Table S1. ***C. elegans*** **strains used in this study**

Strains carrying transgenes			
Strain	**Transgene**	**Genotype**	**Reference**
IT213	*tcer-1 prom:tcer-1ORF:gfp:tcer-1 3'utr*	*unc-119(ed3) III; kpIs(pPK6)*	This study
IT283	*tcer-1 prom:tcer-1ORF:mCherry:tcer-1 3'utr*	*unc-119(ed3) III; kpIs(pPK20)*	This study
IT30	*puf-8 prom:puf-8 ORF:gfp:puf-8 3'utr*	*unc-119(ed3) III; kpIs(pMP15)*	(Ariz et al., 2009)
JH2060	*pie-1 prom:gfp:gld-1 ORF:gld-1 3'utr*	*unc-119(ed3) III; axIs1498*	(Merritt et al., 2008)
IT560	*pie-1 prom:4xcMyc:mCherry:ncbp-2 ORF:cMyc:hip-1 3'utr*	*unc-119(ed3) III; kpIs(pPK46)*	This study
IT305	*pie-1 prom:mCherry:emr-1 ORF:hip-1 3'utr*	*unc-119(ed3) III; kpIs(pPK19)*	This study
XA3507	*pie-1 prom:gfp:lem-2 ORF:pie-1 3'utr*	*unc-119(ed3) III; qaIs3507*	(Galy et al., 2003)
IT293	*tcer-1 prom:tcer-1ORF:mCherry:tcer-1 3'utr &* *pie-1 prom:gfp:lem-2 ORF:pie-1 3'utr*	*unc-119(ed3) III; qaIs3507; kpIs(pPK20)*	This study
IT311	*puf-8 prom:puf-8 ORF:gfp:puf-8 3'utr &* *pie-1 prom:mCherry:emr-1 ORF:hip-1 3'utr*	*unc-119(ed3) III; kpIs(pMP15); kpIs(pPK19)*	This study
IT363	*pie-1 prom:gfp:gld-1 ORF:gld-1 3'utr &* *pie-1 prom:mCherry:emr-1 ORF:hip-1 3'utr*	*unc-119(ed3) III; axIs1498; kpIs(pPK19)*	This study
IT671	*pie-1 prom:4xcMyc:mCherry:ncbp-2 ORF:cMyc:hip-1 3'utr &* *pie-1 prom:gfp:lem-2 ORF:pie-1 3'utr*	*unc-119(ed3) III; kpIs(pPK46); qaIs3507*	This study
IT297	*puf-8 prom:puf-8 ORF:gfp:puf-8 3'utr &* *tcer-1 prom:tcer-1ORF:mCherry:tcer-1 3'utr*	*unc-119(ed3) III; kpIs(pMP15); kpIs(pPK20)*	This study
IT639	*puf-8 prom:puf-8 ORF:gfp:puf-8 3'utr &* *pie-1 prom:4xcMyc:mCherry:ncbp-2 ORF:cMyc:hip-1 3'utr*	*unc-119(ed3) III; kpIs(pMP15); kpIs(pPK46)*	This study
IT539	*puf-8 prom:puf-8 ORF:gfp:puf-8 3'utr*	*puf-8(ok302) unc-4(e120) / mnC1* II; *unc-119(ed3) III; kpIs(pMP15)*	This study
IT549	*puf-8 prom:puf-8 ORF:gfp:puf-8 3'utr*	*tcer-1(tm1452) puf-8(zh17) rol-6(e187) / mnC1* II; *unc-119(ed3) III; kpIs(pMP15)*	This study
IT483	*puf-8 prom:puf-8 ORFΔ3-49aa:gfp:puf-8 3'utr*	*unc-119(ed3) III; kpIs(pPK45)*	This study
IT526	*puf-8 prom:puf-8 ORFΔ3-49aa:gfp:puf-8 3'utr*	*puf-8(ok302) unc-4(e120) / mnC1* II; *unc-119(ed3) III; kpIs(pPK45)*	This study

IT525	*puf-8 prom:puf-8 ORFΔ3-49aa:gfp:puf-8 3'utr*	*tcer-1(tm1452) puf-8(zh17) rol-6(e187) / mnC1* II; *unc-119(ed3) III; kpIs(pPK45)*	This study
IT445	*puf-8 prom:puf-8 ORFΔ51-100aa:gfp:puf-8 3'utr*	*unc-119(ed3) III; kpIs(pPK39)*	This study
IT454	*puf-8 prom:puf-8 ORFΔ51-100aa:gfp:puf-8 3'utr*	*puf-8(ok302) unc-4(e120) / mnC1* II; *unc-119(ed3) III; kpIs(pPK39)*	This study
IT479	*puf-8 prom:puf-8 ORFΔ51-100aa:gfp:puf-8 3'utr*	*tcer-1(tm1452) puf-8(zh17) rol-6(e187) / mnC1* II; *unc-119(ed3) III; kpIs(pPK39)*	This study
IT508	*puf-8 prom:puf-8 ORFΔ111-143aa:gfp:puf-8 3'utr*	*unc-119(ed3) III; kpIs(pPK44)*	This study
IT535	*puf-8 prom:puf-8 ORFΔ111-143aa:gfp:puf-8 3'utr*	*puf-8(ok302) unc-4(e120) / mnC1* II; *unc-119(ed3) III; kpIs(pPK44)*	This study
IT536	*puf-8 prom:puf-8 ORFΔ111-143aa:gfp:puf-8 3'utr*	*tcer-1(tm1452) puf-8(zh17) rol-6(e187) / mnC1* II; *unc-119(ed3) III; kpIs(pPK44)*	This study
IT350	*puf-8 prom:puf-8 ORFΔ3-143aa:gfp:puf-8 3'utr*	*unc-119(ed3) III; kpIs(pPK30)*	This study
IT377	*puf-8 prom:puf-8 ORFΔ3-143aa:gfp:puf-8 3'utr*	*puf-8(ok302) unc-4(e120) / mnC1* II; *unc-119(ed3) III; kpIs(pPK30)*	This study
IT380	*puf-8 prom:puf-8 ORFΔ3-143aa:gfp:puf-8 3'utr*	*tcer-1(tm1452) puf-8(zh17) rol-6(e187) / mnC1* II; *unc-119(ed3) III; kpIs(pPK30)*	This study

