	K1PEP0_CRAGI	40S ribosomal protein S8
m6A	K1QXX7_CRAGI	Myosin heavy chain, non-muscle (Fragment)
m6A	K1QK56_CRAGI	Uncharacterized protein
m6A	K1PNR3_CRAGI	Clathrin heavy chain
m6A	K1PN21_CRAGI	Tubulin beta chain
m6A	K1RG73_CRAGI	Acetyl-CoA carboxylase
m6A	K1RD58_CRAGI	Uncharacterized protein
m6A	K1QU53_CRAGI	NAD(P) transhydrogenase, mitochondrial
m6A	K1R473_CRAGI	Tubulin alpha chain
m6A	K1PH76_CRAGI	Y-box factor-like protein (Fragment)
m6A	K1PE00_CRAGI	Tubulin alpha chain
m6A	K1PJC1_CRAGI	Adipophilin
m6A	K1R6Z7_CRAGI	ATP synthase subunit alpha
m6A	K1R545_CRAGI	Pre-mRNA-processing-splicing factor 8 (Fragment)
m6A	K1RI55_CRAGI	Insulin-like growth factor 2 mRNA-binding protein 3
m6A	K1QGS8_CRAGI	Elongation factor 1-alpha
m6A	K1QFM6_CRAGI	Vitellogenin
m6A	K1R6Q7_CRAGI	DNA topoisomerase I
m6A	K1Q988_CRAGI	Band 4.1-like protein 3
m6A	K1QLS3_CRAGI	Cytochrome b-c1 complex subunit 2, mitochondrial
m6A	K1RWW5_CRAGI	ATP synthase subunit beta
m6A	K1S2N7_CRAGI	Innexin
m6A	K1P421_CRAGI	Histone H2A
m6A	K1RK12_CRAGI	40S ribosomal protein S23
m6A	K1QKD6_CRAGI	Uncharacterized protein
m6A	K1QWZ6_CRAGI	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1
m6A	K1QFN2_CRAGI	Uncharacterized protein
m6A	K1PHW2_CRAGI	Uncharacterized protein

1			
2			
3	m6A	K1PJ06_CRAGI	Importin subunit alpha-1
4	m6A	K1QA13_CRAGI	Calcium-transporting ATPase
5	m6A	K1R0L4_CRAGI	Sodium/potassium-transporting ATPase subunit alpha
6	m6A	K1R115_CRAGI	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial
7	m6A	K1QB61_CRAGI	Protocadherin Fat 4
8	m6A	K1Q4H2_CRAGI	Nodal modulator 3
9	m6A	K1QWK2_CRAGI	MAM domain-containing glycosylphosphatidylinositol anchor protein 2
10	m6A	K1R466_CRAGI	T-complex protein 1 subunit gamma
11	m6A	K1QFW9_CRAGI	Uncharacterized protein
12	m6A	K1R5U4_CRAGI	Acetyl-CoA carboxylase 1
13	m6A	A5LGH1_CRAGI	Voltage-dependent anion channel
14	m6A	K1S4Q2_CRAGI	T-complex protein 1 subunit delta (Fragment)
15	m6A	K1REG6_CRAGI	DNA helicase
16	m6A	K1PUL2_CRAGI	Long-chain-fatty-acid--CoA ligase 1
17	m6A	K1R294_CRAGI	T-complex protein 1 subunit beta
18	m6A	K1PMT6_CRAGI	Heterogeneous nuclear ribonucleoprotein U-like protein 1
19	m6A	K1RGB7_CRAGI	Epidermal retinal dehydrogenase 2
20	m6A	K1R435_CRAGI	Splicing factor, arginine/serine-rich 4
21	m6A	K1R252_CRAGI	Putative methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial
22	m6A	K1QAE5_CRAGI	Uncharacterized protein
23	m6A	K1QIR8_CRAGI	78 kDa glucose-regulated protein
24	m6A	K1QYB3_CRAGI	Ig-like and fibronectin type-III domain-containing protein C25G4.10
25	m6A	K1QJ14_CRAGI	40S ribosomal protein S3a
26	m6A	K1PNQ5_CRAGI	Heat shock protein HSP 90-alpha 1
27	m6A	K1S1S1_CRAGI	Insulin-like growth factor 2 mRNA-binding protein 1
28	m6A	K1QM19_CRAGI	Uncharacterized protein
29	m6A	K1R420_CRAGI	Non-specific serine/threonine protein kinase
30	m6A	K1R4R9_CRAGI	Mitotic apparatus protein p62
31	m6A	K1R0S3_CRAGI	T-complex protein 1 subunit theta
32	m6A	K1RAJ1_CRAGI	T-complex protein 1 subunit alpha
33	m6A	K1QH74_CRAGI	Splicing factor, arginine/serine-rich 1
34	m6A	K1QRL6_CRAGI	Methenyltetrahydrofolate synthetase domain-containing protein
35	m6A	K1QUC6_CRAGI	Uncharacterized protein
36	m6A	K1RIT6_CRAGI	NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial
37	m6A	K1RBF6_CRAGI	Uncharacterized protein yfeX
38	m6A	K1PCS4_CRAGI	Eukaryotic translation initiation factor 2 subunit 3, Y-linked
39	m6A	K1Q620_CRAGI	Uncharacterized protein
40	m6A	K1QWX2_CRAGI	60S acidic ribosomal protein P0
41	m6A	K1PD57_CRAGI	Constitutive coactivator of PPAR-gamma-like protein 1-like protein
42	m6A	K1Q4S5_CRAGI	Cadherin-87A
43	m6A	K1RQA0_CRAGI	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2
44	m6A	K1QMX8_CRAGI	DNA replication licensing factor MCM7
45	m6A	K1QPX8_CRAGI	Alkyl/aryl-sulfatase BDS1
46	m6A	K1QZW0_CRAGI	Polyadenylate-binding protein 2
47	m6A	K1RWX7_CRAGI	Metabotropic glutamate receptor 3
48	m6A	K1RFT1_CRAGI	Band 4.1-like protein 3
49	m6A	K1RNB5_CRAGI	Propionyl-CoA carboxylase beta chain, mitochondrial
50	m6A	K1QBK6_CRAGI	Splicing factor 3B subunit 1
51	m6A	K1Q0Z3_CRAGI	Estradiol 17-beta-dehydrogenase 11
52	m6A	K1R953_CRAGI	Acetyl-CoA carboxylase
53	m6A	K1QNN9_CRAGI	MICOS complex subunit MIC60
54	m6A	K1QXS6_CRAGI	Heterogeneous nuclear ribonucleoprotein A2-like protein 1
55	m6A	K1RJH5_CRAGI	Polyadenylate-binding protein
56	m6A	K1R0Y9_CRAGI	ADP,ATP carrier protein
57	m6A	K1R4D4_CRAGI	40S ribosomal protein SA
58	m6A	K1QWT8_CRAGI	Uncharacterized protein
59	m6A	K1Q0L1_CRAGI	60S ribosomal protein L23a
60	m6A	K1Q260_CRAGI	Nucleolar protein 58
	m6A	K1QT04_CRAGI	Uncharacterized protein
	m6A	K1Q9K6_CRAGI	Histone H3

1			
2			
3	m6A	K1QT21_CRAGI	Putative ATP-dependent RNA helicase DDX5
4	m6A	K1QBN0_CRAGI	Methylcrotonoyl-CoA carboxylase beta chain, mitochondrial
5	m6A	K1PLY1_CRAGI	DNA polymerase
6	m6A	K1QBH0_CRAGI	Uncharacterized protein
7	m6A	K1Q923_CRAGI	Putative ATP-dependent RNA helicase DDX4
8	m6A	K1QG58_CRAGI	Actin
9	m6A	K1QQB6_CRAGI	40S ribosomal protein S14
10	m6A	K1QDX9_CRAGI	Ribosome biogenesis protein BMS1-like protein
11	m6A	K1QF01_CRAGI	40S ribosomal protein S4
12	m6A	K1QLC5_CRAGI	T-complex protein 1 subunit epsilon
13	m6A	K1QY12_CRAGI	Dynamin-1-like protein
14	m6A	K1R0W4_CRAGI	Signal recognition particle subunit SRP72
15	m6A	K1QX26_CRAGI	Endoplasmic
16	m6A	K1QHS8_CRAGI	Ribonucleoside-diphosphate reductase
17	m6A	K1QQ05_CRAGI	Insulin-like growth factor-binding protein complex acid labile chain
18	m6A	K1QFP5_CRAGI	NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial
19	m6A	K1QP17_CRAGI	Caprin-1
20	m6A	K1R7A2_CRAGI	Uncharacterized protein
21	m6A	K1R4L8_CRAGI	Electron transfer flavoprotein-ubiquinone oxidoreductase, mitochondrial
22	m6A	K1R591_CRAGI	Inter-alpha-trypsin inhibitor heavy chain H4
23	m6A	K1R7I9_CRAGI	Heterogeneous nuclear ribonucleoprotein Q
24	m6A	K1QBW8_CRAGI	Uncharacterized protein
25	m6A	K1RSZ6_CRAGI	40S ribosomal protein S7
26	m6A	K1QDZ5_CRAGI	Cytochrome c1, heme protein, mitochondrial
27	m6A	K1PGW7_CRAGI	Transmembrane protein 2
28	m6A	K1QMB9_CRAGI	Eukaryotic translation initiation factor 3 subunit A
29	m6A	K1RNZ6_CRAGI	Eukaryotic translation initiation factor 3 subunit D
30	m6A	K1Q9W5_CRAGI	T-complex protein 1 subunit eta
31	m6A	K1Q404_CRAGI	DNA topoisomerase 2
32	m6A	K1R7J6_CRAGI	Putative sodium/potassium-transporting ATPase subunit beta-2
33	m6A	K1P8W6_CRAGI	60S ribosomal protein L4
34	m6A	K1RSA6_CRAGI	Methylcrotonoyl-CoA carboxylase subunit alpha, mitochondrial
35	m6A	K1RW85_CRAGI	Adenosylhomocysteinase
36	m6A	K1PS27_CRAGI	DNA helicase
37	m6A	K1RH18_CRAGI	Sarcalumenin
38	m6A	K1Q5H6_CRAGI	FACT complex subunit SSRP1
39	m6A	K1PH66_CRAGI	Fibrinolytic enzyme, isozyme C
40	m6A	K1PF10_CRAGI	PAN2-PAN3 deadenylation complex catalytic subunit PAN2
41	m6A	K1Q358_CRAGI	60S acidic ribosomal protein P2
42	m6A	K1PXH5_CRAGI	Putative saccharopine dehydrogenase
43	m6A	K1Q8S0_CRAGI	Nucleolar complex protein 3 homolog
44	m6A	K1QYB6_CRAGI	Delta-1-pyrroline-5-carboxylate synthetase
45	m6A	K1PV79_CRAGI	Importin subunit alpha
46	m6A	K1PV49_CRAGI	RuvB-like helicase
47	m6A	K1PRL4_CRAGI	60S ribosomal protein L38 (Fragment)
48	m6A	K1QL67_CRAGI	60S ribosomal protein L7a
49	m6A	K1PAY7_CRAGI	Propionyl-CoA carboxylase alpha chain, mitochondrial
50	m6A	K1R6L5_CRAGI	NADH-cytochrome b5 reductase
51	m6A	K1R1B1_CRAGI	35 kDa SR repressor protein
52	m6A	K1QHQ6_CRAGI	Acyl-CoA dehydrogenase family member 9, mitochondrial
53	m6A	K1QZU8_CRAGI	Calcium-transporting ATPase
54	m6A	K1RN77_CRAGI	Nuclear autoantigenic sperm protein
55	m6A	K1PZ23_CRAGI	DnaJ-like protein subfamily C member 3
56	m6A	K1R005_CRAGI	Filamin-C (Fragment)
57	m6A	K1RA35_CRAGI	Splicing factor, arginine/serine-rich 7
58	m6A	K1R2V1_CRAGI	Importin subunit beta-1
59	m6A	K1QAH9_CRAGI	H/ACA ribonucleoprotein complex subunit
60	m6A	K1QET2_CRAGI	Coatomer subunit alpha
	m6A	K1RAB9_CRAGI	Epoxide hydrolase 4
	m6A	K1QGK2_CRAGI	Coatomer subunit beta

1			
2			
3	m6A	K1PXN5_CRAGI	T-complex protein 1 subunit zeta
4	m6A	K1QHX2_CRAGI	La-related protein 7
5	m6A	K1PZ08_CRAGI	Ras-related protein Rab-7a
6	m6A	K1RK68_CRAGI	Uncharacterized protein
7	m6A	K1Q0R4_CRAGI	ATP-binding cassette sub-family F member 2
8	m6A	K1QW72_CRAGI	Catalase
9	m6A	K1PPP8_CRAGI	Vigilin
10	m6A	K1QVW3_CRAGI	Alkylglycerone-phosphate synthase
11	m6A	K1PBZ4_CRAGI	Regulator of nonsense transcripts 1
12	m6A	K1Q6W5_CRAGI	FACT complex subunit spt16
13	m6A	K1R5F2_CRAGI	14-3-3 protein epsilon
14	m6A	K1R5F2_CRAGI	14-3-3 protein epsilon
15	m6A	K1R5F2_CRAGI	14-3-3 protein epsilon
16	m6A	K1RLT4_CRAGI	Signal recognition particle subunit SRP68
17	m6A	K1RSS3_CRAGI	Myosin heavy chain, striated muscle
18	m6A	K1RNN9_CRAGI	Cytoskeleton-associated protein 5
19	m6A	K1QN11_CRAGI	Pre-mRNA-processing-splicing factor 8
20	m6A	K1PA54_CRAGI	Replication factor C subunit 3
21	m6A	K1PA54_CRAGI	Replication factor C subunit 3
22	m6A	K1QC78_CRAGI	Ras-related protein Rab-14
23	m6A	K1QW36_CRAGI	60S ribosomal protein L6
24	m6A	K1Q9P5_CRAGI	Mitochondrial-processing peptidase subunit beta
25	m6A	K1Q253_CRAGI	Neutral and basic amino acid transport protein rBAT
26	m6A	K1Q253_CRAGI	Neutral and basic amino acid transport protein rBAT
27	m6A	K1QHK9_CRAGI	Dynein heavy chain, cytoplasmic
28	m6A	K1QFN1_CRAGI	60S ribosomal protein L23
29	m6A	K1P112_CRAGI	ATP synthase subunit gamma, mitochondrial
30	m6A	K1QE71_CRAGI	DNA helicase
31	m6A	K1QE71_CRAGI	DNA helicase
32	m6A	K1PK85_CRAGI	Cullin-associated NEDD8-dissociated protein 1
33	m6A	K1QTD9_CRAGI	Nucleolar protein 56
34	m6A	K1P9N7_CRAGI	14-3-3 protein zeta
35	m6A	K1RG19_CRAGI	Protein FAM98A
36	m6A	K1PMP3_CRAGI	Protoporphyrinogen oxidase
37	m6A	K1PMP3_CRAGI	Protoporphyrinogen oxidase
38	m6A	K1QVN9_CRAGI	T-complex protein 1 subunit eta
39	m6A	K1QG65_CRAGI	rRNA 2'-O-methyltransferase fibrillarin
40	m6A	K1PM76_CRAGI	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial
41	m6A	K1PM50_CRAGI	40S ribosomal protein S16
42	m6A	K1QEF9_CRAGI	Protein-glutamine gamma-glutamyltransferase K
43	m6A	K1RKC1_CRAGI	Far upstream element-binding protein 3
44	m6A	K1RKC1_CRAGI	Far upstream element-binding protein 3
45	m6A	K1PY89_CRAGI	Extracellular superoxide dismutase [Cu-Zn]
46	m6A	K1RIZ3_CRAGI	Bone morphogenetic protein 7
47	m6A	K1RA95_CRAGI	Filamin-A
48	m6A	K1PWZ3_CRAGI	Guanine nucleotide-binding protein subunit beta
49	m6A	K1Q812_CRAGI	NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial
50	m6A	K1Q812_CRAGI	NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial
51	m6A	K1PFS5_CRAGI	Elongation factor 1-gamma
52	m6A	K1PX23_CRAGI	Eukaryotic peptide chain release factor subunit 1
53	m6A	K1QSV1_CRAGI	Uncharacterized protein
54	m6A	K1Q6X5_CRAGI	Protein disulfide-isomerase
55	m6A	K1Q6X5_CRAGI	Protein disulfide-isomerase
56	m6A	K1RAU3_CRAGI	DNA ligase
57	m6A	K1PXG6_CRAGI	Serine/threonine-protein phosphatase
58	m6A	K1RIG6_CRAGI	LSM14-like protein A
59	m6A	K1QWK6_CRAGI	Metalloendopeptidase
60	m6A	K1RCW3_CRAGI	Elongation factor 1-beta
	m6A	K1QK18_CRAGI	Cytochrome b5
	m6A	K1Q056_CRAGI	Calpain-A
	m6A	K1Q9M7_CRAGI	Histone H1-delta
	m6A	K1P7L5_CRAGI	Transmembrane 9 superfamily member
	m6A	K1QSU3_CRAGI	Protein I(2)37Cc
	m6A	K1PLF9_CRAGI	Arginine kinase
	m6A	K1Q1F4_CRAGI	60S ribosomal protein L3 (Fragment)
	m6A	K1R1T8_CRAGI	Nucleolar protein 56
	m6A	K1QGB4_CRAGI	40S ribosomal protein S17
	m6A	K1QJ08_CRAGI	60S ribosomal protein L26
	m6A	K1Q4Y8_CRAGI	Histone H1oo

1			
2			
3	m6A	K1PKF5_CRAGI	Protein-glutamine gamma-glutamyltransferase 4
4	m6A	K1QYT5_CRAGI	Phosphate carrier protein, mitochondrial
5	m6A	K1RHB2_CRAGI	Nucleolar RNA helicase 2
6	m6A	K1RJJ7_CRAGI	Histone H5
7	m6A	K1PS84_CRAGI	Alpha-crystallin B chain
8	m6A	K1R2N0_CRAGI	Histone H4
9	m6A	K1R2N0_CRAGI	Histone H4
10	m6A	K1PZP6_CRAGI	Coatomer subunit gamma
11	m6A	K1RGJ7_CRAGI	Neogenin
12	m6A	K1R9P5_CRAGI	Mitochondrial import receptor subunit TOM70
13	m6A	K1RUM2_CRAGI	Uncharacterized protein
14	m6A	K1RUM2_CRAGI	Uncharacterized protein
15	m6A	K1RJ97_CRAGI	Multifunctional protein ADE2
16	m6A	K1RJS5_CRAGI	Uncharacterized protein
17	m6A	K1QW41_CRAGI	Leucine-zipper-like transcriptional regulator 1
18	m6A	K1R834_CRAGI	60S ribosomal protein L9
19	m6A	K1QLK8_CRAGI	GTP-binding protein SAR1b
20	m6A	K1QLK8_CRAGI	GTP-binding protein SAR1b
21	m6A	K1QDH9_CRAGI	Myosin-11
22	m6A	K1QEF2_CRAGI	ADP-ribosylation factor-like protein 15
23	m6A	K1PUX5_CRAGI	Casein kinase II subunit alpha
24	m6A	K1QLU6_CRAGI	Poly [ADP-ribose] polymerase
25	m6A	K1QLU6_CRAGI	Poly [ADP-ribose] polymerase
26	m6A	K1QUK3_CRAGI	Putative ATP-dependent RNA helicase DDX41
27	m6A	K1S2S8_CRAGI	Signal recognition particle 54 kDa protein
28	m6A	K1PY73_CRAGI	Basic leucine zipper and W2 domain-containing protein 1
29	m6A	K1S6V7_CRAGI	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform
30	m6A	K1QPC6_CRAGI	Nucleolar complex protein 2-like protein
31	m6A	K1QPC6_CRAGI	Nucleolar complex protein 2-like protein
32	m6A	K1QPP2_CRAGI	Elongation factor Tu, mitochondrial
33	m6A	K1QDN1_CRAGI	Heat shock protein 75 kDa, mitochondrial (Fragment)
34	m6A	K1R996_CRAGI	Long-chain-fatty-acid--CoA ligase 4
35	m6A	K1RDW8_CRAGI	Golgi apparatus protein 1
36	m6A	K1S3G2_CRAGI	HMGB1
37	m6A	K1S3G2_CRAGI	HMGB1
38	m6A	K1QR48_CRAGI	Calcium-binding mitochondrial carrier protein SCaMC-2
39	m6A	K1P5V7_CRAGI	Eukaryotic translation initiation factor 3 subunit C
40	m6A	K1PV86_CRAGI	Phosphoglycerate mutase family member 5
41	m6A	K1QWC3_CRAGI	40S ribosomal protein S3
42	m6A	K1PZ70_CRAGI	NADH dehydrogenase [ubiquinone] iron-sulfur protein 6, mitochondrial
43	m6A	K1PZ70_CRAGI	NADH dehydrogenase [ubiquinone] iron-sulfur protein 6, mitochondrial
44	m6A	K1PTL4_CRAGI	Odr-4-like protein
45	m6A	K1QRM1_CRAGI	Nuclear pore protein
46	m6A	K1PVD7_CRAGI	Cytochrome c oxidase subunit 5A, mitochondrial
47	m6A	K1QFR2_CRAGI	Calnexin
48	m6A	K1Q273_CRAGI	60S ribosomal protein L14
49	m6A	K1Q273_CRAGI	60S ribosomal protein L14
50	m6A	K1R0M2_CRAGI	Uncharacterized protein
51	m6A	K1R5W3_CRAGI	Uncharacterized protein
52	m6A	K1QXQ8_CRAGI	DNA helicase
53	m6A	K1QPY8_CRAGI	Extracellular superoxide dismutase [Cu-Zn]
54	m6A	K1Q6V6_CRAGI	Replication factor C subunit 4
55	m6A	K1Q6V6_CRAGI	Replication factor C subunit 4
56	m6A	K1QMS2_CRAGI	Cadherin EGF LAG seven-pass G-type receptor 3
57	m6A	K1Q7T5_CRAGI	Protein disulfide-isomerase
58	m6A	K1QRZ3_CRAGI	40S ribosomal protein S13
59	m6A	K1R4Z3_CRAGI	Malate dehydrogenase, mitochondrial
60	m6A	K1PJ85_CRAGI	26S protease regulatory subunit 6A
	m6A	K1PB87_CRAGI	Uncharacterized protein
	m6A	K1PXU6_CRAGI	60S ribosomal protein L24
	m6A	K1R6S5_CRAGI	40S ribosomal protein S9
	m6A	K1PVH5_CRAGI	Centromere/kinetochore protein zw10-like protein
	m6A	K1R512_CRAGI	Uncharacterized protein
	m6A	K1QK68_CRAGI	Myosin-2 essential light chain
	m6A	K1PUV4_CRAGI	40S ribosomal protein S24
	m6A	K1R5U8_CRAGI	UBX domain-containing protein 4
	m6A	K1PW39_CRAGI	Glycerol-3-phosphate dehydrogenase, mitochondrial
	m6A	K1R790_CRAGI	Retinol dehydrogenase 13
	m6A	K1QT61_CRAGI	NADH dehydrogenase [ubiquinone] flavoprotein 2, mitochondrial (Fragment)

1			
2			
3	m6A	K1RG28_CRAGI	Kinase C and casein kinase substrate in neurons protein 2
4	m6A	K1QKV1_CRAGI	Cytochrome b-c1 complex subunit 6
5	m6A	K1P9S7_CRAGI	Brix domain-containing protein 2
6	m6A	K1QN79_CRAGI	40S ribosomal protein S11
7	m6A	K1QEJ0_CRAGI	Ras GTPase-activating protein-binding protein 2
8	m6A	K1S1X3_CRAGI	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5
9	m6A	K1R9T2_CRAGI	Eukaryotic translation initiation factor 3 subunit B
10	m6A	K1QED7_CRAGI	Replication protein A subunit
11	m6A	K1QK5_CRAGI	Metabotropic glutamate receptor 2
12	m6A	K1RN97_CRAGI	Hemagglutinin/amebocyte aggregation factor
13	m6A	K1PJS7_CRAGI	Poly [ADP-ribose] polymerase
14	m6A	K1R6F5_CRAGI	Putative ATP-dependent RNA helicase DDX23
15	m6A	K1R8R6_CRAGI	Fructose-bisphosphate aldolase
16	m6A	K1QY85_CRAGI	Transport protein Sec31A
17	m6A	K1QF31_CRAGI	Serine/threonine-protein kinase PLK
18	m6A	K1Q5J7_CRAGI	Uncharacterized protein
19	m6A	K1QPF0_CRAGI	Uncharacterized protein
20	m6A	K1P6Y1_CRAGI	Uncharacterized protein
21	m6A	K1QJM1_CRAGI	60S ribosomal protein L30
22	m6A	K1PXD4_CRAGI	Putative ATP-dependent RNA helicase DDX6
23	m6A	K1PH31_CRAGI	Protein arginine N-methyltransferase 1
24	m6A	K1PAM6_CRAGI	Uncharacterized protein
25	m6A	K1RFU6_CRAGI	Proteasome activator complex subunit 3
26	m6A	K1Q324_CRAGI	Heterogeneous nuclear ribonucleoprotein K
27	m6A	K1QRG9_CRAGI	Uncharacterized protein
28	m6A	K1S6H7_CRAGI	Vacuolar protein sorting-associated protein 13C
29	m6A	K1QE94_CRAGI	Alpha-galactosidase
30	m6A	K1Q7Q2_CRAGI	CCAAT/enhancer-binding protein zeta
31	m6A	K1Q7G8_CRAGI	Fatty acid synthase
32	m6A	K1QXH3_CRAGI	Translational activator GCN1
33	m6A	K1P8G1_CRAGI	Heterogeneous nuclear ribonucleoprotein H
34	m6A	K1QKQ8_CRAGI	THO complex subunit 4-A
35	m6A	K1RA63_CRAGI	Transmembrane protein 2
36	m6A	K1QAA2_CRAGI	Uncharacterized protein
37	m6A	K1PLA7_CRAGI	Eukaryotic initiation factor 4A-II (Fragment)
38	m6A	K1QIV3_CRAGI	Uncharacterized protein
39	m6A	K1RAH2_CRAGI	Superoxide dismutase [Cu-Zn]
40	m6A	K1QXA9_CRAGI	Sortilin-related receptor
41	m6A	K1QSD9_CRAGI	Uncharacterized protein
42	m6A	K1Q3W3_CRAGI	NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial
43	m6A	K1R3T3_CRAGI	Transcription factor BTF3
44	m6A	K1QMH5_CRAGI	Small nuclear ribonucleoprotein Sm D1
45	m6A	K1R1R9_CRAGI	Pre-mRNA-processing factor 6
46	m6A	K1PM66_CRAGI	60S ribosomal protein L12
47	m6A	K1Q3W9_CRAGI	FAS-associated factor 2-B
48	m6A	K1P9D0_CRAGI	Stress-70 protein, mitochondrial
49	m6A	K1R4F7_CRAGI	Ras-related protein Rab-6B
50	m6A	K1QGP7_CRAGI	Uncharacterized protein
51	m6A	K1REY2_CRAGI	Dysferlin
52	m6A	K1QSB2_CRAGI	26S protease regulatory subunit 6B
53	m6A	K1RAU8_CRAGI	Eukaryotic translation initiation factor 3 subunit E
54	m6A	K1QAB1_CRAGI	AP-2 complex subunit alpha
55	m6A	K1RFU8_CRAGI	High mobility group protein DSP1
56	m6A	K1QAA8_CRAGI	CAAX prenyl protease 1-like protein
57	m6A	K1PXS8_CRAGI	Calreticulin
58	m6A	K1RV41_CRAGI	Guanine nucleotide-binding protein subunit beta-2-like 1
59	m6A	K1Q5Z6_CRAGI	Eukaryotic translation initiation factor 2 subunit 2
60	m6A	K1QYQ9_CRAGI	Uncharacterized protein
	m6A	K1RCL2_CRAGI	Mitochondrial import inner membrane translocase subunit Tim13-B
	m6A	K1PI50_CRAGI	40S ribosomal protein S26

1			
2			
3	m6A	K1QGP1_CRAGI	Replication factor C subunit 2
4	m6A	K1P541_CRAGI	Alpha-soluble NSF attachment protein
5	m6A	K1Q667_CRAGI	tRNA-splicing ligase RtcB homolog
6	m6A	K1QBM3_CRAGI	Ras-related protein Rab-2
7	m6A	K1R7L4_CRAGI	Neural cell adhesion molecule 1
8	m6A	K1PH13_CRAGI	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3B
9	m6A	K1QAI2_CRAGI	Ufm1-specific protease 2
10	m6A	K1R1JW8_CRAGI	Protein DEK
11	m6A	K1R1JW8_CRAGI	Protein DEK
12	m6A	K1QKG8_CRAGI	Upstream activation factor subunit spp27
13	m6A	K1R150_CRAGI	Ras-related protein Rab-1A
14	m6A	K1PI40_CRAGI	Uncharacterized protein
15	m6A	K1PZT2_CRAGI	Cytochrome c oxidase subunit 5B, mitochondrial
16	m6A	K1PJB0_CRAGI	Heat shock protein 70 B2
17	m6A	K1PJB0_CRAGI	Heat shock protein 70 B2
18	m6A	K1PR25_CRAGI	Regulator of differentiation 1
19	m6A	K1QMV5_CRAGI	Annexin
20	m6A	K1QMV5_CRAGI	Annexin
21	m6A	K1Q0N6_CRAGI	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3A
22	m6A	K1QY58_CRAGI	Eukaryotic translation initiation factor 3 subunit I (Fragment)
23	m6A	K1RIJ1_CRAGI	Synaptobrevin (Fragment)
24	m6A	K1PNC7_CRAGI	AFG3-like protein 2
25	m6A	K1QQR1_CRAGI	Major vault protein
26	m6A	K1QQR1_CRAGI	Major vault protein
27	m6A	K1R5V4_CRAGI	GTP-binding nuclear protein
28	m6A	K1QGA7_CRAGI	Kynurenine formamidase
29	m6A	K1PTV1_CRAGI	Splicing factor 3B subunit 4
30	m6A	K1P3Q5_CRAGI	Programmed cell death 6-interacting protein
31	m6A	K1P3Q5_CRAGI	Programmed cell death 6-interacting protein
32	m6A	K1R2G9_CRAGI	SEC13-like protein
33	m6A	K1PF96_CRAGI	Spliceosome RNA helicase BAT1
34	m6A	K1R1F0_CRAGI	ATP-dependent DNA helicase 2 subunit 1
35	m6A	K1Q5Z1_CRAGI	Uncharacterized protein
36	m6A	K1Q880_CRAGI	Transportin-1
37	m6A	K1PDF8_CRAGI	Splicing factor, arginine/serine-rich 6
38	m6A	K1PDF8_CRAGI	Splicing factor, arginine/serine-rich 6
39	m6A	K1PMY9_CRAGI	Calmodulin
40	m6A	K1PPW8_CRAGI	Coatomer subunit beta
41	m6A	K1QZQ8_CRAGI	Low-density lipoprotein receptor-related protein 8
42	m6A	K1QE43_CRAGI	Uncharacterized protein
43	m6A	K1QE43_CRAGI	Uncharacterized protein
44	m6A	K1RDS1_CRAGI	Splicing factor, arginine/serine-rich 2
45	m6A	K1RAI3_CRAGI	Annexin
46	m6A	K1PCR5_CRAGI	KH domain-containing, RNA-binding, signal transduction-associated protein 2
47	m6A	K1QWP1_CRAGI	Nucleoporin seh1
48	m6A	K1QAL1_CRAGI	Transmembrane emp24 domain-containing protein 7
49	m6A	K1QAL1_CRAGI	Transmembrane emp24 domain-containing protein 7
50	m6A	K1Q2H5_CRAGI	Uncharacterized protein
51	m6A	K1REPO_CRAGI	Uncharacterized protein
52	m6A	K1PKI9_CRAGI	Uncharacterized protein
53	m6A	K1RG79_CRAGI	Neuronal acetylcholine receptor subunit alpha-6
54	m6A	K1Q1L4_CRAGI	Uncharacterized protein
55	m6A	K1Q1L4_CRAGI	Uncharacterized protein
56	m6A	K1QTP6_CRAGI	Cation-transporting ATPase
57	m6A	K1Q615_CRAGI	Peroxiredoxin-1
58	m6A	K1QIZ7_CRAGI	Programmed cell death protein 6
59	m6A	K1R0D7_CRAGI	Eukaryotic translation initiation factor 3 subunit M (Fragment)
60	m6A	K1QTV3_CRAGI	Murinoglobulin-2
	m6A	K1PDL3_CRAGI	Ribosomal protein L19
	m6A	K1QW21_CRAGI	39S ribosomal protein L40, mitochondrial
	m6A	K1Q317_CRAGI	Serine/threonine-protein kinase SRPK1
	m6A	K1QKG9_CRAGI	Cysteine desulfurase, mitochondrial
	m6A	K1PS77_CRAGI	Prostaglandin G/H synthase 1
	m6A	K1QJW6_CRAGI	Translocon-associated protein subunit gamma
	m6A	K1QTV1_CRAGI	Uncharacterized protein
	m6A	K1QTV1_CRAGI	Uncharacterized protein
	m6A	K1QTV6_CRAGI	Eukaryotic translation initiation factor 3 subunit F
	m6A	K1PNY5_CRAGI	Splicing factor, proline-and glutamine-rich
	m6A	K1R100_CRAGI	Metaxin-2
	m6A	K1R8L1_CRAGI	Exportin-2

