**Arnold_FigS1**

A gel image showing protein bands at 45 kDa and 75 kDa. The bands are labeled as CEY-4 and PAB-1. The gel is stained to visualize proteins under different conditions labeled as 1:2000, 1:5000, and 1:10000. The lanes are marked with wild type and cey-1,-4 genotypes.
A

![Bar graph showing mRNA levels](Arnold_FigS2)

- elt-2
- act-1
- egg-1
- cey-1
- cey-4
- cey-2
- cey-3

B

**CEY-1-GFP (live imaging)**

- Distal gonad
- Soma (neurons)

C

- Flag
- ADMA
- 37kDa
- 37kDa

D

- Wild type
- prmt-1
- 45kDa
- 45kDa

E

- Wild type
- prmt-1
- 45kDa
- 42kDa

Arnold_FigS2
A

![Bar chart showing viability at 25°C](Arnold_FigS3)

B

![Bar chart showing viability at 20°C, 25°C, and 26°C](Arnold_FigS3)
Arnold_FigS7

% animals

DA naive  DA cond  DA 60 min delay

wild type  cey-1  cey-4  cey-1,-4

Arnold_FigS7
**Figure A**

Protein concentration [ng/μl] for wild type (n=6) and cey-1,-4 (n=6) strains. The bars show the mean protein concentration with standard error bars. The comparison between the two groups is indicated by a horizontal line labeled "n.s." (not significant).

**Figure B**

Western blot analysis showing protein bands for wild type, cey-1,-4, and elk-1 strains. Protein markers include 100 kDa, 100 kDa, 42 kDa, and 2500, 3000, 3500, 2000, 1500, 1000, 500, 0 ng/μl. Proteins of interest labeled as EEF-2-P, EEF-2, and ACT-1.
A

Absorption (254nm)

monosomes

di-somes

polysomes

submonosomal fractions

mono- and polysomal (5-12)

total (1-12) fractions

B

Arnold_FigS13

*n.s.*

monop- and polysomal mRNA / total mRNA

wild type  cey-1,-4

mRNA:
cyc  oma-2  egl-1  rme-2

Arnold_FigS13
| Strain | Figure | Strain name |
|--------|--------|-------------|
| #928  | S1B    | rrsSi120 [cey-1 pro::cey-1 ORF::GFP::FLAG::cey-1 3'-UTR; unc-119(+)] IV |
| #1143 | 1E     | rrsSi245 [cey-2 pro::GFP::cey-2 ORF::cey-2 3'-UTR; unc-119(+)] I |
| Boag lab | 1E | cey-3 pro::cey-3 ORF::GFP::FLAG(3x)::cey-3 3'UTR |
| #1099 | 6A     | rrsSi235 [rps-1 pro::GFP::rps-1 ORF::rps-1 3'-UTR; unc-119(+)] I |
| #1087 | 1D     | rrsSi228 [cey-1 pro::PEST:GFPH2B::cey-1 3'-UTR; unc-119(+)] I |
| #1090 | 1D     | rrsSi231 [cey-2 pro::PEST:GFPH2B::cey-2 3'-UTR; unc-119(+)] I |
| #1091 | 1D     | rrsSi232 [cey-3 pro::PEST:GFPH2B::cey-3 3'-UTR; unc-119(+)] I |
| #1088 | 1D     | rrsSi229 [cey-4 pro::PEST:GFPH2B::cey-4 3'-UTR; unc-119(+)] I |
| #1092 |        | rrsSi233 [cey-2 pro::FLAG(1x)::cey-2 ORF::cey-2 3'-UTR::operon linker::PEST:GFPH2B: tbb-2 3'UTR; unc-119(+)] I |
| #1308 |        | rrsSi300 [cey-1 pro::FLAG(1x)::cey-1 ORF::cey-1 3'-UTR::operon linker::PEST:GFPH2B: tbb-2 3'UTR; unc-119(+)] I |
| #1335 |        | rrsSi07 [dpy-30 pro::FLAG(1x)::cey-4 ORF::cey-4 3'-UTR::operon linker::PEST:GFPH2B: tbb-2 3'UTR; unc-119(+)] I (*) |
| #1502 |        | rrsSi325 [mex-5 pro::FLAG(1x)::cey-4 ORF::cey-4 3'-UTR::operon linker::PEST:GFPH2B: tbb-2 3'UTR; unc-119(+)] I |
| #1537 |        | rrsSi332 [cey-1 pro::FLAG(1x)::cey-2 ORF::cey-1 3'-UTR::operon linker::PEST:GFPH2B: tbb-2 3'UTR; unc-119(+)] I |
| #1069 |        | cey-2(ok902); cey-3(rr11) |
| #1352 |        | cey-1(rr12) |
Table S2

