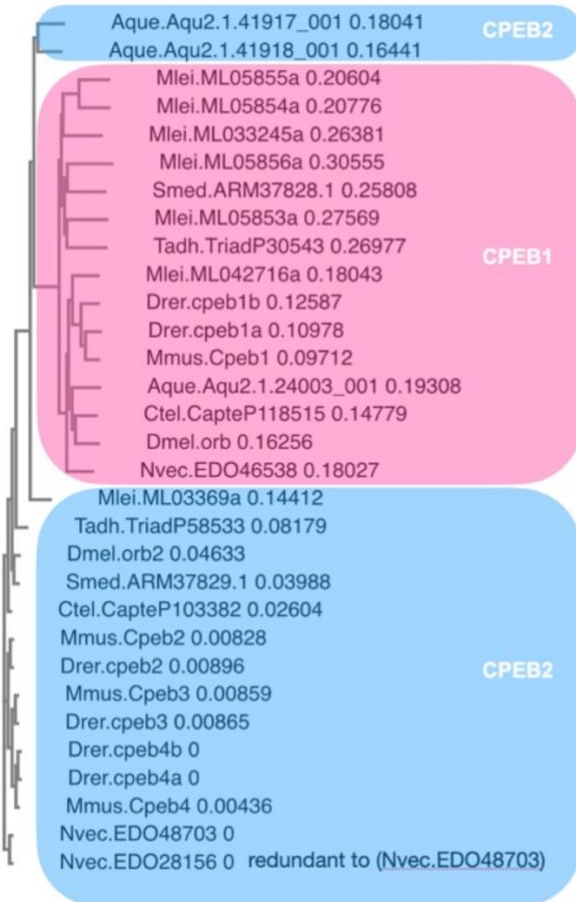
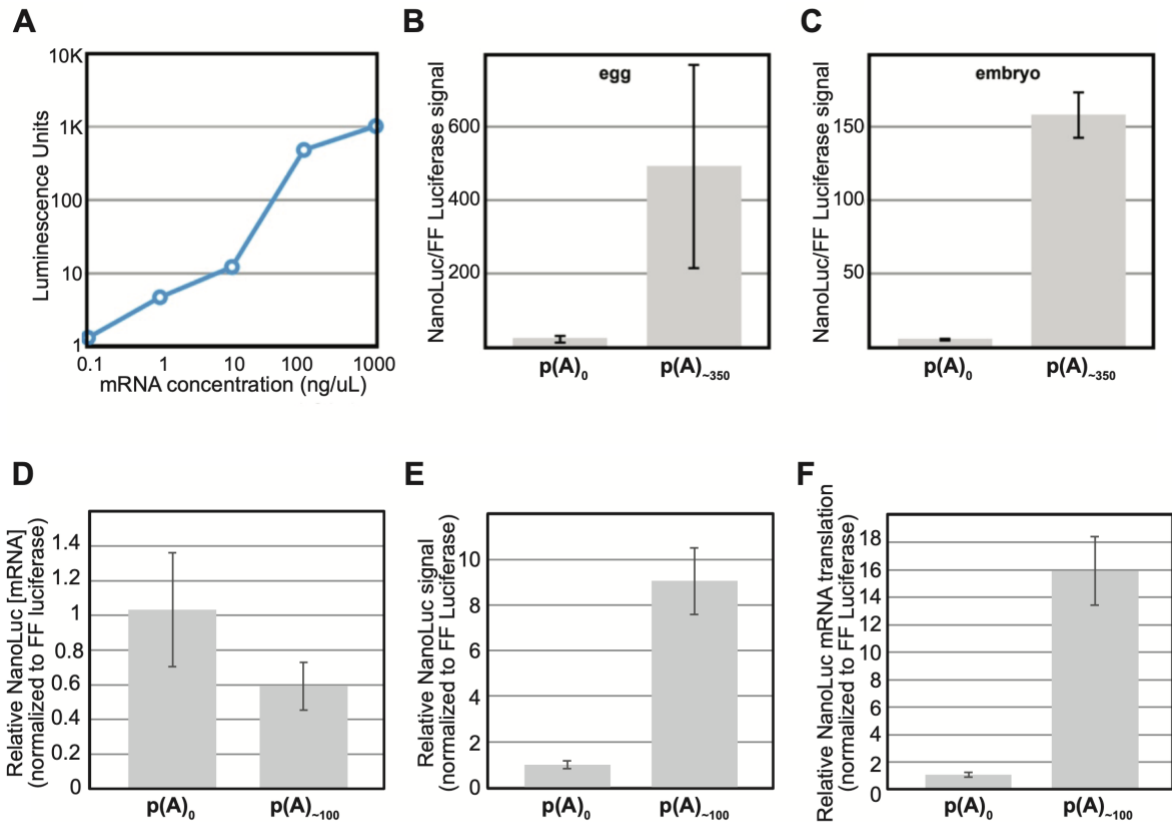


Supplementary Figure S1. Phylogenetic tree (as in Figure 1C) based on similarity to individual RRMs of CPEB1 depicts relationship between CPEB orthologs and close homologs. Bar diagrams of representative proteins in each clade are depicted with the position of RRMs in the clade indicated in red boxes, other RRMs in gray, and ZnF in black. Stems corresponding to CPEB1 (magenta) and CPEB2 (blue) sequences are highlighted. Sequence identifiers are indicated with amino acid positions of RRMs in parentheses.