1			
2			
3	m6A	K1QZ64_CRAGI	Nuclear pore complex protein Nup98-Nup96
4	m6A	K1QWZ8_CRAGI	Catenin beta
5	m6A	K1QAT9_CRAGI	ATP-dependent RNA helicase DDX1
6	m6A	K1P8Y9_CRAGI	Cytochrome b-c1 complex subunit 7
7	m6A	K1PIC5_CRAGI	Transmembrane protein 85
8	m6A	K1QMV7_CRAGI	V-type proton ATPase subunit D
9	m6A	K1RC37_CRAGI	Uncharacterized protein
10	m6A	K1PEY4_CRAGI	26S proteasome non-ATPase regulatory subunit 2
11	m6A	K1RG04_CRAGI	ALK tyrosine kinase receptor
12	m6A	K1QG72_CRAGI	Hemagglutinin/amebocyte aggregation factor
13	m6A	K1RK83_CRAGI	Tyrosine-protein kinase BAZ1B
14	m6A	K1QMT1_CRAGI	DnaJ-like protein subfamily B member 4
15	m6A	K1P811_CRAGI	Pleckstrin-like protein domain-containing family F member 2 (Fragment)
16	m6A	K1R316_CRAGI	Nucleolar complex protein 2-like protein (Fragment)
17	m6A	K1QDB9_CRAGI	Transport protein Sec61 subunit alpha isoform 2 (Fragment)
18	m6A	K1QMJ8_CRAGI	Transcription initiation factor IIA subunit 1
19	m6A	K1R5G4_CRAGI	60S ribosomal protein L31
20	m6A	K1R1W9_CRAGI	Nicalin-1
21	m6A	K1QDA7_CRAGI	Uracil phosphoribosyltransferase
22	m6A	K1QI02_CRAGI	Vesicle-trafficking protein SEC22b
23	m6A	K1QFZ8_CRAGI	Ceramide kinase-like protein
24	m6A	K1Q151_CRAGI	60S ribosomal protein L32
25	m6A	K1QNS4_CRAGI	DnaJ-like protein subfamily C member 9
26	m6A	K1REQ4_CRAGI	Cytochrome c oxidase subunit 6B
27	m6A	K1R4B8_CRAGI	Plexin domain-containing protein 2
28	m6A	K1QC10_CRAGI	GTP-binding protein 1
29	m6A	K1PJY2_CRAGI	Inositol polyphosphate 1-phosphatase
30	m6A	K1R983_CRAGI	Protein transport protein SEC23
31	m6A	K1Q5Y3_CRAGI	Annexin
32	m6A	K1Q1N1_CRAGI	Alpha-mannosidase
33	m6A	K1QNU0_CRAGI	Non-specific serine/threonine protein kinase
34	m6A	K1R1Q8_CRAGI	Ras-related protein Rab-5C
35	m6A	K1RH95_CRAGI	Myosin-IIIB
36	m6A	K1QWE5_CRAGI	Ras-related protein Rab-18-B
37	m6A	K1QCB0_CRAGI	40S ribosomal protein S5
38	m6A	K1Q0I8_CRAGI	Putative splicing factor, arginine/serine-rich 7
39	m6A	K1QXF5_CRAGI	Calcyphosin-like protein
40	m6A	K1R8C6_CRAGI	40S ribosomal protein S12
41	m6A	K1QFA9_CRAGI	Low-density lipoprotein receptor-related protein 2
42	m6A	K1QYF5_CRAGI	Apoptosis-inducing factor 1, mitochondrial
43	m6A	K1QA50_CRAGI	V-type proton ATPase subunit H
44	m6A	K1PY39_CRAGI	Protocadherin Fat 4
45	m6A	K1Q330_CRAGI	Dihydrolipoyl dehydrogenase
46	m6A	K1Q350_CRAGI	Glyceraldehyde-3-phosphate dehydrogenase
47	m6A	K1Q6U7_CRAGI	78 kDa glucose-regulated protein
48	m6A	K1RBI9_CRAGI	Small nuclear ribonucleoprotein Sm D2
49	m6A	K1P0H0_CRAGI	Aspartyl/asparaginyl beta-hydroxylase
50	m6A	K1QSR2_CRAGI	Apoptosis inhibitor 5
51	m6A	K1RDV7_CRAGI	Cell division control protein 2-like protein (Fragment)
52	m6A	K1PD30_CRAGI	Putative histone-binding protein Caf1
53	m6A	K1P7K8_CRAGI	Vesicle-fusing ATPase 1
54	m6A	K1PVZ3_CRAGI	Cold shock domain-containing protein E1
55	m6A	K1RKZ5_CRAGI	DNA damage-binding protein 1
56	m6A	K1R0Z4_CRAGI	Uncharacterized protein
57	m6A	K1Q947_CRAGI	Dynein light chain
58	m6A	K1PU46_CRAGI	Lethal(2) giant larvae-like protein 1
59	m6A	K1Q8K9_CRAGI	KRR1 small subunit processome component-like protein
60	m6A	K1PQZ3_CRAGI	Armadillo repeat-containing protein 4
	m6A	K1QL00_CRAGI	Microsomal glutathione S-transferase 1
	m6A	K1RDM2_CRAGI	60S ribosomal protein L18a

1			
2			
3	m6A	K1Q3V9_CRAGI	Mitochondrial carnitine/acylcarnitine carrier protein
4	m6A	K1QN55_CRAGI	60S acidic ribosomal protein P1
5	m6A	K1R3G0_CRAGI	Transformer-2-like protein beta
6	m6A	K1PWM3_CRAGI	MICOS complex subunit MIC13
7	m6A	K1QKL8_CRAGI	V-type proton ATPase subunit a
8	m6A	K1S6T6_CRAGI	UPF0480 protein C15orf24-like protein
9	m6A	K1R0W0_CRAGI	Ferritin
10	m6A	K1PGK7_CRAGI	Uncharacterized protein
11	m6A	K1QY71_CRAGI	Histone H2B
12	m6A	K1QNT7_CRAGI	Aldehyde dehydrogenase, mitochondrial
13	m6A	K1RJ96_CRAGI	Sphere organelles protein SPH-1
14	m6A	K1RZE2_CRAGI	Isocitrate dehydrogenase [NADP]
15	m6A	K1PPV1_CRAGI	Atlastin-2
16	m6A	K1P9F1_CRAGI	Insulin-like growth factor-binding protein complex acid labile chain
17	m6A	K1QVU0_CRAGI	Synaptojanin-2-binding protein
18	m6A	K1QX44_CRAGI	Ras-related protein Rab-11B
19	m6A	K1QKU6_CRAGI	mRNA export factor
20	m6A	K1QDV6_CRAGI	Protein argonaute-2
21	m6A	K1R5B9_CRAGI	DNA-directed RNA polymerase, mitochondrial
22	m6A	K1RCT2_CRAGI	Translocon-associated protein subunit delta
23	m6A	K1PKD4_CRAGI	40S ribosomal protein S30
24	m6A	K1PP50_CRAGI	Golgi integral membrane protein 4
25	m6A	K1PG60_CRAGI	60S ribosomal protein L17
26	m6A	K1QWJ4_CRAGI	Splicing factor 3B subunit 5
27	m6A	K1RB91_CRAGI	Neutral alpha-glucosidase AB
28	m6A	K1RD12_CRAGI	Uncharacterized protein
29	m6A	K1PQE3_CRAGI	RNA-binding protein Raly
30	m6A	K1Q2Y1_CRAGI	40S ribosomal protein S15
31	m6A	K1PQF1_CRAGI	Neural cell adhesion molecule L1
32	m6A	K1QKJ0_CRAGI	Aldehyde dehydrogenase family 3 member B1
33	m6A	K1PUQ5_CRAGI	Histone H2B
34	m6A	K1Q2W7_CRAGI	Uncharacterized protein
35	m6A	K1Q412_CRAGI	Uncharacterized protein
36	m6A	K1RNH1_CRAGI	60S ribosomal protein L18 (Fragment)
37	m6A	K1QNT4_CRAGI	Anoctamin
38	m6A	K1P8B7_CRAGI	Ubiquitin-conjugating enzyme E2-17 kDa (Fragment)
39	m6A	K1Q1D7_CRAGI	Putative rRNA-processing protein EBP2
40	m6A	K1PY30_CRAGI	Septin-2
41	m6A	K1Q1R1_CRAGI	Exostosin-3
42	m6A	K1RHP3_CRAGI	Proliferation-associated protein 2G4
43	m6A	K1PZI3_CRAGI	SWI/SNF complex subunit SMARCC2
44	m6A	K1QT97_CRAGI	N(G),N(G)-dimethylarginine dimethylaminohydrolase 1
45	m6A	K1QQQ5_CRAGI	Replication factor C subunit 5
46	m6A	K1PA61_CRAGI	Actin-like protein 6A
47	m6A	K1PNL0_CRAGI	Microtubule-associated protein futsch
48	m6A	K1QI28_CRAGI	V-type proton ATPase subunit B
49	m6A	K1PYL5_CRAGI	Uncharacterized protein
50	m6A	K1PJ65_CRAGI	Dual specificity mitogen-activated protein kinase kinase 7
51	m6A	K1QMD8_CRAGI	Proteasome subunit alpha type
52	m6A	K1Q2L4_CRAGI	Transmembrane emp24 domain-containing protein 9
53	m6A	K1Q8C1_CRAGI	Putative RNA-binding protein Luc7-like 2
54	m6A	K1PS71_CRAGI	Uncharacterized protein
55	m6A	K1Q900_CRAGI	Galectin
56	m6A	K1RKR8_CRAGI	Pumilio-like protein 2
57	m6A	K1RKE5_CRAGI	IQ and AAA domain-containing protein 1
58	m6A	K1QRL4_CRAGI	Importin-5
59	m6A	K1PGN0_CRAGI	Fatty-acid amide hydrolase 2
60	m6A	K1RD83_CRAGI	Serine hydroxymethyltransferase
	m6A	K1RFA3_CRAGI	Lamin Dm0
	m6A	K1QAG7_CRAGI	Phosphatidylinositide phosphatase SAC1

1			
2			
3	m6A	K1PJP7_CRAGI	Surfeit locus protein 4
4	m6A	K1PG07_CRAGI	Lupus La-like protein
5	m6A	K1QVS0_CRAGI	Ras-like GTP-binding protein Rho1
6	m6A	K1PWC3_CRAGI	Tetratricopeptide repeat protein 35
7	m6A	K1QZK9_CRAGI	Uncharacterized protein
8	m6A	K1QAG9_CRAGI	Ferritin
9	m6A	K1QAG9_CRAGI	Ferritin
10	m6A	K1QHW8_CRAGI	Ferritin
11	m6A	K1PZF2_CRAGI	Exportin-7
12	m6A	K1RCF4_CRAGI	Translocon-associated protein subunit alpha
13	m6A	K1QVIO_CRAGI	Isocitrate dehydrogenase [NAD] subunit, mitochondrial
14	m6A	K1PX47_CRAGI	Ubiquitin carboxyl-terminal hydrolase
15	m6A	K1P8G6_CRAGI	Vesicular integral-membrane protein VIP36
16	m6A	K1PNZ8_CRAGI	Ribosomal protein L37
17	m6A	K1Q373_CRAGI	Splicing factor, arginine/serine-rich 7
18	m6A	K1R0U6_CRAGI	Uncharacterized protein
19	m6A	K1QAV0_CRAGI	Guanine nucleotide-binding protein G(Q) subunit alpha
20	m6A	K1R8Y1_CRAGI	Obg-like ATPase 1
21	m6A	K1QBY6_CRAGI	Transmembrane protein Tmp21
22	m6A	K1QZ58_CRAGI	Splicing factor U2AF 26 kDa subunit
23	m6A	K1RAE9_CRAGI	ADP-ribosylation factor-like protein 8A
24	m6A	K1RCW5_CRAGI	Eukaryotic translation initiation factor 4 gamma 3
25	m6A	K1PZ89_CRAGI	Mannosyl-oligosaccharide glucosidase
26	m6A	K1PBG6_CRAGI	Uncharacterized protein
27	m6A	K1QPS1_CRAGI	Poly [ADP-ribose] polymerase
28	m6A	K1R1C5_CRAGI	Signal recognition particle receptor subunit beta
29	m6A	K1PVG0_CRAGI	Long-chain fatty acid transport protein 4
30	m6A	K1QXA1_CRAGI	Retinol dehydrogenase 12
31	m6A	K1R481_CRAGI	Epimerase family protein SDR39U1
32	m6A	K1QVP6_CRAGI	Developmentally-regulated GTP-binding protein 1
33	m6A	K1PWB7_CRAGI	Uncharacterized protein
34	m6A	K1PNQ1_CRAGI	Ankyrin repeat domain-containing protein 5
35	m6A	K1Q8C5_CRAGI	Putative ATP-dependent RNA helicase DDX47
36	m6A	K1PR38_CRAGI	TAR DNA-binding protein 43
37	m6A	K1P7Q6_CRAGI	40S ribosomal protein S19
38	m6A	K1RFD2_CRAGI	Adenylate kinase
39	m6A	K1PQJ9_CRAGI	ATP synthase subunit delta, mitochondrial
40	m6A	K1Q4U7_CRAGI	AP-3 complex subunit delta-1
41	m6A	K1QM06_CRAGI	Prohibitin
42	m6A	K1QUW5_CRAGI	U2 snRNP auxiliary factor large subunit
43	m6A	K1PD36_CRAGI	Ubiquitin
44	m6A	K1PBL2_CRAGI	Eukaryotic initiation factor 4A-III
45	m6A	K1R3V8_CRAGI	COP9 signalosome complex subunit 4
46	m6A	K1PII4_CRAGI	YTH domain-containing protein 1
47	m6A	K1PZL0_CRAGI	B-box type zinc finger protein ncl-1
48	m6A	K1REW8_CRAGI	Ribosomal protein L15
49	m6A	K1R9V5_CRAGI	Tetraspanin
50	m6A	K1QPX1_CRAGI	ATPase family AAA domain-containing protein 3
51	m6A	K1QHI2_CRAGI	Heterogeneous nuclear ribonucleoprotein L
52	m6A	K1QZ95_CRAGI	Nuclear pore complex protein
53	m6A	K1R401_CRAGI	Spectrin alpha chain
54	m6A	K1PSA1_CRAGI	Transmembrane 9 superfamily member
55	m6A	K1Q486_CRAGI	Uncharacterized protein
56	m6A	K1PYA0_CRAGI	Cytoplasmic dynein 2 heavy chain 1
57	m6A	K1QLC6_CRAGI	JmjC domain-containing protein 8
58	m6A	K1RDG4_CRAGI	DNA helicase
59	m6A	K1PQY0_CRAGI	Protein quiver
60	m6A	K1QTD5_CRAGI	Low-density lipoprotein receptor-related protein 12
	m6A	K1PSP7_CRAGI	Uncharacterized protein
	m6A	K1QAL3_CRAGI	RNA-binding protein 28
	m6A	K1QND2_CRAGI	Septin-2

1			
2			
3	m6A	K1RMM6_CRAGI	Centromere protein J
4	m6A	K1R1K6_CRAGI	Heat shock protein beta-1
5	m6A	K1R3Z4_CRAGI	5'-3' exoribonuclease 1
6	m6A	K1RB56_CRAGI	Ferritin
7	m6A	K1RIZ9_CRAGI	Band 4.1-like protein 5
8	m6A	K1RFB1_CRAGI	Stomatin-like protein 2 (Fragment)
9	m6A	K1RNI9_CRAGI	Leucine-rich repeat-containing protein 59
10	m6A	K1Q7U7_CRAGI	Basigin
11	m6A	K1RNX0_CRAGI	Small nuclear ribonucleoprotein E
12	m6A	K1P5F7_CRAGI	Metastasis-associated protein MTA1
13	m6A	K1P5F7_CRAGI	Metastasis-associated protein MTA1
14	m6A	K1PVG9_CRAGI	Malectin
15	m6A	K1R247_CRAGI	Condensin complex subunit 1
16	m6A	K1PSN0_CRAGI	Pre-mRNA-processing factor 40-like protein A
17	m6A	K1PZV3_CRAGI	Guanine nucleotide-binding protein-like 3-like protein (Fragment)
18	m6A	K1RWP3_CRAGI	Peptidyl-tRNA hydrolase 2, mitochondrial
19	m6A	K1Q7E4_CRAGI	Ubiquitin-conjugating enzyme E2 N
20	m6A	K1R7E4_CRAGI	Ubiquitin-conjugating enzyme E2 N
21	m6A	K1R7E4_CRAGI	Ubiquitin-conjugating enzyme E2 N
22	m6A	K1RK33_CRAGI	Exportin-1
23	m6A	K1RPP1_CRAGI	Synaptophysin
24	m6A	K1Q5P0_CRAGI	60S ribosomal protein L17
25	m6A	K1PND7_CRAGI	Fatty acid synthase
26	m6A	K1PND7_CRAGI	Fatty acid synthase
27	m6A	K1R0R7_CRAGI	Putative ATP-dependent RNA helicase DHX36
28	m6A	K1QJL6_CRAGI	Microtubule-associated protein RP/EB family member 3
29	m6A	K1QKZ6_CRAGI	Inosine-5'-monophosphate dehydrogenase
30	m6A	Q70MT4_CRAGI	40S ribosomal protein S10
31	m6A	K1RP91_CRAGI	Putative RNA exonuclease NEF-sp
32	m6A	K1PKK7_CRAGI	AP-2 complex subunit mu-1
33	m6A	K1PKK7_CRAGI	AP-2 complex subunit mu-1
34	m6A	K1PLR8_CRAGI	Chromosome transmission fidelity protein 18-like protein (Fragment)
35	m6A	K1PH10_CRAGI	Polyadenylate-binding protein-interacting protein 1
36	m6A	K1P2G0_CRAGI	Strawberry notch-like protein 1
37	m6A	K1P2G0_CRAGI	Strawberry notch-like protein 1
38	m6A	K1PNU2_CRAGI	Histone-arginine methyltransferase CARM1
39	m6A	K1QZJ6_CRAGI	Uncharacterized protein (Fragment)
40	m6A	K1PXB6_CRAGI	Cadherin-23
41	m6A	K1QCK4_CRAGI	CLIP-associating protein 1
42	m6A	K1PPH0_CRAGI	Gamma-tubulin complex component
43	m6A	K1Q105_CRAGI	Ferrochelatase
44	m6A	K1Q105_CRAGI	Ferrochelatase
45	m6A	K1QF52_CRAGI	Uncharacterized protein
46	m6A	K1Q2Z5_CRAGI	Putative ATP-dependent RNA helicase DDX46
47	m6A	K1PXI0_CRAGI	Angiopoietin-4
48	m6A	K1RPF7_CRAGI	60S ribosomal protein L5
49	m6A	K1QV25_CRAGI	Transcription elongation factor B polypeptide 2
50	m6A	K1QV25_CRAGI	Transcription elongation factor B polypeptide 2
51	m6A	K1PUJ1_CRAGI	Radixin
52	m6A	K1QHT0_CRAGI	Deoxyuridine 5'-triphosphate nucleotidohydrolase, mitochondrial
53	m6A	K1QMK5_CRAGI	Kinesin-associated protein 3
54	m6A	K1QQ16_CRAGI	AP complex subunit beta
55	m6A	K1QQ16_CRAGI	AP complex subunit beta
56	m6A	K1QZ49_CRAGI	Adipocyte plasma membrane-associated protein
57	m6A	K1QIB2_CRAGI	Mitogen-activated protein kinase
58	m6A	K1QXH7_CRAGI	DNA replication licensing factor mcm4-B
59	m6A	K1QQV0_CRAGI	Histone H1.2
60	m6A	K1Q61_CRAGI	Acetolactate synthase-like protein
	m6A	K1R5R4_CRAGI	Dynein heavy chain 10, axonemal
	m6A	K1R4J0_CRAGI	MAGUK p55 subfamily member 2
	m6A	K1RR98_CRAGI	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 4-like 2
	m6A	K1Q5E0_CRAGI	Dual specificity protein kinase CLK2
	m6A	K1R275_CRAGI	Putative ATP-dependent RNA helicase DDX52
	m6A	K1RFV5_CRAGI	ATP-dependent RNA helicase DDX1
	m6A	K1QNZ7_CRAGI	Ubiquilin-1
	m6A	K1QZ50_CRAGI	RNA-dependent RNA polymerase
	m6A	K1QH4_CRAGI	Uncharacterized protein
	m6A	K1Q455_CRAGI	Netrin-3
	m6A	K1QQL6_CRAGI	Leucyl-tRNA synthetase, cytoplasmic

1			
2			
3	m6A	K1RZM3_CRAGI	Cartilage acidic protein 1
4	m6A	K1R065_CRAGI	Golgi membrane protein 1
5	m6A	K1RD19_CRAGI	RNA-binding protein 4
6	m6A	K1R969_CRAGI	Uncharacterized protein
7	m6A	K1RE19_CRAGI	V-type proton ATPase subunit S1
8	m6A	K1QGW5_CRAGI	WD repeat and SOF domain-containing protein 1
9	m6A	K1QKI1_CRAGI	Tudor domain-containing protein 1
10	m6A	K1PSH2_CRAGI	28S ribosomal protein S12, mitochondrial
11	m6A	K1QMT2_CRAGI	Signal peptidase complex catalytic subunit SEC11
12	m6A	K1QDI0_CRAGI	Transmembrane protein 49
13	m6A	K1Q8T3_CRAGI	Importin subunit alpha
14	m6A	K1Q525_CRAGI	Mechanosensory protein 2 (Fragment)
15	m6A	K1Q5G6_CRAGI	60 kDa heat shock protein, mitochondrial
16	m6A	K1QHF0_CRAGI	40S ribosomal protein S27
17	m6A	K1Q7X3_CRAGI	Pre-mRNA-splicing factor SYF1
18	m6A	K1RRH1_CRAGI	Chromodomain-helicase-DNA-binding protein Mi-2-like protein
19	m6A	K1Q435_CRAGI	Eukaryotic translation initiation factor 2 subunit 1
20	m6A	K1RNS1_CRAGI	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8
21	m6A	K1QGF9_CRAGI	Rootletin
22	m6A	K1QJ36_CRAGI	Muscle, skeletal receptor tyrosine protein kinase
23	m6A	K1RNU5_CRAGI	Pre-mRNA-splicing factor RBM22
24	m6A	K1R916_CRAGI	Structural maintenance of chromosomes protein
25	m6A	K1RUC9_CRAGI	Uncharacterized protein
26	m6A	K1QR54_CRAGI	Zinc finger RNA-binding protein
27	m6A	K1P9Q2_CRAGI	Signal peptidase complex subunit 3
28	m6A	K1RTR1_CRAGI	ATP-citrate synthase
29	m6A	K1Q050_CRAGI	Centrin-3
30	m6A	K1QPA5_CRAGI	Uncharacterized protein C16orf61-like protein
31	m6A	K1PSY2_CRAGI	Fragile X mental retardation syndrome-related protein 1
32	m6A	K1R7G0_CRAGI	Chromobox-like protein 5
33	m6A	K1QFG2_CRAGI	Telomere-associated protein RIF1
34	m6A	K1QYV5_CRAGI	Cytoplasmic polyadenylation element-binding protein 1-B
35	m6A	K1R1I2_CRAGI	Cation-independent mannose-6-phosphate receptor
36	m6A	K1R255_CRAGI	Heterogeneous nuclear ribonucleoprotein L
37	m6A	K1RB07_CRAGI	60S ribosomal protein L27a
38	m6A	K1RYF2_CRAGI	Enoyl-CoA hydratase domain-containing protein 3, mitochondrial
39	m6A	K1RJ53_CRAGI	Tetratricopeptide repeat protein 12
40	m6A	K1QW73_CRAGI	Glycoprotein 3-alpha-L-fucosyltransferase A
41	m6A	K1RBC9_CRAGI	Transketolase-like protein 2
42	m6A	K1QJ46_CRAGI	Putative methylcrotonoyl-CoA carboxylase beta chain, mitochondrial
43	m6A	K1Q9V2_CRAGI	Antigen KI-67
44	m6A	K1PWQ2_CRAGI	60 kDa neurofilament protein
45	m6A	K1QGF1_CRAGI	Splicing factor 3B subunit 2
46	m6A	K1QTE0_CRAGI	Epidermal retinal dehydrogenase 2
47	m6A	K1PPQ1_CRAGI	14-3-3 protein gamma
48	m6A	K1Q7A7_CRAGI	Putative tyrosinase-like protein tyr-3
49	m6A	K1QHA2_CRAGI	Spectrin beta chain, brain 4
50	m6A	K1Q6U0_CRAGI	Coatomer subunit zeta-1
51	m6A	K1QU16_CRAGI	Protein polybromo-1
52	m6A	K1P7W5_CRAGI	Histone H1-delta
53	m6A	K1QBL6_CRAGI	Tudor domain-containing protein 1
54	m6A	K1QVS1_CRAGI	ER membrane protein complex subunit 3
55	m6A	K1Q1L9_CRAGI	Interferon-induced protein 44-like protein
56	m6A	K1Q109_CRAGI	Neurexin-4
57	m6A	K1PJN7_CRAGI	PC3-like endoprotease variant A
58	m6A	K1RAH1_CRAGI	Uncharacterized protein
59	m6A	K1R472_CRAGI	Synaptobrevin-like protein YKT6
60	m6A	K1QMY9_CRAGI	Uncharacterized protein
	m6A	K1QBT8_CRAGI	Uncharacterized protein
	m6A	K1Q1R2_CRAGI	Caprin-2

1			
2			
3	m6A	K1R8V1_CRAGI	Puratrophin-1
4	m6A	K1PUF0_CRAGI	G-protein coupled receptor moody
5	m6A	K1Q4R2_CRAGI	Zinc finger protein 26
6	m6A	K1QXP9_CRAGI	Uncharacterized protein
7	m6A	K1P6M6_CRAGI	Cerebellin-1
8	A	K1QNA2_CRAGI	Vitellogenin-6
9	A	K1PTY5_CRAGI	Protocadherin Fat 4
10	A	K1QBR5_CRAGI	Uncharacterized protein
11	A	K1PFG1_CRAGI	Uncharacterized protein
12	A	K1P9A4_CRAGI	Beta-1,3-glucan-binding protein
13	A	K1QHI5_CRAGI	Pyruvate carboxylase, mitochondrial
14	A	K1R5B4_CRAGI	Proteasome activator complex subunit 4
15	A	K1QQ94_CRAGI	Uncharacterized protein
16	A	K1QXR4_CRAGI	Pancreatic lipase-related protein 2
17	A	K1RWS2_CRAGI	Transcriptional activator protein Pur-alpha
18	A	K1PNI6_CRAGI	Heterogeneous nuclear ribonucleoprotein A/B
19	A	K1R3U2_CRAGI	Uncharacterized protein
20	A	K1R7V7_CRAGI	Tubulin beta chain
21	A	K1QMX5_CRAGI	Uncharacterized protein
22	A	K1R9B6_CRAGI	H/ACA ribonucleoprotein complex subunit 4
23	A	K1QQ68_CRAGI	Tubulin alpha chain
24	A	K1PQP2_CRAGI	Nucleolin
25	A	K1RLF8_CRAGI	Splicing factor 3B subunit 3
26	A	K1R164_CRAGI	Galectin-4
27	A	K1QVJ8_CRAGI	Piwi-like protein 1
28	A	K1RGT5_CRAGI	Metalloendopeptidase
29	A	K1PH76_CRAGI	Y-box factor-like protein (Fragment)
30	A	K1QII6_CRAGI	Tubulin alpha chain
31	A	K1QSX8_CRAGI	ATPase family AAA domain-containing protein 2B
32	A	K1QK56_CRAGI	Uncharacterized protein
33	A	K1QKB5_CRAGI	Uncharacterized protein
34	A	K1PE00_CRAGI	Tubulin alpha chain
35	A	K1QQ27_CRAGI	Pancreatic lipase-related protein 2
36	A	K1PVA1_CRAGI	Transitional endoplasmic reticulum ATPase
37	A	K1PEP0_CRAGI	40S ribosomal protein S8
38	A	K1QXX7_CRAGI	Myosin heavy chain, non-muscle (Fragment)
39	A	K1RK12_CRAGI	40S ribosomal protein S23
40	A	K1QSQ9_CRAGI	Putative ATP-dependent RNA helicase an3
41	A	K1PNR3_CRAGI	Clathrin heavy chain
42	A	K1QMA4_CRAGI	RRP5-like protein
43	A	K1QHM2_CRAGI	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2
44	A	K1QU53_CRAGI	NAD(P) transhydrogenase, mitochondrial
45	A	K1PJC1_CRAGI	Adipophilin
46	A	K1RG73_CRAGI	Acetyl-CoA carboxylase
47	A	K1QFM6_CRAGI	Vitellogenin
48	A	K1R6Q7_CRAGI	DNA topoisomerase I
49	A	K1R6Z7_CRAGI	ATP synthase subunit alpha
50	A	K1QGS8_CRAGI	Elongation factor 1-alpha
51	A	K1QWZ6_CRAGI	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1
52	A	K1RD58_CRAGI	Uncharacterized protein
53	A	K1QLS3_CRAGI	Cytochrome b-c1 complex subunit 2, mitochondrial
54	A	K1S1S1_CRAGI	Insulin-like growth factor 2 mRNA-binding protein 1
55	A	K1R0L4_CRAGI	Sodium/potassium-transporting ATPase subunit alpha
56	A	K1RWW5_CRAGI	ATP synthase subunit beta
57	A	K1QA13_CRAGI	Calcium-transporting ATPase
58	A	K1QFN2_CRAGI	Uncharacterized protein
59	A	K1R545_CRAGI	Pre-mRNA-processing-splicing factor 8 (Fragment)
60	A	K1R252_CRAGI	Putative methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial
	A	K1PMT6_CRAGI	Heterogeneous nuclear ribonucleoprotein U-like protein 1
	A	K1RGB7_CRAGI	Epidermal retinal dehydrogenase 2

1			
2			
3	A	K1R466_CRAGI	T-complex protein 1 subunit gamma
4	A	K1R294_CRAGI	T-complex protein 1 subunit beta
5	A	K1RIT6_CRAGI	NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial
6	A	K1QIR8_CRAGI	78 kDa glucose-regulated protein
7			
8	A	K1RI55_CRAGI	Insulin-like growth factor 2 mRNA-binding protein 3
9	A	K1QH74_CRAGI	Splicing factor, arginine/serine-rich 1
10	A	K1S2N7_CRAGI	Innexin
11	A	K1R435_CRAGI	Splicing factor, arginine/serine-rich 4
12	A	K1R5U4_CRAGI	Acetyl-CoA carboxylase 1
13	A	K1QBK6_CRAGI	Splicing factor 3B subunit 1
14	A	K1Q988_CRAGI	Band 4.1-like protein 3
15	A	K1R420_CRAGI	Non-specific serine/threonine protein kinase
16	A	A5LGH1_CRAGI	Voltage-dependent anion channel
17	A	K1PHW2_CRAGI	Uncharacterized protein
18	A	K1REG6_CRAGI	DNA helicase
19	A	K1QAE5_CRAGI	Uncharacterized protein
20	A	K1QWT8_CRAGI	Uncharacterized protein
21	A	K1QRL6_CRAGI	Methenyltetrahydrofolate synthetase domain-containing protein
22	A	K1QYB3_CRAGI	Ig-like and fibronectin type-III domain-containing protein C25G4.10
23	A	K1QKD6_CRAGI	Uncharacterized protein
24	A	K1R115_CRAGI	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial
25	A	K1S4Q2_CRAGI	T-complex protein 1 subunit delta (Fragment)
26	A	K1QWK2_CRAGI	MAM domain-containing glycosylphosphatidylinositol anchor protein 2
27	A	K1R0S3_CRAGI	T-complex protein 1 subunit theta
28	A	K1QFW9_CRAGI	Uncharacterized protein
29	A	K1Q0Z3_CRAGI	Estradiol 17-beta-dehydrogenase 11
30	A	K1PNQ5_CRAGI	Heat shock protein HSP 90-alpha 1
31	A	K1RBF6_CRAGI	Uncharacterized protein yfeX
32	A	K1R4D4_CRAGI	40S ribosomal protein SA
33	A	K1QJ14_CRAGI	40S ribosomal protein S3a
34	A	K1PUL2_CRAGI	Long-chain-fatty-acid--CoA ligase 1
35	A	K1RFT1_CRAGI	Band 4.1-like protein 3
36	A	K1PJ06_CRAGI	Importin subunit alpha-1
37	A	K1QT21_CRAGI	Putative ATP-dependent RNA helicase DDX5
38	A	K1QM19_CRAGI	Uncharacterized protein
39	A	K1QXS6_CRAGI	Heterogeneous nuclear ribonucleoprotein A2-like protein 1
40	A	K1QMX8_CRAGI	DNA replication licensing factor MCM7
41	A	K1PD57_CRAGI	Constitutive coactivator of PPAR-gamma-like protein 1-like protein
42	A	K1R953_CRAGI	Acetyl-CoA carboxylase
43	A	K1RJH5_CRAGI	Polyadenylate-binding protein
44	A	K1RSZ6_CRAGI	40S ribosomal protein S7
45	A	K1R7A2_CRAGI	Uncharacterized protein
46	A	K1QUC6_CRAGI	Uncharacterized protein
47	A	K1QWX2_CRAGI	60S acidic ribosomal protein P0
48	A	K1RNB5_CRAGI	Propionyl-CoA carboxylase beta chain, mitochondrial
49	A	K1PCS4_CRAGI	Eukaryotic translation initiation factor 2 subunit 3, Y-linked
50	A	K1Q923_CRAGI	Putative ATP-dependent RNA helicase DDX4
51	A	K1QPX8_CRAGI	Alkyl/aryl-sulfatase BDS1
52	A	K1R4R9_CRAGI	Mitotic apparatus protein p62
53	A	K1RAJ1_CRAGI	T-complex protein 1 subunit alpha
54	A	K1Q0L1_CRAGI	60S ribosomal protein L23a
55	A	K1Q620_CRAGI	Uncharacterized protein
56	A	K1QG58_CRAGI	Actin
57	A	K1Q4H2_CRAGI	Nodal modulator 3
58	A	K1Q260_CRAGI	Nucleolar protein 58
59	A	K1QF01_CRAGI	40S ribosomal protein S4
60	A	K1PUM2_CRAGI	Histone H2A
	A	K1QNN9_CRAGI	MICOS complex subunit MIC60
	A	K1RQA0_CRAGI	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2
	A	K1QZW0_CRAGI	Polyadenylate-binding protein 2