| Accession | Peptides | Score | Tags | Description | Summed peptide ion abundance |
|-----------|----------|-------|------|-------------|-------------------------------|
|           |          |       |      |             | CEY-1 +/RNAse | CEY-1 -/RNAse | wild type ctrl |
| RS3A_CAEEL | 17       | 838.34 |      | RPS-1       | 1.20E+05 | 2.59E+05 | 3.04E+04 |
| R8L_CAEEL  | 15       | 813.31 |      | RPL-8       | 1.23E+05 | 2.88E+05 | 4.82E+04 |
| RS8_CAEEL  | 13       | 733.52 |      | RPS-8       | 7.67E+04 | 2.85E+05 | 5.49E+04 |
| RL13_CAEEL | 13       | 649.94 |      | RPL-13      | 8.15E+04 | 2.73E+05 | 3.70E+04 |
| O18240_CAEEL | 13     | 630.39 |      | RPS-18      | 1.17E+05 | 2.88E+05 | 4.88E+04 |
| RS17_CAEEL | 12       | 607.13 |      | RPS-17      | 7.80E+04 | 1.99E+05 | 2.64E+04 |
| RL10_CAEEL | 11       | 550.09 |      | RPL-10      | 4.70E+04 | 9.67E+04 | 1.30E+04 |
| RS12_CAEEL | 8        | 523.37 |      | RPS-12      | 9.41E+04 | 2.48E+05 | 3.57E+04 |
| RL19_CAEEL | 12       | 513.95 |      | RPL-19      | 5.21E+04 | 1.41E+05 | 1.31E+04 |
| RS7_CAEEL  | 11       | 509.24 |      | RPS-7       | 6.62E+04 | 1.49E+05 | 2.15E+04 |
| RS13_CAEEL | 12       | 455.13 |      | RPS-13      | 5.12E+04 | 1.53E+05 | 1.91E+04 |
| RLA1_CAEEL | 7        | 453.79 |      | RLA-1       | 2.47E+05 | 3.09E+05 | 5.92E+04 |
| Q20206_CAEEL | 11     | 415.23 |      | RPS-11      | 3.77E+04 | 1.27E+05 | 2.20E+04 |
| Q8WQA8_CAEEL | 8      | 398.64 |      | RPS-20      | 4.68E+04 | 1.13E+05 | 2.24E+04 |
| RS14_CAEEL | 6        | 396.76 |      | RPS-14      | 3.74E+04 | 9.79E+04 | 1.34E+04 |
| RL7_CAEEL  | 11       | 376.49 |      | RPL-7       | 7.31E+04 | 1.45E+05 | 2.81E+04 |
| R23A2_CAEEL | 9       | 374.41 |      | RPL-25.2    | 4.98E+04 | 2.29E+05 | 1.34E+04 |
| O01869_CAEEL | 6      | 346.71 |      | RPS-10      | 5.65E+04 | 1.40E+05 | 2.24E+04 |
| RS9_CAEEL  | 11       | 340.91 |      | RPS-9       | 2.50E+04 | 7.45E+04 | 1.41E+04 |
| RL31_CAEEL | 7        | 308.05 |      | RPL-31      | 3.04E+04 | 8.03E+04 | 6732.43 |
| RL26_CAEEL | 7        | 301.68 |      | RPL-26      | 4.12E+04 | 2.53E+05 | 2.64E+04 |
| RL35A_CAEEL | 8       | 281.34 |      | RPL-33      | 3.00E+04 | 8.50E+04 | 1.49E+04 |
| RL13A_CAEEL | 8       | 280.75 |      | RPL-16      | 2.61E+04 | 4.84E+04 | 3064.33 |
| RL37A_CAEEL | 6       | 271.68 |      | RPL-43      | 7263.06  | 4.17E+04 | 7036.81 |
| RS25_CAEEL | 6        | 268.22 |      | RPS-25      | 5.61E+04 | 1.68E+05 | 3.26E+04 |
| RL27_CAEEL | 5        | 268.16 |      | RPL-27      | 7457.44  | 9.60E+04 | 1.03E+04 |
| RS23_CAEEL | 5        | 260.62 |      | RPS-23      | 6.16E+04 | 1.59E+05 | 1.23E+04 |
| RL36_CAEEL | 5        | 255.67 |      | RPL-36      | 4.18E+04 | 1.33E+05 | 8340.94 |
| Q22716_CAEEL | 5     | 245.06 |      | RPL-32      | 2.60E+04 | 7.04E+04 | 1954.95 |
| A3QMC5_CAEEL | 5       | 228.86 |      | RPL-34      | 2.29E+04 | 9.23E+04 | 1.33E+04 |
| Q9U1X9_CAEEL | 5       | 220.07 |      | RLA-2       | 1.92E+04 | 5.98E+04 | 7131.92 |
| O62388_CAEEL | 7      | 219.11 |      | W01D2.1     | 6413.02  | 2.06E+04 | 2303.11 |
| P90983_CAEEL | 5      | 213.51 |      | RPS-29      | 1602.78  | 4.72E+04 | 1180.4  |
| RL35_CAEEL | 5        | 207.9  |      | RPL-35      | 2.51E+04 | 9.16E+04 | 4887.81 |
| Q9XSWS4_CAEEL | 4     | 202.89 |      | RPL_30      | 1.91E+04 | 5.39E+04 | 7841.98 |
| RS27A_CAEEL | 2        | 201.41 |      | UBL-1       | 2.27E+04 | 9.91E+04 | 9931.76 |
| R23A1_CAEEL | 4        | 196.18 |      | RPL-25.1    | 2.80E+04 | 6.02E+04 | 1.17E+04 |
| O17218_CAEEL | 3      | 138.96 |      | RPS-22      | 1.22E+04 | 6.18E+04 | 1.78E+04 |
| RL38_CAEEL | 2        | 122.93 |      | RPL-38      | 1.37E+04 | 7.19E+04 | 2481.09 |
| RL44_CAEEL | 5        | 120.84 |      | RPL-41      | 1.17E+04 | 5.02E+04 | 2626.83 |
| Q18231_CAEEL | 3      | 89.82  |      | RPS-30      | 7607.51  | 2.40E+04 | 1854.05 |
| RT07_CAEEL | 2        | 82.33  |      | MRPS-7      | 2122.53  | 2717.21  | 0       |
| Accession   | Score   | Description | Kda       | Mda       | Gda       |
|-------------|---------|-------------|-----------|-----------|-----------|
| Q9U302_CAEEL| 32.14   | PAB-1       | 9.89E+04  | 5.51E+06  | 1.20E+05  |
| Q9XW17_CAEEL| 214.94  | CAR-1       | 3.22E+05  | 5.04E+06  | 3.34E+05  |
| CGH1_CAEEL  | 2093.3  | CGH-1       | 5.17E+04  | 1.70E+06  | 3.89E+04  |
| P91306_CAEEL| 1832.24 | CEY-2       | 5.95E+04  | 1.07E+07  | 6.19E+04  |
| P91398_CAEEL| 1673.54 | CEY-3       | 3.39E+04  | 3.82E+06  | 4.56E+04  |
| Q19579_CAEEL| 1461.93 | PAB-2       | 2.24E+04  | 1.24E+06  | 2.89E+04  |
| Q8WQD8_CAEEL| 1411.73 | CAH-4       | 2.31E+04  | 1.60E+05  | 1.41E+04  |
| O62213_CAEEL| 1392.65 | CEY-1       | 3.30E+07  | 2.87E+07  | 4.98E+04  |