No matches from non-animal species

Supplementary Figure S2. Phylogram showing relationship between CPEBs from the five major animal lineages based on neighbor joining association of sequence matches to CPEB Zinc Finger motif BLAST searches. Sequences corresponding to CPEB1 orthologs are shaded in pink, and those corresponding to CPEB2 orthologs in blue. No hits were found in non-animal sequences.



Supplementary Figure S3. The poly(A) tail enhances expression of reporter mRNA in *N. vectensis* eggs and embryos. **(A)** Luminescence units (y-axis) generated from eggs of *N. vectensis* 6 hours post-injection of different concentrations (x-axis) of *in vitro*-synthesized unpolyadenylated firefly luciferase mRNAs. **(B-C)** Translation level of unpolyadenylated (poly(A)₀; first column) and polyadenylated (poly(A)₃₅₀; second column) NanoLuc mRNA relative to unpolyadenylated firefly (FF) luciferase mRNAs 6 hours after co-injection [25 ng/μl ea.] into *N. vectensis* eggs (B) and embryos (C). **(D-F)** Results from a single batch of injected *N. vectensis* eggs reveals close relative abundance of non-polyadenylated (poly(A)₀) and polyadenylated (poly(A)₋₁₀₀) NanoLuc reporter mRNA 6 hours post-injection (D), whereas NanoLuc mRNA translation in the same batch of injected eggs was 16-fold higher for polyadenylated transcripts than poly(A)₀ counterparts (E and F). **(D)** The abundance of injected NanoLuc reporter mRNAs is shown normalized to co-injected Firefly Luciferase (FF Luciferase) mRNA reporter without a poly(A) tail. **(E)** NanoLuc luminescence activity in eggs relative to that of FF Luciferase in eggs from the batch as in (D) 6 post-injection of reporter mRNAs. **(F)** Relative levels of poly(A)- and poly(A)+ NanoLuc mRNA translation calculated from the ratio of normalized luminescence in (E) to corresponding mRNA abundance in (D).

>XM_001629488.2 (Nv_c-mos)

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TAACGGAAGTAAATTTCAATGAAACTGAATATAATGTAGTGTATTCCTATTTGCTGTGCTACTTTATTTTGGCGATG
TTATGAAAAATAAACTTCTGTATGGTGCCTAA

-3' UTR region in amplicon: 178 nts.

>XM_032362260.1 (Nv_GLD2)

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TGTTAAAAACTGTTATCGTTAATGGCGTTGATGTTCAATGGCAAGGCA**CAGCGTCTACTCCAGACACGAGAATCTGA**
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3'UTR region in amplicon: 170 nt

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TATCATACTGGAACAATACTCTGAGCCACTACACTGGATTTGAGCTTCATGACCTCAAACATGCATACAAGATCTG
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AATAGCACAAAAGACATTACAG

3'UTR region in amplicon: 93 nts.

Predicted based on reference: 219 nts.

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TCCCAGCTCAAGAAAATGTCGACGTCCTCACAAAAGCTAAGCATGGCCAAAATACTCGCTTTGGACGCGCCGCTTTG
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TGAAGCTTTCACGGCGCTTCCCAAGCCCGAACGGCCGGCCTCAAAGCCCGAGCCCATGGACATGGCTGATTTTAGTG
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CAGCTTGTAGGAGTTGGTGTCTATGCTTCTTGCTTCCAAATATGAAGAGATGTTTGCCCCTGAGATAGGCGACTTTGT
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TCTTGACAGCCAGGACCAATCTTAGTTTATAATAAGCATAGAAGCAATTTATAAAGGGTTATAGGGTGGGTAGGGTG
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3'UTR region in amplicon: 96 nts.

Predicted based on reference: 116 nts.

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TTAATCAGCTTTAAAAAATAAGGTATCAGATTACCCAAATTTAGATTACCCATATTGAGAAACATATCATTTCATC
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TGTAATATTCAACACTATCAACAAGTAAAGTTAGCTGCATAAGGGGAC

Observed 3'UTR region in amplicon: 224 nt.

Predicted based on reference: 232 nt

>ML4553_cuf_38 transcript (ML455312a; M. leidyi cyclin homolog 4)