1			
2			
3	A	K1QBN0_CRAGI	Methylcrotonoyl-CoA carboxylase beta chain, mitochondrial
4	A	K1Q8S0_CRAGI	Nucleolar complex protein 3 homolog
5	A	K1RH18_CRAGI	Sarcalumenin
6	A	K1QQ05_CRAGI	Insulin-like growth factor-binding protein complex acid labile chain
7	A	K1QT04_CRAGI	Uncharacterized protein
8	A	K1RLC5_CRAGI	T-complex protein 1 subunit epsilon
9	A	K1Q9K6_CRAGI	Histone H3
10	A	K1QBW8_CRAGI	Uncharacterized protein
11	A	K1Q9W5_CRAGI	T-complex protein 1 subunit eta
12	A	K1R0Y9_CRAGI	ADP,ATP carrier protein
13	A	K1QP17_CRAGI	Caprin-1
14	A	K1QYB6_CRAGI	Delta-1-pyrroline-5-carboxylate synthetase
15	A	K1R7I9_CRAGI	Heterogeneous nuclear ribonucleoprotein Q
16	A	K1QMB9_CRAGI	Eukaryotic translation initiation factor 3 subunit A
17	A	K1PM50_CRAGI	40S ribosomal protein S16
18	A	K1P8W6_CRAGI	60S ribosomal protein L4
19	A	K1PXH5_CRAGI	Putative saccharopine dehydrogenase
20	A	K1PBZ4_CRAGI	Regulator of nonsense transcripts 1
21	A	K1R4L8_CRAGI	Electron transfer flavoprotein-ubiquinone oxidoreductase, mitochondrial
22	A	K1QFP5_CRAGI	NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial
23	A	K1RIG6_CRAGI	LSM14-like protein A
24	A	K1R591_CRAGI	Inter-alpha-trypsin inhibitor heavy chain H4
25	A	K1RSA6_CRAGI	Methylcrotonoyl-CoA carboxylase subunit alpha, mitochondrial
26	A	K1R1B1_CRAGI	35 kDa SR repressor protein
27	A	K1QZU8_CRAGI	Calcium-transporting ATPase
28	A	K1QX26_CRAGI	Endoplasmic
29	A	K1Q358_CRAGI	60S acidic ribosomal protein P2
30	A	K1P112_CRAGI	ATP synthase subunit gamma, mitochondrial
31	A	K1QHS8_CRAGI	Ribonucleoside-diphosphate reductase
32	A	K1PXN5_CRAGI	T-complex protein 1 subunit zeta
33	A	K1R7J6_CRAGI	Putative sodium/potassium-transporting ATPase subunit beta-2
34	A	K1Q5H6_CRAGI	FACT complex subunit SSRP1
35	A	K1QTD9_CRAGI	Nucleolar protein 56
36	A	K1QC78_CRAGI	Ras-related protein Rab-14
37	A	K1Q9M7_CRAGI	Histone H1-delta
38	A	K1RNZ6_CRAGI	Eukaryotic translation initiation factor 3 subunit D
39	A	K1QAH9_CRAGI	H/ACA ribonucleoprotein complex subunit
40	A	K1RLT4_CRAGI	Signal recognition particle subunit SRP68
41	A	K1RWX7_CRAGI	Metabotropic glutamate receptor 3
42	A	K1RA35_CRAGI	Splicing factor, arginine/serine-rich 7
43	A	K1QE71_CRAGI	DNA helicase
44	A	K1PS27_CRAGI	DNA helicase
45	A	K1Q4Y8_CRAGI	Histone H1oo
46	A	K1PGW7_CRAGI	Transmembrane protein 2
47	A	K1RAB9_CRAGI	Epoxide hydrolase 4
48	A	K1Q9P5_CRAGI	Mitochondrial-processing peptidase subunit beta
49	A	K1QL67_CRAGI	60S ribosomal protein L7a
50	A	K1PLY1_CRAGI	DNA polymerase
51	A	K1R996_CRAGI	Long-chain-fatty-acid--CoA ligase 4
52	A	K1Q404_CRAGI	DNA topoisomerase 2
53	A	K1QBH0_CRAGI	Uncharacterized protein
54	A	K1R0W4_CRAGI	Signal recognition particle subunit SRP72
55	A	K1RN77_CRAGI	Nuclear autoantigenic sperm protein
56	A	K1PA54_CRAGI	Replication factor C subunit 3
57	A	K1Q4S5_CRAGI	Cadherin-87A
58	A	K1QEF2_CRAGI	ADP-ribosylation factor-like protein 15
59	A	K1QYT5_CRAGI	Phosphate carrier protein, mitochondrial
60	A	K1QDX9_CRAGI	Ribosome biogenesis protein BMS1-like protein
	A	K1QB61_CRAGI	Protocadherin Fat 4
	A	K1R0D7_CRAGI	Eukaryotic translation initiation factor 3 subunit M (Fragment)

1			
2			
3	A	K1PM76_CRAGI	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial
4	A	K1PRL4_CRAGI	60S ribosomal protein L38 (Fragment)
5	A	K1RW85_CRAGI	Adenosylhomocysteinase
6	A	K1PAY7_CRAGI	Propionyl-CoA carboxylase alpha chain, mitochondrial
7	A	K1PZ08_CRAGI	Ras-related protein Rab-7a
8	A	K1QY12_CRAGI	Dynamin-1-like protein
9	A	K1QFN1_CRAGI	60S ribosomal protein L23
10	A	K1RDW8_CRAGI	Golgi apparatus protein 1
11	A	K1RSS3_CRAGI	Myosin heavy chain, striated muscle
12	A	K1QGK2_CRAGI	Coatomer subunit beta
13	A	K1PV79_CRAGI	Importin subunit alpha
14	A	K1QN79_CRAGI	40S ribosomal protein S11
15	A	K1PV49_CRAGI	RuvB-like helicase
16	A	K1QG65_CRAGI	rRNA 2'-O-methyltransferase fibrillar
17	A	K1PK85_CRAGI	Cullin-associated NEDD8-dissociated protein 1
18	A	K1QVN9_CRAGI	T-complex protein 1 subunit eta
19	A	K1QGB4_CRAGI	40S ribosomal protein S17
20	A	K1QK18_CRAGI	Cytochrome b5
21	A	K1QVW3_CRAGI	Alkylglycerone-phosphate synthase
22	A	K1QN11_CRAGI	Pre-mRNA-processing-splicing factor 8
23	A	K1RJS5_CRAGI	Uncharacterized protein
24	A	K1Q6W5_CRAGI	FACT complex subunit spt16
25	A	K1QQB6_CRAGI	40S ribosomal protein S14
26	A	K1PKF5_CRAGI	Protein-glutamine gamma-glutamyltransferase 4
27	A	K1PH66_CRAGI	Fibrinolytic enzyme, isozyme C
28	A	K1PY89_CRAGI	Extracellular superoxide dismutase [Cu-Zn]
29	A	K1QUK3_CRAGI	Putative ATP-dependent RNA helicase DDX41
30	A	K1R2V1_CRAGI	Importin subunit beta-1
31	A	K1PV86_CRAGI	Phosphoglycerate mutase family member 5
32	A	K1QJ08_CRAGI	60S ribosomal protein L26
33	A	K1QLU6_CRAGI	Poly [ADP-ribose] polymerase
34	A	K1QDN1_CRAGI	Heat shock protein 75 kDa, mitochondrial (Fragment)
35	A	K1QPP2_CRAGI	Elongation factor Tu, mitochondrial
36	A	K1R834_CRAGI	60S ribosomal protein L9
37	A	K1R005_CRAGI	Filamin-C (Fragment)
38	A	K1QET2_CRAGI	Coatomer subunit alpha
39	A	K1RKC1_CRAGI	Far upstream element-binding protein 3
40	A	K1RG19_CRAGI	Protein FAM98A
41	A	K1Q056_CRAGI	Calpain-A
42	A	K1QKJ0_CRAGI	Aldehyde dehydrogenase family 3 member B1
43	A	K1QDZ5_CRAGI	Cytochrome c1, heme protein, mitochondrial
44	A	K1PPP8_CRAGI	Vigilin
45	A	K1RHB2_CRAGI	Nucleolar RNA helicase 2
46	A	K1PH31_CRAGI	Protein arginine N-methyltransferase 1
47	A	K1Q6V6_CRAGI	Replication factor C subunit 4
48	A	K1PI50_CRAGI	40S ribosomal protein S26
49	A	K1PX23_CRAGI	Eukaryotic peptide chain release factor subunit 1
50	A	K1QFZ8_CRAGI	Ceramide kinase-like protein
51	A	K1S2S8_CRAGI	Signal recognition particle 54 kDa protein
52	A	K1R1T8_CRAGI	Nucleolar protein 56
53	A	K1QRZ3_CRAGI	40S ribosomal protein S13
54	A	K1PMP3_CRAGI	Protoporphyrinogen oxidase
55	A	K1P9N7_CRAGI	14-3-3 protein zeta
56	A	K1Q0R4_CRAGI	ATP-binding cassette sub-family F member 2
57	A	K1QWC3_CRAGI	40S ribosomal protein S3
58	A	K1Q812_CRAGI	NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial
59	A	K1P5V7_CRAGI	Eukaryotic translation initiation factor 3 subunit C
60	A	K1R2N0_CRAGI	Histone H4
	A	K1QLK8_CRAGI	GTP-binding protein SAR1b
	A	K1QHX2_CRAGI	La-related protein 7

1			
2			
3	A	K1S6V7_CRAGI	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform
4	A	K1Q3W9_CRAGI	FAS-associated factor 2-B
5	A	K1QG72_CRAGI	Hemagglutinin/amebocyte aggregation factor
6	A	K1QHQ6_CRAGI	Acyl-CoA dehydrogenase family member 9, mitochondrial
7	A	K1QFR2_CRAGI	Calnexin
8	A	K1S1X3_CRAGI	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5
9	A	K1PWZ3_CRAGI	Guanine nucleotide-binding protein subunit beta
10	A	K1QW41_CRAGI	Leucine-zipper-like transcriptional regulator 1
11	A	K1RK68_CRAGI	Uncharacterized protein
12	A	K1RA95_CRAGI	Filamin-A
13	A	K1QMV5_CRAGI	Annexin
14	A	K1QW72_CRAGI	Catalase
15	A	K1QXQ8_CRAGI	DNA helicase
16	A	K1P7L5_CRAGI	Transmembrane 9 superfamily member
17	A	K1P8G1_CRAGI	Heterogeneous nuclear ribonucleoprotein H
18	A	K1PZ23_CRAGI	DnaJ-like protein subfamily C member 3
19	A	K1RIZ3_CRAGI	Bone morphogenetic protein 7
20	A	K1RNN9_CRAGI	Cytoskeleton-associated protein 5
21	A	K1R6L5_CRAGI	NADH-cytochrome b5 reductase
22	A	K1R5F2_CRAGI	14-3-3 protein epsilon
23	A	K1P9D0_CRAGI	Stress-70 protein, mitochondrial
24	A	K1RGJ7_CRAGI	Neogenin
25	A	K1PZP6_CRAGI	Coatmer subunit gamma
26	A	K1RJ97_CRAGI	Multifunctional protein ADE2
27	A	K1R6F5_CRAGI	Putative ATP-dependent RNA helicase DDX23
28	A	K1PS84_CRAGI	Alpha-crystallin B chain
29	A	K1P9S7_CRAGI	Brix domain-containing protein 2
30	A	K1PI40_CRAGI	Uncharacterized protein
31	A	K1QAI2_CRAGI	Ufm1-specific protease 2
32	A	K1REP0_CRAGI	Uncharacterized protein
33	A	K1QJM1_CRAGI	60S ribosomal protein L30
34	A	K1S3G2_CRAGI	HMGB1
35	A	K1PXD4_CRAGI	Putative ATP-dependent RNA helicase DDX6
36	A	K1RJJ7_CRAGI	Histone H5
37	A	K1Q3W3_CRAGI	NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial
38	A	K1RJW8_CRAGI	Protein DEK
39	A	K1RN97_CRAGI	Hemagglutinin/amebocyte aggregation factor
40	A	K1QW36_CRAGI	60S ribosomal protein L6
41	A	K1RA63_CRAGI	Transmembrane protein 2
42	A	K1R9T2_CRAGI	Eukaryotic translation initiation factor 3 subunit B
43	A	K1PM66_CRAGI	60S ribosomal protein L12
44	A	K1Q273_CRAGI	60S ribosomal protein L14
45	A	K1PXG6_CRAGI	Serine/threonine-protein phosphatase
46	A	K1QPC6_CRAGI	Nucleolar complex protein 2-like protein
47	A	K1RCW3_CRAGI	Elongation factor 1-beta
48	A	K1Q324_CRAGI	Heterogeneous nuclear ribonucleoprotein K
49	A	K1PLA7_CRAGI	Eukaryotic initiation factor 4A-II (Fragment)
50	A	K1RBI9_CRAGI	Small nuclear ribonucleoprotein Sm D2
51	A	K1RCL2_CRAGI	Mitochondrial import inner membrane translocase subunit Tim13-B
52	A	K1QKV1_CRAGI	Cytochrome b-c1 complex subunit 6
53	A	K1QVU0_CRAGI	Synaptojanin-2-binding protein
54	A	K1QRG9_CRAGI	Uncharacterized protein
55	A	K1PZ70_CRAGI	NADH dehydrogenase [ubiquinone] iron-sulfur protein 6, mitochondrial
56	A	K1Q350_CRAGI	Glyceraldehyde-3-phosphate dehydrogenase
57	A	K1PXU6_CRAGI	60S ribosomal protein L24
58	A	K1QZQ8_CRAGI	Low-density lipoprotein receptor-related protein 8
59	A	K1RUM2_CRAGI	Uncharacterized protein
60	A	K1REY2_CRAGI	Dysferlin
	A	K1Q6X5_CRAGI	Protein disulfide-isomerase
	A	K1QWK6_CRAGI	Metalloendopeptidase

1			
2			
3	A	K1QDH9_CRAGI	Myosin-11
4	A	K1QQR1_CRAGI	Major vault protein
5	A	K1RAH2_CRAGI	Superoxide dismutase [Cu-Zn]
6	A	K1PH13_CRAGI	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3B
7	A	K1PY73_CRAGI	Basic leucine zipper and W2 domain-containing protein 1
8	A	K1Q7T5_CRAGI	Protein disulfide-isomerase
9	A	K1PFS5_CRAGI	Elongation factor 1-gamma
10	A	K1PW39_CRAGI	Glycerol-3-phosphate dehydrogenase, mitochondrial
11	A	K1R1C5_CRAGI	Signal recognition particle receptor subunit beta
12	A	K1Q1F4_CRAGI	60S ribosomal protein L3 (Fragment)
13	A	K1QNS4_CRAGI	DnaJ-like protein subfamily C member 9
14	A	K1QY85_CRAGI	Transport protein Sec31A
15	A	K1QWP1_CRAGI	Nucleoporin seh1
16	A	K1RAU3_CRAGI	DNA ligase
17	A	K1R5W3_CRAGI	Uncharacterized protein
18	A	K1QF31_CRAGI	Serine/threonine-protein kinase PLK
19	A	K1Q667_CRAGI	tRNA-splicing ligase RtcB homolog
20	A	K1QRM1_CRAGI	Nuclear pore protein
21	A	K1R790_CRAGI	Retinol dehydrogenase 13
22	A	K1R0M2_CRAGI	Uncharacterized protein
23	A	K1QNT7_CRAGI	Aldehyde dehydrogenase, mitochondrial
24	A	K1QIV3_CRAGI	Uncharacterized protein
25	A	K1QR48_CRAGI	Calcium-binding mitochondrial carrier protein SCaMC-2
26	A	K1R4F7_CRAGI	Ras-related protein Rab-6B
27	A	K1PIC5_CRAGI	Transmembrane protein 85
28	A	K1RKZ5_CRAGI	DNA damage-binding protein 1
29	A	K1QW21_CRAGI	39S ribosomal protein L40, mitochondrial
30	A	K1PB87_CRAGI	Uncharacterized protein
31	A	K1R150_CRAGI	Ras-related protein Rab-1A
32	A	K1PVZ3_CRAGI	Cold shock domain-containing protein E1
33	A	K1QSD9_CRAGI	Uncharacterized protein
34	A	K1PPW8_CRAGI	Coatomer subunit beta
35	A	K1QKG9_CRAGI	Cysteine desulfurase, mitochondrial
36	A	K1RK83_CRAGI	Tyrosine-protein kinase BAZ1B
37	A	K1QE94_CRAGI	Alpha-galactosidase
38	A	K1RIJ1_CRAGI	Synaptobrevin (Fragment)
39	A	K1PJB0_CRAGI	Heat shock protein 70 B2
40	A	K1R6S5_CRAGI	40S ribosomal protein S9
41	A	K1PAM6_CRAGI	Uncharacterized protein
42	A	K1QY71_CRAGI	Histone H2B
43	A	K1P6Y1_CRAGI	Uncharacterized protein
44	A	K1PNY5_CRAGI	Splicing factor, proline-and glutamine-rich
45	A	K1PDL3_CRAGI	Ribosomal protein L19
46	A	K1RDG4_CRAGI	DNA helicase
47	A	K1RV41_CRAGI	Guanine nucleotide-binding protein subunit beta-2-like 1
48	A	K1QMH5_CRAGI	Small nuclear ribonucleoprotein Sm D1
49	A	K1R4Z3_CRAGI	Malate dehydrogenase, mitochondrial
50	A	K1R3T3_CRAGI	Transcription factor BTF3
51	A	K1QAB1_CRAGI	AP-2 complex subunit alpha
52	A	K1QSU3_CRAGI	Protein I(2)37Cc
53	A	K1PEY4_CRAGI	26S proteasome non-ATPase regulatory subunit 2
54	A	K1PU46_CRAGI	Lethal(2) giant larvae-like protein 1
55	A	K1Q0N6_CRAGI	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3A
56	A	K1QGP1_CRAGI	Replication factor C subunit 2
57	A	K1QDV6_CRAGI	Protein argonaute-2
58	A	K1S6H7_CRAGI	Vacuolar protein sorting-associated protein 13C
59	A	K1PF10_CRAGI	PAN2-PAN3 deadenylation complex catalytic subunit PAN2
60	A	K1Q1L4_CRAGI	Uncharacterized protein
	A	K1PWC3_CRAGI	Tetratricopeptide repeat protein 35
	A	K1QKL8_CRAGI	V-type proton ATPase subunit a

1			
2			
3	A	K1QT61_CRAGI	NADH dehydrogenase [ubiquinone] flavoprotein 2, mitochondrial (Fragment)
4	A	K1Q7G8_CRAGI	Fatty acid synthase
5	A	K1QX44_CRAGI	Ras-related protein Rab-11B
6	A	K1P7K8_CRAGI	Vesicle-fusing ATPase 1
7	A	K1QHK9_CRAGI	Dynein heavy chain, cytoplasmic
8	A	K1Q7Q2_CRAGI	CCAAT/enhancer-binding protein zeta
9	A	K1Q880_CRAGI	Transportin-1
10	A	K1Q253_CRAGI	Neutral and basic amino acid transport protein rBAT
11	A	K1QGA7_CRAGI	Kynurenine formamidase
12	A	K1QAL3_CRAGI	RNA-binding protein 28
13	A	K1PXS8_CRAGI	Calreticulin
14	A	K1QTP6_CRAGI	Cation-transporting ATPase
15	A	K1PR25_CRAGI	Regulator of differentiation 1
16	A	K1PA61_CRAGI	Actin-like protein 6A
17	A	K1QAA8_CRAGI	CAAX prenyl protease 1-like protein
18	A	K1PY30_CRAGI	Septin-2
19	A	K1R100_CRAGI	Metaxin-2
20	A	K1PTL4_CRAGI	Odr-4-like protein
21	A	K1QA50_CRAGI	V-type proton ATPase subunit H
22	A	K1PVH5_CRAGI	Centromere/kinetochore protein zw10-like protein
23	A	K1PUQ5_CRAGI	Histone H2B
24	A	K1RFB1_CRAGI	Stomatin-like protein 2 (Fragment)
25	A	K1QAA2_CRAGI	Uncharacterized protein
26	A	K1PNC7_CRAGI	AFG3-like protein 2
27	A	K1PJS7_CRAGI	Poly [ADP-ribose] polymerase
28	A	K1PLF9_CRAGI	Arginine kinase
29	A	K1RC37_CRAGI	Uncharacterized protein
30	A	K1PKD4_CRAGI	40S ribosomal protein S30
31	A	K1RDS1_CRAGI	Splicing factor, arginine/serine-rich 2
32	A	K1Q5Z1_CRAGI	Uncharacterized protein
33	A	K1PF96_CRAGI	Spliceosome RNA helicase BAT1
34	A	K1QTW6_CRAGI	Eukaryotic translation initiation factor 3 subunit F
35	A	K1RAU8_CRAGI	Eukaryotic translation initiation factor 3 subunit E
36	A	K1RAI3_CRAGI	Annexin
37	A	K1PUX5_CRAGI	Casein kinase II subunit alpha
38	A	K1PDF8_CRAGI	Splicing factor, arginine/serine-rich 6
39	A	K1QXH3_CRAGI	Translational activator GCN1
40	A	K1PQE3_CRAGI	RNA-binding protein Raly
41	A	K1QWE5_CRAGI	Ras-related protein Rab-18-B
42	A	K1R5G4_CRAGI	60S ribosomal protein L31
43	A	K1RCT2_CRAGI	Translocon-associated protein subunit delta
44	A	K1RFU6_CRAGI	Proteasome activator complex subunit 3
45	A	K1ROW0_CRAGI	Ferritin
46	A	K1Q5Z6_CRAGI	Eukaryotic translation initiation factor 2 subunit 2
47	A	K1RKE5_CRAGI	IQ and AAA domain-containing protein 1
48	A	K1P8G6_CRAGI	Vesicular integral-membrane protein VIP36
49	A	K1P3Q5_CRAGI	Programmed cell death 6-interacting protein
50	A	K1Q615_CRAGI	Peroxiredoxin-1
51	A	K1RG04_CRAGI	ALK tyrosine kinase receptor
52	A	K1QQK5_CRAGI	Metabotropic glutamate receptor 2
53	A	K1R3G0_CRAGI	Transformer-2-like protein beta
54	A	K1QCB0_CRAGI	40S ribosomal protein S5
55	A	K1REQ4_CRAGI	Cytochrome c oxidase subunit 6B
56	A	K1QHI2_CRAGI	Heterogeneous nuclear ribonucleoprotein L
57	A	K1PSH2_CRAGI	28S ribosomal protein S12, mitochondrial
58	A	K1R9P5_CRAGI	Mitochondrial import receptor subunit TOM70
59	A	K1PGK7_CRAGI	Uncharacterized protein
60	A	K1QPF0_CRAGI	Uncharacterized protein
	A	K1QT00_CRAGI	ATP synthase subunit alpha, mitochondrial
	A	K1RG28_CRAGI	Kinase C and casein kinase substrate in neurons protein 2

1			
2			
3	A	K1PMY9_CRAGI	Calmodulin
4	A	K1R1Q8_CRAGI	Ras-related protein Rab-5C
5	A	K1RPP1_CRAGI	Synaptophysin
6	A	K1RFU8_CRAGI	High mobility group protein DSP1
7	A	K1PJ85_CRAGI	26S protease regulatory subunit 6A
8	A	K1R2G9_CRAGI	SEC13-like protein
9			
10	A	K1QJW6_CRAGI	Translocon-associated protein subunit gamma
11	A	K1R5B9_CRAGI	DNA-directed RNA polymerase, mitochondrial
12	A	K1R8C6_CRAGI	40S ribosomal protein S12
13	A	K1QSR2_CRAGI	Apoptosis inhibitor 5
14	A	K1Q5E0_CRAGI	Dual specificity protein kinase CLK2
15	A	K1QBM3_CRAGI	Ras-related protein Rab-2
16	A	K1Q8K9_CRAGI	KRR1 small subunit processome component-like protein
17	A	K1QNU0_CRAGI	Non-specific serine/threonine protein kinase
18	A	K1RDM2_CRAGI	60S ribosomal protein L18a
19	A	K1RD12_CRAGI	Uncharacterized protein
20	A	K1QGP7_CRAGI	Uncharacterized protein
21	A	K1PBL2_CRAGI	Eukaryotic initiation factor 4A-III
22	A	K1QAT9_CRAGI	ATP-dependent RNA helicase DDX1
23	A	K1QWJ4_CRAGI	Splicing factor 3B subunit 5
24	A	K1Q412_CRAGI	Uncharacterized protein
25	A	K1R8R6_CRAGI	Fructose-bisphosphate aldolase
26	A	K1RWP3_CRAGI	Peptidyl-tRNA hydrolase 2, mitochondrial
27	A	K1PGN0_CRAGI	Fatty-acid amide hydrolase 2
28	A	K1PUV4_CRAGI	40S ribosomal protein S24
29	A	K1PJY2_CRAGI	Inositol polyphosphate 1-phosphatase
30	A	K1QWZ8_CRAGI	Catenin beta
31	A	K1R1F0_CRAGI	ATP-dependent DNA helicase 2 subunit 1
32	A	K1PN47_CRAGI	Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial
33	A	K1QYQ9_CRAGI	Uncharacterized protein
34	A	K1PNZ8_CRAGI	Ribosomal protein L37
35	A	K1PVD7_CRAGI	Cytochrome c oxidase subunit 5A, mitochondrial
36	A	K1QEJ0_CRAGI	Ras GTPase-activating protein-binding protein 2
37	A	K1PYL5_CRAGI	Uncharacterized protein
38	A	K1QQQ5_CRAGI	Replication factor C subunit 5
39	A	K1RFA3_CRAGI	Lamin Dm0
40	A	K1RRH1_CRAGI	Chromodomain-helicase-DNA-binding protein Mi-2-like protein
41	A	K1Q2Y1_CRAGI	40S ribosomal protein S15
42	A	K1RIZ9_CRAGI	Band 4.1-like protein 5
43	A	K1QVI0_CRAGI	Isocitrate dehydrogenase [NAD] subunit, mitochondrial
44	A	K1PS77_CRAGI	Prostaglandin G/H synthase 1
45	A	K1QZK9_CRAGI	Uncharacterized protein
46	A	K1R9V5_CRAGI	Tetraspanin
47	A	K1PPV1_CRAGI	Atlastin-2
48	A	K1R0Z4_CRAGI	Uncharacterized protein
49	A	K1R1R9_CRAGI	Pre-mRNA-processing factor 6
50	A	K1QKU6_CRAGI	mRNA export factor
51	A	K1PCR5_CRAGI	KH domain-containing, RNA-binding, signal transduction-associated protein 2
52	A	K1R7L4_CRAGI	Neural cell adhesion molecule 1
53	A	K1QAL1_CRAGI	Transmembrane emp24 domain-containing protein 7
54	A	K1QB65_CRAGI	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1
55	A	K1QVP6_CRAGI	Developmentally-regulated GTP-binding protein 1
56	A	K1QNT4_CRAGI	Anoctamin
57	A	K1QMT1_CRAGI	DnaJ-like protein subfamily B member 4
58	A	K1RCF4_CRAGI	Translocon-associated protein subunit alpha
59	A	K1QJL6_CRAGI	Microtubule-associated protein RP/EB family member 3
60	A	K1QPY8_CRAGI	Extracellular superoxide dismutase [Cu-Zn]
	A	K1R5V4_CRAGI	GTP-binding nuclear protein
	A	K1RNU5_CRAGI	Pre-mRNA-splicing factor RBM22
	A	K1QK68_CRAGI	Myosin-2 essential light chain

1			
2			
3	A	K1QED7_CRAGI	Replication protein A subunit
4	A	K1QPS1_CRAGI	Poly [ADP-ribose] polymerase
5	A	K1PD36_CRAGI	Ubiquitin
6	A	K1R4B8_CRAGI	Plexin domain-containing protein 2
7	A	K1RHP3_CRAGI	Proliferation-associated protein 2G4
8	A	K1QE43_CRAGI	Uncharacterized protein
9	A	K1R3I6_CRAGI	Nucleolar complex protein 2-like protein (Fragment)
10	A	K1QMJ8_CRAGI	Transcription initiation factor IIA subunit 1
11	A	K1QXF5_CRAGI	Calcyphosin-like protein
12	A	K1R512_CRAGI	Uncharacterized protein
13	A	K1QM06_CRAGI	Prohibitin
14	A	K1R275_CRAGI	Putative ATP-dependent RNA helicase DDX52
15	A	K1QSB2_CRAGI	26S protease regulatory subunit 6B
16	A	K1QBW6_CRAGI	Tudor domain-containing protein 1
17	A	K1PZT2_CRAGI	Cytochrome c oxidase subunit 5B, mitochondrial
18	A	K1QIZ7_CRAGI	Programmed cell death protein 6
19	A	K1QDA7_CRAGI	Uracil phosphoribosyltransferase
20	A	K1R401_CRAGI	Spectrin alpha chain
21	A	K1P541_CRAGI	Alpha-soluble NSF attachment protein
22	A	K1PND7_CRAGI	Fatty acid synthase
23	A	K1R8L1_CRAGI	Exportin-2
24	A	K1QEF9_CRAGI	Protein-glutamine gamma-glutamyltransferase K
25	A	K1Q2W7_CRAGI	Uncharacterized protein
26	A	K1RYM7_CRAGI	LAG1 longevity assurance-like protein 6
27	A	K1PY09_CRAGI	Uncharacterized protein
28	A	K1Q105_CRAGI	Ferrochelatase
29	A	K1PD30_CRAGI	Putative histone-binding protein Caf1
30	A	K1QDB9_CRAGI	Transport protein Sec61 subunit alpha isoform 2 (Fragment)
31	A	K1QTW3_CRAGI	Murinoglobulin-2
32	A	K1PVG9_CRAGI	Malectin
33	A	K1Q3V9_CRAGI	Mitochondrial carnitine/acylcarnitine carrier protein
34	A	K1QVS0_CRAGI	Ras-like GTP-binding protein Rho1
35	A	K1PX68_CRAGI	Tyrosine-protein phosphatase non-receptor type 6
36	A	K1RPF7_CRAGI	60S ribosomal protein L5
37	A	K1QZ64_CRAGI	Nuclear pore complex protein Nup98-Nup96
38	A	K1QSV1_CRAGI	Uncharacterized protein
39	A	K1Q2L4_CRAGI	Transmembrane emp24 domain-containing protein 9
40	A	K1RMM6_CRAGI	Centromere protein J
41	A	K1QKK2_CRAGI	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 11, mitochondrial
42	A	K1PNV6_CRAGI	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit DAD1
43	A	K1PNQ1_CRAGI	Ankyrin repeat domain-containing protein 5
44	A	K1QKQ8_CRAGI	THO complex subunit 4-A
45	A	K1QAG9_CRAGI	Ferritin
46	A	K1QHW8_CRAGI	Ferritin
47	A	K1RFV5_CRAGI	ATP-dependent RNA helicase DDX1
48	A	K1RNH1_CRAGI	60S ribosomal protein L18 (Fragment)
49	A	K1PPQ1_CRAGI	14-3-3 protein gamma
50	A	K1QQV0_CRAGI	Histone H1.2
51	A	K1Q1R1_CRAGI	Exostosin-3
52	A	K1QYF5_CRAGI	Apoptosis-inducing factor 1, mitochondrial
53	A	K1RZE2_CRAGI	Isocitrate dehydrogenase [NADP]
54	A	K1QL00_CRAGI	Microsomal glutathione S-transferase 1
55	A	K1QTV1_CRAGI	Uncharacterized protein
56	A	K1RZM3_CRAGI	Cartilage acidic protein 1
57	A	K1Q0I8_CRAGI	Putative splicing factor, arginine/serine-rich 7
58	A	K1RP91_CRAGI	Putative RNA exonuclease NEF-sp
59	A	K1PG60_CRAGI	60S ribosomal protein L17
60	A	K1QTP4_CRAGI	5'-3' exoribonuclease
	A	K1RG79_CRAGI	Neuronal acetylcholine receptor subunit alpha-6
	A	K1Q947_CRAGI	Dynein light chain