| G5EDV3_CAEEL| 1292.14 | CEY-4       | 2.11E+04  | 1.17E+06  | 4811.64   |
| O02089_CAEEL| 879.68  | MSRA-1      | 2.29E+04  | 2.19E+05  | 1579.89   |
| Q9XUW5_CAEEL| 865.95  | F58E10.3    | 1.69E+05  | 8.96E+04  | 3.13E+04  |
| PCCA_CAEEL  | 709.09  | PCCA-1      | 1.91E+04  | 1.74E+05  | 1.68E+05  |
| Q8MXR6_CAEEL| 661.53  | SQD-1       | 1.95E+05  | 5.51E+04  | 7.49E+04  |
| DKC1_CAEEL  | 613.23  | K01G5.5     | 9173.24   | 1.20E+05  | 7523.09   |
| D5MCN2_CAEEL| 604.26  | LARP-1      | 1414.81   | 7.56E+04  | 1.04E+04  |
| H2Kyr1_CAEEL| 586.51  | VIG-1       | 6.67E+04  | 1.02E+05  | 1.58E+04  |
| Q94271_CAEEL| 465.16  | ASP-14      | 1.57E+05  | 931.43    | 3146.47   |
| GLD1_CAEEL  | 445.29  | GLD-1       | 4736.04   | 1.27E+05  | 5716.97   |
| Q18490_CAEEL| 434.72  | C35D10.13   | 316.5     | 1.13E+05  | 545.02    |
| MYO4_CAEEL  | 430.99  | UNC-54      | 3.11E+05  | 1.68E+04  | 3434.74   |
| Q20277_CAEEL| 390.14  | FIPR-21     | 4.04E+05  | 7.02E+05  | 5.72E+04  |
| FBRL_CAEEL  | 369.18  | FIB-1       | 7.37E+04  | 4.07E+04  | 4825.66   |
| G1K0V8_CAEEL| 296.64  | IFF-1       | 3.69E+04  | 1.45E+04  | 6942.51   |
| GAR1_CAEEL  | 289.54  | Y66H1A.4    | 1.52E+04  | 5.94E+04  | 1866.14   |
| Q94230_CAEEL| 282.77  | PLP-1       | 1342.86   | 3.67E+04  | 185.68    |
| Q9N3F4_CAEEL| 276.73  | VBH-1       | 9.51E+04  | 2.50E+04  | 1.13E+04  |
| MEL47_CAEEL | 256.85  | MEL-47      | 128.22    | 3.73E+04  | 1420.83   |
| IF4E3_CAEEL | 229.5   | IFE-3       | 6612.3    | 5.00E+04  | 1056.53   |
| O61880_CAEEL| 219.68  | F59B1.2     | 1.26E+05  | 2.09E+05  | 5580.79   |
| Q21740_CAEEL| 219.51  | EDC-3       | 82.18     | 2.79E+04  | 184.29    |
| Q95YC6_CAEEL| 216.17  | C45B2.1     | 3.86E+05  | 2.83E+05  | 2.00E+04  |
| NHP2_CAEEL  | 207.47  | Y48A6B.3    | 1.30E+04  | 5.40E+04  | 1.05E+04  |
| Q21832_CAEEL| 151.71  | RNP-4       | 200.74    | 3.39E+04  | 1077.31   |
| Q20898_CAEEL| 150.73  | IFET-1      | 2603.01   | 6.01E+04  | 3548.16   |
| NOP10_CAEEL | 148.73  | C25A1.6     | 8.86      | 3.61E+04  | 3950.43   |
| O76616_CAEEL| 142.69  | Y23H5A.3    | 30.06     | 1.13E+04  | 615.11    |
| Q20448_CAEEL| 139.2   | 2TF-7       | 1852.2    | 1.37E+04  | 584.22    |
| SMD2_CAEEL  | 138.95  | SNR-4       | 8598.32   | 1.86E+04  | 1824.47   |
| G5EDE4_CAEEL| 126.75  | W08E3.2     | 413.86    | 2.40E+04  | 0         |
| Q17407_CAEEL| 108.42  | T27E9.1a    | 2855.68   | 4050.76   | 0         |
| O45012_CAEEL| 108.41  | NOL-5       | 639.06    | 6466.18   | 244.7     |
| M1ZJ32_CAEEL| 103.33  | SNR-3       | 1067.21   | 1.64E+04  | 581.59    |
| ODB2_CAEEL  | 92.64   | ZK669.4     | 10.66     | 2430.89   | 163.99    |
| SAHH_CAEEL  | 91.74   | AHCY-1      | 9525.78   | 1899.79   | 0.08      |
| IF5A2_CAEEL | 85.56   | IFF-2       | 1.24E+04  | 3871.42   | 1494.24   |
| RSMB_CAEEL  | 84.84   | SNR-2       | 1192.22   | 1.23E+04  | 3267.49   |
| Gene         | Conf. | Score change | Fold change | Fold change | Mean change | Max change |
|--------------|-------|--------------|-------------|-------------|-------------|------------|
| MYO2_CAEEL   | 3     | 82.74        | 2.44E+04    | 2.28E+04    | 559.63      |
| O45713_CAEEL | 2     | 79.72        | 5241.94     | 828.89      | 437.66      |
| Q18494_CAEEL | 2     | 79.52        | 1378.99     | 5327.85     | 161.96      |
| H2KZC9_CAEEL | 3     | 75.99        | 4798.14     | 1.20E+04    | 1168.87     |
| Q86MP4_CAEEL | 3     | 74.7         | 0           | 6763.26     | 4008.3      |
| Q9XUS4_CAEEL | 2     | 70.17        | 306.36      | 1.56E+04    | 4177.95     |
| SUCA_CAEEL   | 3     | 63.79        | 207.24      | 8295.48     | 3955.17     |
| RSP3_CAEEL   | 2     | 61.86        | 1.87E+04    | 3199.36     | 1.82E+04    |
| Q9NA98_CAEEL | 2     | 59.58        | 4717.06     | 1146.44     | 0           |
| O16303_CAEEL | 2     | 59.39        | 2935.68     | 5718.93     | 0           |
| G5EEE4_CAEEL | 4     | 59.06        | 4022.79     | 4.87E+04    | 3110.35     |
| ALH13_CAEEL  | 2     | 55.37        | 3.46E+04    | 5.13E+04    | 558.67      |
| GNL3_CAEEL   | 3     | 54.89        | 6309.97     | 5.56E+04    | 776.05      |
| Q9U334_CAEEL | 2     | 54.52        | 1.01E+04    | 1.08E+04    | 602.23      |
| O44633_CAEEL | 2     | 53.12        | 1272.41     | 1.03E+05    | 2315.26     |
| Q966A5_CAEEL | 3     | 53.07        | 3.68E+05    | 4.90E+05    | 3.90E+04    |
| H2L0J8_CAEEL | 2     | 52.62        | 1522.94     | 4.07E+04    | 457.29      |
| Q965K2_CAEEL | 2     | 51.94        | 0           | 4677.86     | 573.44      |
| O45021_CAEEL | 2     | 51.1         | 1.51E+04    | 1487.48     | 874.26      |
| O62131_CAEEL | 2     | 50.82        | 3231.94     | 6391.15     | 530.64      |