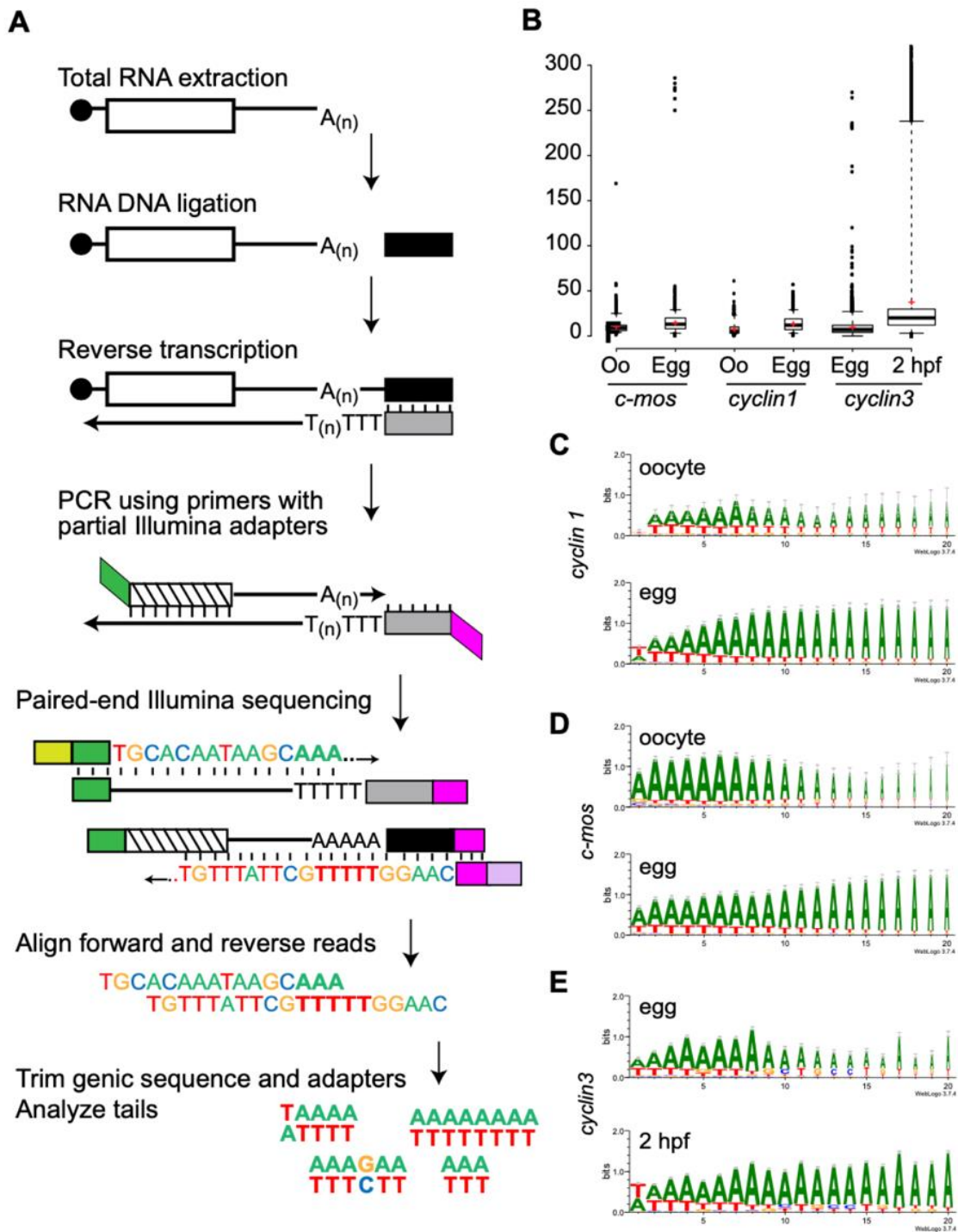
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ACCAACCCCTTAAGTATCAGAGTGGACACCAAGAAGCCGTCTCCAAACAGAAGCAGATCGCGTCCCGATCGCAGCG
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CAAGTTGAAGTTTGAATGGTATCAGTAACAAGTATGATATGATAATTAATTGATTATTAATTATCCAATTGGTTGAT
ATTACTTTTGTACTTGACTCAACCCTC

3'UTR region in amplicon: 191 nt

Supplementary Figure S4. Reference cDNA sequences for targets of cytoplasmic polyadenylation identified in this study. Sequences obtained from NCBI (<https://www.ncbi.nlm.nih.gov/>; XM_ prefix), SIMRbase (<https://simrbase.stowers.org/>; NVERTX prefix), and the Mnemiopsis Genome Portal (<https://research.nhgri.nih.gov/mnemiopsis/>; ML prefix) are shown. The predicted open reading frames (highlighted in gray), putative Cytoplasmic Polyadenylation Elements (UUUUA; red font), as well as Cleavage and Polyadenylation Signals (underlined) are indicated. Highlighted in yellow are regions validated from Sanger sequencing of cloned poly(A) tail length assay (PAT) amplicons, along with the number of nucleotides in that segment. The predicted 3'-end length of reference sequences including regions not covered in PAT amplicons (potentially due to alternative/rare cleavage and polyadenylation sites) that were cloned and analyzed by Sanger sequencing are also indicated when present.

Supplementary Figure S5. (A-B) Sequence of 3'-end amplicon cDNA clones from oocytes and eggs of *N. vectensis* (A), as well as *M. leidyi* zygotes and 2-cell stage embryos (B). Sequence that matches genic reference is shown in black font, whereas the rest is presumed to represent poly(A) tails (green font). Non-A nucleotides in poly(A) tails are shown in red and composition of tails summarized in parentheses. There is sequence downstream of the highlighted region at the end of the oocyte *cyclin3* read that matches genic reference. This is presumed to be amplification from a longer 3'UTR with indicated sequence (red and green font) that does not match our genic reference.