1			
2			
3	A	K1RJ91_CRAGI	Ubiquitin-associated protein 2
4	A	K1Q2Z5_CRAGI	Putative ATP-dependent RNA helicase DDX46
5	A	K1PYA0_CRAGI	Cytoplasmic dynein 2 heavy chain 1
6	A	K1QAV0_CRAGI	Guanine nucleotide-binding protein G(Q) subunit alpha
7	A	K1RKR8_CRAGI	Pumilio-like protein 2
8	A	K1QZI3_CRAGI	Myosin-le
9	A	K1R5R4_CRAGI	Dynein heavy chain 10, axonemal
10	A	K1QKG8_CRAGI	Upstream activation factor subunit spp27
11	A	K1P8I1_CRAGI	Pleckstrin-like protein domain-containing family F member 2 (Fragment)
12	A	K1Q1N1_CRAGI	Alpha-mannosidase
13	A	K1PXB6_CRAGI	Cadherin-23
14	A	K1QXA9_CRAGI	Sortilin-related receptor
15	A	K1PVG0_CRAGI	Long-chain fatty acid transport protein 4
16	A	K1PBG6_CRAGI	Uncharacterized protein
17	A	K1PP50_CRAGI	Golgi integral membrane protein 4
18	A	K1QCQ5_CRAGI	Succinate--CoA ligase [ADP-forming] subunit beta, mitochondrial
19	A	K1PK87_CRAGI	Putative E3 ubiquitin-protein ligase TRIP12
20	A	K1Q373_CRAGI	Splicing factor, arginine/serine-rich 7
21	A	K1Q151_CRAGI	60S ribosomal protein L32
22	A	K1QZ95_CRAGI	Nuclear pore complex protein
23	A	K1PPH0_CRAGI	Gamma-tubulin complex component
24	A	K1R0R7_CRAGI	Putative ATP-dependent RNA helicase DHX36
25	A	K1R247_CRAGI	Condensin complex subunit 1
26	A	K1QIB2_CRAGI	Mitogen-activated protein kinase
27	A	K1QG61_CRAGI	Acetolactate synthase-like protein
28	A	K1RBC9_CRAGI	Transketolase-like protein 2
29	A	K1RCW5_CRAGI	Eukaryotic translation initiation factor 4 gamma 3
30	A	K1PQZ3_CRAGI	Armadillo repeat-containing protein 4
31	A	K1PYJ8_CRAGI	Uncharacterized protein
32	A	K1QQP1_CRAGI	Programmed cell death protein 4
33	A	K1PQY0_CRAGI	Protein quiver
34	A	K1PLC6_CRAGI	Nucleolar protein 14
35	A	K1QV25_CRAGI	Transcription elongation factor B polypeptide 2
36	A	K1QZ50_CRAGI	RNA-dependent RNA polymerase
37	A	K1QXH7_CRAGI	DNA replication licensing factor mcm4-B
38	A	K1PDE4_CRAGI	Protein arginine N-methyltransferase
39	A	K1QT36_CRAGI	Golgi resident protein GCP60
40	A	K1PZ89_CRAGI	Mannosyl-oligosaccharide glucosidase
41	A	K1Q7A7_CRAGI	Putative tyrosinase-like protein tyr-3
42	A	K1R481_CRAGI	Epimerase family protein SDR39U1
43	A	K1RJ35_CRAGI	All-trans-retinol 13,14-reductase
44	A	Q70MT4_CRAGI	40S ribosomal protein S10
45	A	K1REV3_CRAGI	DNA polymerase delta subunit 2
46	A	K1P9F1_CRAGI	Insulin-like growth factor-binding protein complex acid labile chain
47	A	K1PJ65_CRAGI	Dual specificity mitogen-activated protein kinase kinase 7
48	A	K1Q2T0_CRAGI	ADP-dependent glucokinase
49	A	K1PZI3_CRAGI	SWI/SNF complex subunit SMARCC2
50	A	K1Q8C5_CRAGI	Putative ATP-dependent RNA helicase DDX47
51	A	K1QZ58_CRAGI	Splicing factor U2AF 26 kDa subunit
52	A	K1RR98_CRAGI	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 4-like 2
53	A	K1QMT2_CRAGI	Signal peptidase complex catalytic subunit SEC11
54	A	K1PWM3_CRAGI	MICOS complex subunit MIC13
55	A	K1QMM4_CRAGI	Leucine zipper transcription factor-like protein 1
56	A	K1QMV7_CRAGI	V-type proton ATPase subunit D
57	A	K1QKI1_CRAGI	Tudor domain-containing protein 1
58	A	K1P0H0_CRAGI	Aspartyl/asparaginyl beta-hydroxylase
59	A	K1PVQ8_CRAGI	Eukaryotic translation initiation factor 3 subunit K
60	A	K1Q5P0_CRAGI	60S ribosomal protein L17
	A	K1QJ36_CRAGI	Muscle, skeletal receptor tyrosine protein kinase
	A	K1PHS4_CRAGI	Ribosome-binding protein 1

1			
2			
3	A	K1QQB4_CRAGI	Long-chain-fatty-acid--CoA ligase 1
4	A	K1QYM4_CRAGI	D-beta-hydroxybutyrate dehydrogenase, mitochondrial
5	A	K1P2G0_CRAGI	Strawberry notch-like protein 1
6	A	K1QCT0_CRAGI	Sideroflexin
7	A	K1QFG2_CRAGI	Telomere-associated protein RIF1
8	A	K1Q5J7_CRAGI	Uncharacterized protein
9	A	K1QKA9_CRAGI	Piwi-like protein 2
10	A	K1P7Q6_CRAGI	40S ribosomal protein S19
11	A	K1QYV5_CRAGI	Cytoplasmic polyadenylation element-binding protein 1-B
12	A	K1QG84_CRAGI	THO complex subunit 2
13	A	K1R7G0_CRAGI	Chromobox-like protein 5
14	A	K1QHX4_CRAGI	Uncharacterized protein
15	A	K1QBY6_CRAGI	Transmembrane protein Tmp21
16	A	K1PKK7_CRAGI	AP-2 complex subunit mu-1
17	A	K1P9V5_CRAGI	General transcription factor IIF subunit 1
18	A	K1Q9V2_CRAGI	Antigen KI-67
19	A	K1PNU2_CRAGI	Histone-arginine methyltransferase CARM1
20	A	K1Q109_CRAGI	Neurexin-4
21	A	K1P9Q2_CRAGI	Signal peptidase complex subunit 3
22	A	K1QCN0_CRAGI	Signal recognition particle 9 kDa protein
23	A	K1Q7E4_CRAGI	Ubiquitin-conjugating enzyme E2 N
24	A	K1Q5G6_CRAGI	60 kDa heat shock protein, mitochondrial
25	A	K1RUW0_CRAGI	E3 SUMO-protein ligase RanBP2
26	A	K1RB91_CRAGI	Neutral alpha-glucosidase AB
27	A	K1QGF1_CRAGI	Splicing factor 3B subunit 2
28	A	K1Q525_CRAGI	Mechanosensory protein 2 (Fragment)
29	A	K1RDB3_CRAGI	F-box/WD repeat-containing protein 1A
30	A	K1QI28_CRAGI	V-type proton ATPase subunit B
31	A	K1R4J0_CRAGI	MAGUK p55 subfamily member 2
32	A	K1Q9T7_CRAGI	Afadin-and alpha-actinin-binding protein
33	A	K1RNH6_CRAGI	Toll-like receptor 3
34	A	K1PZC0_CRAGI	Structural maintenance of chromosomes protein
35	A	K1PT69_CRAGI	Uncharacterized protein
36	A	K1RE67_CRAGI	Methylated-DNA--protein-cysteine methyltransferase
37	A	K1QCX5_CRAGI	Cyclic AMP-dependent transcription factor ATF-2
38	A	K1QBT8_CRAGI	Uncharacterized protein
39	A	K1RFF1_CRAGI	Uncharacterized protein
40	A	K1RS40_CRAGI	Uncharacterized protein
41	A	K1R8V1_CRAGI	Puratrophin-1
42			
43			
44			
45			
46			
47			
48			
49			
50			
51			
52			
53			
54			
55			
56			
57			
58			
59			
60			

1
2
3 **Data S2:** Identified proteins by RNA pull down coupled with mass spectrometry with m6A or A-oligo, in nuclear or cytosolic protein extracts

4 Proteins identified in cytosolic extracts

5	Oligo	Accession	Description
6	m6A	K1QNA2_CRAGI	Vitellogenin-6
7	m6A	K1QVJ8_CRAGI	Piwi-like protein 1
8	m6A	K1QQ94_CRAGI	Uncharacterized protein
10	m6A	K1QHK9_CRAGI	Dynein heavy chain, cytoplasmic
11	m6A	K1QQ68_CRAGI	Tubulin alpha chain
12	m6A	K1RLF8_CRAGI	Splicing factor 3B subunit 3
13	m6A	K1R473_CRAGI	Tubulin alpha chain
14	m6A	K1QII6_CRAGI	Tubulin alpha chain
15	m6A	K1PNR3_CRAGI	Clathrin heavy chain
17	m6A	K1R7V7_CRAGI	Tubulin beta chain
18	m6A	K1PNI6_CRAGI	Heterogeneous nuclear ribonucleoprotein A/B
19	m6A	K1QMX5_CRAGI	Uncharacterized protein
20	m6A	K1QHI5_CRAGI	Pyruvate carboxylase, mitochondrial
21	m6A	K1PE00_CRAGI	Tubulin alpha chain
22	m6A	K1R294_CRAGI	T-complex protein 1 subunit beta
23	m6A	K1S4Q2_CRAGI	T-complex protein 1 subunit delta (Fragment)
24	m6A	K1PQP2_CRAGI	Nucleolin
25	m6A	K1R466_CRAGI	T-complex protein 1 subunit gamma
26	m6A	K1PN21_CRAGI	Tubulin beta chain
27	m6A	K1R164_CRAGI	Galectin-4
28	m6A	K1S2N7_CRAGI	Innexin
29	m6A	K1R6Z7_CRAGI	ATP synthase subunit alpha
30	m6A	K1R5B4_CRAGI	Proteasome activator complex subunit 4
31	m6A	K1PVA1_CRAGI	Transitional endoplasmic reticulum ATPase
32	m6A	K1QFW9_CRAGI	Uncharacterized protein
33	m6A	K1R0S3_CRAGI	T-complex protein 1 subunit theta
34	m6A	K1QMA4_CRAGI	RRP5-like protein
35	m6A	K1R3U2_CRAGI	Uncharacterized protein
36	m6A	K1Q9W5_CRAGI	T-complex protein 1 subunit eta
37	m6A	K1QBK6_CRAGI	Splicing factor 3B subunit 1
38	m6A	K1R545_CRAGI	Pre-mRNA-processing-splicing factor 8 (Fragment)
39	m6A	K1RAJ1_CRAGI	T-complex protein 1 subunit alpha
40	m6A	K1RWS2_CRAGI	Transcriptional activator protein Pur-alpha
41	m6A	K1Q350_CRAGI	Glyceraldehyde-3-phosphate dehydrogenase
42	m6A	K1RGT5_CRAGI	Metalloendopeptidase
43	m6A	K1PJ85_CRAGI	26S protease regulatory subunit 6A
44	m6A	K1S6V7_CRAGI	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform
45	m6A	K1S1S1_CRAGI	Insulin-like growth factor 2 mRNA-binding protein 1
46	m6A	K1RZE2_CRAGI	Isocitrate dehydrogenase [NADP]
47	m6A	K1PNQ5_CRAGI	Heat shock protein HSP 90-alpha 1
48	m6A	K1R866_CRAGI	Puromycin-sensitive aminopeptidase
49	m6A	K1P9D0_CRAGI	Stress-70 protein, mitochondrial
50	m6A	K1QXX7_CRAGI	Myosin heavy chain, non-muscle (Fragment)
51	m6A	K1RG73_CRAGI	Acetyl-CoA carboxylase
52	m6A	K1R420_CRAGI	Non-specific serine/threonine protein kinase
53	m6A	K1PXN5_CRAGI	T-complex protein 1 subunit zeta
54	m6A	K1QGS8_CRAGI	Elongation factor 1-alpha
55	m6A	K1RLC5_CRAGI	T-complex protein 1 subunit epsilon
56	m6A	K1R6Q7_CRAGI	DNA topoisomerase I
57	m6A	K1RW85_CRAGI	Adenosylhomocysteinase
58	m6A	K1QSX8_CRAGI	ATPase family AAA domain-containing protein 2B
59	m6A	K1R4Z3_CRAGI	Malate dehydrogenase, mitochondrial
60	m6A	K1PEY4_CRAGI	26S proteasome non-ATPase regulatory subunit 2
	m6A	K1RI55_CRAGI	Insulin-like growth factor 2 mRNA-binding protein 3
	m6A	K1PK85_CRAGI	Cullin-associated NEDD8-dissociated protein 1
	m6A	K1R9B6_CRAGI	H/ACA ribonucleoprotein complex subunit 4
	m6A	K1R252_CRAGI	Putative methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial

1			
2			
3	m6A	K1RK12_CRAGI	40S ribosomal protein S23
4	m6A	K1QVN9_CRAGI	T-complex protein 1 subunit eta
5	m6A	K1PLF9_CRAGI	Arginine kinase
6	m6A	Q8TA69_CRAGI	Actin 2
7	m6A	K1QG58_CRAGI	Actin
8	m6A	K1QSB2_CRAGI	26S protease regulatory subunit 6B
9	m6A	K1R401_CRAGI	Spectrin alpha chain
10	m6A	K1Q112_CRAGI	26S protease regulatory subunit 7
11	m6A	K1Q419_CRAGI	D-3-phosphoglycerate dehydrogenase (Fragment)
12	m6A	K1R401_CRAGI	Spectrin alpha chain
13	m6A	K1R401_CRAGI	Spectrin alpha chain
14	m6A	K1R401_CRAGI	Spectrin alpha chain
15	m6A	K1R401_CRAGI	Spectrin alpha chain
16	m6A	K1R401_CRAGI	Spectrin alpha chain
17	m6A	K1R401_CRAGI	Spectrin alpha chain
18	m6A	K1R401_CRAGI	Spectrin alpha chain
19	m6A	K1R401_CRAGI	Spectrin alpha chain
20	m6A	K1R401_CRAGI	Spectrin alpha chain
21	m6A	K1R401_CRAGI	Spectrin alpha chain
22	m6A	K1R401_CRAGI	Spectrin alpha chain
23	m6A	K1R401_CRAGI	Spectrin alpha chain
24	m6A	K1R401_CRAGI	Spectrin alpha chain
25	m6A	K1R401_CRAGI	Spectrin alpha chain
26	m6A	K1R401_CRAGI	Spectrin alpha chain
27	m6A	K1R401_CRAGI	Spectrin alpha chain
28	m6A	K1R401_CRAGI	Spectrin alpha chain
29	m6A	K1R401_CRAGI	Spectrin alpha chain
30	m6A	K1R401_CRAGI	Spectrin alpha chain
31	m6A	K1R401_CRAGI	Spectrin alpha chain
32	m6A	K1R401_CRAGI	Spectrin alpha chain
33	m6A	K1R401_CRAGI	Spectrin alpha chain
34	m6A	K1R401_CRAGI	Spectrin alpha chain
35	m6A	K1R401_CRAGI	Spectrin alpha chain
36	m6A	K1R401_CRAGI	Spectrin alpha chain
37	m6A	K1R401_CRAGI	Spectrin alpha chain
38	m6A	K1R401_CRAGI	Spectrin alpha chain
39	m6A	K1R401_CRAGI	Spectrin alpha chain
40	m6A	K1R401_CRAGI	Spectrin alpha chain
41	m6A	K1R401_CRAGI	Spectrin alpha chain
42	m6A	K1R401_CRAGI	Spectrin alpha chain
43	m6A	K1R401_CRAGI	Spectrin alpha chain
44	m6A	K1R401_CRAGI	Spectrin alpha chain
45	m6A	K1R401_CRAGI	Spectrin alpha chain
46	m6A	K1R401_CRAGI	Spectrin alpha chain
47	m6A	K1R401_CRAGI	Spectrin alpha chain
48	m6A	K1R401_CRAGI	Spectrin alpha chain
49	m6A	K1R401_CRAGI	Spectrin alpha chain
50	m6A	K1R401_CRAGI	Spectrin alpha chain
51	m6A	K1R401_CRAGI	Spectrin alpha chain
52	m6A	K1R401_CRAGI	Spectrin alpha chain
53	m6A	K1R401_CRAGI	Spectrin alpha chain
54	m6A	K1R401_CRAGI	Spectrin alpha chain
55	m6A	K1R401_CRAGI	Spectrin alpha chain
56	m6A	K1R401_CRAGI	Spectrin alpha chain
57	m6A	K1R401_CRAGI	Spectrin alpha chain
58	m6A	K1R401_CRAGI	Spectrin alpha chain
59	m6A	K1R401_CRAGI	Spectrin alpha chain
60	m6A	K1R401_CRAGI	Spectrin alpha chain
	m6A	K1R2V1_CRAGI	Importin subunit beta-1
	m6A	K1QZW0_CRAGI	Polyadenylate-binding protein 2
	m6A	K1R4R9_CRAGI	Mitotic apparatus protein p62
	m6A	K1QWK2_CRAGI	MAM domain-containing glycosylphosphatidylinositol anchor protein 2
	m6A	K1R2D6_CRAGI	Plastin-3
	m6A	K1QB04_CRAGI	26S proteasome non-ATPase regulatory subunit 3
	m6A	K1RH70_CRAGI	6-phosphogluconate dehydrogenase, decarboxylating
	m6A	K1QGK2_CRAGI	Coatomer subunit beta
	m6A	K1QUE6_CRAGI	26S proteasome non-ATPase regulatory subunit 6
	m6A	K1R7I9_CRAGI	Heterogeneous nuclear ribonucleoprotein Q
	m6A	K1PND7_CRAGI	Fatty acid synthase

1		
2		
3	m6A	K1QI28_CRAGI V-type proton ATPase subunit B
4	m6A	K1Q2H5_CRAGI Uncharacterized protein
5	m6A	K1QLT5_CRAGI 26S protease regulatory subunit 4
6	m6A	K1R4I2_CRAGI 26S proteasome non-ATPase regulatory subunit 3
7	m6A	K1QQR1_CRAGI Major vault protein
8	m6A	K1RAU3_CRAGI DNA ligase
9	m6A	K1PFG1_CRAGI Uncharacterized protein
10	m6A	K1RBC9_CRAGI Transketolase-like protein 2
11	m6A	K1QT21_CRAGI Putative ATP-dependent RNA helicase DDX5
12	m6A	K1PKK7_CRAGI AP-2 complex subunit mu-1
13	m6A	K1Q358_CRAGI 60S acidic ribosomal protein P2
14	m6A	K1PS71_CRAGI Uncharacterized protein
15	m6A	K1QHA2_CRAGI Spectrin beta chain, brain 4
16	m6A	K1REG6_CRAGI DNA helicase
17	m6A	A7M7T7_CRAGI Non-selenium glutathione peroxidase
18	m6A	K1QHX2_CRAGI La-related protein 7
19	m6A	K1RJ97_CRAGI Multifunctional protein ADE2
20	m6A	K1RNZ6_CRAGI Eukaryotic translation initiation factor 3 subunit D
21	m6A	K1PAY7_CRAGI Propionyl-CoA carboxylase alpha chain, mitochondrial
22	m6A	K1QQ27_CRAGI Pancreatic lipase-related protein 2
23	m6A	K1Q9K6_CRAGI Histone H3
24	m6A	K1R083_CRAGI Aspartate aminotransferase, mitochondrial
25	m6A	K1PEP0_CRAGI 40S ribosomal protein S8
26	m6A	K1PU26_CRAGI Malate dehydrogenase (Fragment)
27	m6A	K1QF01_CRAGI 40S ribosomal protein S4
28	m6A	K1QDN1_CRAGI Heat shock protein 75 kDa, mitochondrial (Fragment)
29	m6A	K1QBH0_CRAGI Uncharacterized protein
30	m6A	K1Q9V3_CRAGI V-type proton ATPase catalytic subunit A
31	m6A	K1PJC1_CRAGI Adipophilin
32	m6A	K1Q330_CRAGI Dihydrolipoyl dehydrogenase
33	m6A	K1S3Y1_CRAGI 2-amino-3-ketobutyrate coenzyme A ligase, mitochondrial (Fragment)
34	m6A	K1R2Q9_CRAGI Aspartate aminotransferase
35	m6A	K1QEF2_CRAGI ADP-ribosylation factor-like protein 15
36	m6A	K1PVH5_CRAGI Centromere/kinetochore protein zw10-like protein
37	m6A	K1PG07_CRAGI Lupus La-like protein
38	m6A	K1QMX8_CRAGI DNA replication licensing factor MCM7
39	m6A	K1P7K8_CRAGI Vesicle-fusing ATPase 1
40	m6A	K1QQL6_CRAGI Leucyl-tRNA synthetase, cytoplasmic
41	m6A	K1PY89_CRAGI Extracellular superoxide dismutase [Cu-Zn]
42	m6A	K1QKA9_CRAGI Piwi-like protein 2
43	m6A	K1QHI6_CRAGI Dynein heavy chain 5, axonemal
44	m6A	K1QBF7_CRAGI Hypoxia up-regulated protein 1
45	m6A	K1RTR1_CRAGI ATP-citrate synthase
46	m6A	K1PZF2_CRAGI Exportin-7
47	m6A	K1PPP8_CRAGI Vigilin
48	m6A	K1RN77_CRAGI Nuclear autoantigenic sperm protein
49	m6A	K1PV49_CRAGI RuvB-like helicase
50	m6A	K1QXQ8_CRAGI DNA helicase
51	m6A	K1P2G0_CRAGI Strawberry notch-like protein 1
52	m6A	K1QRQ2_CRAGI Glutamate dehydrogenase 1, mitochondrial
53	m6A	K1QHS8_CRAGI Ribonucleoside-diphosphate reductase
54	m6A	K1QX26_CRAGI Endoplasmin
55	m6A	K1QGB4_CRAGI 40S ribosomal protein S17
56	m6A	K1RJJ7_CRAGI Histone H5
57	m6A	K1QY85_CRAGI Transport protein Sec31A
58	m6A	K1Q6W3_CRAGI Talin-1
59	m6A	K1R3V8_CRAGI COP9 signalosome complex subunit 4
60	m6A	K1QY12_CRAGI Dynamin-1-like protein
	m6A	K1PYA0_CRAGI Cytoplasmic dynein 2 heavy chain 1
	m6A	K1PF10_CRAGI PAN2-PAN3 deadenylation complex catalytic subunit PAN2

1		
2		
3	m6A	K1PNP4_CRAGI 26S proteasome non-ATPase regulatory subunit 11
4	m6A	K1QMB9_CRAGI Eukaryotic translation initiation factor 3 subunit A
5	m6A	K1QC10_CRAGI GTP-binding protein 1
6	m6A	K1QK56_CRAGI Uncharacterized protein
7	m6A	K1PJP9_CRAGI 26S proteasome non-ATPase regulatory subunit 1
8	m6A	K1PUL2_CRAGI Long-chain-fatty-acid--CoA ligase 1
9	m6A	K1Q7Q2_CRAGI CCAAT/enhancer-binding protein zeta
10	m6A	K1Q7Q2_CRAGI CCAAT/enhancer-binding protein zeta
11	m6A	K1QQK1_CRAGI 26S proteasome non-ATPase regulatory subunit 12
12	m6A	K1R3T3_CRAGI Transcription factor BTF3
13	m6A	K1PK93_CRAGI GDP-L-fucose synthetase
14	m6A	K1PF96_CRAGI Spliceosome RNA helicase BAT1
15	m6A	K1PM50_CRAGI 40S ribosomal protein S16
16	m6A	K1PX47_CRAGI Ubiquitin carboxyl-terminal hydrolase
17	m6A	K1PX47_CRAGI Ubiquitin carboxyl-terminal hydrolase
18	m6A	K1QMV7_CRAGI V-type proton ATPase subunit D
19	m6A	K1RAL0_CRAGI Aspartate aminotransferase, cytoplasmic
20	m6A	K1RAL0_CRAGI Aspartate aminotransferase, cytoplasmic
21	m6A	K1P9N7_CRAGI 14-3-3 protein zeta
22	m6A	K1QBR5_CRAGI Uncharacterized protein
23	m6A	K1PVW0_CRAGI S-adenosylmethionine synthase
24	m6A	K1PY73_CRAGI Basic leucine zipper and W2 domain-containing protein 1
25	m6A	K1PY73_CRAGI Basic leucine zipper and W2 domain-containing protein 1
26	m6A	K1QBL6_CRAGI Tudor domain-containing protein 1
27	m6A	K1Q9M7_CRAGI Histone H1-delta
28	m6A	K1S151_CRAGI Rab GDP dissociation inhibitor
29	m6A	K1RM80_CRAGI Citrate synthase
30	m6A	K1R115_CRAGI Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial
31	m6A	K1R115_CRAGI Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial
32	m6A	K1R5D5_CRAGI U3 small nucleolar RNA-associated protein 6-like protein
33	m6A	K1QSR2_CRAGI Apoptosis inhibitor 5
34	m6A	K1P5D4_CRAGI Cysteine synthase
35	m6A	K1PE57_CRAGI Severin
36	m6A	K1P8I1_CRAGI Pleckstrin-like protein domain-containing family F member 2 (Fragment)
37	m6A	K1P8I1_CRAGI Pleckstrin-like protein domain-containing family F member 2 (Fragment)
38	m6A	K1Q5G9_CRAGI SUMO-activating enzyme subunit 2
39	m6A	K1PVZ3_CRAGI Cold shock domain-containing protein E1
40	m6A	K1R4D4_CRAGI 40S ribosomal protein SA
41	m6A	K1QXH3_CRAGI Translational activator GCN1
42	m6A	K1PI02_CRAGI Talin-1
43	m6A	K1PI02_CRAGI Talin-1
44	m6A	K1P3Q5_CRAGI Programmed cell death 6-interacting protein
45	m6A	K1PKF5_CRAGI Protein-glutamine gamma-glutamyltransferase 4
46	m6A	K1QFZ8_CRAGI Ceramide kinase-like protein
47	m6A	K1PJF4_CRAGI Isoleucyl-tRNA synthetase, cytoplasmic
48	m6A	K1PV79_CRAGI Importin subunit alpha
49	m6A	K1QMD3_CRAGI Glycerol-3-phosphate dehydrogenase [NAD(+)]
50	m6A	K1QMD3_CRAGI Glycerol-3-phosphate dehydrogenase [NAD(+)]
51	m6A	K1RDV7_CRAGI Cell division control protein 2-like protein (Fragment)
52	m6A	K1P8W6_CRAGI 60S ribosomal protein L4
53	m6A	K1P112_CRAGI ATP synthase subunit gamma, mitochondrial
54	m6A	K1R5F2_CRAGI 14-3-3 protein epsilon
55	m6A	K1R5F2_CRAGI 14-3-3 protein epsilon
56	m6A	K1QBW8_CRAGI Uncharacterized protein
57	m6A	K1PZP6_CRAGI Coatomer subunit gamma
58	m6A	K1PAR4_CRAGI Unc-45-like protein A
59	m6A	K1QRZ3_CRAGI 40S ribosomal protein S13
60	m6A	K1QQB6_CRAGI 40S ribosomal protein S14
	m6A	K1QE71_CRAGI DNA helicase
	m6A	K1RJM8_CRAGI SAGA-associated factor 11 homolog
	m6A	K1RK33_CRAGI Exportin-1
	m6A	K1PPW8_CRAGI Coatomer subunit beta
	m6A	K1QRK9_CRAGI Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial
	m6A	K1Q273_CRAGI 60S ribosomal protein L14
	m6A	K1PLY1_CRAGI DNA polymerase
	m6A	K1PYR4_CRAGI 26S proteasome non-ATPase regulatory subunit 1
	m6A	K1QPC6_CRAGI Nucleolar complex protein 2-like protein
	m6A	K1QP17_CRAGI Caprin-1
	m6A	K1R2N0_CRAGI Histone H4

1		
2		
3	m6A	K1Q5G6_CRAGI 60 kDa heat shock protein, mitochondrial
4	m6A	K1RIG6_CRAGI LSM14-like protein A
5	m6A	K1QY71_CRAGI Histone H2B
6	m6A	K1QAB1_CRAGI AP-2 complex subunit alpha
7	m6A	K1QAF3_CRAGI Alanine aminotransferase 2
8	m6A	K1QI97_CRAGI Adenylyl cyclase-associated protein
9	m6A	K1PD57_CRAGI Constitutive coactivator of PPAR-gamma-like protein 1-like protein
10	m6A	K1Q0L1_CRAGI 60S ribosomal protein L23a
11	m6A	K1R8C6_CRAGI Epidermal retinal dehydrogenase 2
12	m6A	K1R8C6_CRAGI Epidermal retinal dehydrogenase 2
13	m6A	K1R0Y9_CRAGI ADP,ATP carrier protein
14	m6A	K1R0Y9_CRAGI ADP,ATP carrier protein
15	m6A	K1QXF5_CRAGI Calcyphosin-like protein
16	m6A	K1PA54_CRAGI Replication factor C subunit 3
17	m6A	K1PS27_CRAGI DNA helicase
18	m6A	K1R8C6_CRAGI 40S ribosomal protein S12
19	m6A	K1R8C6_CRAGI 40S ribosomal protein S12
20	m6A	K1Q880_CRAGI Transportin-1
21	m6A	K1PXD4_CRAGI Putative ATP-dependent RNA helicase DDX6
22	m6A	K1P421_CRAGI Histone H2A
23	m6A	K1RL00_CRAGI Proteasome-associated protein ECM29-like protein
24	m6A	K1PI50_CRAGI 40S ribosomal protein S26
25	m6A	K1PI50_CRAGI 40S ribosomal protein S26
26	m6A	K1RCW5_CRAGI Eukaryotic translation initiation factor 4 gamma 3
27	m6A	K1R0W4_CRAGI Signal recognition particle subunit SRP72
28	m6A	K1QN11_CRAGI Pre-mRNA-processing-splicing factor 8
29	m6A	K1R8R6_CRAGI Fructose-bisphosphate aldolase
30	m6A	K1R8R6_CRAGI Fructose-bisphosphate aldolase
31	m6A	K1QVE8_CRAGI Phosphoacetylglucosamine mutase
32	m6A	K1R5B9_CRAGI DNA-directed RNA polymerase, mitochondrial
33	m6A	K1Q880_CRAGI Transportin-1
34	m6A	K1QA50_CRAGI V-type proton ATPase subunit H
35	m6A	K1R3V0_CRAGI CAD protein
36	m6A	K1R3V0_CRAGI CAD protein
37	m6A	K1PFK8_CRAGI Uncharacterized protein
38	m6A	K1PSN0_CRAGI Pre-mRNA-processing factor 40-like protein A
39	m6A	K1QL67_CRAGI 60S ribosomal protein L7a
40	m6A	K1QE32_CRAGI Very long-chain specific acyl-CoA dehydrogenase, mitochondrial
41	m6A	K1QQ16_CRAGI AP complex subunit beta
42	m6A	K1QN79_CRAGI 40S ribosomal protein S11
43	m6A	K1P8B7_CRAGI Ubiquitin-conjugating enzyme E2-17 kDa (Fragment)
44	m6A	K1P8B7_CRAGI Ubiquitin-conjugating enzyme E2-17 kDa (Fragment)
45	m6A	K1RHB2_CRAGI Nucleolar RNA helicase 2
46	m6A	K1QWC3_CRAGI 40S ribosomal protein S3
47	m6A	K1Q4E1_CRAGI N-acetyl-D-glucosamine kinase
48	m6A	K1Q6F7_CRAGI V-type proton ATPase subunit C
49	m6A	K1R3I6_CRAGI Nucleolar complex protein 2-like protein (Fragment)
50	m6A	K1R3I6_CRAGI Nucleolar complex protein 2-like protein (Fragment)
51	m6A	K1PFS5_CRAGI Elongation factor 1-gamma
52	m6A	K1PBZ4_CRAGI Regulator of nonsense transcripts 1
53	m6A	K1RV41_CRAGI Guanine nucleotide-binding protein subunit beta-2-like 1
54	m6A	K1QKV1_CRAGI Cytochrome b-c1 complex subunit 6
55	m6A	K1S2Y0_CRAGI Uncharacterized protein
56	m6A	K1S2Y0_CRAGI Uncharacterized protein
57	m6A	K1QKK5_CRAGI Vacuolar protein sorting-associated protein 4B
58	m6A	K1Q8S0_CRAGI Nucleolar complex protein 3 homolog
59	m6A	K1QWK6_CRAGI Metalloendopeptidase
60	m6A	K1PH31_CRAGI Protein arginine N-methyltransferase 1
	m6A	K1R834_CRAGI 60S ribosomal protein L9
	m6A	K1RDG4_CRAGI DNA helicase
	m6A	K1R591_CRAGI Inter-alpha-trypsin inhibitor heavy chain H4
	m6A	K1Q9P5_CRAGI Mitochondrial-processing peptidase subunit beta
	m6A	K1QLS3_CRAGI Cytochrome b-c1 complex subunit 2, mitochondrial
	m6A	K1QNT7_CRAGI Aldehyde dehydrogenase, mitochondrial
	m6A	K1QDX9_CRAGI Ribosome biogenesis protein BMS1-like protein
	m6A	K1S6G3_CRAGI Ubiquitin-like modifier-activating enzyme 1
	m6A	K1R8S7_CRAGI Phospholipase A-2-activating protein
	m6A	K1QFN1_CRAGI 60S ribosomal protein L23
	m6A	K1Q5Z6_CRAGI Eukaryotic translation initiation factor 2 subunit 2