**Tags**

- **=1 peptide**
- **>5x fold change**
- **>10 fold change**
- **highest in CEY-1/4 - RNase**
- **highest in CEY-1/4 + RNase**
- **highest in N2**
- **confidence< 50**
Table S3

| Accession   | Peptides | Score       | Tags | Description       | Summed peptide ion abundance |
|-------------|----------|-------------|------|-------------------|-------------------------------|
|             |          |             |      |                   | CEY-4 + RNAse | CEY-4 - RNAse | wild type ctrl |
| RL4_CAEEL   | 33       | 1963.59     | RPL-4| 7.23E+05          | 6.54E+05   | 1.42E+05        |
| RS3_CAEEL   | 22       | 1282.38     | RPS-3| 2.73E+05          | 3.92E+05   | 5.86E+04        |
| RL5_CAEEL   | 19       | 1151.56     | RPL-5| 2.53E+05          | 3.52E+05   | 5.84E+04        |
| RS3A_CAEEL  | 23       | 1123.67     | RPS-1| 5.86E+05          | 3.78E+05   | 3.20E+04        |
| RL3_CAEEL   | 22       | 1068.35     | RPL-3| 2.65E+05          | 2.78E+05   | 5.29E+04        |
| RL8_CAEEL   | 17       | 1040.61     | RPL-8| 2.82E+05          | 2.74E+05   | 3.68E+04        |
| RLA0_CAEEL  | 18       | 1001.35     | RPA-0| 2.53E+05          | 2.86E+05   | 3.74E+04        |
| RS6_CAEEL   | 16       | 1001.23     | RPS-6| 1.52E+05          | 1.35E+05   | 2.62E+04        |
| RS15_CAEEL  | 13       | 799.1       | RPS-15| 9.50E+04          | 1.47E+05   | 1.20E+04        |
| RS7_CAEEL   | 13       | 757.65      | RPS-7| 2.01E+05          | 2.28E+05   | 2.80E+04        |
| RL10_CAEEL  | 14       | 723.34      | RPL-10| 1.17E+05          | 1.10E+05   | 2.22E+04        |
| RS16_CAEEL  | 12       | 691.76      | RPS-16| 1.54E+05          | 1.91E+05   | 1.58E+04        |
| RS12_CAEEL  | 11       | 684.41      | RPS-12| 3.74E+05          | 3.48E+05   | 4.36E+04        |
| RS17_CAEEL  | 14       | 683.69      | RPS-17| 2.50E+05          | 2.39E+05   | 2.28E+04        |
| O18240_CAEEL| 14       | 680.29      | RPS-18| 2.88E+05          | 3.38E+05   | 3.52E+04        |
| RL6_CAEEL   | 13       | 667.74      | RPL-6| 1.76E+05          | 2.26E+05   | 3.47E+04        |
| RL13_CAEEL  | 13       | 647.35      | RPL-13| 1.94E+05          | 2.07E+05   | 3.94E+04        |
| RL7A_CAEEL  | 17       | 630.19      | RPL-7A| 1.66E+05          | 1.28E+05   | 3.00E+04        |
| RS5_CAEEL   | 11       | 620.68      | RPS-5| 1.36E+05          | 2.04E+05   | 3.63E+04        |
| RL19_CAEEL  | 13       | 599.47      | RPL-19| 1.15E+05          | 1.27E+05   | 2.40E+04        |
| RS13_CAEEL  | 13       | 596.3       | RPS-13| 1.64E+05          | 1.65E+05   | 2.31E+04        |
| Q8WQA8_CAEEL| 12       | 589.45      | RPS-20| 1.84E+05          | 2.03E+05   | 2.34E+04        |
| RL7_CAEEL   | 13       | 584.19      | RPL-7| 2.19E+05          | 1.83E+05   | 3.72E+04        |
| RS21_CAEEL  | 8        | 580.42      | RPS-21| 2.28E+05          | 2.24E+05   | 3.36E+04        |
| RLA1_CAEEL  | 6        | 576.37      | RLA-1| 7.18E+05          | 4.68E+05   | 1.07E+05        |
| RL17_CAEEL  | 13       | 561.55      | RPL-17| 2.97E+05          | 2.13E+05   | 4.04E+04        |
| RL10A_CAEEL | 9        | 554.88      | RPL-10A| 1.06E+05         | 2.20E+05   | 3.15E+04        |
| Q20206_CAEEL| 11       | 553.9       | RPS-11| 1.30E+05          | 1.08E+05   | 1.43E+04        |
| RS19_CAEEL  | 11       | 485         | RPS-19| 2.50E+05          | 1.86E+05   | 4.15E+04        |
| RS14_CAEEL  | 8        | 446.12      | RPS-14| 1.38E+05          | 1.54E+05   | 2.97E+04        |
| O01869_CAEEL| 7        | 433.66      | RPS-10| 1.63E+05          | 1.70E+05   | 2.03E+04        |
| RL35A_CAEEL | 10       | 422.26      | RPL-33| 8.33E+04          | 7.28E+04   | 1.23E+04        |
| RS25_CAEEL  | 7        | 401.66      | RPS-25| 1.89E+05          | 1.66E+05   | 2.86E+04        |
| Q22716_CAEEL| 8        | 380.18      | RPL-32| 6.06E+04          | 5.17E+04   | 4155.61         |
| RS26_CAEEL  | 5        | 375.47      | RPS-26| 1.61E+05          | 1.44E+05   | 1.11E+04        |
| RL11_CAEEL  | 9        | 370.94      | RPL-11.1| 1.25E+05         | 9.83E+04   | 1.78E+04        |
| RL18A_CAEEL | 9        | 352.1       | RPL-20| 5.37E+04          | 6.69E+04   | 9293.01         |
| O17218_CAEEL| 4        | 346.78      | RPS-22| 2.88E+04          | 1.03E+05   | 1.66E+04        |
| R23A2_CAEEL | 8        | 335.65      | RPL-25.2| 1.08E+05         | 1.02E+05   | 1.82E+04        |
| RS23_CAEEL  | 6        | 325.55      | RPS-23| 1.06E+05          | 1.02E+05   | 1.82E+04        |
| RL26_CAEEL  | 8        | 319.79      | RPL-26| 8.25E+04          | 1.87E+05   | 1.65E+04        |
| RL13A_CAEEL | 8        | 318.86      | RPL-16| 5.48E+04          | 6.21E+04   | 3284.68         |
| Protein ID  | Score | Environment | Value 1  | Value 2  | Value 3  |
|------------|-------|-------------|----------|----------|----------|
| RL31_CAEEL | 6     | RPL-31      | 1.21E+05 | 8.33E+04 | 5781.92  |
| RL22_CAEEL | 6     | RPL-22      | 1.65E+05 | 1.20E+05 | 2.49E+04 |
| Q9XWS4_CAEEL | 5   | RPL-30      | 6.43E+04 | 6.42E+04 | 8360.82  |
| A3OMC5_CAEEL | 6   | RPL-34      | 9.79E+04 | 6.83E+04 | 1.67E+04 |
| RS27A_CAEEL | 3    | UBL-1       | 1.70E+05 | 1.01E+05 | 1.40E+04 |
| P90983_CAEEL | 5   | RPS-29      | 4.765.88 | 3.90E+04 | 769.58   |
| RS27_CAEEL  | 4    | RPS-27      | 2.89E+04 | 5.80E+04 | 5917.36  |
| RL35_CAEEL  | 6    | RPL-35      | 6.36E+04 | 9.18E+04 | 1.49E+04 |
| RL38_CAEEL  | 3    | RPL-38      | 6.35E+04 | 6.91E+04 | 6824.36  |
| RL44_CAEEL  | 4    | RPL-41      | 1.81E+04 | 2.65E+04 | 1011.38  |
| Q18231_CAEEL | 3  | RPS-30      | 1.62E+04 | 1.33E+04 | 2170.1   |
| Q23155_CAEEL | 2   | MRPS-11     | 5823.49  | 2972.62  | 748.17   |
| RT07_CAEEL  | 2    | MRPS-7      | 3593.36  | 648.88   | 0        |
| RL40_CAEEL  | 2    | UBQ-2       | 9051.73  | 6458.58  | 1125.02  |
| Others proteins |
| G5EDV3_CAEEL | 47  | CEY-4       | 3.58E+07 | 4.18E+07 | 1.55E+05 |
| Q9U302_CAEEL | 54  | PAB-1       | 1.11E+05 | 6.23E+06 | 1.26E+05 |
| Q9XW17_CAEEL | 31  | CAR-1       | 2.89E+05 | 4.93E+04 | 3.34E+05 |
| P91306_CAEEL | 20  | CEY-2       | 5.44E+04 | 1.39E+07 | 6.75E+04 |