Supplementary Figure S6. Poly(A) tail length and composition assessed by Amplicon-EZ

sequencing. (A) Generation of Amplicon-EZ sequence reads corresponding to 3'-ends of mRNAs

involves the same initial steps as in (Figure 2K), but with modified primers that include adapters for

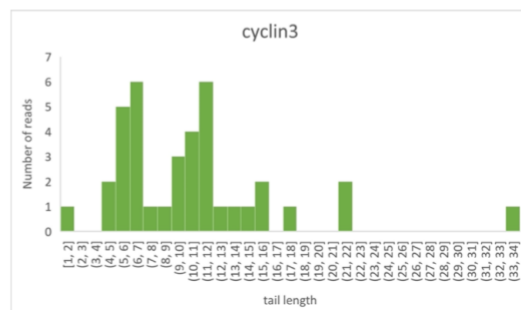
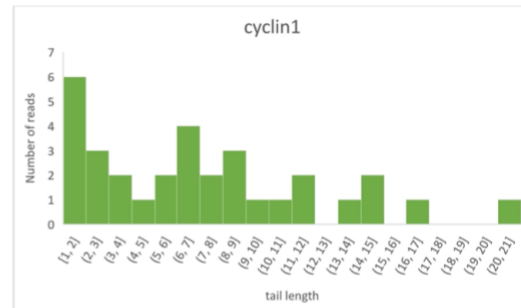
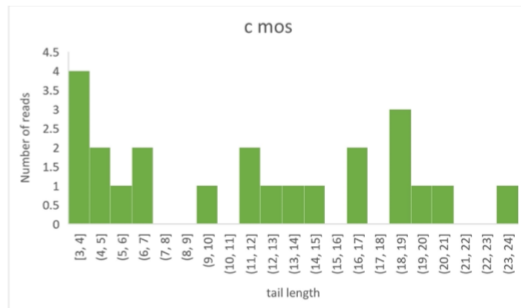
Illumina sequencing (green and magenta) and is followed by alignment of paired-end reads and trimming

of adapters and genic sequence. **(B)** Box plot of poly(A) tail lengths measured using Amplicon-EZ from ovary (Oo), egg, and 2 hours post-fertilization RNA samples. Thick horizontal lines represent medians; red crosses represent sample means; box limits indicate the 25th and 75th percentiles; whiskers extend to 5th and 95th percentiles; outliers are represented by dots; and width of the boxes is proportional to the square root of the sample size (n= 3249, 3285, 631, 2381, 12804, and 17482 from left to right of the plot). Plot was generated in BoxPloTR (<http://shiny.chemgrid.org/boxplotr/>). **(C-E)** Sequence logos for the first 20 nucleotides of poly(A) tail sequence as obtained from Amplicon-EZ analysis of *N. vectensis cyclin1* (C), *c-mos* (D), and *cyclin3* (E) mRNAs. Sequence logos generated by the WebLogo 3 server (Crooks et al., 2004) for all sequences with poly(A) tails longer than 5 nucleotides.

cyclin1 sequences	Length
UUAAAAAGAAAAAUAAAAU	21
AAGAAAAAGAAAAAAC	17
AAAAAAAAGAAAAA	15
UUUAAAAAUAAAA	15
AAAUUUAAAAAU	14
AAAAAGAAAAU	12
AUAAAAAGGAU	12
GAAAAAGAAA	11
AUUUUAAAA	10
AGAAAAAU	9
AUGAGAAU	9
AAAAAAAU	9
GGAAAAU	8
UUGAAAAU	8
AAAAAC	7
AAUAGAA	7
AAAAAA	7
ACAAAA	7
AAAAU	6
AAAAU	6
AAGAA	5
AACU	4
AAU	4
AAA	3
AAA	3
AAA	3
AU	2
AU	2
AU	2
AU	2
A	1
U	1
average:	7.5625
standard deviation:	5.066891266

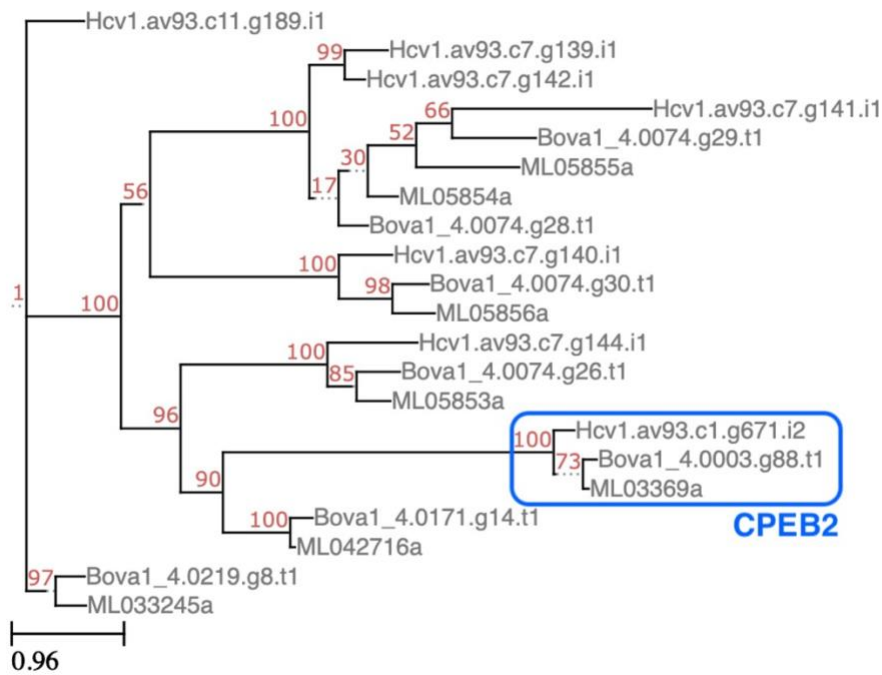
cyclin3 sequences	Length
UAUCAAUUAUAAAAUAAUUAUAAAAAUAAAAU	34
AUAAAAAAAUAAAAAAAU	22
UAUACAUCUAAAAUAGAAAA	22
AAUAAAAAAAUAAAAA	18
AAUAAUAAUAAAAAU	16
AAUUAAAAAUAAAAU	16
AAAAAAUAAAAAAU	15
AUUUAAAAAAAU	14
UUUUAAAAAAAU	13
AAAAAUAAU	12
AAACUUAAAAU	12
UACUAGAAAAU	12
UUUAUAAAAAU	12
UUCUAAAAAAU	12
UAAAAUAAAAU	12
AAAAAAUAAU	11
AAAAAAUAAU	11
AAGAAAAAU	11
AAAAAUAAAAU	11
UUAAAAAAC	10
ACAAAAAAU	10
AAAAAAAU	10
UUAAAAAU	9
UUAAAAAU	8
AAAAAA	7
AAAAAA	7
AAAAAC	7
AAAAAU	7
AAAAAU	7
AAAAAU	7
AAAAAC	6
AAAAU	6
AAAAU	6
AAAAAC	6
AAAAA	6
AAAA	5
AAAA	5
U	1
average:	10.94736842
standard deviation:	5.959082863