1		
2		
3	m6A	K1R6C2_CRAGI Peroxisomal 3,2-trans-enoyl-CoA isomerase
4	m6A	K1Q0R4_CRAGI ATP-binding cassette sub-family F member 2
5	m6A	K1P5V7_CRAGI Eukaryotic translation initiation factor 3 subunit C
6	m6A	K1PGW7_CRAGI Transmembrane protein 2
7	m6A	K1RKC1_CRAGI Far upstream element-binding protein 3
8	m6A	K1QHY1_CRAGI Eosinophil peroxidase
9	m6A	K1QLK8_CRAGI GTP-binding protein SAR1b
10	m6A	K1QRG9_CRAGI Uncharacterized protein
11	m6A	K1QRW4_CRAGI Coronin
12	m6A	K1QKI1_CRAGI Tudor domain-containing protein 1
13	m6A	K1QRM1_CRAGI Nuclear pore protein
14	m6A	K1RBZ5_CRAGI Ran GTPase-activating protein 1
15	m6A	K1RLT4_CRAGI Signal recognition particle subunit SRP68
16	m6A	K1R7N6_CRAGI Eukaryotic translation initiation factor 6
17	m6A	K1P5F7_CRAGI Metastasis-associated protein MTA1
18	m6A	K1RCW3_CRAGI Elongation factor 1-beta
19	m6A	K1R2H9_CRAGI WD repeat-containing protein 35
20	m6A	K1Q1K8_CRAGI Elongation factor 1-beta
21	m6A	K1QTD9_CRAGI Nucleolar protein 56
22	m6A	K1QBW6_CRAGI Tudor domain-containing protein 1
23	m6A	K1QFR9_CRAGI Spectrin beta chain
24	m6A	K1P9S7_CRAGI Brix domain-containing protein 2
25	m6A	K1QEK7_CRAGI Ubiquitin carboxyl-terminal hydrolase
26	m6A	K1PAM6_CRAGI Uncharacterized protein
27	m6A	K1S3G2_CRAGI HMGB1
28	m6A	K1QI11_CRAGI Pyruvate dehydrogenase E1 component subunit alpha type II, mitochondrial
29	m6A	K1QF31_CRAGI Serine/threonine-protein kinase PLK
30	m6A	K1QDA7_CRAGI Uracil phosphoribosyltransferase
31	m6A	K1QKN4_CRAGI Dynein heavy chain 6, axonemal
32	m6A	K1RNH1_CRAGI 60S ribosomal protein L18 (Fragment)
33	m6A	K1QK11_CRAGI Dynein heavy chain 7, axonemal
34	m6A	K1QED7_CRAGI Replication protein A subunit
35	m6A	K1PB82_CRAGI Electron transfer flavoprotein subunit beta
36	m6A	K1PPQ1_CRAGI 14-3-3 protein gamma
37	m6A	K1R8T6_CRAGI Cullin-1
38	m6A	K1Q7E4_CRAGI Ubiquitin-conjugating enzyme E2 N
39	m6A	K1RSZ6_CRAGI 40S ribosomal protein S7
40	m6A	K1Q1S3_CRAGI Myosin-VI
41	m6A	K1QH70_CRAGI Leucine-rich repeat-containing protein 40
42	m6A	K1QZ13_CRAGI Myosin-Ie
43	m6A	K1Q4Z4_CRAGI Bifunctional purine biosynthesis protein PURH
44	m6A	K1Q5H6_CRAGI FACT complex subunit SSRP1
45	m6A	K1PKL8_CRAGI Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit alpha isoform
46	m6A	K1QUC6_CRAGI Uncharacterized protein
47	m6A	K1QPP2_CRAGI Elongation factor Tu, mitochondrial
48	m6A	K1QMH5_CRAGI Small nuclear ribonucleoprotein Sm D1
49	m6A	K1PZD9_CRAGI 26S proteasome non-ATPase regulatory subunit 11
50	m6A	K1PBU0_CRAGI L-fucose kinase
51	m6A	K1QYB6_CRAGI Delta-1-pyrroline-5-carboxylate synthetase
52	m6A	K1PMP3_CRAGI Protoporphyrinogen oxidase
53	m6A	K1Q2E0_CRAGI AP-1 complex subunit mu-1
54	m6A	K1QEF9_CRAGI Protein-glutamine gamma-glutamyltransferase K
55	m6A	K1QGE4_CRAGI Proteasome endopeptidase complex (Fragment)
56	m6A	K1Q6V6_CRAGI Replication factor C subunit 4
57	m6A	K1QYT7_CRAGI COP9 signalosome complex subunit 7a
58	m6A	K1PWP4_CRAGI Phenylalanyl-tRNA synthetase alpha chain
59	m6A	K1PWD9_CRAGI Uncharacterized protein
60	m6A	K1QAH9_CRAGI H/ACA ribonucleoprotein complex subunit
	m6A	K1PS13_CRAGI Coatomer subunit beta (Fragment)
	m6A	K1QJ33_CRAGI Aminoacyl tRNA synthetase complex-interacting multifunctional protein 2

1		
2		
3	m6A	K1QRL6_CRAGI Methenyltetrahydrofolate synthetase domain-containing protein
4	m6A	K1PU46_CRAGI Lethal(2) giant larvae-like protein 1
5	m6A	K1R7J6_CRAGI Putative sodium/potassium-transporting ATPase subunit beta-2
6	m6A	K1QYV6_CRAGI NMDA receptor-regulated protein 1
7	m6A	K1R6E9_CRAGI Dihydrolipoamide acetyltransferase component of pyruvate dehydrogenase complex
8	m6A	K1P7L9_CRAGI Nucleolar GTP-binding protein 1
9	m6A	K1PIB7_CRAGI Phenylalanyl-tRNA synthetase beta chain
10	m6A	K1PX23_CRAGI Eukaryotic peptide chain release factor subunit 1
11	m6A	K1QDV6_CRAGI Protein argonaute-2
12	m6A	K1R5G4_CRAGI 60S ribosomal protein L31
13	m6A	K1R9T2_CRAGI Eukaryotic translation initiation factor 3 subunit B
14	m6A	K1PW99_CRAGI Protein OSCP1
15	m6A	K1R1F0_CRAGI ATP-dependent DNA helicase 2 subunit 1
16	m6A	K1Q260_CRAGI Nucleolar protein 58
17	m6A	K1QFS4_CRAGI Actin-related protein 2
18	m6A	K1QLZ1_CRAGI Actin-related protein 3
19	m6A	K1Q6X5_CRAGI Protein disulfide-isomerase
20	m6A	K1PJB0_CRAGI Heat shock protein 70 B2
21	m6A	K1Q8K2_CRAGI Importin subunit alpha
22	m6A	K1PKF6_CRAGI 26S proteasome non-ATPase regulatory subunit 13
23	m6A	K1QGL9_CRAGI Mannose-1-phosphate guanyltransferase beta
24	m6A	K1RGJ7_CRAGI Neogenin
25	m6A	K1PUJ1_CRAGI Radixin
26	m6A	K1Q811_CRAGI Alpha-centractin
27	m6A	K1QWZ0_CRAGI Tetratricopeptide repeat protein 38
28	m6A	K1PRL4_CRAGI 60S ribosomal protein L38 (Fragment)
29	m6A	K1Q9I1_CRAGI TRAF2 and NCK-interacting protein kinase
30	m6A	K1QVR0_CRAGI 26S proteasome non-ATPase regulatory subunit 8
31	m6A	K1QK68_CRAGI Myosin-2 essential light chain
32	m6A	K1QMH2_CRAGI DNA polymerase
33	m6A	K1PD36_CRAGI Ubiquitin
34	m6A	K1Q4V0_CRAGI Myosin-VIIa
35	m6A	K1QBT2_CRAGI Proteasome subunit beta
36	m6A	K1PXU6_CRAGI 60S ribosomal protein L24
37	m6A	K1Q329_CRAGI Pyruvate dehydrogenase E1 component subunit beta, mitochondrial
38	m6A	K1QDH9_CRAGI Myosin-11
39	m6A	K1QW36_CRAGI 60S ribosomal protein L6
40	m6A	K1Q4Y8_CRAGI Histone H1oo
41	m6A	K1PM66_CRAGI 60S ribosomal protein L12
42	m6A	K1Q4U7_CRAGI AP-3 complex subunit delta-1
43	m6A	K1QPY8_CRAGI Extracellular superoxide dismutase [Cu-Zn]
44	m6A	K1QIP0_CRAGI 26S proteasome non-ATPase regulatory subunit 5
45	m6A	K1QW72_CRAGI Catalase
46	m6A	K1QMD8_CRAGI Proteasome subunit alpha type
47	m6A	K1PZC0_CRAGI Structural maintenance of chromosomes protein
48	m6A	K1RBI9_CRAGI Small nuclear ribonucleoprotein Sm D2
49	m6A	K1QCQ5_CRAGI Succinate--CoA ligase [ADP-forming] subunit beta, mitochondrial
50	m6A	K1ROL4_CRAGI Sodium/potassium-transporting ATPase subunit alpha
51	m6A	K1QKG9_CRAGI Cysteine desulfurase, mitochondrial
52	m6A	K1PPK1_CRAGI Actin-related protein 2/3 complex subunit 4
53	m6A	K1PUQ5_CRAGI Histone H2B
54	m6A	K1RFU6_CRAGI Proteasome activator complex subunit 3
55	m6A	K1Q615_CRAGI Peroxiredoxin-1
56	m6A	K1RIT6_CRAGI NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial
57	m6A	K1PQZ3_CRAGI Armadillo repeat-containing protein 4
58	m6A	K1QW41_CRAGI Leucine-zipper-like transcriptional regulator 1
59	m6A	K1PNS2_CRAGI 33 kDa inner dynein arm light chain, axonemal
60	m6A	K1QQP1_CRAGI Programmed cell death protein 4
	m6A	K1QQC1_CRAGI Dynein light chain roadblock
	m6A	K1P6F0_CRAGI HEAT repeat-containing protein 2

1		
2		
3	m6A	K1QHM2_CRAGI Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2
4	m6A	K1QY58_CRAGI Eukaryotic translation initiation factor 3 subunit I (Fragment)
5	m6A	K1PLA7_CRAGI Eukaryotic initiation factor 4A-II (Fragment)
6	m6A	K1R8I8_CRAGI Acetyltransferase component of pyruvate dehydrogenase complex
7	m6A	K1R2L7_CRAGI Glutaminyl-tRNA synthetase (Fragment)
8	m6A	K1QSD9_CRAGI Uncharacterized protein
9	m6A	K1R008_CRAGI Proteasome subunit alpha type
10	m6A	K1QBL3_CRAGI Putative phosphoglycerate mutase
11	m6A	K1R6S5_CRAGI 40S ribosomal protein S9
12	m6A	K1R6S5_CRAGI 40S ribosomal protein S9
13	m6A	K1QNS4_CRAGI DnaJ-like protein subfamily C member 9
14	m6A	K1QNS4_CRAGI DnaJ-like protein subfamily C member 9
15	m6A	K1Q7X3_CRAGI Pre-mRNA-splicing factor SYF1
16	m6A	K1QG65_CRAGI rRNA 2'-O-methyltransferase fibrillarin
17	m6A	K1QU53_CRAGI NAD(P) transhydrogenase, mitochondrial
18	m6A	K1RU04_CRAGI Actin, cytoplasmic
19	m6A	K1RAH6_CRAGI Ubiquitin-conjugating enzyme E2-17 kDa
20	m6A	K1RAH6_CRAGI Ubiquitin-conjugating enzyme E2-17 kDa
21	m6A	K1PTV1_CRAGI Splicing factor 3B subunit 4
22	m6A	K1PCR5_CRAGI KH domain-containing, RNA-binding, signal transduction-associated protein 2
23	m6A	K1QYH6_CRAGI COP9 signalosome complex subunit 3
24	m6A	K1QH74_CRAGI Splicing factor, arginine/serine-rich 1
25	m6A	K1QH74_CRAGI Splicing factor, arginine/serine-rich 1
26	m6A	K1PX83_CRAGI Dynein heavy chain 5, axonemal
27	m6A	K1QJF7_CRAGI Coronin
28	m6A	K1PNX0_CRAGI Methionyl-tRNA synthetase, cytoplasmic
29	m6A	K1Q1L4_CRAGI Uncharacterized protein
30	m6A	K1PH10_CRAGI Polyadenylate-binding protein-interacting protein 1
31	m6A	K1PH10_CRAGI Polyadenylate-binding protein-interacting protein 1
32	m6A	K1QCL6_CRAGI Proteasomal ubiquitin receptor ADRM1
33	m6A	K1Q1Q9_CRAGI Alpha-aminoadipic semialdehyde synthase, mitochondrial
34	m6A	K1QVP6_CRAGI Developmentally-regulated GTP-binding protein 1
35	m6A	K1QNU0_CRAGI Non-specific serine/threonine protein kinase
36	m6A	K1Q6U0_CRAGI Coatomer subunit zeta-1
37	m6A	K1Q6U0_CRAGI Coatomer subunit zeta-1
38	m6A	K1S058_CRAGI Transcription factor RFX3
39	m6A	K1R488_CRAGI Actin-related protein 2/3 complex subunit
40	m6A	K1Q4G7_CRAGI Tubulin gamma chain
41	m6A	K1PDL3_CRAGI Ribosomal protein L19
42	m6A	K1PBL2_CRAGI Eukaryotic initiation factor 4A-III
43	m6A	K1QE83_CRAGI CCR4-NOT transcription complex subunit 1
44	m6A	K1QE83_CRAGI CCR4-NOT transcription complex subunit 1
45	m6A	K1R1Q8_CRAGI Ras-related protein Rab-5C
46	m6A	K1ROP8_CRAGI CTP synthase
47	m6A	K1QJ46_CRAGI Putative methylcrotonoyl-CoA carboxylase beta chain, mitochondrial
48	m6A	K1QJ46_CRAGI Putative methylcrotonoyl-CoA carboxylase beta chain, mitochondrial
49	m6A	K1QG70_CRAGI Katanin p60 ATPase-containing subunit A1
50	m6A	K1RBF6_CRAGI Uncharacterized protein yfeX
51	m6A	K1RZM3_CRAGI Cartilage acidic protein 1
52	m6A	K1R5V4_CRAGI GTP-binding nuclear protein
53	m6A	K1QZX9_CRAGI Uncharacterized protein
54	m6A	K1Q6U7_CRAGI 78 kDa glucose-regulated protein
55	m6A	K1Q6U7_CRAGI 78 kDa glucose-regulated protein
56	m6A	K1R195_CRAGI Protein DJ-1
57	m6A	K1Q317_CRAGI Serine/threonine-protein kinase SRPK1
58	m6A	K1QJE9_CRAGI Uncharacterized protein
59	m6A	K1PD30_CRAGI Putative histone-binding protein Caf1
60	m6A	K1QJM1_CRAGI 60S ribosomal protein L30
	m6A	K1RHP3_CRAGI Proliferation-associated protein 2G4
	m6A	K1PMJ9_CRAGI Cleavage stimulation factor 77 kDa subunit
	m6A	K1RAU8_CRAGI Eukaryotic translation initiation factor 3 subunit E
	m6A	K1RIS2_CRAGI 3-oxoacyl-[acyl-carrier-protein] reductase
	m6A	K1PLM3_CRAGI Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial
	m6A	K1PWU5_CRAGI Cytosolic carboxypeptidase 1
	m6A	K1QFF0_CRAGI Vacuolar protein sorting-associated protein 35 (Fragment)
	m6A	K1P6C4_CRAGI Poly [ADP-ribose] polymerase
	m6A	K1RG19_CRAGI Protein FAM98A
	m6A	K1QCB0_CRAGI 40S ribosomal protein S5
	m6A	K1PCH8_CRAGI Nucleoporin p54

1		
2		
3	m6A	K1Q2Y1_CRAGI 40S ribosomal protein S15
4	m6A	K1QGW4_CRAGI Density-regulated protein
5	m6A	K1R6H7_CRAGI Uncharacterized protein
6	m6A	K1R0D7_CRAGI Eukaryotic translation initiation factor 3 subunit M (Fragment)
7	m6A	K1PPI6_CRAGI Synaptobrevin-like protein YKT6
8	m6A	K1RMW3_CRAGI Protein kinase C
9	m6A	K1QV25_CRAGI Transcription elongation factor B polypeptide 2
10	m6A	K1QC27_CRAGI Hydroxysteroid dehydrogenase-like protein 2
11	m6A	K1RAT9_CRAGI Tubulin-specific chaperone D
12	m6A	K1RAT9_CRAGI Tubulin-specific chaperone D
13	m6A	K1QWJ4_CRAGI Splicing factor 3B subunit 5
14	m6A	K1PZ08_CRAGI Ras-related protein Rab-7a
15	m6A	K1PZ08_CRAGI Ras-related protein Rab-7a
16	m6A	K1QMQ1_CRAGI TBC1 domain family member 10B
17	m6A	K1R811_CRAGI Ribonucleoside-diphosphate reductase small chain
18	m6A	K1P8G1_CRAGI Heterogeneous nuclear ribonucleoprotein H
19	m6A	K1R983_CRAGI Protein transport protein SEC23
20	m6A	K1R983_CRAGI Protein transport protein SEC23
21	m6A	K1QDI4_CRAGI Superoxide dismutase [Cu-Zn]
22	m6A	K1RDM2_CRAGI 60S ribosomal protein L18a
23	m6A	K1QYI9_CRAGI Arginyl-tRNA synthetase, cytoplasmic (Fragment)
24	m6A	K1QVS0_CRAGI Ras-like GTP-binding protein Rho1
25	m6A	K1QVS0_CRAGI Ras-like GTP-binding protein Rho1
26	m6A	K1PJS7_CRAGI Poly [ADP-ribose] polymerase
27	m6A	K1QRD0_CRAGI Cytoplasmic dynein 1 light intermediate chain 1
28	m6A	K1R0R7_CRAGI Putative ATP-dependent RNA helicase DHX36
29	m6A	K1Q1F1_CRAGI Serine/threonine-protein kinase 31
30	m6A	K1Q1F1_CRAGI Serine/threonine-protein kinase 31
31	m6A	K1QI32_CRAGI Synaptotagmin-like protein 5
32	m6A	K1PMY9_CRAGI Calmodulin
33	m6A	K1PXG6_CRAGI Serine/threonine-protein phosphatase
34	m6A	K1QW61_CRAGI WD repeat-containing protein 19
35	m6A	K1P2B8_CRAGI GDP-mannose 4,6 dehydratase
36	m6A	K1QYT5_CRAGI Phosphate carrier protein, mitochondrial
37	m6A	K1QYT5_CRAGI Phosphate carrier protein, mitochondrial
38	m6A	K1RIZ9_CRAGI Band 4.1-like protein 5
39	m6A	K1QT97_CRAGI N(G),N(G)-dimethylarginine dimethylaminohydrolase 1
40	m6A	K1QKF8_CRAGI S-(hydroxymethyl)glutathione dehydrogenase
41	m6A	K1REJ2_CRAGI Lon protease homolog, mitochondrial
42	m6A	K1R1B1_CRAGI 35 kDa SR repressor protein
43	m6A	K1R1B1_CRAGI 35 kDa SR repressor protein
44	m6A	K1PRK2_CRAGI Small glutamine-rich tetratricopeptide repeat-containing protein beta
45	m6A	K1QAT9_CRAGI ATP-dependent RNA helicase DDX1
46	m6A	K1PFV9_CRAGI 4-trimethylaminobutyraldehyde dehydrogenase
47	m6A	K1QLP5_CRAGI Coatomer subunit delta
48	m6A	K1PIH2_CRAGI V-type proton ATPase subunit E
49	m6A	K1RBU9_CRAGI Non-specific serine/threonine protein kinase
50	m6A	K1RBU9_CRAGI Non-specific serine/threonine protein kinase
51	m6A	K1QGP1_CRAGI Replication factor C subunit 2
52	m6A	K1PJ96_CRAGI Uncharacterized protein
53	m6A	K1QHH0_CRAGI Protein henna
54	m6A	K1ROW0_CRAGI Ferritin
55	m6A	K1ROW0_CRAGI Ferritin
56	m6A	K1Q6W5_CRAGI FACT complex subunit spt16
57	m6A	K1QEZ5_CRAGI MON2-like protein
58	m6A	K1RJW8_CRAGI Protein DEK
59	m6A	K1P752_CRAGI UPF0195 protein FAM96B
60	m6A	K1RP91_CRAGI Putative RNA exonuclease NEF-sp
	m6A	K1QSZ6_CRAGI Uncharacterized protein
	m6A	K1RD83_CRAGI Serine hydroxymethyltransferase
	m6A	K1R5W3_CRAGI Uncharacterized protein
	m6A	K1S211_CRAGI Poly(A) RNA polymerase gld-2-like protein A
	m6A	K1QTW6_CRAGI Eukaryotic translation initiation factor 3 subunit F
	m6A	K1QEJ0_CRAGI Ras GTPase-activating protein-binding protein 2
	m6A	K1R1R9_CRAGI Pre-mRNA-processing factor 6
	m6A	K1QJL2_CRAGI CCR4-NOT transcription complex subunit 10
	m6A	K1PUV4_CRAGI 40S ribosomal protein S24
	m6A	K1RH58_CRAGI Alpha-actinin, sarcomeric
	m6A	K1PQI4_CRAGI Enolase-phosphatase E1

1		
2		
3	m6A	K1R7D7_CRAGI Poly(A)-specific ribonuclease PARN
4	m6A	K1PS84_CRAGI Alpha-crystallin B chain
5	m6A	K1QQV0_CRAGI Histone H1.2
6	m6A	K1QPJ9_CRAGI Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B
7	m6A	K1QZX3_CRAGI Vacuolar protein sorting-associated protein VTA1-like protein
8	m6A	K1R517_CRAGI Superkiller viralicidic activity 2-like 2
9	m6A	K1RJS5_CRAGI Uncharacterized protein
10	m6A	K1S3Q9_CRAGI MAK16-like protein (Fragment)
11	m6A	K1PKD4_CRAGI 40S ribosomal protein S30
12	m6A	K1PGZ0_CRAGI Thyroid adenoma-associated protein
13	m6A	K1REV3_CRAGI DNA polymerase delta subunit 2
14	m6A	K1QGF1_CRAGI Splicing factor 3B subunit 2
15	m6A	K1R8B2_CRAGI Isovaleryl-CoA dehydrogenase, mitochondrial
16	m6A	K1PR25_CRAGI Regulator of differentiation 1
17	m6A	K1PZ23_CRAGI DnaJ-like protein subfamily C member 3
18	m6A	K1PLG1_CRAGI Putative ribosomal RNA methyltransferase NOP2
19	m6A	K1PNY5_CRAGI Splicing factor, proline-and glutamine-rich
20	m6A	K1RG79_CRAGI Neuronal acetylcholine receptor subunit alpha-6
21	m6A	K1PRB6_CRAGI Apolipoprotein D
22	m6A	K1PTR3_CRAGI Oxysterol-binding protein
23	m6A	K1Q1F4_CRAGI 60S ribosomal protein L3 (Fragment)
24	m6A	Q70MT4_CRAGI 40S ribosomal protein S10
25	m6A	K1Q662_CRAGI Actin-interacting protein 1
26	m6A	K1R2G9_CRAGI SEC13-like protein
27	m6A	K1PRV7_CRAGI Profilin
28	m6A	K1QWZ6_CRAGI Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1
29	m6A	K1R9S5_CRAGI Cytosolic Fe-S cluster assembly factor NUBP2 homolog
30	m6A	K1QUK0_CRAGI NEDD8-activating enzyme E1 catalytic subunit
31	m6A	K1PTE3_CRAGI Uncharacterized protein
32	m6A	K1Q6M6_CRAGI 6-phosphofructokinase
33	m6A	K1QZN3_CRAGI Myosin-Ia
34	m6A	K1PB94_CRAGI ATP-binding cassette sub-family E member 1
35	m6A	K1RNN9_CRAGI Cytoskeleton-associated protein 5
36	m6A	K1PZL0_CRAGI B-box type zinc finger protein ncl-1
37	m6A	K1RKZ5_CRAGI DNA damage-binding protein 1
38	m6A	K1R138_CRAGI Nuclear pore glycoprotein p62
39	m6A	K1Q9D7_CRAGI Sorting nexin-2
40	m6A	K1R6F1_CRAGI Proteasome subunit alpha type
41	m6A	K1QKQ5_CRAGI N-terminal acetyltransferase B complex subunit MDM20
42	m6A	K1PDC6_CRAGI Proteasome subunit beta
43	m6A	A5LGH1_CRAGI Voltage-dependent anion channel
44	m6A	K1PF60_CRAGI 3-ketoacyl-CoA thiolase, mitochondrial
45	m6A	K1R924_CRAGI RNA-binding protein 45
46	m6A	K1RTQ6_CRAGI Fructose-bisphosphate aldolase
47	m6A	K1Q888_CRAGI Translin
48	m6A	K1R255_CRAGI Heterogeneous nuclear ribonucleoprotein L
49	m6A	K1QIZ7_CRAGI Programmed cell death protein 6
50	m6A	K1QI48_CRAGI Inositol hexakisphosphate and diphosphoinositol-pentakisphosphate kinase
51	m6A	K1PWB9_CRAGI EH domain-containing protein 1
52	m6A	K1QZ84_CRAGI Thioredoxin domain-containing protein 3-like protein
53	m6A	K1PJY4_CRAGI Calcium-binding protein 39
54	m6A	K1PBC0_CRAGI Non-neuronal cytoplasmic intermediate filament protein
55	m6A	K1PRD5_CRAGI Trifunctional purine biosynthetic protein adenosine-3
56	m6A	K1QXH7_CRAGI DNA replication licensing factor mcm4-B
57	m6A	K1Q719_CRAGI Serine/threonine-protein kinase OSR1
58	m6A	K1QV87_CRAGI Catenin alpha-2
59	m6A	K1PBH3_CRAGI Dynein heavy chain 3, axonemal
60	m6A	K1R4M7_CRAGI Serine/threonine protein phosphatase 2A regulatory subunit
	m6A	K1R3A0_CRAGI Transcription initiation factor IIB
	m6A	K1QQQ5_CRAGI Replication factor C subunit 5

1		
2		
3	m6A	K1RJ70_CRAGI Cytosolic non-specific dipeptidase
4	m6A	K1QNY7_CRAGI Transport protein Sec24C
5	m6A	K1R481_CRAGI Epimerase family protein SDR39U1
6	m6A	K1QRE1_CRAGI COP9 signalosome complex subunit 6
7	m6A	K1RA63_CRAGI Transmembrane protein 2
8	m6A	K1QHT0_CRAGI Deoxyuridine 5'-triphosphate nucleotidohydrolase, mitochondrial
9	m6A	K1PQA3_CRAGI Pseudouridylate synthase 7-like protein
10	m6A	K1PII4_CRAGI YTH domain-containing protein 1
11	m6A	K1P8S5_CRAGI Condensin complex subunit 3
12	m6A	K1QMT1_CRAGI DnaJ-like protein subfamily B member 4
13	m6A	K1PN10_CRAGI Intron-binding protein aquarius
14	m6A	K1PCR9_CRAGI Proteasome endopeptidase complex
15	m6A	K1PZI3_CRAGI SWI/SNF complex subunit SMARCC2
16	m6A	K1RIZ3_CRAGI Bone morphogenetic protein 7
17	m6A	K1QMY1_CRAGI Aconitate hydratase, mitochondrial
18	m6A	K1R3W9_CRAGI Replication protein A 14 kDa subunit
19	m6A	K1PLD4_CRAGI Dynein heavy chain 2, axonemal
20	m6A	K1QC78_CRAGI Ras-related protein Rab-14
21	m6A	K1PTV5_CRAGI Programmed cell death protein 10
22	m6A	K1RGG1_CRAGI Alanyl-tRNA synthetase, cytoplasmic
23	m6A	K1R3R4_CRAGI Cytosolic Fe-S cluster assembly factor NUBP1 homolog
24	m6A	K1R266_CRAGI Retinal dehydrogenase 1
25	m6A	K1QGC9_CRAGI Acetyl-coenzyme A synthetase
26	m6A	K1Q7T5_CRAGI Protein disulfide-isomerase
27	m6A	K1QKQ8_CRAGI THO complex subunit 4-A
28	m6A	K1QR54_CRAGI Zinc finger RNA-binding protein
29	m6A	K1PEW1_CRAGI Sorting nexin
30	m6A	K1PFL3_CRAGI Dihydropteridine reductase
31	m6A	K1QC11_CRAGI AP-1 complex subunit gamma
32	m6A	K1QQI3_CRAGI Rab-like protein 5
33	m6A	K1R916_CRAGI Structural maintenance of chromosomes protein
34	m6A	K1PF37_CRAGI Thioredoxin domain-containing protein 9
35	m6A	K1PJW0_CRAGI Talin-1
36	m6A	K1PUX5_CRAGI Casein kinase II subunit alpha
37	m6A	K1QB86_CRAGI Dynamin-1
38	m6A	K1QWX0_CRAGI 26S proteasome non-ATPase regulatory subunit 14
39	m6A	K1QBM3_CRAGI Ras-related protein Rab-2
40	m6A	K1RG04_CRAGI ALK tyrosine kinase receptor
41	m6A	K1PXH5_CRAGI Putative saccharopine dehydrogenase
42	m6A	K1Q407_CRAGI Ras GTPase-activating protein 1
43	m6A	K1PYK7_CRAGI RNA-binding protein 39
44	m6A	K1PZR3_CRAGI U2 small nuclear ribonucleoprotein A
45	m6A	K1RBJ3_CRAGI DnaJ-like protein subfamily C member 13
46	m6A	K1Q324_CRAGI Heterogeneous nuclear ribonucleoprotein K
47	m6A	K1PA61_CRAGI Actin-like protein 6A
48	m6A	K1PWS8_CRAGI Mitotic spindle assembly checkpoint protein MAD2A
49	m6A	K1PL64_CRAGI Poly(A) polymerase gamma
50	m6A	K1RB97_CRAGI Kinetochores-associated protein 1
51	m6A	K1R6S7_CRAGI Mannose-1-phosphate guanyltransferase alpha-A
52	m6A	K1RK83_CRAGI Tyrosine-protein kinase BAZ1B
53	m6A	K1QSA2_CRAGI Short-chain specific acyl-CoA dehydrogenase, mitochondrial
54	m6A	K1RFU8_CRAGI High mobility group protein DSP1
55	m6A	K1QV46_CRAGI Tetratricopeptide repeat protein 21B
56	m6A	K1R8W3_CRAGI S-phase kinase-associated protein 1
57	m6A	K1RFF7_CRAGI Protein lethal(2)essential for life
58	m6A	K1R1T8_CRAGI Nucleolar protein 56
59	m6A	K1PNG7_CRAGI Sorting nexin-33
60	m6A	K1PCV0_CRAGI Severin
	m6A	K1QVX4_CRAGI Glycogen synthase kinase-3 beta
	m6A	K1P9V5_CRAGI General transcription factor IIF subunit 1