| YM67_CAEEL  | 22   | K12H4.7     | 9.14E+06 | 5.46E+06 | 4.32E+04 |
| CGH1_CAEEL  | 32   | CGH-1       | 5.62E+04 | 1.47E+06 | 2.69E+04 |
| P91398_CAEEL | 19  | CEY-3       | 6.31E+04 | 4.83E+06 | 5.45E+04 |
| Q19579_CAEEL | 25  | PAB-2       | 3.37E+04 | 1.17E+06 | 4.09E+04 |
| GBLP_CAEEL  | 18   | RACK-1      | 5.25E+05 | 6.15E+05 | 8.48E+04 |
| DKC1_CAEEL  | 18   | K01G5.5     | 1.01E+04 | 3.98E+05 | 1.65E+04 |
| Q8WQD8_CAEEL | 14  | CAH-4       | 1.39E+06 | 1.47E+05 | 4.19E+04 |
| Q9XUW5_CAEEL | 19  | F58E10.3    | 1.07E+05 | 5.42E+04 | 1.83E+04 |
| GLD1_CAEEL  | 16   | GLD-1       | 5.076.07 | 2.63E+05 | 1.39E+04 |
| O02089_CAEEL | 10  | MSRA-1      | 7828.31  | 1.59E+05 | 1503.79  |
| Q8MXR6_CAEEL | 11  | SQD-1       | 5.43E+04 | 4.23E+05 | 6.52E+04 |
| MEL47_CAEEL | 13   | MEL-47      | 5319.37  | 1.54E+05 | 1.10E+04 |
| YZVL_CAEEL  | 12   | K07C5.4     | 4981.51  | 1.07E+05 | 1.69E+04 |
| EIF3A_CAEEL  | 16   | EGL-45      | 1.94E+05 | 1.50E+05 | 2.62E+04 |
| RO60_CAEEL  | 14   | ROP-1       | 2.60E+04 | 8.68E+04 | 6251.13  |
| Q21740_CAEEL | 8   | EDC-3       | 312.47   | 6.49E+04 | 350.6    |
| O45012_CAEEL | 8   | NOL-5       | 5137.3   | 4.04E+04 | 1213.8   |
| Q18490_CAEEL | 9   | C35D10.13   | 9017.96  | 1.54E+05 | 3161.09  |
| Q20277_CAEEL | 5   | FIPR-21     | 1.72E+05 | 2.67E+05 | 1.75E+04 |
| Q9N3F4_CAEEL | 9   | VBH-1       | 1.46E+05 | 4.16E+04 | 1.32E+04 |
| IF4E3_CAEEL  | 6    | IFE-3       | 1567.62  | 9.94E+04 | 2008.83  |
| O76616_CAEEL | 6   | Y23H5A.3    | 458.44   | 4.03E+04 | 817.87   |
| Q20057_CAEEL | 3   | F35G12.11   | 576.43   | 4.10E+04 | 283.56   |
| NH2P_CAEEL  | 6    | Y48AB6.3    | 1.73E+04 | 1.61E+05 | 9527.66  |
| GAR1_CAEEL  | 6    | Y66H1A.4    | 8246.91  | 1.21E+05 | 2782.61  |
| D5MCN2_CAEEL | 7   | LARP-1      | 3.10E+05 | 2.63E+05 | 1755.47  |
| Q94230_CAEEL | 7   | PLP-1       | 1373.52  | 4.28E+04 | 290.26   |
| ODB2_CAEEL  | 5    | ZK669.4     | 421.92   | 2.75E+04 | 1428.7   |
| Gene Symbol | Species | Gene Name | Homo sapiens | Homo sapiens | Homo sapiens | Homo sapiens |
|-------------|---------|-----------|--------------|--------------|--------------|--------------|
| NOP10_CAEEL | 4       | C25A1.6   | 249.96       | 5.00E+04     | 0.12         |
| Q17407_CAEEL | 4       | T27E9.1a  | 5597.62      | 1.98E+04     | 3719.14      |
| Q20898_CAEEL | 7       | IFET-1    | 2549.01      | 5.39E+04     | 559.81       |
| MYO4_CAEEL | 5       | UNC-54    | 1.84E+04     | 1.00E+04     | 322.87       |
| P91453_CAEEL | 8       | T19B4.5   | 3.08E+04     | 9797.9       | 3813.85      |
| O62213_CAEEL | 4       | CEY-1     | 1.56E+04     | 1.27E+04     | 774.44       |
| Q94271_CAEEL | 4       | ASP-14    | 1.72E+04     | 2499.48      | 1842.37      |
| Q9U2X0_CAEEL | 4       | PRMT-1    | 1.56E+04     | 1.40E+04     | 140.09       |
| EIF3C_CAEEL | 3       | EIF-3     | 8618.62      | 4373.58      | 1718.24      |
| T5R1_CAEEL | 4       | TAG-151   | 9835.96      | 399.61       | 154.95       |
| ITJ4C6_CAEEL | 4       | K0F7S.15  | 8336.33      | 2502.25      | 992.21       |
| P91223_CAEEL | 3       | F07E5.5   | 71.44        | 8678.71      | 0            |
| YQ58_CAEEL | 3       | C16C10.8  | 1.20E+06     | 3.03E+04     | 4318.42      |
| LIN41_CAEEL | 2       | LIN-41    | 3601.14      | 7263.32      | 523.37       |
| O01806_CAEEL | 3       | C44E4.4   | 2117.33      | 7419.46      | 177.42       |
| DMN2_CAEEL | 2       | Y73F4A.1  | 6439.86      | 8689.51      | 0            |
| B6VQ85_CAEEL | 6       | C23H4.6   | 2.17E+05     | 2.38E+05     | 2.90E+04     |
| SMD2_CAEEL | 2       | SNR-4     | 1007.89      | 1.41E+04     | 487.59       |
| NH2L1_CAEEL | 2       | M28.5     | 1.86E+04     | 161.08       | 161.08       |
| BNYN1_CAEEL | 2       | BYN-1     | 5677.28      | 1743.01      | 106.13       |
| Q23359_CAEEL | 3       | OMA-2     | 12.55        | 1.51E+04     | 830.35       |
| Q20448_CAEEL | 2       | ZTF-7     | 829.13       | 9745.79      | 124.8        |
| H2FLK6_CAEEL | 4       | LEA-1     | 289.87       | 1.09E+04     | 6933.22      |
| G5EFM7_CAEEL | 2       | F18C12.3  | 3610.85      | 71.6         | 2584.59      |
| ATPB_CAEEL | 2       | ATP-2     | 5403.34      | 4261.5       | 1041.76      |
| Q21323_CAEEL | 3       | RNP-3     | 163.73       | 1.11E+04     | 1373         |
| OLA1_CAEEL | 2       | TAG-210   | 946.79       | 3906.58      | 461.39       |
| H9G340_CAEEL | 2       | MPST-3    | 7714.84      | 311.34       | 243.52       |
| G5EDE4_CAEEL | 2       | W08E3.2   | 254.45       | 4813.82      | 62.44        |
| Q0G828_CAEEL | 2       | F04F8.11  | 3836.36      | 4445.36      | 5.13         |
| LTIV_CAEEL | 2       | T23B6.3   | 7582.97      | 1272.74      | 524.1        |
| O61880_CAEEL | 2       | F59B1.2   | 7031.69      | 3.60E+04     | 2237.45      |
| METK5_CAEEL | 3       | SAMS-5    | 9658.74      | 8660.12      | 1779.37      |
| RUXF_CAEEL | 2       | SNR-5     | 1.20E+04     | 872.01       | 0            |
| Q20878_CAEEL | 5       | F56D5.9   | 1.28E+05     | 9.83E+05     | 9.72E+04     |
| D1MN65_CAEEL | 2       | IFE-1     | 5277.7       | 131.21       |
| RSMB_CAEEL | 2       | SNR-2     | 591.14       | 1.58E+04     | 1248.53      |
| MED12_CAEEL | 3       | DPY-22    | 6956.49      | 214.47       | 4643.34      |
| M1ZK05_CAEEL | 4       | SEC-16    | 7713.54      | 6.52E+04     | 8831.31      |
| MYO2_CAEEL | 2       | MYO-2     | 8590.38      | 2446.91      | 0            |
| G5EBX1_CAEEL | 4       | UNC-53    | 2393.6       | 2.72E+05     | 1.65E+04     |
| EIF3I_CAEEL | 2       | EIF-3.1   | 2198.92      | 695.81       |
| Q94174_CAEEL | 3       | BICD-1    | 2.11E+04     | 3.82E+04     | 3070.6       |
| Q814C5_CAEEL | 2       | FAAH-4    | 3.13E+05     | 2.48E+05     | 1873.46      |
| O62102_CAEEL | 2       | PBS-2     | 3.86E+04     | 2.76E+04     | 679.6        |
| G5ECY5_CAEEL | 2       | CSP-2     | 1.70E+04     | 1.26E+04     | 592.77       |
| DYP27_CAEEL | 3       | DPY-27    | 4915.97      | 8606.28      | 1197.02      |
| YKA3_CAEEL | 3       | B0303.3   | 2.00E+04     | 2.78E+04     | 600.33       |
### Tags