cmos sequences	Length
AAAUUUAAAAAAUAAAAUAAAC	24
AAUAAUAAUAAUAAAAAAU	21
AAUAAAAUAAAAUAAAAU	20
UAUAAAAUAAUAAAAAU	19
UUUAAAAUUUUCAAAAU	19
UAUAAAAAAACAAAAAU	19
AAAUUUAAAAAAAU	17
AAAAUUUUUAAAAAU	17
UAAUUUAAAAAAAC	15
AAUUUUAAAAAAU	14
AUUUUUAAAAAC	13
AAUAAAAAAC	12
AAAAUAAAAAU	12
AAAAUUAAU	10
UAUAAU	7
UUAAAAU	7
AAAAAC	6
UAAU	5
AAAAU	5
AAAC	4
AAU	3
AAU	3
ACU	3
average:	11.95652174
standard deviation:	6.724975572

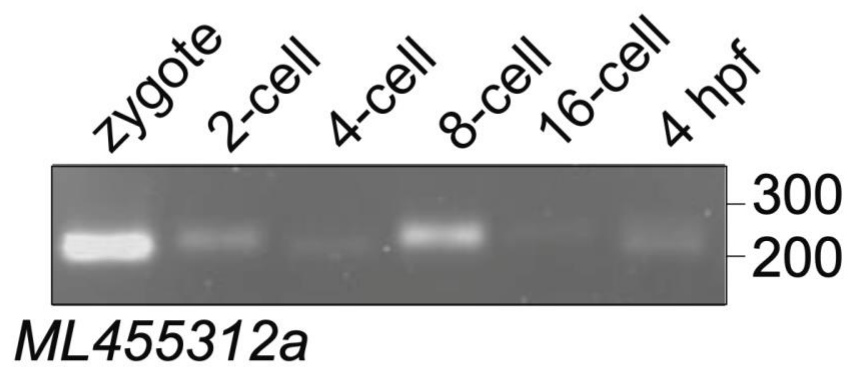


Supplementary Figure S8. Non-templated sequence in the 3'-end of *N. vectensis* egg mRNA reads

(NCBI BioProject: PRJNA956458 obtained using Oxford Nanopore Technology Direct RNA sequencing. Genic sequence for *cyclin1*, *cyclin3*, and *c-mos* was recognized by sequence alignment and the remainder of the 3' end of individual reads (after removal of adapter oligo sequence, when present) is shown for each mRNA read. Graphs summarizing the observed length of tails using this method is shown for each of the three genes.



Supplementary Figure S9. Phylogram showing position of CPEBs within Ctenophora. CPEBs from *Hormiphora californensis* and *Beroe ovata* were identified via reciprocal BLAST between human CPEB protein sequences (CPEB1, NP_001275748.1; and CPEB4, AAH36899.1) and the protein models of these two ctenophore species and aligned with *Mnemiopsis leidyi* CPEBs using MAFFT (default parameters). The position of CPEBs was calculated according to maximum-likelihood analysis using IQ-TREE (default parameters with automatic model finding and 1000 bootstraps) and the phylogram generated using ETE toolkit (<http://etetoolkit.org/>; Huerta-Cepas et al., 2016). Scale bar represents substitutions per amino acid position.



Supplementary Figure S10. Detailed analysis of changes in poly(A) tail length for *M. leidyi cyclin* homolog *ML455312a* using the method described in (Figure 2K) during each of the first four cleavages and at 4-hpf. Position of DNA size markers is shown on the right.

Supplementary Tables

Supplementary Table S1. CPEBs orthologs found in genomes of 44 animal species, including

representatives from 14 animal phyla, but not in genomes from species outside the Metazoa (modified from Paps and Holland (2018)).