1		
2		
3	m6A	K1Q904_CRAGI PAN2-PAN3 deadenylation complex subunit PAN3
4	m6A	K1REC3_CRAGI Exportin-5
5	m6A	K1P137_CRAGI Actin-related protein 2/3 complex subunit 5
6	m6A	K1QBT8_CRAGI Uncharacterized protein
7	m6A	K1PZN1_CRAGI Calcium/calmodulin-dependent protein kinase type II delta chain
8	m6A	K1QVZ2_CRAGI Uncharacterized protein
9	m6A	K1REPO_CRAGI Uncharacterized protein
10	m6A	K1QHX0_CRAGI Double-stranded RNA-specific editase 1
11	m6A	K1PVL5_CRAGI tRNA 2'-phosphotransferase 1
12	m6A	K1Q6Y2_CRAGI Uncharacterized protein
13	m6A	K1Q6Y2_CRAGI Uncharacterized protein
14	m6A	K1PMQ4_CRAGI Microtubule-associated serine/threonine-protein kinase-like protein
15	m6A	K1PQR9_CRAGI Squamous cell carcinoma antigen recognized by T-cells 3
16	m6A	K1R150_CRAGI Ras-related protein Rab-1A
17	m6A	K1R150_CRAGI Ras-related protein Rab-1A
18	m6A	K1PNU2_CRAGI Histone-arginine methyltransferase CARM1
19	m6A	K1PEX5_CRAGI Protein hu-li tai shao
20	m6A	K1PDF0_CRAGI Protein disulfide-isomerase A6
21	m6A	K1PDF0_CRAGI Protein disulfide-isomerase A6
22	m6A	K1QC22_CRAGI 40S ribosomal protein S19
23	m6A	K1PUF0_CRAGI G-protein coupled receptor moody
24	m6A	K1S422_CRAGI Katanin p80 WD40 repeat-containing subunit B1
25	m6A	K1S422_CRAGI Katanin p80 WD40 repeat-containing subunit B1
26	m6A	K1PI41_CRAGI Flap endonuclease 1
27	m6A	K1R0N8_CRAGI Flap endonuclease GEN-like protein 1
28	m6A	K1RXR4_CRAGI Arrestin domain-containing protein 3
29	m6A	K1PXX6_CRAGI Uncharacterized protein
30	m6A	K1QXP9_CRAGI Uncharacterized protein
31	m6A	K1QXP9_CRAGI Uncharacterized protein
32	m6A	K1RJB4_CRAGI Ubiquitin carboxyl-terminal hydrolase 1
33	A	K1QNA2_CRAGI Vitellogenin-6
34	A	K1QHK9_CRAGI Dynein heavy chain, cytoplasmic
35	A	K1PNR3_CRAGI Clathrin heavy chain
36	A	K1QVJ8_CRAGI Piwi-like protein 1
37	A	K1QVJ8_CRAGI Piwi-like protein 1
38	A	K1R7V7_CRAGI Tubulin beta chain
39	A	K1QQ94_CRAGI Uncharacterized protein
40	A	K1RLF8_CRAGI Splicing factor 3B subunit 3
41	A	K1QQ68_CRAGI Tubulin alpha chain
42	A	K1S2N7_CRAGI Innexin
43	A	K1S2N7_CRAGI Innexin
44	A	K1R164_CRAGI Galectin-4
45	A	K1QMX5_CRAGI Uncharacterized protein
46	A	K1QHI5_CRAGI Pyruvate carboxylase, mitochondrial
47	A	K1PQP2_CRAGI Nucleolin
48	A	K1PN21_CRAGI Tubulin beta chain
49	A	K1PAG1_CRAGI Dynein beta chain, ciliary
50	A	K1PAG1_CRAGI Dynein beta chain, ciliary
51	A	K1QII6_CRAGI Tubulin alpha chain
52	A	K1R5B4_CRAGI Proteasome activator complex subunit 4
53	A	K1QFW9_CRAGI Uncharacterized protein
54	A	K1R473_CRAGI Tubulin alpha chain
55	A	K1R473_CRAGI Tubulin alpha chain
56	A	K1PK85_CRAGI Cullin-associated NEDD8-dissociated protein 1
57	A	K1R294_CRAGI T-complex protein 1 subunit beta
58	A	K1PE00_CRAGI Tubulin alpha chain
59	A	K1PNI6_CRAGI Heterogeneous nuclear ribonucleoprotein A/B
60	A	K1PYA0_CRAGI Cytoplasmic dynein 2 heavy chain 1
	A	K1R466_CRAGI T-complex protein 1 subunit gamma
	A	K1S4Q2_CRAGI T-complex protein 1 subunit delta (Fragment)
	A	K1QMA4_CRAGI RRP5-like protein
	A	K1R5R4_CRAGI Dynein heavy chain 10, axonemal
	A	K1RZE2_CRAGI Isocitrate dehydrogenase [NADP]
	A	K1QGS8_CRAGI Elongation factor 1-alpha
	A	K1QXX7_CRAGI Myosin heavy chain, non-muscle (Fragment)
	A	K1S6V7_CRAGI Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform
	A	K1R866_CRAGI Puromycin-sensitive aminopeptidase
	A	K1QBK6_CRAGI Splicing factor 3B subunit 1
	A	K1R3U2_CRAGI Uncharacterized protein

1		
2		
3	A	K1QNW9_CRAGI Bifunctional aminoacyl-tRNA synthetase
4	A	K1R545_CRAGI Pre-mRNA-processing-splicing factor 8 (Fragment)
5	A	K1R6Z7_CRAGI ATP synthase subunit alpha
6	A	K1R6Q7_CRAGI DNA topoisomerase I
7	A	K1R0S3_CRAGI T-complex protein 1 subunit theta
8	A	K1RAJ1_CRAGI T-complex protein 1 subunit alpha
9	A	K1PNQ5_CRAGI Heat shock protein HSP 90-alpha 1
10	A	K1PVA1_CRAGI Transitional endoplasmic reticulum ATPase
11	A	K1QHI6_CRAGI Dynein heavy chain 5, axonemal
12	A	K1Q7G8_CRAGI Fatty acid synthase
13	A	K1R401_CRAGI Spectrin alpha chain
14	A	K1PND7_CRAGI Fatty acid synthase
15	A	K1RGT5_CRAGI Metalloendopeptidase
16	A	K1PLF9_CRAGI Arginine kinase
17	A	K1QET2_CRAGI Coatomer subunit alpha
18	A	K1QSB2_CRAGI 26S protease regulatory subunit 6B
19	A	K1R9B6_CRAGI H/ACA ribonucleoprotein complex subunit 4
20	A	K1R512_CRAGI Uncharacterized protein
21	A	K1RK12_CRAGI 40S ribosomal protein S23
22	A	K1QQR1_CRAGI Major vault protein
23	A	K1R420_CRAGI Non-specific serine/threonine protein kinase
24	A	K1Q9W5_CRAGI T-complex protein 1 subunit eta
25	A	K1QSX8_CRAGI ATPase family AAA domain-containing protein 2B
26	A	K1Q350_CRAGI Glyceraldehyde-3-phosphate dehydrogenase
27	A	K1PJ85_CRAGI 26S protease regulatory subunit 6A
28	A	K1Q923_CRAGI Putative ATP-dependent RNA helicase DDX4
29	A	K1PJ06_CRAGI Importin subunit alpha-1
30	A	K1RLC5_CRAGI T-complex protein 1 subunit epsilon
31	A	K1R278_CRAGI Tubulin beta chain
32	A	K1R8L1_CRAGI Exportin-2
33	A	K1PEY4_CRAGI 26S proteasome non-ATPase regulatory subunit 2
34	A	K1RWS2_CRAGI Transcriptional activator protein Pur-alpha
35	A	K1RG73_CRAGI Acetyl-CoA carboxylase
36	A	K1QLK6_CRAGI E3 ubiquitin-protein ligase HUWE1
37	A	K1PXN5_CRAGI T-complex protein 1 subunit zeta
38	A	K1P9D0_CRAGI Stress-70 protein, mitochondrial
39	A	K1QR72_CRAGI Dipeptidyl peptidase 3
40	A	K1R4Z3_CRAGI Malate dehydrogenase, mitochondrial
41	A	K1Q988_CRAGI Band 4.1-like protein 3
42	A	K1QB04_CRAGI 26S proteasome non-ATPase regulatory subunit 3
43	A	K1QRL4_CRAGI Importin-5
44	A	K1Q112_CRAGI 26S protease regulatory subunit 7
45	A	K1QXR4_CRAGI Pancreatic lipase-related protein 2
46	A	K1RH70_CRAGI 6-phosphogluconate dehydrogenase, decarboxylating
47	A	K1PH66_CRAGI Fibrinolytic enzyme, isozyme C
48	A	K1PTY5_CRAGI Protocadherin Fat 4
49	A	K1Q114_CRAGI 40S ribosomal protein S3a
50	A	K1QBN0_CRAGI Methylcrotonoyl-CoA carboxylase beta chain, mitochondrial
51	A	K1QMD3_CRAGI Glycerol-3-phosphate dehydrogenase [NAD(+)]
52	A	K1QVN9_CRAGI T-complex protein 1 subunit eta
53	A	K1RN77_CRAGI Nuclear autoantigenic sperm protein
54	A	K1QSQ9_CRAGI Putative ATP-dependent RNA helicase an3
55	A	K1RI55_CRAGI Insulin-like growth factor 2 mRNA-binding protein 3
56	A	K1S1S1_CRAGI Insulin-like growth factor 2 mRNA-binding protein 1
57	A	K1PH76_CRAGI Y-box factor-like protein (Fragment)
58	A	K1QWP8_CRAGI Actin-2
59	A	K1R252_CRAGI Putative methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial
60	A	K1QEA6_CRAGI Phosphoenolpyruvate carboxykinase [GTP]
	A	K1RNB5_CRAGI Propionyl-CoA carboxylase beta chain, mitochondrial
	A	K1RJH5_CRAGI Polyadenylate-binding protein

1		
2		
3	A	K1PLY1_CRAGI DNA polymerase
4	A	K1R5U4_CRAGI Acetyl-CoA carboxylase 1
5	A	K1PF10_CRAGI PAN2-PAN3 deadenylation complex catalytic subunit PAN2
6	A	K1QBR5_CRAGI Uncharacterized protein
7	A	K1QVS3_CRAGI Thimet oligopeptidase
8	A	K1RFT1_CRAGI Band 4.1-like protein 3
9	A	K1R2V1_CRAGI Importin subunit beta-1
10	A	K1RW85_CRAGI Adenosylhomocysteinase
11	A	K1QWT8_CRAGI Uncharacterized protein
12	A	K1PFG1_CRAGI Uncharacterized protein
13	A	K1QWX2_CRAGI 60S acidic ribosomal protein P0
14	A	K1R1M7_CRAGI Ubiquitin-like modifier-activating enzyme 1
15	A	K1QK11_CRAGI Dynein heavy chain 7, axonemal
16	A	K1RWW5_CRAGI ATP synthase subunit beta
17	A	K1RJ97_CRAGI Multifunctional protein ADE2
18	A	K1RWD4_CRAGI Actin, cytoplasmic
19	A	K1R3V0_CRAGI CAD protein
20	A	K1QHA2_CRAGI Spectrin beta chain, brain 4
21	A	K1REG6_CRAGI DNA helicase
22	A	K1R4I2_CRAGI 26S proteasome non-ATPase regulatory subunit 3
23	A	K1RTR1_CRAGI ATP-citrate synthase
24	A	K1QGK2_CRAGI Coatomer subunit beta
25	A	K1Q9Z6_CRAGI 26S proteasome non-ATPase regulatory subunit 7
26	A	K1QQL6_CRAGI Leucyl-tRNA synthetase, cytoplasmic
27	A	K1Q330_CRAGI Dihydrolipoyl dehydrogenase
28	A	K1QUE6_CRAGI 26S proteasome non-ATPase regulatory subunit 6
29	A	K1QY12_CRAGI Dynamin-1-like protein
30	A	K1Q3S7_CRAGI Cytosolic carboxypeptidase 1
31	A	K1RSZ6_CRAGI 40S ribosomal protein S7
32	A	K1PJF4_CRAGI Isoleucyl-tRNA synthetase, cytoplasmic
33	A	K1Q9V3_CRAGI V-type proton ATPase catalytic subunit A
34	A	K1RBC9_CRAGI Transketolase-like protein 2
35	A	K1PPP8_CRAGI Vigilin
36	A	K1PX47_CRAGI Ubiquitin carboxyl-terminal hydrolase
37	A	K1QX26_CRAGI Endoplasmic
38	A	K1PZP6_CRAGI Coatomer subunit gamma
39	A	K1QE71_CRAGI DNA helicase
40	A	K1QBH0_CRAGI Uncharacterized protein
41	A	K1QCC1_CRAGI Phosphoglycerate kinase
42	A	K1PJP9_CRAGI 26S proteasome non-ATPase regulatory subunit 1
43	A	K1QIR8_CRAGI 78 kDa glucose-regulated protein
44	A	K1Q4I9_CRAGI D-3-phosphoglycerate dehydrogenase (Fragment)
45	A	K1RNZ6_CRAGI Eukaryotic translation initiation factor 3 subunit D
46	A	K1R3V8_CRAGI COP9 signalosome complex subunit 4
47	A	K1PUL2_CRAGI Long-chain-fatty-acid--CoA ligase 1
48	A	K1QHX2_CRAGI La-related protein 7
49	A	K1QDN1_CRAGI Heat shock protein 75 kDa, mitochondrial (Fragment)
50	A	K1PZF2_CRAGI Exportin-7
51	A	K1PMT6_CRAGI Heterogeneous nuclear ribonucleoprotein U-like protein 1
52	A	K1RCW5_CRAGI Eukaryotic translation initiation factor 4 gamma 3
53	A	K1R7I9_CRAGI Heterogeneous nuclear ribonucleoprotein Q
54	A	K1QYB6_CRAGI Delta-1-pyrroline-5-carboxylate synthetase
55	A	K1P3Q5_CRAGI Programmed cell death 6-interacting protein
56	A	K1Q2H5_CRAGI Uncharacterized protein
57	A	K1QBF7_CRAGI Hypoxia up-regulated protein 1
58	A	K1PW06_CRAGI Filamin-C
59	A	K1QHS8_CRAGI Ribonucleoside-diphosphate reductase
60	A	K1RL00_CRAGI Proteasome-associated protein ECM29-like protein
	A	K1QQ16_CRAGI AP complex subunit beta
	A	K1R4R9_CRAGI Mitotic apparatus protein p62

1		
2		
3	A	K1QXH3_CRAGI Translational activator GCN1
4	A	K1P5D4_CRAGI Cysteine synthase
5	A	K1RM80_CRAGI Citrate synthase
6	A	K1PVH5_CRAGI Centromere/kinetochore protein zw10-like protein
7	A	K1QQ27_CRAGI Pancreatic lipase-related protein 2
8	A	K1QMX8_CRAGI DNA replication licensing factor MCM7
9	A	K1QK56_CRAGI Uncharacterized protein
10	A	K1QMB9_CRAGI Eukaryotic translation initiation factor 3 subunit A
11	A	K1R0W4_CRAGI Signal recognition particle subunit SRP72
12	A	K1QLT5_CRAGI 26S protease regulatory subunit 4
13	A	K1QSR2_CRAGI Apoptosis inhibitor 5
14	A	K1QKA9_CRAGI Piwi-like protein 2
15	A	K1RJM8_CRAGI SAGA-associated factor 11 homolog
16	A	K1QQB6_CRAGI 40S ribosomal protein S14
17	A	K1PE57_CRAGI Severin
18	A	K1PKK7_CRAGI AP-2 complex subunit mu-1
19	A	K1QXS6_CRAGI Heterogeneous nuclear ribonucleoprotein A2-like protein 1
20	A	K1R5F2_CRAGI 14-3-3 protein epsilon
21	A	K1Q4V0_CRAGI Myosin-VIIa
22	A	K1QA50_CRAGI V-type proton ATPase subunit H
23	A	K1QWK2_CRAGI MAM domain-containing glycosylphosphatidylinositol anchor protein 2
24	A	K1PV49_CRAGI RuvB-like helicase
25	A	K1QAB1_CRAGI AP-2 complex subunit alpha
26	A	K1RK33_CRAGI Exportin-1
27	A	K1PCS4_CRAGI Eukaryotic translation initiation factor 2 subunit 3, Y-linked
28	A	K1RSA6_CRAGI Methylcrotonoyl-CoA carboxylase subunit alpha, mitochondrial
29	A	K1PI02_CRAGI Talin-1
30	A	K1PNP4_CRAGI 26S proteasome non-ATPase regulatory subunit 11
31	A	K1RAL0_CRAGI Aspartate aminotransferase, cytoplasmic
32	A	K1QXQ8_CRAGI DNA helicase
33	A	K1QI28_CRAGI V-type proton ATPase subunit B
34	A	K1Q9K6_CRAGI Histone H3
35	A	K1S151_CRAGI Rab GDP dissociation inhibitor
36	A	K1P2G0_CRAGI Strawberry notch-like protein 1
37	A	K1QI97_CRAGI Adenylyl cyclase-associated protein
38	A	K1QBW6_CRAGI Tudor domain-containing protein 1
39	A	K1PEP0_CRAGI 40S ribosomal protein S8
40	A	K1QG84_CRAGI THO complex subunit 2
41	A	K1PJM2_CRAGI Histone H2A
42	A	K1PU26_CRAGI Malate dehydrogenase (Fragment)
43	A	A7M7T7_CRAGI Non-selenium glutathione peroxidase
44	A	K1PWW9_CRAGI 26S proteasome non-ATPase regulatory subunit 3
45	A	K1QF01_CRAGI 40S ribosomal protein S4
46	A	K1QZW0_CRAGI Polyadenylate-binding protein 2
47	A	K1RAU3_CRAGI DNA ligase
48	A	K1PVW0_CRAGI S-adenosylmethionine synthase
49	A	K1QBL6_CRAGI Tudor domain-containing protein 1
50	A	K1QE32_CRAGI Very long-chain specific acyl-CoA dehydrogenase, mitochondrial
51	A	K1PY73_CRAGI Basic leucine zipper and W2 domain-containing protein 1
52	A	K1S2Y0_CRAGI Uncharacterized protein
53	A	K1QEF2_CRAGI ADP-ribosylation factor-like protein 15
54	A	K1PV79_CRAGI Importin subunit alpha
55	A	K1R083_CRAGI Aspartate aminotransferase, mitochondrial
56	A	K1QMH2_CRAGI DNA polymerase
57	A	K1QL67_CRAGI 60S ribosomal protein L7a
58	A	K1QDV6_CRAGI Protein argonaute-2
59	A	K1QU53_CRAGI NAD(P) transhydrogenase, mitochondrial
60	A	K1RIZ9_CRAGI Band 4.1-like protein 5
	A	K1R2Q9_CRAGI Aspartate aminotransferase
	A	K1Q4E1_CRAGI N-acetyl-D-glucosamine kinase

1		
2		
3	A	K1R916_CRAGI Structural maintenance of chromosomes protein
4	A	K1R2N0_CRAGI Histone H4
5	A	K1P7K8_CRAGI Vesicle-fusing ATPase 1
6	A	K1PJC1_CRAGI Adipophilin
7	A	K1QVR0_CRAGI 26S proteasome non-ATPase regulatory subunit 8
8	A	K1Q6X5_CRAGI Protein disulfide-isomerase
9	A	K1Q6X5_CRAGI Protein disulfide-isomerase
10	A	K1QGB4_CRAGI 40S ribosomal protein S17
11	A	K1QT21_CRAGI Putative ATP-dependent RNA helicase DDX5
12	A	K1Q7Q2_CRAGI CCAAT/enhancer-binding protein zeta
13	A	K1Q6W3_CRAGI Talin-1
14	A	K1R4D4_CRAGI 40S ribosomal protein SA
15	A	K1R4D4_CRAGI 40S ribosomal protein SA
16	A	K1QH70_CRAGI Leucine-rich repeat-containing protein 40
17	A	K1Q880_CRAGI Transportin-1
18	A	K1PS71_CRAGI Uncharacterized protein
19	A	K1PAY7_CRAGI Propionyl-CoA carboxylase alpha chain, mitochondrial
20	A	K1PAY7_CRAGI Propionyl-CoA carboxylase alpha chain, mitochondrial
21	A	K1QPP2_CRAGI Elongation factor Tu, mitochondrial
22	A	K1PX23_CRAGI Eukaryotic peptide chain release factor subunit 1
23	A	K1QRG9_CRAGI Uncharacterized protein
24	A	K1PIB7_CRAGI Phenylalanyl-tRNA synthetase beta chain
25	A	K1R115_CRAGI Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial
26	A	K1R115_CRAGI Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial
27	A	K1PF96_CRAGI Spliceosome RNA helicase BAT1
28	A	K1QFN1_CRAGI 60S ribosomal protein L23
29	A	K1R0D7_CRAGI Eukaryotic translation initiation factor 3 subunit M (Fragment)
30	A	K1R0D7_CRAGI Eukaryotic translation initiation factor 3 subunit M (Fragment)
31	A	K1PK93_CRAGI GDP-L-fucose synthetase
32	A	K1R2D6_CRAGI Plastin-3
33	A	K1Q358_CRAGI 60S acidic ribosomal protein P2
34	A	K1QMV7_CRAGI V-type proton ATPase subunit D
35	A	K1R953_CRAGI Acetyl-CoA carboxylase
36	A	K1PPQ1_CRAGI 14-3-3 protein gamma
37	A	K1PPQ1_CRAGI 14-3-3 protein gamma
38	A	K1QYV6_CRAGI NMDA receptor-regulated protein 1
39	A	K1PH31_CRAGI Protein arginine N-methyltransferase 1
40	A	K1RDV7_CRAGI Cell division control protein 2-like protein (Fragment)
41	A	K1PBZ4_CRAGI Regulator of nonsense transcripts 1
42	A	K1PD57_CRAGI Constitutive coactivator of PPAR-gamma-like protein 1-like protein
43	A	K1PD57_CRAGI Constitutive coactivator of PPAR-gamma-like protein 1-like protein
44	A	K1PVZ3_CRAGI Cold shock domain-containing protein E1
45	A	K1PLA7_CRAGI Eukaryotic initiation factor 4A-II (Fragment)
46	A	K1Q1S3_CRAGI Myosin-VI
47	A	K1QY85_CRAGI Transport protein Sec31A
48	A	K1QH74_CRAGI Splicing factor, arginine/serine-rich 1
49	A	K1RB97_CRAGI Kinetochores-associated protein 1
50	A	K1RB97_CRAGI Kinetochores-associated protein 1
51	A	K1REC3_CRAGI Exportin-5
52	A	K1R3T3_CRAGI Transcription factor BTF3
53	A	K1Q9J5_CRAGI Importin-4
54	A	K1Q0R4_CRAGI ATP-binding cassette sub-family F member 2
55	A	K1Q0R4_CRAGI ATP-binding cassette sub-family F member 2
56	A	K1QD40_CRAGI Importin-7
57	A	K1R5B9_CRAGI DNA-directed RNA polymerase, mitochondrial
58	A	K1PD30_CRAGI Putative histone-binding protein Caf1
59	A	K1QRW4_CRAGI Coronin
60	A	K1RDG4_CRAGI DNA helicase
	A	K1QHY1_CRAGI Eosinophil peroxidase
	A	K1QLS3_CRAGI Cytochrome b-c1 complex subunit 2, mitochondrial
	A	K1Q5G9_CRAGI SUMO-activating enzyme subunit 2
	A	K1QED7_CRAGI Replication protein A subunit
	A	K1S3Y1_CRAGI 2-amino-3-ketobutyrate coenzyme A ligase, mitochondrial (Fragment)
	A	K1PGW7_CRAGI Transmembrane protein 2
	A	K1R7N6_CRAGI Eukaryotic translation initiation factor 6
	A	K1QRL6_CRAGI Methenyltetrahydrofolate synthetase domain-containing protein
	A	K1PN10_CRAGI Intron-binding protein aquarius
	A	K1QNT7_CRAGI Aldehyde dehydrogenase, mitochondrial
	A	K1QLZ1_CRAGI Actin-related protein 3

1		
2		
3	A	K1R9T2_CRAGI Eukaryotic translation initiation factor 3 subunit B
4	A	K1PS27_CRAGI DNA helicase
5	A	K1Q5G6_CRAGI 60 kDa heat shock protein, mitochondrial
6	A	K1QRM1_CRAGI Nuclear pore protein
7	A	K1QGC9_CRAGI Acetyl-coenzyme A synthetase
8	A	K1RLT4_CRAGI Signal recognition particle subunit SRP68
9	A	K1PAR4_CRAGI Unc-45-like protein A
10	A	K1QVE8_CRAGI Phosphoacetylglucosamine mutase
11	A	K1Q4Z4_CRAGI Bifunctional purine biosynthesis protein PURH
12	A	K1P8W6_CRAGI 60S ribosomal protein L4
13	A	K1P8W6_CRAGI 60S ribosomal protein L4
14	A	K1P8W6_CRAGI 60S ribosomal protein L4
15	A	K1QQK1_CRAGI 26S proteasome non-ATPase regulatory subunit 12
16	A	K1RIT6_CRAGI NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial
17	A	K1R2L7_CRAGI Glutaminyl-tRNA synthetase (Fragment)
18	A	K1QRQ2_CRAGI Glutamate dehydrogenase 1, mitochondrial
19	A	K1RKZ5_CRAGI DNA damage-binding protein 1
20	A	K1QC10_CRAGI GTP-binding protein 1
21	A	K1QC10_CRAGI GTP-binding protein 1
22	A	K1PGZ0_CRAGI Thyroid adenoma-associated protein
23	A	K1QUK0_CRAGI NEDD8-activating enzyme E1 catalytic subunit
24	A	K1QQP1_CRAGI Programmed cell death protein 4
25	A	K1PM50_CRAGI 40S ribosomal protein S16
26	A	K1PJS7_CRAGI Poly [ADP-ribose] polymerase
27	A	K1PJS7_CRAGI Poly [ADP-ribose] polymerase
28	A	K1QX37_CRAGI Enolase
29	A	K1QCA7_CRAGI Valyl-tRNA synthetase
30	A	K1Q811_CRAGI Alpha-centractin
31	A	K1Q811_CRAGI Alpha-centractin
32	A	K1QRZ3_CRAGI 40S ribosomal protein S13
33	A	K1QG70_CRAGI Katanin p60 ATPase-containing subunit A1
34	A	K1QW36_CRAGI 60S ribosomal protein L6
35	A	K1R8S7_CRAGI Phospholipase A-2-activating protein
36	A	K1P9N7_CRAGI 14-3-3 protein zeta
37	A	K1P9N7_CRAGI 14-3-3 protein zeta
38	A	K1PG07_CRAGI Lupus La-like protein
39	A	K1QFZ8_CRAGI Ceramide kinase-like protein
40	A	K1Q1Q9_CRAGI Alpha-amino adipic semialdehyde synthase, mitochondrial
41	A	K1PX83_CRAGI Dynein heavy chain 5, axonemal
42	A	K1PCV0_CRAGI Severin
43	A	K1QP17_CRAGI Caprin-1
44	A	K1QP17_CRAGI Caprin-1
45	A	K1PS13_CRAGI Coatomer subunit beta (Fragment)
46	A	K1Q273_CRAGI 60S ribosomal protein L14
47	A	K1PBU0_CRAGI L-fucose kinase
48	A	K1QVV5_CRAGI Periostin
49	A	K1P112_CRAGI ATP synthase subunit gamma, mitochondrial
50	A	K1P112_CRAGI ATP synthase subunit gamma, mitochondrial
51	A	K1QKN4_CRAGI Dynein heavy chain 6, axonemal
52	A	K1P2B8_CRAGI GDP-mannose 4,6 dehydratase
53	A	K1QC11_CRAGI AP-1 complex subunit gamma
54	A	K1QPD6_CRAGI Ubiquitin conjugation factor E4 B
55	A	K1QPD6_CRAGI Ubiquitin conjugation factor E4 B
56	A	K1QWZ0_CRAGI Tetratricopeptide repeat protein 38
57	A	K1QKF8_CRAGI S-(hydroxymethyl)glutathione dehydrogenase
58	A	K1RD83_CRAGI Serine hydroxymethyltransferase
59	A	K1R1F0_CRAGI ATP-dependent DNA helicase 2 subunit 1
60	A	K1QMD8_CRAGI Proteasome subunit alpha type
	A	K1Q8S0_CRAGI Nucleolar complex protein 3 homolog
	A	K1PI50_CRAGI 40S ribosomal protein S26
	A	K1R8T6_CRAGI Cullin-1
	A	K1P6F0_CRAGI HEAT repeat-containing protein 2
	A	K1PXG6_CRAGI Serine/threonine-protein phosphatase
	A	K1QG65_CRAGI rRNA 2'-O-methyltransferase fibrillarin
	A	K1R5W3_CRAGI Uncharacterized protein
	A	K1QB60_CRAGI Uncharacterized protein
	A	K1R5D5_CRAGI U3 small nucleolar RNA-associated protein 6-like protein
	A	K1REJ2_CRAGI Lon protease homolog, mitochondrial
	A	K1PLD4_CRAGI Dynein heavy chain 2, axonemal

1		
2		
3	A	K1QPC6_CRAGI Nucleolar complex protein 2-like protein
4	A	K1PQZ3_CRAGI Armadillo repeat-containing protein 4
5	A	K1Q6F7_CRAGI V-type proton ATPase subunit C
6	A	K1RPF7_CRAGI 60S ribosomal protein L5
7	A	K1QHQ6_CRAGI Acyl-CoA dehydrogenase family member 9, mitochondrial
8	A	K1PFS5_CRAGI Elongation factor 1-gamma
9	A	K1PPW8_CRAGI Coatomer subunit beta
10	A	K1QGE4_CRAGI Proteasome endopeptidase complex (Fragment)
11	A	K1QDX9_CRAGI Ribosome biogenesis protein BMS1-like protein
12	A	K1Q8K2_CRAGI Importin subunit alpha
13	A	K1Q8K2_CRAGI Importin subunit alpha
14	A	K1Q8K2_CRAGI Importin subunit alpha
15	A	K1Q8K2_CRAGI Importin subunit alpha
16	A	K1Q8K2_CRAGI Importin subunit alpha
17	A	K1Q8K2_CRAGI Importin subunit alpha
18	A	K1Q8K2_CRAGI Importin subunit alpha
19	A	K1Q8K2_CRAGI Importin subunit alpha
20	A	K1Q8K2_CRAGI Importin subunit alpha
21	A	K1Q8K2_CRAGI Importin subunit alpha
22	A	K1Q8K2_CRAGI Importin subunit alpha
23	A	K1Q8K2_CRAGI Importin subunit alpha
24	A	K1Q8K2_CRAGI Importin subunit alpha
25	A	K1Q8K2_CRAGI Importin subunit alpha
26	A	K1Q8K2_CRAGI Importin subunit alpha
27	A	K1Q8K2_CRAGI Importin subunit alpha
28	A	K1Q8K2_CRAGI Importin subunit alpha
29	A	K1Q8K2_CRAGI Importin subunit alpha
30	A	K1Q8K2_CRAGI Importin subunit alpha
31	A	K1Q8K2_CRAGI Importin subunit alpha
32	A	K1Q8K2_CRAGI Importin subunit alpha
33	A	K1Q8K2_CRAGI Importin subunit alpha
34	A	K1Q8K2_CRAGI Importin subunit alpha
35	A	K1Q8K2_CRAGI Importin subunit alpha
36	A	K1Q8K2_CRAGI Importin subunit alpha
37	A	K1Q8K2_CRAGI Importin subunit alpha
38	A	K1Q8K2_CRAGI Importin subunit alpha
39	A	K1Q8K2_CRAGI Importin subunit alpha
40	A	K1Q8K2_CRAGI Importin subunit alpha
41	A	K1Q8K2_CRAGI Importin subunit alpha
42	A	K1Q8K2_CRAGI Importin subunit alpha
43	A	K1Q8K2_CRAGI Importin subunit alpha
44	A	K1Q8K2_CRAGI Importin subunit alpha
45	A	K1Q8K2_CRAGI Importin subunit alpha
46	A	K1Q8K2_CRAGI Importin subunit alpha
47	A	K1Q8K2_CRAGI Importin subunit alpha
48	A	K1Q8K2_CRAGI Importin subunit alpha
49	A	K1Q8K2_CRAGI Importin subunit alpha
50	A	K1Q8K2_CRAGI Importin subunit alpha
51	A	K1Q8K2_CRAGI Importin subunit alpha
52	A	K1Q8K2_CRAGI Importin subunit alpha
53	A	K1Q8K2_CRAGI Importin subunit alpha
54	A	K1Q8K2_CRAGI Importin subunit alpha
55	A	K1Q8K2_CRAGI Importin subunit alpha
56	A	K1Q8K2_CRAGI Importin subunit alpha
57	A	K1Q8K2_CRAGI Importin subunit alpha
58	A	K1Q8K2_CRAGI Importin subunit alpha
59	A	K1Q8K2_CRAGI Importin subunit alpha
60	A	K1Q8K2_CRAGI Importin subunit alpha
	A	K1R3I6_CRAGI Nucleolar complex protein 2-like protein (Fragment)
	A	K1QJF7_CRAGI Coronin
	A	K1PKF5_CRAGI Protein-glutamine gamma-glutamyltransferase 4
	A	K1R266_CRAGI Retinal dehydrogenase 1
	A	K1Q3F9_CRAGI Armadillo repeat-containing protein 8
	A	K1QSZ6_CRAGI Uncharacterized protein
	A	K1P8B7_CRAGI Ubiquitin-conjugating enzyme E2-17 kDa (Fragment)
	A	K1QLK8_CRAGI GTP-binding protein SAR1b
	A	K1QF31_CRAGI Serine/threonine-protein kinase PLK
	A	K1RKC1_CRAGI Far upstream element-binding protein 3
	A	K1PHE1_CRAGI Putative ubiquitin carboxyl-terminal hydrolase FAF-X
	A	K1QOL1_CRAGI 60S ribosomal protein L23a