- **=1 peptide**
- **>5x fold change**
- **>10 fold change**
- **highest in CEY-1/4 - RNase**
- **highest in CEY-1/4 + RNase**
- **highest in N2**
- **confidence< 50**
| Wormbase ID   | Name      | cey-1,-4 / wild type (mRNA) | cey-1,-4 / wild type (RPF) |
|--------------|-----------|----------------------------|---------------------------|
| WBGene00000386 | cdc-25.1  | 0.78                       | 0.43                      |
| WBGene00000465 | cpg-1     | 0.87                       | 0.35                      |
| WBGene00000866 | cyb-2.1   | 1.12                       | 0.33                      |
| WBGene00000867 | cyb-2.2   | 1.24                       | 0.32                      |
| WBGene00000870 | cyp-1     | 1.06                       | 0.48                      |
| WBGene00000913 | daf-18    | 0.96                       | 0.36                      |
| WBGene00001372 | exo-3     | 0.95                       | 0.5                       |
| WBGene00001569 | gel-12    | 0.93                       | 0.3                       |
| WBGene00001606 | gln-5     | 0.96                       | 0.37                      |
| WBGene00001647 | gna-2     | 0.93                       | 0.48                      |
| WBGene00003184 | mei-2     | 1.06                       | 0.43                      |
| WBGene00003229 | mex-3     | 1.10                       | 0.45                      |
| WBGene00003865 | oma-2     | 0.76                       | 0.32                      |
| WBGene00004027 | pie-1     | 1.06                       | 0.49                      |
| WBGene00004086 | pph-4.2   | 1.01                       | 0.44                      |
| WBGene00004217 | ptr-2     | 0.97                       | 0.48                      |
| WBGene00004239 | puf-3     | 0.95                       | 0.5                       |
| WBGene00004352 | rgs-9     | 0.90                       | 0.33                      |
| WBGene00004374 | rme-2     | 0.84                       | 0.49                      |
| WBGene00004819 | skr-13    | 0.73                       | 0.5                       |
| WBGene00004984 | spn-4     | 1.01                       | 0.25                      |
| WBGene00006619 | try-1     | 0.79                       | 0.45                      |
| WBGene00007643 | C17E4.3   | 1.01                       | 0.27                      |
| WBGene00008218 | nasp-2    | 0.92                       | 0.48                      |
| WBGene00008219 | C50B6.3   | 1.20                       | 0.46                      |
| WBGene00009035 | F22B3.4   | 0.84                       | 0.42                      |
| WBGene00010351 | cdb-1     | 0.88                       | 0.41                      |
| WBGene00010353 | H021I2.5  | 0.98                       | 0.29                      |
| WBGene00010492 | meg-1     | 1.08                       | 0.29                      |
| WBGene00010493 | meg-2     | 1.01                       | 0.37                      |
| WBGene00010621 | K07A12.2  | 0.87                       | 0.46                      |
| WBGene00010674 | K08E7.6   | 1.03                       | 0.03                      |
| WBGene00010939 | M163.7    | 1.00                       | 0.21                      |
| WBGene00011320 | T01C3.3   | 0.95                       | 0.42                      |
| WBGene00011352 | rskn-1    | 0.92                       | 0.44                      |
| WBGene00011501 | rmd-1     | 0.80                       | 0.41                      |
| WBGene00011986 | T24D1.3   | 0.96                       | 0.46                      |
| WBGene00012077 | T27A8.5   | 1.07                       | 0.25                      |
| WBGene00012220 | W03C9.2   | 0.89                       | 0.41                      |
| WBGene00012328 | W07G1.1   | 1.13                       | 0.17                      |
| WBGene00013380 | Y62E10A.14| 0.81                       | 0.36                      |
| WBGene00013862 | wdr-5.3   | 1.24                       | 0.5                       |
| WBGene00014117 | clec-91   | 0.87                       | 0.49                      |
| WBGene00015083 | egg-1     | 0.81                       | 0.41                      |
| WBGene00015102 | cpg-2     | 0.82                       | 0.44                      |
| WBGene00016263 | C30F12.4  | 1.03                       | 0.45                      |
| WBGene00016440 | C35D10.2  | 1.48                       | 0.46                      |
| Gene ID           | Gene Symbol | Expression Value | z Score |
|------------------|-------------|------------------|---------|
| WBGene00016485   | C36C9.1     | 0.71             | 0.37    |
| WBGene00017548   | F18A1.7     | 0.94             | 0.38    |
| WBGene00017843   | F26G5.1     | 0.76             | 0.47    |
| WBGene00017986   | F32D1.7     | 1.09             | 0.33    |
| WBGene00019095   | F59A7.8     | 1.09             | 0.39    |
| WBGene00019606   | clec-88     | 0.86             | 0.36    |
| WBGene00019811   | egg-2       | 0.91             | 0.47    |
| WBGene00020035   | egg-5       | 1.05             | 0.42    |
| WBGene00020652   | egg-4       | 1.01             | 0.42    |
| WBGene00020910   | W01A11.2    | 1.04             | 0.49    |
| WBGene00021035   | W05F2.3     | 0.79             | 0.42    |
| WBGene00021056   | W06B4.1     | 0.85             | 0.44    |
| WBGene00021206   | Y17G9B.9    | 0.90             | 0.38    |
| WBGene00021891   | Y54G2A.27   | 1.48             | 0.48    |
Supplementary Figure and Table legends