Deuterostomia	
<i>Saccoglossus kowalevskii</i>	Skow_10916m Skow_22287m
<i>Strongylocentrotus purpuratus</i>	Spur_015450_Cpeb1 Spur_001293_Cpeb2
<i>Branchiostoma floridae</i>	Bflo_260831047
<i>Ciona intestinalis</i>	Cint_003938 Cint_024148 Cint_003274
<i>Ciona savignyi</i>	Csav_004444 Csav_013417 Csav_004446 Csav_004445 Csav_013416 Csav_013415
<i>Botryllus schlosseri</i>	Bsch_g10689 Bsch_g8517 Bsch_g25882 Bsch_g45408 Bsch_g63388
<i>Oikopleura dioica</i>	Odio_015065001
<i>Danio rerio</i>	Drer_008454_cytoplasmic_polyadenylation_element_binding_protein_1b_Source_ZFIN_Acc_ZDB_GENE_990927_1_cpeb1b Drer_053117_Uncharacterized_protein_Source_UniProtKB_TrEMBL_Acc_E7FA11_cpeb1a Drer_045932_cytoplasmic_polyadenylation_element_binding_protein_1a_Source_ZFIN_Acc_ZDB_GENE_080723_42_cpeb1a Drer_056691_cytoplasmic_polyadenylation_element_binding_protein_4_Source_ZFIN_Acc_ZDB_GENE_040426_1557_cpeb4 Drer_060103_cytoplasmic_polyadenylation_element_binding_protein_3_Source_ZFIN_Acc_ZDB_GENE_090312_68_cpeb3 Drer_052604_cytoplasmic_polyadenylation_element_binding_protein_2_Source_HGNC_Symbol_Acc_21745_CPEB2 Drer_074474_cytoplasmic_polyadenylation_element_binding_protein_4_Source_HGNC_Symbol_Acc_21747_CPEB4_3_of_3 Drer_060495_cytoplasmic_polyadenylation_element_binding_protein_4_Source_HGNC_Symbol_Acc_21747_CPEB4_2_of_3
<i>Xenopus (Silurana) tropicalis</i>	Xtro_023343 Xtro_059795 Xtro_026614 Xtro_043840 Xtro_027833
<i>Gallus gallus</i>	Ggal_003366 Ggal_011187 Ggal_023384 Ggal_022748
<i>Anolis carolinensis</i>	Acar_0000309 Acar_00014820 Acar_00020487 Acar_00006260 Acar_00011854
<i>Homo sapiens</i>	Hsap_Ensembl0260836_RP11_152F13_10 Hsap_Ensembl0214575_cytoplasmic_polyadenylation_element_binding_protein_1_Source_HGNC_Symbol_Acc_21744_CPEB1 Hsap_Ensembl0107864_cytoplasmic_polyadenylation_element_binding_protein_3_Source_HGNC_Symbol_Acc_21746_CPEB3 Hsap_Ensembl0113742_cytoplasmic_polyadenylation_element_binding_protein_4_Source_HGNC_Symbol_Acc_21747_CPEB4 Hsap_Ensembl0137449_cytoplasmic_polyadenylation_element_binding_protein_2_Source_HGNC_Symbol_Acc_21745_CPEB2
Ecdysozoa	
<i>Trichinella spiralis</i>	Tspi_316973214 Tspi_316969994 Tspi_316978840 Tspi_316956776
<i>Romanomermis culicivoxax</i>	Rcul_t24732 Rcul_t40503 Rcul_t00011 Rcul_t00012 Rcul_t01824
<i>Caenorhabditis elegans</i>	Cele_000772_cpb_3_Protein_CPB_3_cpb_3_mRNA_complete_cds_Source_RefSeq_mRNA_Acc_NM_059279 Cele_000770_cpb_1_Protein_CPB_1_cpb_1_mRNA_complete_cds_Source_RefSeq_mRNA_Acc_NM_066650 Cele_001481_fog_1_Protein_FOG_1_isoform_b_Source_RefSeq_mRNA_Acc_NM_001026621 Cele_000771_cpb_2_Protein_CPB_2_cpb_2_mRNA_complete_cds_Source_RefSeq_mRNA_Acc_NM_062835
<i>Brugia malayi</i>	Bmal_170571749 Bmal_170579891 Bmal_170596242 Bmal_170582725
<i>Strigamia maritima</i>	Smar_004137 Smar_004113
<i>Mesobuthus martensii</i> (scorpion)	Mmar_MMa39152 Mmar_MMa28869 Mmar_MMa28867 Mmar_MMa45969
<i>Stegodyphus mimosarum</i> (spider)	Smim_72406_cytoplasmic_polyadenylation_element_binding_protein_putative_Ixodes_scapularis_gi_241829409_ref_XP_002414761_6e_175_501 Smim_56756_PREDICTED_probable_RNA_binding_protein_orb2_like_isoform_Acyrtosiphon_pisum_gi_328721760_ref_XP_003247398_0_0_575 Smim_27690_cytoplasmic_polyadenylation_element_binding_protein_putative_Ixodes_scapularis_gi_241560350_ref_XP_002400996_2e_85_260 Smim_27683_A_Chain_A_Solution_Structure_Of_Rna_Binding_Domain_In_Cytoplasmic_Polyadenylation_Element_Binding_Protein_3_gi_159164253_pdb_2DNL_A_5e_40_136
<i>Ixodes scapularis</i> (tick)	Isca_ISCW023425-PA Isca_ISCW010113-PA
<i>Daphnia pulex</i>	Dpul_326182 Dpul_308504
<i>Zootermopsis nevadensis</i>	Znev_12790 Znev_18107
<i>Tribolium castaneum</i> (beetle)	Tcas_270001277 Tcas_270015159
<i>Drosophila melanogaster</i>	Dmel_0004882_orb_oo18_RNA_binding_protein_Source_FlyBase_0004882 Dmel_0264307_orb2
Lophotrochozoa	
<i>Adineta vaga</i>	Avag_50023001 Avag_12615001 Avag_47368001 Avag_01285001 Avag_12616001 Avag_49767001 Avag_04121001 Avag_07376001 Avag_00865001 Avag_15043001 Avag_65428001 Avag_61392001 Avag_18987001 Avag_04122001 Avag_11453001 Avag_59612001 Avag_19009001 Avag_27103001 Avag_50024001 Avag_01286001 Avag_49768001
<i>Gyrodactylus salaris</i>	Gsal_4058_cytoplasmic_polyadenylation_element_binding_protein_1 Gsal_1072_cytoplasmic_polyadenylation_element_binding_protein_2
<i>Schistosoma japonicum</i>	Sjap_0065230 Sjap_0032030 Sjap_0029950