1		
2		
3	A	K1R008_CRAGI Proteasome subunit alpha type
4	A	K1QBG8_CRAGI Proteasome subunit beta type-4
5	A	K1R8B2_CRAGI Isovaleryl-CoA dehydrogenase, mitochondrial
6	A	K1RNN9_CRAGI Cytoskeleton-associated protein 5
7	A	K1QYG7_CRAGI Glucosamine--fructose-6-phosphate aminotransferase [isomerizing] 1
8	A	K1PFK8_CRAGI Uncharacterized protein
9	A	K1PRD5_CRAGI Trifunctional purine biosynthetic protein adenosine-3
10	A	K1PBH3_CRAGI Dynein heavy chain 3, axonemal
11	A	K1QVK0_CRAGI Transaldolase
12	A	K1PAM6_CRAGI Uncharacterized protein
13	A	K1Q948_CRAGI Alpha-1,4 glucan phosphorylase
14	A	K1RGG1_CRAGI Alanyl-tRNA synthetase, cytoplasmic
15	A	K1Q9P5_CRAGI Mitochondrial-processing peptidase subunit beta
16	A	K1QTE3_CRAGI ATP-binding cassette sub-family F member 1
17	A	K1PZ08_CRAGI Ras-related protein Rab-7a
18	A	K1RGJ7_CRAGI Neogenin
19	A	K1RK68_CRAGI Uncharacterized protein
20	A	K1QEF9_CRAGI Protein-glutamine gamma-glutamyltransferase K
21	A	K1RHB2_CRAGI Nucleolar RNA helicase 2
22	A	K1QAF3_CRAGI Alanine aminotransferase 2
23	A	K1PB94_CRAGI ATP-binding cassette sub-family E member 1
24	A	K1R488_CRAGI Actin-related protein 2/3 complex subunit
25	A	K1QC65_CRAGI DNA polymerase alpha subunit B
26	A	K1PCR9_CRAGI Proteasome endopeptidase complex
27	A	K1RFU6_CRAGI Proteasome activator complex subunit 3
28	A	K1R9R5_CRAGI Proteasome subunit alpha type
29	A	K1PRQ5_CRAGI Ubiquitin-like modifier-activating enzyme 1
30	A	K1Q1L4_CRAGI Uncharacterized protein
31	A	K1Q982_CRAGI Malignant fibrous histiocytoma-amplified sequence 1
32	A	K1PKF6_CRAGI 26S proteasome non-ATPase regulatory subunit 13
33	A	K1QBT2_CRAGI Proteasome subunit beta
34	A	K1P5Z3_CRAGI Lysosomal aspartic protease
35	A	K1P7L9_CRAGI Nucleolar GTP-binding protein 1
36	A	K1Q9M7_CRAGI Histone H1-delta
37	A	K1PS84_CRAGI Alpha-crystallin B chain
38	A	K1R6C2_CRAGI Peroxisomal 3,2-trans-enoyl-CoA isomerase
39	A	K1PZC0_CRAGI Structural maintenance of chromosomes protein
40	A	K1PMJ9_CRAGI Cleavage stimulation factor 77 kDa subunit
41	A	K1R4M7_CRAGI Serine/threonine protein phosphatase 2A regulatory subunit
42	A	K1S3G2_CRAGI HMGB1
43	A	K1PB82_CRAGI Electron transfer flavoprotein subunit beta
44	A	K1PWP4_CRAGI Phenylalanyl-tRNA synthetase alpha chain
45	A	K1QNS4_CRAGI DnaJ-like protein subfamily C member 9
46	A	K1Q7E4_CRAGI Ubiquitin-conjugating enzyme E2 N
47	A	K1R6F1_CRAGI Proteasome subunit alpha type
48	A	K1Q667_CRAGI tRNA-splicing ligase RtcB homolog
49	A	K1QWC3_CRAGI 40S ribosomal protein S3
50	A	K1RAH6_CRAGI Ubiquitin-conjugating enzyme E2-17 kDa
51	A	K1RIM7_CRAGI Methionine aminopeptidase 2
52	A	K1PXS8_CRAGI Calreticulin
53	A	K1RIG6_CRAGI LSM14-like protein A
54	A	K1R168_CRAGI Dynein heavy chain 2, axonemal
55	A	K1R591_CRAGI Inter-alpha-trypsin inhibitor heavy chain H4
56	A	K1QK11_CRAGI Tudor domain-containing protein 1
57	A	K1RNB6_CRAGI Alpha-aminoadipic semialdehyde dehydrogenase
58	A	K1ROY9_CRAGI ADP,ATP carrier protein
59	A	K1QE83_CRAGI CCR4-NOT transcription complex subunit 1
60	A	K1QFR9_CRAGI Spectrin beta chain
	A	K1RAP8_CRAGI Malic enzyme
	A	K1PK49_CRAGI Myosin-Ic

1		
2		
3	A	K1QAH9_CRAGI H/ACA ribonucleoprotein complex subunit
4	A	K1PYR4_CRAGI 26S proteasome non-ATPase regulatory subunit 1
5	A	K1R8C6_CRAGI 40S ribosomal protein S12
6	A	K1PY89_CRAGI Extracellular superoxide dismutase [Cu-Zn]
7	A	K1Q662_CRAGI Actin-interacting protein 1
8	A	K1Q4G7_CRAGI Tubulin gamma chain
9	A	K1R472_CRAGI Synaptobrevin-like protein YKT6
10	A	K1PS69_CRAGI Importin-9
11	A	K1QDU9_CRAGI 3-phosphoinositide-dependent protein kinase 1
12	A	K1PFU5_CRAGI Ubiquitin-conjugating enzyme E2 C
13	A	K1QKG8_CRAGI Upstream activation factor subunit spp27
14	A	K1ROP8_CRAGI CTP synthase
15	A	K1QZX9_CRAGI Uncharacterized protein
16	A	K1QTD9_CRAGI Nucleolar protein 56
17	A	K1PIP8_CRAGI Proteasome subunit beta
18	A	K1RBF6_CRAGI Uncharacterized protein yfeX
19	A	K1PW99_CRAGI Protein OSCP1
20	A	K1PWB9_CRAGI EH domain-containing protein 1
21	A	K1PU46_CRAGI Lethal(2) giant larvae-like protein 1
22	A	K1QYH6_CRAGI COP9 signalosome complex subunit 3
23	A	K1Q6I1_CRAGI Ubiquitin-conjugating enzyme E2 L3
24	A	K1PF60_CRAGI 3-ketoacyl-CoA thiolase, mitochondrial
25	A	K1PQD4_CRAGI Phosphoglucomutase-1
26	A	K1PSNO_CRAGI Pre-mRNA-processing factor 40-like protein A
27	A	K1R834_CRAGI 60S ribosomal protein L9
28	A	K1RBU9_CRAGI Non-specific serine/threonine protein kinase
29	A	K1QHM2_CRAGI Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2
30	A	K1QW73_CRAGI Glycoprotein 3-alpha-L-fucosyltransferase A
31	A	K1Q7X3_CRAGI Pre-mRNA-splicing factor SYF1
32	A	K1PUJ1_CRAGI Radixin
33	A	K1R8I8_CRAGI Acetyltransferase component of pyruvate dehydrogenase complex
34	A	K1PRL4_CRAGI 60S ribosomal protein L38 (Fragment)
35	A	K1Q0G7_CRAGI Developmentally-regulated GTP-binding protein 2
36	A	K1PBN1_CRAGI Phospholipase
37	A	K1QJ33_CRAGI Aminoacyl tRNA synthetase complex-interacting multifunctional protein 2
38	A	A5LGH1_CRAGI Voltage-dependent anion channel
39	A	K1PUV4_CRAGI 40S ribosomal protein S24
40	A	K1QJE9_CRAGI Uncharacterized protein
41	A	K1R005_CRAGI Filamin-C (Fragment)
42	A	K1RGB7_CRAGI Epidermal retinal dehydrogenase 2
43	A	K1PPJ6_CRAGI Nicotinamide phosphoribosyltransferase
44	A	K1PEW1_CRAGI Sorting nexin
45	A	K1QDH9_CRAGI Myosin-11
46	A	K1QPJ9_CRAGI Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B
47	A	K1R9S5_CRAGI Cytosolic Fe-S cluster assembly factor NUBP2 homolog
48	A	K1PTV1_CRAGI Splicing factor 3B subunit 4
49	A	K1Q5H6_CRAGI FACT complex subunit SSRP1
50	A	K1RN05_CRAGI Transportin-3
51	A	K1PDE4_CRAGI Protein arginine N-methyltransferase
52	A	K1Q9G3_CRAGI Isocitrate dehydrogenase [NAD] subunit, mitochondrial
53	A	K1R2H9_CRAGI WD repeat-containing protein 35
54	A	K1PA61_CRAGI Actin-like protein 6A
55	A	K1QQT2_CRAGI Uncharacterized protein y4x0
56	A	K1PJG8_CRAGI Timeless-like protein
57	A	K1QJM1_CRAGI 60S ribosomal protein L30
58	A	K1QK68_CRAGI Myosin-2 essential light chain
59	A	K1R517_CRAGI Superkiller viralicidic activity 2-like 2
60	A	K1Q6V6_CRAGI Replication factor C subunit 4
	A	K1Q888_CRAGI Translin
	A	K1QQC1_CRAGI Dynein light chain roadblock

1		
2		
3	A	K1Q1F4_CRAGI 60S ribosomal protein L3 (Fragment)
4	A	K1Q2E0_CRAGI AP-1 complex subunit mu-1
5	A	K1Q155_CRAGI THO complex subunit 1
6	A	K1R3M4_CRAGI Ubiquitin-like modifier-activating enzyme 1
7	A	K1PML4_CRAGI Pre-mRNA-processing factor 39
8	A	K1QEK7_CRAGI Ubiquitin carboxyl-terminal hydrolase
9	A	K1QDI4_CRAGI Superoxide dismutase [Cu-Zn]
10	A	K1Q1Z3_CRAGI Seryl-tRNA synthetase, cytoplasmic
11	A	K1Q4X8_CRAGI DNA mismatch repair protein Msh2
12	A	K1Q4X8_CRAGI DNA mismatch repair protein Msh2
13	A	K1P5F7_CRAGI Metastasis-associated protein MTA1
14	A	K1R7J6_CRAGI Putative sodium/potassium-transporting ATPase subunit beta-2
15	A	K1R7J6_CRAGI Putative sodium/potassium-transporting ATPase subunit beta-2
16	A	K1QNY7_CRAGI Transport protein Sec24C
17	A	K1QKQ5_CRAGI N-terminal acetyltransferase B complex subunit MDM20
18	A	K1PH10_CRAGI Polyadenylate-binding protein-interacting protein 1
19	A	K1Q329_CRAGI Pyruvate dehydrogenase E1 component subunit beta, mitochondrial
20	A	K1Q329_CRAGI Pyruvate dehydrogenase E1 component subunit beta, mitochondrial
21	A	K1QI08_CRAGI Ribose-phosphate pyrophosphokinase 1
22	A	K1QV87_CRAGI Catenin alpha-2
23	A	K1PXD4_CRAGI Putative ATP-dependent RNA helicase DDX6
24	A	K1QCQ5_CRAGI Succinate--CoA ligase [ADP-forming] subunit beta, mitochondrial
25	A	K1QCQ5_CRAGI Succinate--CoA ligase [ADP-forming] subunit beta, mitochondrial
26	A	K1QCL6_CRAGI Proteasomal ubiquitin receptor ADRM1
27	A	K1PFV9_CRAGI 4-trimethylaminobutyraldehyde dehydrogenase
28	A	K1PTR3_CRAGI Oxysterol-binding protein
29	A	K1R1T8_CRAGI Nucleolar protein 56
30	A	K1QUC6_CRAGI Uncharacterized protein
31	A	K1QUC6_CRAGI Uncharacterized protein
32	A	K1QCM0_CRAGI Rho GDP-dissociation inhibitor 1
33	A	K1QNZ3_CRAGI Serine/threonine-protein phosphatase
34	A	K1QKG9_CRAGI Cysteine desulfurase, mitochondrial
35	A	K1RUW0_CRAGI E3 SUMO-protein ligase RanBP2
36	A	K1QPZ1_CRAGI Actin-related protein 2/3 complex subunit 3
37	A	K1QHT0_CRAGI Deoxyuridine 5'-triphosphate nucleotidohydrolase, mitochondrial
38	A	K1QHT0_CRAGI Deoxyuridine 5'-triphosphate nucleotidohydrolase, mitochondrial
39	A	K1Q5I4_CRAGI COP9 signalosome complex subunit 2
40	A	K1PLW6_CRAGI Bifunctional purine biosynthesis protein PURH
41	A	K1PWU5_CRAGI Cytosolic carboxypeptidase 1
42	A	K1P9S7_CRAGI Brix domain-containing protein 2
43	A	K1P9S7_CRAGI Brix domain-containing protein 2
44	A	K1Q260_CRAGI Nucleolar protein 58
45	A	K1PKL8_CRAGI Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit alpha isoform
46	A	K1S1X3_CRAGI SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5
47	A	K1Q3F4_CRAGI Inorganic pyrophosphatase
48	A	K1P7J8_CRAGI 6-phosphofructokinase
49	A	K1QXR6_CRAGI Protein farnesyltransferase/geranylgeranyltransferase type-1 subunit alpha
50	A	K1QXR6_CRAGI Protein farnesyltransferase/geranylgeranyltransferase type-1 subunit alpha
51	A	K1Q4Q8_CRAGI Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial
52	A	K1RA63_CRAGI Transmembrane protein 2
53	A	K1Q8T3_CRAGI Importin subunit alpha
54	A	K1QMT1_CRAGI DnaJ-like protein subfamily B member 4
55	A	K1RBT5_CRAGI Ran GTPase-activating protein 1
56	A	K1RBT5_CRAGI Ran GTPase-activating protein 1
57	A	K1PST9_CRAGI Brefeldin A-inhibited guanine nucleotide-exchange protein 1
58	A	K1QWJ4_CRAGI Splicing factor 3B subunit 5
59	A	K1QYT7_CRAGI COP9 signalosome complex subunit 7a
60	A	K1R7D7_CRAGI Poly(A)-specific ribonuclease PARN
	A	K1QZI3_CRAGI Myosin-le
	A	K1PNX0_CRAGI Methionyl-tRNA synthetase, cytoplasmic
	A	K1Q324_CRAGI Heterogeneous nuclear ribonucleoprotein K
	A	K1QY71_CRAGI Histone H2B
	A	K1QDA7_CRAGI Uracil phosphoribosyltransferase
	A	K1RAU8_CRAGI Eukaryotic translation initiation factor 3 subunit E
	A	K1QRD0_CRAGI Cytoplasmic dynein 1 light intermediate chain 1
	A	K1Q719_CRAGI Serine/threonine-protein kinase OSR1
	A	K1RJJ7_CRAGI Histone H5
	A	K1P8Y3_CRAGI Sulfotransferase 1C4
	A	K1QMY1_CRAGI Aconitate hydratase, mitochondrial

1		
2		
3	A	K1RBI9_CRAGI Small nuclear ribonucleoprotein Sm D2
4	A	K1QEJ0_CRAGI Ras GTPase-activating protein-binding protein 2
5	A	K1Q5Z6_CRAGI Eukaryotic translation initiation factor 2 subunit 2
6	A	K1RGS1_CRAGI WD repeat-containing protein 19
7	A	K1R195_CRAGI Protein DJ-1
8	A	K1R8Y1_CRAGI Obg-like ATPase 1
9	A	K1RRH1_CRAGI Chromodomain-helicase-DNA-binding protein Mi-2-like protein
10	A	K1PM66_CRAGI 60S ribosomal protein L12
11	A	K1PKQ3_CRAGI Uncharacterized protein
12	A	K1QIB2_CRAGI Mitogen-activated protein kinase
13	A	K1PSN4_CRAGI Tetratricopeptide repeat protein 39C
14	A	K1PT09_CRAGI Uncharacterized protein
15	A	K1S0I4_CRAGI Methylthioribose-1-phosphate isomerase
16	A	K1Q9I1_CRAGI TRAF2 and NCK-interacting protein kinase
17	A	K1R5G4_CRAGI 60S ribosomal protein L31
18	A	K1R7F6_CRAGI Cystathionine gamma-lyase
19	A	K1QGP1_CRAGI Replication factor C subunit 2
20	A	K1Q4S7_CRAGI Calreticulin
21	A	K1RTQ6_CRAGI Fructose-bisphosphate aldolase
22	A	K1QN79_CRAGI 40S ribosomal protein S11
23	A	K1R6E9_CRAGI Dihydrolipoamide acetyltransferase component of pyruvate dehydrogenase complex
24	A	K1PXU6_CRAGI 60S ribosomal protein L24
25	A	K1PVA0_CRAGI Cullin-5
26	A	K1QSZ4_CRAGI Serine--pyruvate aminotransferase
27	A	K1RNH1_CRAGI 60S ribosomal protein L18 (Fragment)
28	A	K1PIH2_CRAGI V-type proton ATPase subunit E
29	A	K1QG08_CRAGI Phosphatidylinositol-binding clathrin assembly protein LAP
30	A	K1RVR1_CRAGI Telomerase protein component 1
31	A	K1Q9D7_CRAGI Sorting nexin-2
32	A	K1PDC6_CRAGI Proteasome subunit beta
33	A	K1R1E2_CRAGI Arp2/3 complex 34 kDa subunit
34	A	K1PCR5_CRAGI KH domain-containing, RNA-binding, signal transduction-associated protein 2
35	A	K1P8S5_CRAGI Condensin complex subunit 3
36	A	K1PCH8_CRAGI Nucleoporin p54
37	A	K1QY58_CRAGI Eukaryotic translation initiation factor 3 subunit I (Fragment)
38	A	K1Q947_CRAGI Dynein light chain
39	A	K1Q615_CRAGI Peroxiredoxin-1
40	A	K1QC78_CRAGI Ras-related protein Rab-14
41	A	K1QET6_CRAGI Neurobeachin
42	A	K1PG48_CRAGI Dynein-1-beta heavy chain, flagellar inner arm I1 complex
43	A	K1R9P5_CRAGI Mitochondrial import receptor subunit TOM70
44	A	K1PGV8_CRAGI Nucleoprotein TPR
45	A	K1PRV7_CRAGI Profilin
46	A	K1QIZ7_CRAGI Programmed cell death protein 6
47	A	K1Q4U7_CRAGI AP-3 complex subunit delta-1
48	A	K1QGL9_CRAGI Mannose-1-phosphate guanyltransferase beta
49	A	K1PBL2_CRAGI Eukaryotic initiation factor 4A-III
50	A	K1R3A0_CRAGI Transcription initiation factor IIB
51	A	K1P7Q2_CRAGI Elongation factor 1-gamma
52	A	K1PNU2_CRAGI Histone-arginine methyltransferase CARM1
53	A	K1PWP8_CRAGI Echinoderm microtubule-associated protein-like 1
54	A	K1QV46_CRAGI Tetratricopeptide repeat protein 21B
55	A	K1QKQ9_CRAGI Dynein heavy chain 7, axonemal
56	A	K1PR47_CRAGI Eukaryotic translation initiation factor 2A
57	A	K1S058_CRAGI Transcription factor RFX3
58	A	K1QEG3_CRAGI Heat shock 70 kDa protein 12B
59	A	K1R481_CRAGI Epimerase family protein SDR39U1
60	A	K1QBF3_CRAGI Trpc4-associated protein
	A	K1PUX5_CRAGI Casein kinase II subunit alpha
	A	K1QK98_CRAGI IST1-like protein

1		
2		
3	A	K1RDV2_CRAGI Myotrophin-like protein
4	A	K1PDL3_CRAGI Ribosomal protein L19
5	A	K1S2S8_CRAGI Signal recognition particle 54 kDa protein
6	A	K1QZ11_CRAGI Geranylgeranyl transferase type-2 subunit alpha
7	A	K1QU47_CRAGI Dual oxidase 2
8	A	K1QXF9_CRAGI Acyl-protein thioesterase 2
9	A	K1PL64_CRAGI Poly(A) polymerase gamma
10	A	K1RQJ6_CRAGI Enhancer of mRNA-decapping protein 4
11	A	K1QLP5_CRAGI Coatomer subunit delta
12	A	K1PJB0_CRAGI Heat shock protein 70 B2
13	A	K1Q404_CRAGI DNA topoisomerase 2
14	A	K1QJA7_CRAGI Histone chaperone asf1-B
15	A	K1RP91_CRAGI Putative RNA exonuclease NEF-sp
16	A	K1PZD9_CRAGI 26S proteasome non-ATPase regulatory subunit 11
17	A	K1QI32_CRAGI Synaptotagmin-like protein 5
18	A	K1RK83_CRAGI Tyrosine-protein kinase BAZ1B
19	A	K1QQG2_CRAGI ATP-dependent RNA helicase DHX8
20	A	K1PUQ5_CRAGI Histone H2B
21	A	K1QW72_CRAGI Catalase
22	A	K1R2U8_CRAGI Universal stress protein A-like protein
23	A	K1PY30_CRAGI Septin-2
24	A	K1Q8C5_CRAGI Putative ATP-dependent RNA helicase DDX47
25	A	K1QNP9_CRAGI Putative deoxyribose-phosphate aldolase
26	A	K1PDF0_CRAGI Protein disulfide-isomerase A6
27	A	K1R1R9_CRAGI Pre-mRNA-processing factor 6
28	A	K1Q3G8_CRAGI Chaperone activity of bc1 complex-like, mitochondrial
29	A	K1QBH4_CRAGI ATP-dependent RNA helicase DDX42
30	A	K1PEM0_CRAGI Ubiquitin-like modifier-activating enzyme 5
31	A	K1QD23_CRAGI Acetyl-CoA acetyltransferase B, mitochondrial
32	A	K1RJ96_CRAGI Sphere organelles protein SPH-1
33	A	K1R1B1_CRAGI 35 kDa SR repressor protein
34	A	K1QCB0_CRAGI 40S ribosomal protein S5
35	A	K1RGZ8_CRAGI Wings apart-like protein
36	A	K1Q107_CRAGI Histidine triad nucleotide-binding protein 1
37	A	K1QYM1_CRAGI Thymidylate synthase
38	A	K1QYT5_CRAGI Phosphate carrier protein, mitochondrial
39	A	K1QJT3_CRAGI COP9 signalosome complex subunit 1
40	A	K1QAU8_CRAGI Peptidyl-prolyl cis-trans isomerase E
41	A	K1RG28_CRAGI Kinase C and casein kinase substrate in neurons protein 2
42	A	K1R2S4_CRAGI NEDD8-activating enzyme E1 regulatory subunit (Fragment)
43	A	K1Q4Y8_CRAGI Histone H1oo
44	A	K1PYQ1_CRAGI Protein phosphatase 1 regulatory subunit 7
45	A	K1RWE5_CRAGI Thioredoxin-like protein 1
46	A	K1QJL2_CRAGI CCR4-NOT transcription complex subunit 10
47	A	K1P6C4_CRAGI Poly [ADP-ribose] polymerase
48	A	K1PNL0_CRAGI Microtubule-associated protein futsch
49	A	K1QSA2_CRAGI Short-chain specific acyl-CoA dehydrogenase, mitochondrial
50	A	K1QU30_CRAGI MON2-like protein
51	A	K1Q317_CRAGI Serine/threonine-protein kinase SRPK1
52	A	K1RGE2_CRAGI Prostaglandin reductase 1
53	A	K1RIB1_CRAGI Arginyl-tRNA synthetase, cytoplasmic
54	A	K1ROW0_CRAGI Ferritin
55	A	K1P8T5_CRAGI Glycerol-3-phosphate dehydrogenase [NAD(+)]
56	A	K1QQD8_CRAGI Putative ATP-dependent RNA helicase DDX43
57	A	K1QMH5_CRAGI Small nuclear ribonucleoprotein Sm D1
58	A	K1QS22_CRAGI UPF0160 protein MYG1, mitochondrial (Fragment)
59	A	K1QHP8_CRAGI Uncharacterized protein
60	A	K1PXM3_CRAGI Chromatin assembly factor 1 subunit A
	A	K1QF45_CRAGI Alpha-tocopherol transfer-like protein
	A	K1QC27_CRAGI Hydroxysteroid dehydrogenase-like protein 2

1		
2		
3	A	Q70MT4_CRAGI 40S ribosomal protein S10
4	A	K1PQB4_CRAGI Acyl-CoA dehydrogenase family member 10
5	A	K1PZI3_CRAGI SWI/SNF complex subunit SMARCC2
6	A	K1PNS2_CRAGI 33 kDa inner dynein arm light chain, axonemal
7	A	K1RG36_CRAGI Phosphoribosylformylglycinamide synthase (Fragment)
8	A	K1QMQ0_CRAGI Putative exonuclease mut-7-like protein
9	A	K1QD80_CRAGI Protein quaking-B
10	A	K1R0M2_CRAGI Uncharacterized protein
11	A	K1QKI4_CRAGI Lysine--tRNA ligase
12	A	K1PPH6_CRAGI Kelch domain-containing protein 8B
13	A	K1QBE2_CRAGI Syntaxin-5
14	A	K1RHP3_CRAGI Proliferation-associated protein 2G4
15	A	K1PZU1_CRAGI Hsc70-interacting protein
16	A	K1RMW3_CRAGI Protein kinase C
17	A	K1R1Q8_CRAGI Ras-related protein Rab-5C
18	A	K1PPK1_CRAGI Actin-related protein 2/3 complex subunit 4
19	A	K1R8Y9_CRAGI Translin-associated protein X
20	A	K1QW41_CRAGI Leucine-zipper-like transcriptional regulator 1
21	A	K1Q1G2_CRAGI Elongator complex protein 1
22	A	K1RA79_CRAGI E3 ubiquitin-protein ligase HECTD1
23	A	K1RZM3_CRAGI Cartilage acidic protein 1
24	A	K1QD81_CRAGI Ubiquitin conjugation factor E4 A
25	A	K1PMY9_CRAGI Calmodulin
26	A	K1RU04_CRAGI Actin, cytoplasmic
27	A	K1QND2_CRAGI Septin-2
28	A	K1PR25_CRAGI Regulator of differentiation 1
29	A	K1QV25_CRAGI Transcription elongation factor B polypeptide 2
30	A	K1RJ70_CRAGI Cytosolic non-specific dipeptidase
31	A	K1R751_CRAGI Nuclear pore complex protein Nup88
32	A	K1QDK0_CRAGI Engulfment and cell motility protein 2
33	A	K1PLV6_CRAGI F-actin-capping protein subunit alpha
34	A	K1QWN2_CRAGI Elongation factor 1-delta
35	A	K1RRP7_CRAGI Uncharacterized protein
36	A	K1R6H7_CRAGI Uncharacterized protein
37	A	K1REP0_CRAGI Uncharacterized protein
38	A	K1R0L4_CRAGI Sodium/potassium-transporting ATPase subunit alpha
39	A	K1R0V5_CRAGI Cell differentiation protein RCD1-like protein
40	A	K1R2N1_CRAGI Glutathione reductase
41	A	K1PRB6_CRAGI Apolipoprotein D
42	A	K1QMF1_CRAGI Isocitrate dehydrogenase [NAD] subunit gamma, mitochondrial
43	A	K1R5E7_CRAGI Cathepsin L
44	A	K1PMI0_CRAGI Charged multivesicular body protein 4b
45	A	K1QZN3_CRAGI Myosin-IId
46	A	K1S0N3_CRAGI Glutamate receptor-interacting protein 1
47	A	K1RDM2_CRAGI 60S ribosomal protein L18a
48	A	K1R0R7_CRAGI Putative ATP-dependent RNA helicase DHX36
49	A	K1QWX0_CRAGI 26S proteasome non-ATPase regulatory subunit 14
50	A	K1PQA3_CRAGI Pseudouridylate synthase 7-like protein
51	A	K1Q7K0_CRAGI Putative serine carboxypeptidase CPVL
52	A	K1R7N8_CRAGI Proteasome endopeptidase complex
53	A	K1QCL7_CRAGI Uncharacterized protein
54	A	K1QQB3_CRAGI Glycyl-tRNA synthetase
55	A	K1RFU8_CRAGI High mobility group protein DSP1
56	A	K1PJW0_CRAGI Talin-1
57	A	K1RBJ3_CRAGI DnaJ-like protein subfamily C member 13
58	A	K1PRV2_CRAGI Threonine synthase-like 1
59	A	K1R347_CRAGI Tetratricopeptide repeat protein 38
60	A	K1S422_CRAGI Katanin p80 WD40 repeat-containing subunit B1
	A	K1QK18_CRAGI Cytochrome b5
	A	K1QJU3_CRAGI Cell division cycle protein 20-like protein

1		
2		
3	A	K1QRM9_CRAGI Acidic leucine-rich nuclear phosphoprotein 32 family member A
4	A	K1R373_CRAGI ATP-binding cassette sub-family F member 3
5	A	K1RE81_CRAGI Transport protein Sec24B
6	A	K1QW21_CRAGI 39S ribosomal protein L40, mitochondrial
7	A	K1PLG1_CRAGI Putative ribosomal RNA methyltransferase NOP2
8	A	K1R712_CRAGI Transforming growth factor-beta receptor-associated protein 1
9	A	K1R712_CRAGI Transforming growth factor-beta receptor-associated protein 1
10	A	K1Q1K8_CRAGI Elongation factor 1-beta
11	A	K1PNK5_CRAGI Ras GTPase-activating-like protein IQGAP1
12	A	K1Q1F1_CRAGI Serine/threonine-protein kinase 31
13	A	K1QFS4_CRAGI Actin-related protein 2
14	A	K1PUK3_CRAGI Armadillo repeat-containing protein 6
15	A	K1PI41_CRAGI Flap endonuclease 1
16	A	K1PI41_CRAGI Flap endonuclease 1
17	A	K1QU96_CRAGI Pre-rRNA-processing protein TSR1-like protein
18	A	K1QFK8_CRAGI Target of Myb protein 1
19	A	K1R4Q3_CRAGI Spectrin beta chain, brain 1
20	A	K1R4Q3_CRAGI Spectrin beta chain, brain 1
21	A	K1QMS7_CRAGI Malonyl CoA-acyl carrier protein transacylase, mitochondrial
22	A	K1P8Q1_CRAGI Putative methyltransferase TARBP1
23	A	K1RXV8_CRAGI PAT1-like protein 1
24	A	K1PXH5_CRAGI Putative saccharopine dehydrogenase
25	A	K1PXH5_CRAGI Putative saccharopine dehydrogenase
26	A	K1QWP1_CRAGI Nucleoporin seh1
27	A	K1RDF6_CRAGI Long-chain specific acyl-CoA dehydrogenase, mitochondrial
28	A	K1QYH5_CRAGI Ubiquitin carboxyl-terminal hydrolase 14
29	A	K1S0J9_CRAGI Uncharacterized protein
30	A	K1R247_CRAGI Condensin complex subunit 1
31	A	K1R247_CRAGI Condensin complex subunit 1
32	A	K1QKZ6_CRAGI Inosine-5'-monophosphate dehydrogenase
33	A	K1QQ48_CRAGI Serine/threonine-protein kinase N2
34	A	K1RIZ3_CRAGI Bone morphogenetic protein 7
35	A	K1PVQ8_CRAGI Eukaryotic translation initiation factor 3 subunit K
36	A	K1QMQ1_CRAGI TBC1 domain family member 10B
37	A	K1QMQ1_CRAGI TBC1 domain family member 10B
38	A	K1QFF0_CRAGI Vacuolar protein sorting-associated protein 35 (Fragment)
39	A	K1Q435_CRAGI Eukaryotic translation initiation factor 2 subunit 1
40	A	K1Q435_CRAGI Eukaryotic translation initiation factor 2 subunit 1
41	A	K1QNZ7_CRAGI Ubiquilin-1
42	A	K1QYI6_CRAGI Cullin-3-B
43	A	K1PFV4_CRAGI Eukaryotic translation initiation factor 4E
44	A	K1QVV1_CRAGI Ribose-5-phosphate isomerase
45	A	K1RT39_CRAGI Glutaredoxin-3
46	A	K1PNG7_CRAGI Sorting nexin-33
47	A	K1PYK7_CRAGI RNA-binding protein 39
48	A	K1QCP3_CRAGI Crooked neck-like protein 1
49	A	K1QSV4_CRAGI RNA helicase
50	A	K1QSV4_CRAGI RNA helicase
51	A	K1R811_CRAGI Ribonucleoside-diphosphate reductase small chain
52	A	K1R944_CRAGI Tetratricopeptide repeat protein 37
53	A	K1QS07_CRAGI Proteasome subunit beta type-3
54	A	K1PZV3_CRAGI Guanine nucleotide-binding protein-like 3-like protein (Fragment)
55	A	K1PZV3_CRAGI Guanine nucleotide-binding protein-like 3-like protein (Fragment)
56	A	K1QNU0_CRAGI Non-specific serine/threonine protein kinase
57	A	K1R3R4_CRAGI Cytosolic Fe-S cluster assembly factor NUBP1 homolog
58	A	K1R3R4_CRAGI Cytosolic Fe-S cluster assembly factor NUBP1 homolog
59	A	K1RJS5_CRAGI Uncharacterized protein
60	A	K1RNK8_CRAGI Rho GTPase-activating protein 17
	A	K1RG79_CRAGI Neuronal acetylcholine receptor subunit alpha-6
	A	K1QVF8_CRAGI Uncharacterized protein in QAH/OAS sulfhydrylase 3'region (Fragment)
	A	K1Q4C3_CRAGI Fumarylacetoacetase
	A	K1R7T0_CRAGI GMP synthase [glutamine-hydrolyzing]
	A	K1QX22_CRAGI 4-hydroxyphenylpyruvate dioxygenase
	A	K1RIS2_CRAGI 3-oxoacyl-[acyl-carrier-protein] reductase
	A	K1Q407_CRAGI Ras GTPase-activating protein 1
	A	K1R9I0_CRAGI Myosin-VIIa
	A	K1Q0N9_CRAGI Uncharacterized protein
	A	K1PUE8_CRAGI Serine/threonine-protein phosphatase 4 regulatory subunit 3
	A	K1PSY2_CRAGI Fragile X mental retardation syndrome-related protein 1
	A	K1RA35_CRAGI Splicing factor, arginine/serine-rich 7