Figure S1. Specificity of the CEY-4 antibody

The CEY-4 antibody (obtained from sdix, affinity purified, rabbit, polyclonal) was tested at different dilutions (1:2000, 1:5000, 1:10000) on either wild-type or cey-1,-4 protein extract. The antibody is specific as the signal disappears in the absence of CEY-4.

Figure S2. Characteristics of CEY proteins

(A) qRT-PCR analysis on wild type and germline-less glp-4(bn2) mutants showed that cey-2 and cey-3 are only expressed in the germline. Controls include soma-specific elt-2, ubiquitously expressed act-1 and germline-specific egg-1. Error bars represent SEM. (B) Fluorescent micrographs of GFP-CEY-1 (live animals) and of CEY-4 immunostainings. The gonad and somatic structures are outlined by a dotted and solid line, respectively. Asterisk indicates the distal end of the gonad. CEY-1 and CEY-4 proteins are cytoplasmic in both the soma (intestine and neurons) and the germline. Scale bar = 20 µm. (C-D) IPs performed on CEY-1 (FLAG-CEY-1), CEY-2 (FLAG-CEY-2), and CEY-4 (endogenous), revealed that the RG/RGG repeats in CEY-1 and CEY-4 are asymmetrically di-methylated (ADMA). (C) CEY-2 has no RG/RGG repeats and consistently showed no ADMA signal. (D) The ADMA mark depends on prmt-1. In addition, the amount of CEY-4 protein increased upon the loss of ADMA. This was confirmed by western blot analysis of total protein (E).

Figure S3. CEY-2 and CEY-3 have a predominant role in producing progeny

The number of progeny per animal (n = 8-10) was counted at the indicated temperature. Error bars represent SEM. Two asterisks denotes p-value<0.01 by t-test. Three asterisks denotes p-value<0.005 by t-test. (A) The loss of either cey-2 or cey-3 caused a significant reduction of viable progeny at 25°C. (B) Consistently, knocking out both cey-2 and cey-3 simultaneously caused a strong decrease in progeny number at all three tested temperatures. The cey-1,-4 double mutant only started showing severe fertility defects at 26°C.

Figure S4. Global analysis of mRNAs bound by CEY proteins

(A) Pairwise correlation heatmaps for FLAG IPs performed on FLAG-CEY-1, -2, and -4 and their respective MYC IP controls performed in duplicates. (B-D) Scatter plots comparing MYC
IPs and FLAG IPs for CEY-1 (B), CEY-2 (C) and CEY-4 (D). (E) Scatter plot for the highly expressed genes (>8, log2 scale), highlighting in red those that were depleted by more than 2.25 fold in the FLAG IPs performed on FLAG-CEY-2 compared to the respective MYC control IPs. (F) Scatter plot comparing expression in the gonad to expression in the soma (glp-4(bn2)) for the same genes as in (E) highlighting the identical subset of genes as in (E).

**Figures S5 and S6. Mass-spectrometry data on the interaction partners of CEY-1 and CEY-4 in the presence or absence of RNA**

The log2 ratio of the protein abundances from the RNase treated CEY-1 or CEY-4 IP to the non-treated CEY-1 or CEY-4 IP is plotted on the X-axis. The proteins are ranked according to their abundance on the Y-axis. The data points are labeled with the gene names. Proteins quantified with two or more peptides are shown. Ribosomal proteins are marked in red circles. A group of proteins either shown (see Fig. 2A) or suspected to undergo RNA-dependent interactions with CEY-1 and CEY-4 are marked with green squares. The protein used for the IP (either CEY-1 or CEY-4) is marked with a blue square.

**Figure S7. Neurological functions do not appear to be compromised in the cey-1,-4 mutant**

Neither the two single mutants (cey-1 and cey-4) nor the double mutant (cey-1,-4) showed deficiencies in chemotaxis (DA naive), learning (DA cond) or memory (DA 60 min delay). “cond”: conditioned; “DA”: diacetyl.