<i>Schistosoma mansoni</i>	Sman_070360_Putative_cytoplasmic_polyadenylation_element_binding_protein_Cpeb_Source_UniProtKB_TrEMBL_Acc_G4V T97 Sman_012950_Putative_cytoplasmic_polyadenylation_element_binding_protein_Cpeb_Source_UniProtKB_TrEMBL_Acc_G4V EX4 Sman_136410_Putative_cytoplasmic_polyadenylation_element_binding_protein_Cpeb_Source_UniProtKB_TrEMBL_Acc_G4V EX5 Sman_137460_Cytoplasmic_polyadenylation_element_binding_protein_Cpeb_putative_Source_UniProtKB_TrEMBL_Acc_G4L W19
<i>Hymenolepis microstoma</i>	Hmic_0079100
<i>Echinococcus granulosus</i>	Egra_08380 Egra_00993
<i>Echinococcus multilocularis</i>	Emul_08189 Emul_03389
<i>Crassostrea gigas</i>	Cgig_14557_Cytoplasmic_polyadenylation_element_binding_protein_4_Source_UniProtKB_TrEMBL_Acc_K1Q726 Cgig_19114_Cytoplasmic_polyadenylation_element_binding_protein_1_B_Source_UniProtKB_TrEMBL_Acc_K1QYV5
<i>Pinctada fucata</i>	Pfuc_154180_1_28450_t1 Pfuc_1867_1_37153_t1 Pfuc_36185_1_26743_t1
<i>Lottia gigantea</i>	Lgig_213887 Lgig_115324
<i>Capitella teleta</i>	Ctel_118515 Ctel_103382
<i>Helobdella robusta</i>	Hrob_111676 Hrob_79994 Hrob_69117 Hrob_66900
Cnidaria	
<i>Nematostella vectensis</i>	Nvec_39034 Nvec_34062 Nvec_57237 RRM_1
<i>Acropora digitifera</i>	Adig_13400 Adig_10936
<i>Hydra magnipapillata</i>	Hmag_224246 Hmag_210731 Hmag_202650
Placozoa	
<i>Trichoplax adhaerens</i>	Tadh_30543 Tadh_58533
Porifera	
<i>Amphimedon queenslandica</i>	Aque_228234 Aque_215503
<i>Oscarella carmela</i> (incomplete?)	OcarG_3927 OcarG_1845
Ctenophora	
<i>Mnemiopsis leidyi</i>	Mley_ML033245a Mley_ML05854a Mley_ML05855a Mley_ML05856a Mley_ML03369a Mley_ML042716a
<i>Pleurobrachia bachei</i>	Pbac_3462211 Pbac_3463340 Pbac_3460394 Pbac_3479762 Pbac_3475771
Non-Metazoan Eukaryotes	
<i>Chlamydomonas reinhardtii</i>	
<i>Physcomitrella patens</i>	
<i>Selaginella moellendorffii</i>	
<i>Amborella trichopoda</i>	
<i>Arabidopsis thaliana</i>	
<i>Emiliana huxleyii</i>	
<i>Bigeloviella natans</i>	
<i>Reticulomyxa filosa</i>	
<i>Thecamonas trahens</i> ATCC 50062	
<i>Fonticula alba</i>	
<i>Spizellomyces punctatus</i>	
<i>Allomyces macrogynus</i>	
<i>Saccharomyces cerevisiae</i>	
<i>Sphaeroforma arctica</i>	
<i>Creolimax fragrantissima</i>	
<i>Capsaspora owczarzaki</i>	
<i>Monosiga brevicollis</i>	
<i>Salpingoeca rosetta</i>	

Supplementary Table S2. Percent nucleotide composition of 5' halves, 3' halves, and full poly(A) tails obtained from Amplicon-EZ reads of *N. vectensis* *c-mos*, *cyclin1*, and *cyclin3* mRNAs. Average from all three mRNAs including both developmental stages tested for each is shown at the bottom.