1		
2		
3	A	K1QW39_CRAGI Neurobeachin
4	A	K1QJ19_CRAGI Importin-13
5	A	K1R3M6_CRAGI Ubiquitin-conjugating enzyme E2-22 kDa
6	A	K1RCR8_CRAGI Carbonyl reductase [NADPH] 1
7	A	K1R1JW8_CRAGI Protein DEK
8	A	K1R2G9_CRAGI SEC13-like protein
9	A	K1PLF8_CRAGI Diacylglycerol kinase
10	A	K1PWV7_CRAGI Uncharacterized protein
11	A	K1R3W9_CRAGI Replication protein A 14 kDa subunit
12	A	K1P8G1_CRAGI Heterogeneous nuclear ribonucleoprotein H
13	A	K1R2S2_CRAGI Peptidylprolyl isomerase
14	A	K1PNY5_CRAGI Splicing factor, proline-and glutamine-rich
15	A	K1P7Q6_CRAGI 40S ribosomal protein S19
16	A	K1PZN1_CRAGI Calcium/calmodulin-dependent protein kinase type II delta chain
17	A	K1PBC0_CRAGI Non-neuronal cytoplasmic intermediate filament protein
18	A	K1QNN9_CRAGI MICOS complex subunit MIC60
19	A	K1QJ46_CRAGI Putative methylcrotonoyl-CoA carboxylase beta chain, mitochondrial
20	A	K1R2G7_CRAGI Ran-binding protein 3
21	A	K1RJG6_CRAGI Heterogeneous nuclear ribonucleoprotein 27C
22	A	K1QZ58_CRAGI Splicing factor U2AF 26 kDa subunit
23	A	K1QCU0_CRAGI Eukaryotic translation initiation factor 3 subunit G
24	A	K1PH25_CRAGI Methionyl-tRNA synthetase, cytoplasmic
25	A	K1RN97_CRAGI Hemagglutinin/amebocyte aggregation factor
26	A	K1Q6M6_CRAGI 6-phosphofructokinase
27	A	K1PPL6_CRAGI Malonyl-CoA decarboxylase, mitochondrial
28	A	K1R9Q4_CRAGI Uncharacterized protein
29	A	K1QPX8_CRAGI Alkyl/aryl-sulfatase BDS1
30	A	K1PJP2_CRAGI Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15
31	A	K1RRZ9_CRAGI MKI67 FHA domain-interacting nucleolar phosphoprotein-like protein
32	A	K1S6R2_CRAGI N-acetyltransferase 11
33	A	K1PJY4_CRAGI Calcium-binding protein 39
34	A	K1Q1G9_CRAGI Putative ATP-dependent RNA helicase DHX37
35	A	K1RA95_CRAGI Filamin-A
36	A	K1Q865_CRAGI Trafficking protein particle complex subunit 4
37	A	K1RFQ4_CRAGI Tetratricopeptide repeat protein 27
38	A	K1QRD4_CRAGI S-formylglutathione hydrolase
39	A	K1Q9Z4_CRAGI Aldehyde dehydrogenase
40	A	K1QB76_CRAGI Uncharacterized protein
41	A	K1Q2Y1_CRAGI 40S ribosomal protein S15
42	A	K1S3Q9_CRAGI MAK16-like protein (Fragment)
43	A	K1RAF8_CRAGI Uncharacterized protein
44	A	K1QE44_CRAGI UPF0663 transmembrane protein C17orf28
45	A	K1PN44_CRAGI Casein kinase II subunit beta
46	A	K1PWR4_CRAGI Signal recognition particle receptor subunit alpha
47	A	K1QDS1_CRAGI 3-hydroxyacyl-CoA dehydrogenase type-2
48	A	K1R924_CRAGI RNA-binding protein 45
49	A	K1QWZ6_CRAGI Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1
50	A	K1PSH2_CRAGI 28S ribosomal protein S12, mitochondrial
51	A	K1QKL1_CRAGI DNA-directed RNA polymerases I, II, and III subunit RPABC3
52	A	K1RCY7_CRAGI Eukaryotic peptide chain release factor GTP-binding subunit ERF3B
53	A	K1Q6U7_CRAGI 78 kDa glucose-regulated protein
54	A	K1R2E8_CRAGI Prolyl endopeptidase
55	A	K1R4M1_CRAGI Intraflagellar transport protein 52-like protein
56	A	K1RB91_CRAGI Neutral alpha-glucosidase AB
57	A	K1Q056_CRAGI Calpain-A
58	A	K1REW8_CRAGI Ribosomal protein L15
59	A	K1QQQ5_CRAGI Replication factor C subunit 5
60	A	K1QLC6_CRAGI JmjC domain-containing protein 8
	A	K1QFP5_CRAGI NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial
	A	K1Q7H0_CRAGI ATP-dependent DNA helicase II subunit 2

1		
2		
3	A	K1PYW7_CRAGI CDK5 regulatory subunit-associated protein 3
4	A	K1QVD0_CRAGI Small nuclear ribonucleoprotein Sm D3
5	A	K1QAT9_CRAGI ATP-dependent RNA helicase DDX1
6	A	K1R920_CRAGI Eukaryotic translation initiation factor 1A, X-chromosomal
7	A	K1QQG7_CRAGI DNA-directed RNA polymerase subunit
8	A	K1R0T1_CRAGI V-type proton ATPase subunit G
9	A	K1PD36_CRAGI Ubiquitin
10	A	K1QHI2_CRAGI Heterogeneous nuclear ribonucleoprotein L
11	A	K1RED7_CRAGI Poly(RC)-binding protein 3
12	A	K1QRE1_CRAGI COP9 signalosome complex subunit 6
13	A	K1QHS9_CRAGI Tubulin polyglutamylase TTLL13
14	A	K1R6Y8_CRAGI Uncharacterized protein
15	A	K1RC37_CRAGI Uncharacterized protein
16	A	K1PBG6_CRAGI Uncharacterized protein
17	A	K1R150_CRAGI Ras-related protein Rab-1A
18	A	K1QVS0_CRAGI Ras-like GTP-binding protein Rho1
19	A	K1R716_CRAGI Putative isovaleryl-CoA dehydrogenase
20	A	K1Q113_CRAGI Ornithine aminotransferase
21	A	K1Q151_CRAGI 60S ribosomal protein L32
22	A	K1QMY8_CRAGI Dedicator of cytokinesis protein 9
23	A	K1PR93_CRAGI 3-hydroxyisobutyrate dehydrogenase
24	A	K1QZX3_CRAGI Vacuolar protein sorting-associated protein VTA1-like protein
25	A	K1Q3W3_CRAGI NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial
26	A	K1RHA5_CRAGI Nucleoside diphosphate kinase
27	A	K1RG61_CRAGI Cytosolic carboxypeptidase 2
28	A	K1RSK5_CRAGI Kelch-like protein 6
29	A	K1Q105_CRAGI Ferrochelatase
30	A	K1QCS7_CRAGI Leucine-rich repeat-containing protein 16A
31	A	K1PWR0_CRAGI Protein SET
32	A	K1RIA0_CRAGI Molybdopterin molybdenumtransferase
33	A	K1RC43_CRAGI U4/U6 small nuclear ribonucleoprotein Prp31
34	A	K1S185_CRAGI Counting factor associated protein D
35	A	K1PFL3_CRAGI Dihydropteridine reductase
36	A	K1QIU2_CRAGI Putative tRNA (cytidine(32)/guanosine(34)-2'-O)-methyltransferase
37	A	K1S6H7_CRAGI Vacuolar protein sorting-associated protein 13C
38	A	K1QMM4_CRAGI Leucine zipper transcription factor-like protein 1
39	A	K1PEX5_CRAGI Protein hu-li tai shao
40	A	K1PUM5_CRAGI Cytoplasmic aconitate hydratase
41	A	K1QE49_CRAGI DnaJ-like protein subfamily A member 1
42	A	K1QGF1_CRAGI Splicing factor 3B subunit 2
43	A	K1P8Z2_CRAGI Histidyl-tRNA synthetase, cytoplasmic
44	A	K1QFN2_CRAGI Uncharacterized protein
45	A	K1QI48_CRAGI Inositol hexakisphosphate and diphosphoinositol-pentakisphosphate kinase
46	A	K1PZ93_CRAGI Dihydropyrimidine dehydrogenase [NADP(+)]
47	A	K1QN99_CRAGI Regulator of nonsense transcripts 2
48	A	K1QXX2_CRAGI Ubiquitin-conjugating enzyme E2 Q2
49	A	K1Q6U0_CRAGI Coatomer subunit zeta-1
50	A	K1P8F1_CRAGI Uncharacterized protein
51	A	K1RTD6_CRAGI UDP-glucose:glycoprotein glucosyltransferase 1
52	A	K1RKE5_CRAGI IQ and AAA domain-containing protein 1
53	A	K1QKD6_CRAGI Uncharacterized protein
54	A	K1QN55_CRAGI 60S acidic ribosomal protein P1
55	A	K1RGT9_CRAGI 60S ribosomal protein L13a
56	A	K1PZ23_CRAGI DnaJ-like protein subfamily C member 3
57	A	K1PCC8_CRAGI Serine/threonine-protein kinase 25
58	A	K1PKD4_CRAGI 40S ribosomal protein S30
59	A	K1RXA0_CRAGI cAMP-dependent protein kinase regulatory subunit
60	A	K1QAL3_CRAGI RNA-binding protein 28
	A	K1Q6J3_CRAGI Eukaryotic translation initiation factor 2-alpha kinase 4
	A	K1S049_CRAGI Putative RNA-binding protein 16

1		
2		
3	A	K1RBT3_CRAGI ATP-dependent RNA helicase SUV3-like protein, mitochondrial
4	A	K1QFS8_CRAGI Importin-9
5	A	K1QVF4_CRAGI Heterogeneous nuclear ribonucleoprotein L
6	A	K1PGD2_CRAGI Putative aminopeptidase NPEPL1
7	A	K1QUT5_CRAGI Amine oxidase
8	A	K1QAG0_CRAGI Serine-threonine kinase receptor-associated protein
9	A	K1PHS4_CRAGI Ribosome-binding protein 1
10	A	K1RMS0_CRAGI Translation initiation factor eIF-2B subunit beta
11	A	K1R604_CRAGI DCC-interacting protein 13-alpha
12	A	K1PQE3_CRAGI RNA-binding protein Raly
13	A	K1PQH6_CRAGI Cullin-4A
14	A	K1PM29_CRAGI Glucose-6-phosphate 1-dehydrogenase
15	A	K1QNK4_CRAGI 3-oxoacyl-[acyl-carrier-protein] reductase
16	A	K1PD41_CRAGI DNA primase
17	A	K1PTV5_CRAGI Programmed cell death protein 10
18	A	K1PV35_CRAGI Kyphoscoliosis peptidase
19	A	K1Q4J3_CRAGI Nuclear cap-binding protein subunit 1
20	A	K1RJV3_CRAGI TRS85-like protein
21	A	K1QM61_CRAGI Uncharacterized protein
22	A	K1PKI9_CRAGI Uncharacterized protein
23	A	K1QPB0_CRAGI U3 small nucleolar RNA-associated protein 6-like protein
24	A	K1PF70_CRAGI MON2-like protein (Fragment)
25	A	K1RFF7_CRAGI Protein lethal(2)essential for life
26	A	K1PG60_CRAGI 60S ribosomal protein L17
27	A	K1Q189_CRAGI F-box/WD repeat-containing protein 9
28	A	K1QBM3_CRAGI Ras-related protein Rab-2
29	A	K1PNP9_CRAGI Bullous pemphigoid antigen 1, isoforms 1/2/3/4
30	A	K1QIJ3_CRAGI Nuclear pore complex protein Nup85
31	A	K1QX44_CRAGI Ras-related protein Rab-11B
32	A	K1QLD7_CRAGI Kinetochores protein NDC80-like protein
33	A	K1QUD7_CRAGI Conserved oligomeric Golgi complex subunit 3 (Fragment)
34	A	K1Q9Z5_CRAGI Peptidyl-prolyl cis-trans isomerase
35	A	K1RLT0_CRAGI D-erythrulose reductase
36	A	K1PG98_CRAGI rRNA-processing protein FCF1-like protein
37	A	K1QKQ8_CRAGI THO complex subunit 4-A
38	A	K1RB07_CRAGI 60S ribosomal protein L27a
39	A	K1PEZ6_CRAGI Kyphoscoliosis peptidase
40	A	D7EZH1_CRAGI Cystatin B-like protein
41	A	K1RJ53_CRAGI Tetratricopeptide repeat protein 12
42	A	K1QQH9_CRAGI DNA (Cytosine-5)-methyltransferase 1 (Fragment)
43	A	K1PL63_CRAGI TBC1 domain family member 15
44	A	K1PG17_CRAGI 60S ribosomal protein L21
45	A	K1QQ99_CRAGI Uncharacterized protein
46	A	K1RG04_CRAGI ALK tyrosine kinase receptor
47	A	K1PZP3_CRAGI Conserved oligomeric Golgi complex subunit 2
48	A	K1QH68_CRAGI Syntenin-1
49	A	K1S4H5_CRAGI Adenosylhomocysteinase
50	A	K1R4L8_CRAGI Electron transfer flavoprotein-ubiquinone oxidoreductase, mitochondrial
51	A	K1RFD2_CRAGI Adenylate kinase
52	A	K1PB87_CRAGI Uncharacterized protein
53	A	K1PM74_CRAGI DNA mismatch repair protein Msh6
54	A	K1RR99_CRAGI Rho guanine nucleotide exchange factor 12
55	A	K1QGQ5_CRAGI Superoxide dismutase
56	A	K1PBB1_CRAGI Stress-induced-phosphoprotein 1
57	A	K1Q681_CRAGI Clustered mitochondria protein homolog
58	A	K1PQR9_CRAGI Squamous cell carcinoma antigen recognized by T-cells 3
59	A	K1QSV1_CRAGI Uncharacterized protein
60	A	K1QKY7_CRAGI Uncharacterized protein
	A	K1QBJ7_CRAGI Uncharacterized protein
	A	K1S5H7_CRAGI Cell division cycle 5-related protein

1			
2			
3	A	K1RHJ9_CRAGI	Suppressor of G2 allele of SKP1-like protein
4	A	K1R2Z2_CRAGI	Methyltransferase-like protein 13
5	A	K1QHY6_CRAGI	Rap1 GTPase-GDP dissociation stimulator 1-A
6	A	K1Q1L1_CRAGI	Kinesin-associated protein 3
7	A	K1R3Z4_CRAGI	5'-3' exoribonuclease 1
8	A	K1P951_CRAGI	Fanconi anemia group D2 protein
9	A	K1PKD7_CRAGI	6-phosphogluconolactonase
10	A	K1QN54_CRAGI	Brain protein 16
11	A	K1QYD0_CRAGI	UBX domain-containing protein 1
12	A	K1QCY6_CRAGI	40S ribosomal protein S28
13	A	K1QZ29_CRAGI	Uncharacterized protein
14	A	K1R136_CRAGI	Phosphatidylinositol transfer protein alpha isoform
15	A	K1R969_CRAGI	Uncharacterized protein
16	A	K1R1E4_CRAGI	Serine/threonine-protein kinase Chk2
17	A	K1QVL1_CRAGI	Serine/threonine-protein phosphatase 4 regulatory subunit 4
18	A	K1QYD8_CRAGI	Trans-1,2-dihydrobenzene-1,2-diol dehydrogenase
19	A	K1Q927_CRAGI	Neurofibromin
20	A	K1QAU3_CRAGI	WD repeat-containing protein 63
21	A	K1Q8P7_CRAGI	Aspartyl aminopeptidase
22	A	K1QZ64_CRAGI	Nuclear pore complex protein Nup98-Nup96
23	A	K1PLR8_CRAGI	Chromosome transmission fidelity protein 18-like protein (Fragment)
24	A	K1P752_CRAGI	UPF0195 protein FAM96B
25	A	K1QAY3_CRAGI	Dipeptidyl-peptidase 1 (Fragment)
26	A	K1R669_CRAGI	Uncharacterized protein
27	A	K1PWS8_CRAGI	Mitotic spindle assembly checkpoint protein MAD2A
28	A	K1PK87_CRAGI	Putative E3 ubiquitin-protein ligase TRIP12
29	A	K1QKU6_CRAGI	mRNA export factor
30	A	K1QQV0_CRAGI	Histone H1.2
31	A	K1QR54_CRAGI	Zinc finger RNA-binding protein
32	A	K1PE13_CRAGI	Uncharacterized protein
33	A	K1QUW5_CRAGI	U2 snRNP auxiliary factor large subunit
34	A	K1PTH4_CRAGI	ADP-ribosylation factor
35	A	K1Q3C3_CRAGI	Lambda-crystallin-like protein
36	A	K1RE82_CRAGI	Uncharacterized protein
37	A	K1P486_CRAGI	Heat shock 70 kDa protein 12A
38	A	K1R7A4_CRAGI	Peptidylprolyl isomerase
39	A	K1PEC8_CRAGI	Actin-related protein 8
40	A	K1RAR8_CRAGI	Protein FAM49B
41	A	K1QZD2_CRAGI	Tudor domain-containing protein 7
42	A	K1QM54_CRAGI	Activator of 90 kDa heat shock protein ATPase-like protein 1
43	A	K1Q904_CRAGI	PAN2-PAN3 deadenylation complex subunit PAN3
44	A	K1P6N8_CRAGI	Ubiquitin carboxyl-terminal hydrolase 7
45	A	K1RBM7_CRAGI	Ubiquitin-conjugating enzyme E2 variant 1
46	A	K1PV92_CRAGI	Hsp90 co-chaperone Cdc37
47	A	K1PQU8_CRAGI	Sperm-associated antigen 6
48	A	K1QUK4_CRAGI	Protein SET
49	A	K1QJ85_CRAGI	Glutathione S-transferase A
50	A	K1QJW3_CRAGI	Heat shock 70 kDa protein 12B
51	A	K1QNW5_CRAGI	MAK10-like protein
52	A	K1QZ84_CRAGI	Thioredoxin domain-containing protein 3-like protein
53	A	K1QXH7_CRAGI	DNA replication licensing factor mcm4-B
54	A	K1Q1L9_CRAGI	Interferon-induced protein 44-like protein
55	A	K1RGD5_CRAGI	F-box only protein 36
56	A	K1Q3B4_CRAGI	DNA topoisomerase
57	A	K1P8Z1_CRAGI	Uncharacterized protein
58	A	K1PYA2_CRAGI	Host cell factor
59	A	K1PZR3_CRAGI	U2 small nuclear ribonucleoprotein A
60	A	K1QB69_CRAGI	Uncharacterized protein
	A	K1PI78_CRAGI	Golgi-specific brefeldin A-resistance guanine nucleotide exchange factor 1
	A	K1RKK2_CRAGI	Phosphatidylinositol-4-phosphate 5-kinase type-1 alpha

1			
2			
3	A	K1QLS5_CRAGI	Uncharacterized protein
4	A	K1QFI3_CRAGI	Apoptosis-inducing factor 3
5	A	K1QKB1_CRAGI	Tryptophanyl-tRNA synthetase, cytoplasmic
6	A	K1REU2_CRAGI	WD repeat and HMG-box DNA-binding protein 1
7	A	K1QUK3_CRAGI	Putative ATP-dependent RNA helicase DDX41
8	A	K1QBT8_CRAGI	Uncharacterized protein
9	A	K1QBT8_CRAGI	Uncharacterized protein
10	A	K1QVX4_CRAGI	Glycogen synthase kinase-3 beta
11	A	K1PF20_CRAGI	Gamma-tubulin complex component
12	A	K1RFG1_CRAGI	Lipoxygenase-like protein domain-containing protein 1
13	A	K1PCI8_CRAGI	Cullin-2
14	A	K1PC18_CRAGI	Cullin-2
15	A	K1QS27_CRAGI	UBX domain-containing protein 6
16	A	K1RFF1_CRAGI	Uncharacterized protein
17	A	K1Q4N9_CRAGI	Uncharacterized protein
18	A	K1QJN8_CRAGI	AP-3 complex subunit beta
19	A	K1PXA0_CRAGI	Uncharacterized protein
20	A	K1PXA0_CRAGI	Uncharacterized protein
21	A	K1QA13_CRAGI	Calcium-transporting ATPase
22	A	K1QXY4_CRAGI	Kinase
23	A	K1PBW4_CRAGI	Uncharacterized protein
24	A	K1PUF0_CRAGI	G-protein coupled receptor moody
25	A	K1QMY9_CRAGI	Uncharacterized protein
26	A	K1QMY9_CRAGI	Uncharacterized protein
27	A	K1QZ54_CRAGI	Coiled-coil domain-containing protein 39
28	A	K1QWU8_CRAGI	Uncharacterized protein
29	A	K1Q3L1_CRAGI	Kielin/chordin-like protein
30	A	K1PGR2_CRAGI	G patch domain-containing protein 1
31	A	K1PGR2_CRAGI	G patch domain-containing protein 1
32	A	K1RXP9_CRAGI	Ventricular zone-expressed PH domain-containing-like protein 1
33	A	K1PIB2_CRAGI	Uncharacterized protein
34	A	K1R4U3_CRAGI	Uncharacterized protein
35			
36			
37			
38			
39			
40			
41			
42			
43			
44			
45			
46			
47			
48			
49			
50			
51			
52			
53			
54			
55			
56			
57			
58			
59			
60			

Data S3: Complete list of GO terms of clustered genes of m6A interacting proteins (p-value<0,05)

	Cluster	term_ID	description	log10 p-value	Class
1					
2					
3					
4					
5					
6	cluster1	GO:0006172	ADP biosynthetic process	-2,848	Biological process
7	cluster1	GO:0006886	intracellular protein transport	-6,1176	Biological process
8	cluster1	GO:0015031	protein transport	-1,6944	Biological process
9					
10	cluster1	GO:0006511	ubiquitin-dependent protein catabolic process	-1,8071	Biological process
11	cluster1	GO:0030833	regulation of actin filament polymerization	-2,5256	Biological process
12	cluster1	GO:0006563	L-serine metabolic process	-2,3716	Biological process
13	cluster1	GO:0006544	glycine metabolic process	-2,0706	Biological process
14	cluster1	GO:0016192	vesicle-mediated transport	-3,119	Biological process
15	cluster1	GO:0006429	leucyl-tRNA aminoacylation	-2,1763	Biological process
16	cluster1	GO:0006413	translational initiation	-1,3708	Biological process
17					
18	cluster1	GO:0006122	mitochondrial electron transport, ubiquinol to cytochrome c	-1,9328	Biological process
19	cluster1	GO:0048280	vesicle fusion with Golgi apparatus	-2,3699	Biological process
20	cluster1	GO:0006888	ER to Golgi vesicle-mediated transport	-1,4737	Biological process
21	cluster1	GO:0030117	membrane coat	-3,0546	Cellular component
22	cluster1	GO:0030127	COPII vesicle coat	-1,6994	Cellular component
23	cluster1	GO:0030131	clathrin adaptor complex	-1,5595	Cellular component
24	cluster1	GO:0005737	cytoplasm	-2,3551	Cellular component
25					
26	cluster1	GO:0031105	septin complex	-2,0349	Cellular component
27	cluster1	GO:0005850	eukaryotic translation initiation factor 2 complex	-2,6924	Cellular component
28	cluster1	GO:0005856	cytoskeleton	-1,6967	Cellular component
29					
30	cluster1	GO:0005750	mitochondrial respiratory chain complex III	-1,9328	Cellular component
31	cluster1	GO:0000139	Golgi membrane	-1,4267	Cellular component
32	cluster1	GO:0003743	translation initiation factor activity	-2,6564	Molecular function
33	cluster1	GO:0004372	glycine hydroxymethyltransferase activity	-2,3716	Molecular function
34	cluster1	GO:0005488	binding	-1,66	Molecular function
35	cluster1	GO:0008565	protein transporter activity	-2,7964	Molecular function
36	cluster1	GO:0004823	leucine-tRNA ligase activity	-2,1763	Molecular function
37					
38	cluster1	GO:0008242	omega peptidase activity	-2,0158	Molecular function
39	cluster1	GO:0008536	Ran GTPase binding	-1,4396	Molecular function
40	cluster1	GO:0005525	GTP binding	-1,9855	Molecular function
41					
42	cluster1	GO:0016813	hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in linear amidines	-1,9675	Molecular function
43	cluster1	GO:0002161	aminoacyl-tRNA editing activity	-1,4387	Molecular function
44	cluster1	GO:0016776	phosphotransferase activity, phosphate group as acceptor	-2,0567	Molecular function
45	cluster1	GO:0005543	phospholipid binding	-1,3689	Molecular function
46	cluster1	GO:0004017	adenylate kinase activity	-2,2504	Molecular function
47	cluster1	GO:0019205	nucleobase-containing compound kinase activity	-1,9387	Molecular function
48	cluster1	GO:0019904	protein domain specific binding	-1,4245	Molecular function
49	cluster1	GO:0004843	thiol-dependent ubiquitin-specific protease activity	-1,6596	Molecular function
50	cluster1	GO:0003779	actin binding	-1,33	Molecular function
51					
52	cluster 2	GO:0006376	mRNA splice site selection	-2,2802	Biological process
53	cluster 2	GO:0016192	vesicle-mediated transport	-1,9467	Biological process
54	cluster 2	GO:0006511	ubiquitin-dependent protein catabolic process	-1,895	Biological process
55	cluster 2	GO:0051603	proteolysis involved in cellular protein catabolic process	-1,4434	Biological process
56	cluster 2	GO:0006281	DNA repair	-1,946	Biological process
57	cluster 2	GO:0006164	purine nucleotide biosynthetic process	-1,9132	Biological process
58	cluster 2	GO:0006606	protein import into nucleus	-1,6687	Biological process
59	cluster 2	GO:0006367	transcription initiation from RNA polymerase II promoter	-1,8729	Biological process
60	cluster 2	GO:0045893	positive regulation of transcription, DNA-templated	-1,8902	Biological process
	cluster 2	GO:0051276	chromosome organization	-1,9322	Biological process
	cluster 2	GO:0005685	U1 snRNP	-2,0889	Cellular component
	cluster 2	GO:0005694	chromosome	-1,6569	Cellular component
	cluster 2	GO:0019773	proteasome core complex, alpha-subunit complex	-1,7608	Cellular component
	cluster 2	GO:0005839	proteasome core complex	-1,4434	Cellular component
	cluster 2	GO:0005643	nuclear pore	-1,5471	Cellular component
	cluster 2	GO:0003938	IMP dehydrogenase activity	-2,5964	Molecular function
	cluster 2	GO:0005488	binding	-5,6024	Molecular function
	cluster 2	GO:0008536	Ran GTPase binding	-3,3815	Molecular function
	cluster 2	GO:0008565	protein transporter activity	-1,3099	Molecular function
	cluster 2	GO:0017056	structural constituent of nuclear pore	-2,5981	Molecular function
	cluster 2	GO:0016844	strictosidine synthase activity	-2,4472	Molecular function
	cluster 2	GO:0042578	phosphoric ester hydrolase activity	-2,0068	Molecular function
	cluster 2	GO:0008641	small protein activating enzyme activity	-1,8257	Molecular function
	cluster 2	GO:0003729	mRNA binding	-1,9507	Molecular function
	cluster 2	GO:0000166	nucleotide binding	-1,9175	Molecular function
	cluster 2	GO:0030554	adenyl nucleotide binding	-1,4276	Molecular function
	cluster 2	GO:0004175	endopeptidase activity	-1,4434	Molecular function
	cluster 2	GO:0004298	threonine-type endopeptidase activity	-1,4434	Molecular function
	cluster 3	GO:0006184	(obsolete) GTP catabolic process	-1,3497	Biological process
	cluster 3	GO:0007156	homophilic cell adhesion via plasma membrane adhesion molecules	-1,6645	Biological process
	cluster 3	GO:0008152	metabolic process	-1,9382	Biological process

1					
2					
3					
4	cluster 3	GO:0015986	ATP synthesis coupled proton transport	-4,8627	Biological process
5	cluster 3	GO:0006096	glycolytic process	-1,4156	Biological process
6	cluster 3	GO:0051258	protein polymerization	-2,6757	Biological process
7	cluster 3	GO:0044262	cellular carbohydrate metabolic process	-2,0966	Biological process
8	cluster 3	GO:0006388	tRNA splicing, via endonucleolytic cleavage and ligation	-1,523	Biological process
9	cluster 3	GO:0006879	cellular iron ion homeostasis	-1,4857	Biological process
10	cluster 3	GO:0007017	microtubule-based process	-2,4915	Biological process
11	cluster 3	GO:0006412	translation	-2,0331	Biological process
12	cluster 3	GO:0006122	mitochondrial electron transport, ubiquinol to cytochrome c	-2,0662	Biological process
13	cluster 3	GO:0000276	mitochondrial proton-transporting ATP synthase complex, coupling factor F(o)	-4,1068	Cellular component
14	cluster 3	GO:0005750	mitochondrial respiratory chain complex III	-2,0662	Cellular component
15	cluster 3	GO:0045261	proton-transporting ATP synthase complex, catalytic core F(1)	-2,0025	Cellular component
16	cluster 3	GO:0005874	microtubule	-2,2282	Cellular component
17	cluster 3	GO:0005882	intermediate filament	-1,9067	Cellular component
18	cluster 3	GO:0043231	intracellular membrane-bounded organelle	-2,1492	Cellular component
19	cluster 3	GO:0005852	eukaryotic translation initiation factor 3 complex	-1,6821	Cellular component
20	cluster 3	GO:0005737	cytoplasm	-1,9776	Cellular component
21	cluster 3	GO:0005840	ribosome	-2,0503	Cellular component
22	cluster 3	GO:0043234	protein complex	-2,6757	Cellular component
23	cluster 3	GO:0004739	pyruvate dehydrogenase (acetyl-transferring) activity	-2,8179	Molecular function
24	cluster 3	GO:0016624	oxidoreductase activity, acting on the aldehyde or oxo group of donors, disulfide as acceptor	-2,0554	Molecular function
25	cluster 3	GO:0005200	structural constituent of cytoskeleton	-2,3865	Molecular function
26	cluster 3	GO:0005525	GTP binding	-1,9304	Molecular function
27	cluster 3	GO:0015078	hydrogen ion transmembrane transporter activity	-3,0193	Molecular function
28	cluster 3	GO:0046961	proton-transporting ATPase activity, rotational mechanism	-1,6263	Molecular function
29	cluster 3	GO:0046933	proton-transporting ATP synthase activity, rotational mechanism	-1,7326	Molecular function
30	cluster 3	GO:0004775	succinate-CoA ligase (ADP-forming) activity	-2,3995	Molecular function
31	cluster 3	GO:0046912	transferase activity, transferring acyl groups, acyl groups converted into alkyl on transfer	-2,3982	Molecular function
32	cluster 3	GO:0016874	ligase activity	-1,4798	Molecular function
33	cluster 3	GO:0048037	cofactor binding	-1,6628	Molecular function
34	cluster 3	GO:0008199	ferric iron binding	-1,4607	Molecular function
35	cluster 3	GO:0005544	calcium-dependent phospholipid binding	-1,6049	Molecular function
36	cluster 3	GO:0003878	ATP citrate synthase activity	-2,3995	Molecular function
37	cluster 3	GO:0003735	structural constituent of ribosome	-1,9881	Molecular function
38					
39					
40					
41					
42					
43					
44					
45					
46					
47					
48					
49					
50					
51					
52					
53					
54					
55					
56					
57					
58					
59					
60					

Table S1: Transitions used for each compound. A: first transition, B: second transition

Nucleoside	Retention time (min)	MRM precursor (m/z)	MRM product (m/z)		Collision Energy (V)	
			A	B	A	B
A	3.07	268.0	135.9	119.0	-30	-12
m⁶A	2.12	282.0	150.1	123.1	-17	-46

For Review Only

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Table S2: Correspondence between development stages in our study, and the GigaTON database.

Development stages : This Study	Development stages : GigaTON [53]
Oocytes	E (Eggs)
2/8 Cells	TC (Two Cell embryos)
	FC (Four Cell embryos)
	EM (Early Morula)
Morula	M (Morula)
Blastula	B (Blastula)
	RM (Rotary Movement)
	FS (Free Swimming)
Gastrula	EG (Early Gastrula)
	G (Gastrula)
	T (Trochophore) 1
	T2
Trochophore	T3
	T4
	T5
	ED (Early D larvae) 1
	ED2
D larvae	D (D larvae)1
	D2
	D3
	D4
	D5
Spat	S (Spat)
Juvenile	J (Juvenile)