	C. elegans		***S. cerevisiae***		**Mouse NIH3T3**		**Drosophila S2**	
Spearman correlation:	**R**	**P**	**R**	**P**	**R**	**P**	**R**	**P**
Poly(A) *vs* abundance	-0.24	$<10^{-174}$	-0.24	$<10^{-57}$	-0.27	$<10^{-53}$	-0.05	$<10^{-3}$
Poly(A) *vs* F_{op} (or TR)	-0.32	$<10^{-250}$	-0.17	$<10^{-25}$	-0.19	$<10^{-31}$	-0.09	$<10^{-10}$
Poly(A) *vs* RE	-0.29	$<10^{-16}$	-0.09	$<10^{-8}$	-0.08	$<10^{-6}$		
Poly(A) *vs* ORF	0.30	$<10^{-258}$						
Poly(A) *vs* 3'UTR	0.21	$<10^{-114}$						
Poly(A) *vs* half-life			-0.11	$<10^{-9}$	-0.14	$<10^{-16}$		
Poly(A) *vs* CPI			0.2	$<10^{-29}$				
F_{op} (or TR) *vs* abundance	0.37	$<10^{-250}$	0.7	$<10^{-250}$	0.45	$<10^{-162}$	0.37	$<10^{-163}$
F_{op} (or TR) *vs* half-life			0.28	$<10^{-51}$	0.2	$<10^{-33}$		
F_{op} (or TR) *vs* RE	0.41	$<10^{-16}$	0.47	$<10^{-187}$	0.44	$<10^{-153}$		
Abundance measured by mTail-seq *vs* RNA-seq	0.84	$<10^{-16}$						

Supplementary Table 1. Spearman correlation values for poly(A) tail length, frequency of optimal codons (F_{op}) or NIH3T3 translation rates (TR), abundance, ribosome enrichment (RE), open reading frame (ORF) length, 3' untranslated region (3'UTR) length, codon protection index (CPI), and other features in *C. elegans*, *S. cerevisiae*, *M. musculus* NIH3T3 and Drosophila S2 cells. Source data for *C. elegans* calculations are online and in **Supplementary Data Sets 1, 2 and 3;** references and details for the source data used for calculations in other species are in **Supplementary Table 2.**