<i>c-mos</i> (oocyte)	5' half	3' half	total
A	75	92	83.5
U	12	4	8
C	5	1	3
G	9	3	6

<i>c-mos</i> (egg)	5' half	3' half	total
A	69	92	80.5
U	24	6	15
C	3	1	2
G	4	1	2.5

<i>cyclin 1</i> (oocyte)	5' half	3' half	total
A	42	80	61
U	39	14	26.5
C	6	1	3.5
G	12	5	8.5

<i>cyclin 1</i> (egg)	5' half	3' half	total
A	63	94	78.5
U	30	4	17
C	3	0	1.5
G	4	1	2.5

<i>cyclin 3</i> (egg)	5' half	3' half	total
A	55	86	70.5
U	27	7	17
C	7	3	5
G	10	4	7

<i>cyclin 3</i> (2 HPF)	5' half	3' half	total
A	71	92	81.5
U	22	6	14
C	5	2	3.5
G	3	1	2

Average (All)	5' half	3' half	total
A	62.50	89.33	75.92
U	25.67	6.83	16.25
C	4.83	1.33	3.08
G	7.00	2.50	4.75

Supplementary Table S3. Identification of CPEBs in three different ctenophores. CPEB1 and CPEB2 orthologs identified in reference sequences (left column) of *Mnemiopsis leidyi* (top), *Hormiphora californensis* (center), and *Beroe ovata* (bottom). Transcripts or gene models concluded to correspond to individual genes are grouped in individual rows. Top match from reciprocal BLASTP analyses with human proteins and corresponding E-values (center columns) are included. Glutamine (Q)-rich regions identified as included in at least three of four consecutive positions are indicated (right column).

	Transcript ID	Top Hs Match (RefSeq proteins)	BLASTP E-val (vs. Hs Match)	Potential Prion Motifs (minimum 3 Q in 4 AA stretch)
M. leidyi CPEBs (TBLASTN vs. NHGRI Gene models 2.2)	MI-CPEB1a (ML042716)	CPEB1	1E-129	QQQQQPQ; QVPQQSQPDQ
	MI-CPEB1b (ML05853a)	CPEB1	1E-71	-
	MI-CPEB1c (ML05854a)	CPEB1	1E-60	-
	MI-CPEB1d (ML05855a)	CPEB1	4E-54	-
	MI-CPEB1e (ML05856a)	CPEB1	2E-61	-
	MI-CPEB1f (ML033245a)	CPEB1	6E-78	-
	MI-CPEB2 (ML03369a)	CPEB4	6E-142	
TBLASTN vs. Hcv1av93_transcripts .fasta	Hcv1.av93.c11.g189.i1	CPEB1	7E-72	-
	Hcv1.av93.c11.g188.i1		8E-68	
	Hcv1.av93.c7.g144.i1	CPEB1	1E-63	-
	Hcv1.av93.c7.g142.i1	CPEB1	1E-60	QQQMTPSLQLQ; QKQQQYHPQQHSQQHSQQQQ
	Hcv1.av93.c7.g139.i1	CPEB1	3E-54	-
	Hcv1.av93.c7.g141.i1	CPEB1	2E-40	-
	Hcv1.av93.c7.g140.i1	CPEB1	5E-39	QQQQQPQQ; QQSYYQQQ; QEQQ; QNKQQPQAAPTQQQQ
	Hcv1.av93.c1.g671.i2	CPEB4	8E-140	QQQHQQQ; N-rich
	Hcv1.av93.c1.g671.i1		7E-135	
Hcv1.av93.c1.g671.i3		4E-131		
TBLASTN vs. Bova1.4 cds	Bova1_4.0171.g14.t1	CPEB1	2E-107	QQQ; QPQPQQHQ; QQQPPPQQPQQPPQ
	Bova1_4.0219.g8.t1	CPEB1	5E-74	-
	Bova1_4.0074.g29.t1	CPEB1	4E-77	-
	Bova1_4.0074.g26.t1	CPEB1	3E-64	-
	Bova1_4.0074.g28.t1	CPEB1	5E-59	-
	Bova1_4.0074.g29.t1	CPEB1	1E-47	-
	Bova1_4.0003.g88.t3	CPEB3	9E-137	-
	Bova1_4.0003.g88.t4		2E-135	
	Bova1_4.0003.g88.t2		4E-134	
Bova1_4.0003.g88.t1		5E-134		

Supplementary Files (available at https://github.com/Irouhana/cpeb_evolution)

Supplementary File S1. Protein sequences with homology to human CPEB1 that were identified in BLAST searches against reference sequences from animal and non-animal species. Redundant sequences were removed and only longer isoforms were retained.

Supplementary File S2. Amplicon-EZ reads of 3'-ends of *Nv_c-mos*, *Nv_cyclin1*, and *Nv_cyclin3* mRNAs from stages analyzed in (Figure 2 M-O) and (Supplementary Figure S6).

Supplementary File S3. *N. vectensis* egg transcriptome sequences generated using Oxford Nanopore Direct RNA-sequencing (available for download under NCBI BioProject: PRJNA956458).

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