**Figure S8. Additional polysome profiling data**

(A) Extract was treated with puromycin prior to loading on sucrose gradients. In the presence of puromycin, the majority of polysomes were lost, suggesting that they correspond to actively translating/elongating ribosomes. Indicated are the positions of mono- and disomes (two ribosomes), and of polysomes. (B-C) Wild-type and cey-1,-4 mutant animals were heat-shocked for 4 h at 30°C and compared to control animals. (B) Polysome profiles for wild type showed a decrease of polysomes as a response to heat stress. (C) Similar to wild type, cey-1,-4 mutants responded to heat shock by a further reduction of translating ribosomes. (D-E) Polysome profiling was performed on wild type (previously published in [29]) and germlineless (glp-4(bn2)) mutants. RNA was isolated either from sucrose fractions containing monosomes and polysomes (termed polysomal mRNA) or from all sucrose fractions (termed
total mRNA). The global abundance of transcripts was measured by microarray analysis. Polysomal mRNAs were then plotted against total mRNAs. The red diagonal demarcates transcripts that were more than two-fold depleted from polysomal fractions (to the right of the line). Most mRNAs found below the two-fold cutoff in wild type disappeared upon removal of the germline (E). (F-G) FLAG-tagged CEY-1 and CEY-4 were partially able to restore polysomes in the cey-1,-4 mutant. (H) The polysome profile of the cey-4 single mutant showed a decrease of large polysomes and an increase of mono-, di-, and trisomes. (I) Loss of CEY-1 caused a slight decrease of large polysomes but no increase of mono-, di-, or trisomes.

Figure S9. Total protein levels and EEF-2 phosphorylation status remain unchanged in the cey-1,-4 mutant

(A) Protein was extracted from an equal amount of wild-type and cey-1,-4 mutant animals. The total volume (not shown) and concentration of mutant extract were not affected in the cey-1,-4 mutant. (B) Western blot analysis of EEF-2 and its phosphorylated (inactive) form (EEF-2-P) in wild-type, cey-1,-4 mutant, and efk-1 (EEF-2 kinase homologue in C. elegans) mutant animals. Both EEF-2 and EEF-2-P levels remained unchanged in wild type and cey-1,-4 mutant. As expected, the EEF-2-P signal was lost in efk-1 mutant animals. ACT-1 was used as a loading control.

Figure S10. RNA sequencing and ribosome profiling data

Pairwise correlation plots shown for the mRNA sequencing data (A) and the ribosome profiling data (B). Axes are in log2 scale. “1”: first replicate, “2”: second replicate. “RPF”: ribosome protected fragment. In all cases the replicates correlated very well.

Figure S11. RPFs mapped to the transcriptome show no difference in wild type and cey-1,-4 mutant

Ribosome profiling was performed in duplicates for both wild type and cey-1,-4. The positions of the 5′ ends of the reads for ribosome protected fragments (RPFs) were used for counting. Only genes with an annotated 3′UTR or 5′UTR of at least 50 bp were used. To reduce the impact of highly expressed transcripts, we normalized the coverage of each transcript by its expression (coverageNorm=coverage/(expression+8) *avgExpression). The pseudocount of 8 was used to reduce the impact of transcripts with very low expression levels.
avgExpression denotes the average transcript expression and was used as a global constant to scale back the counts. Three nucleotide periodicity and depletion of RPFs from 5'UTRs and 3'UTRs supports that they originate from mRNAs undergoing translation. "rep": replicate.

**Figure S12. Selecting specific subsets of transcripts**

The three different subsets of mRNAs ("germline-specific", "ribosome-depleted", "ribosome-enriched") marked in Fig. 7 were selected as follows. (A) The "germline-specific" mRNA subset was selected by plotting gene expression data derived from germline-less *glp-4(bn2)* animals (soma) against those derived from dissected gonads (gonad). mRNAs were arbitrarily selected as being "germline-specific" if they were more than 22-fold enriched in gonads (green). (B) Consistent with the finding that most ribosome-depleted mRNAs were found in the germline (Fig. S7D-E), germline-specific genes showed a bias towards ribosome-depletion (green). (C) The "ribosome-depleted" mRNA subset was selected by plotting polysomal mRNA versus total mRNA (described in Fig. S7D-E). The chosen cutoff represents transcripts depleted at least two-fold from polysomal fractions (red). (D) In magenta are marked mRNAs that show similar mRNA abundance between wild-type and *cey-1,-4* mutant animals, but are more than two-fold reduced in ribosomal association in the mutants. This group of mRNAs encodes many regulators of oocyte-to-embryo transition; see Table S3. These changes were real, as marked genes were expressed at both the mRNA and RPF level in wild type and *cey-1,-4* mutant animals shown by wild-type mRNA vs *cey-1,-4* mRNA or wild-type RPF vs *cey-1,-4* RPF plots (E-F). (G) The "ribosome-enriched" mRNA subset was selected by plotting polysomal mRNA versus total mRNA (described in Fig. S7D-E). The chosen cutoff represents transcripts enriched at least 1.4-fold in polysomal fractions (blue). As expected this subset was absent from germline-expressed transcripts (H).

**Figure S13. The distribution of mRNAs in submonosomal versus mono- and polysomal fractions**

(A) Fractions 1-12 from a polysome profiling experiment were pooled and RNA was extracted (total mRNA). Fractions 5-12 were pooled and RNA was extracted (mono- and polysomal mRNA). (B) qRT-PCR analysis for germline-specific mRNAs. The values for mono- and polysomal mRNA were divided by the values of total mRNA. *rme-2* mRNA levels appeared to drop in mono- and polysomal fractions in *cey-1,-4* mutants compared to wild type. This was not the case for *oma-2* and *egg-1* mRNAs. Asterisk denotes *p*-value<0.05 by *t*-test. Error bars represent SEM.
Table S1. Summary of acquired transgenic strains used in this study

(*) the ubiquitous *dpy-30* promoter had to be used instead of the *cey-4* promoter (also ubiquitous) due to cloning problems.

Tables S2 and S3. Mass-spectrometry data

List of interacting proteins identified by massspec following FLAG IPs performed on either FLAG-tagged CEY-1 or CEY-4. IPs were performed with and without RNAse treatment. Proteins were divided into “ribosomal proteins” and “others”. “peptides”: number of unique peptides used for the quantification; “score”: sum of the peptide ion scores from MASCOT; “summed peptide ion abundance”: relative protein quantification was done with the program Progenesis LC-MS. All peptide ion abundances for a protein were summed up and listed in the table.

Table S4. Transcripts down-regulated predominantly at the RPF level in the *cey-1,-4* mutant encode many oocyte-to-embryo transition regulators

Shown are the expression changes at the mRNA level and the level of translation (RPFs) for the subset of genes marked in magenta in Fig. S11D. Genes (*rme-2, oma-2, egg-1*) validated by qRT-PCR are highlighted in yellow.