Other strains

Strain	**Genotype**	**Reference**
IT60	*puf-8(zh17) unc-4(e120) / mnC1* II	(Ariz et al., 2009)
JH1500	*puf-8(ok302) unc-4(e120) / mnC1* II	(Subramaniam and Seydoux, 2003)
IT325	*tcer-1(tm1452)* II	This study
IT168	*tcer-1(tm1452) puf-8(zh17) rol-6(e187) / mnC1* II	This study
IT668	*ZK1127.6(tm2782)* II	This study
IT235	*ZK1127.6(tm2782) puf-8(zh17) rol-6(e187) / mnC1* II	This study

Table S2. Sequences of PCR primers used for generating the transgene constructs described in this study

Name	Sequence
KS109	TCTGGTACCGGAAATCACCTTTCCCGAGT
KS1222	TCTGCCGGCCTCCCCATCAATGTTCTTTC
KS1223	TCTCCGCGGCGGAAAGTGATTGACCCGTA
KS2132	TCTGGATCCCGAATCTCATAGTC
KS2133	TGAGATTCGGGATCCACGTA
KS2134	TCTCCCGGGTTGCTTTCTGCGATCCCGCT
KS2135	TCTCCCGGGATGAGTAAAGGAGAAGAACTTTTCAC
KS2315	TCTCCGCGGGCTGTATCCTACACCAACAG
KS2316	TCTGTCGACCAACAAGAGCGGGATCGCAG
KS2326	TCTGTCGACTTATTTGTATAGTTCATCCATGC
KS2361	TCTGGGCCCACAACAAGAGCGGGATCGC
KS2944	TCTCCCGGGATGGTCTCAAAGGGTGAAGA
KS2945	TCTGTCGACTTACTTATACAATTCATCCATGC
KS2978	TCTACTAGTCTTATACAATTCATCCATGC
KS3022	TCTAGATCTCTATGAGTCGTCCGATTTCAAT
KS3175	TCTGCGGCCGCCTAGGCGTAGTCTGGGACGTCGTATGGGTATTTGTATAGTTCATCCATGCC
KS3303	TCTGCAGGTACCGGGCCCACTCATCAGGAACGCAGATTAC
KS3304	TCTGCAGGGCCCCACCAAGCGCATTCTCAAAG
KS3320	TCTGCAGGGCCCTCGTGAGATCCCTGCATATC
KS3526	CAAATGGGATCCGAGCAGAAGCTCATCTCCGAGGAGGACCTCATGGTCTCAAAGGGTGAAGA
KS3551	TCTGCAGGTACCGGGCCCGGTAGAAATATGACGGCCAT
KS3609	TCTGCAGGGCCCTCTAATGTCGGTCATGTCTTG
KS3612	TCTGCAGGGCCCGATAGTACTCAAGACATGACC

KS3675	TCTGCAGGGCCCACCAATCCAAAAAATGAACGCC
KS3703	TATAAGACTAGTATGGTCTTCGATCCAAGAAC
KS3704	CCTTAAGGCGCCTTAGAGGTCCTCCTCGGAGATGAGCTTCTGCTCACCTTTTTGAGCAATAGCGC
KS3709	TCTGACAGATCTGAGCAGAAGCTCATCTCCGAGGAGGACCTCGAGCAGAAGCTCATCTCCGAGGAGG
KS3710	GTCAGAGGATCCGAGGTCCTCCTCGGAGATGAGCTTCTGCTCGAGGTCCTCCTCGGAGATGAGCTTC

Table S3. Sequences of PCR primers used for RNA quantitation

RNA	Primer name	Sequence	Fold enrichment with MBP::PUF-8*
cyb-2.1	2241	ATGTTGCGAGTTACTACAAGC	3.79
	3087	TCTCCCGGGTTCCATTTCTGATGTTTCAGCTTC	
fbf-1	1666	TCTCTAATCGACATGGACCAATC	
	1662	GTTACGATCAATCTCGGTAG	
fbf-2	2665	GCTCGCCATCAACAGAATCA	
	2666	ATCCATGTTCTGGAGACTGG	
egg-5	3321	TCTCCCGGGATGGCGTTGAACAGCGAAGTG	4.58
	2900	GCTCCATTCCTCCGATGATGG	
hip-1	2409	TCAGAAGGCCGATATCGAGC	5.15
	2410	TGTTGTGGGACAGAAGCTCC	
mex-3	1086	TCTCCATGGGCATGAAGGAAGAACAAATCGC	
	1087	TCTCTCGAGTTATCCATTGATCGGCACGAG	
mex-5	1030	TCTCCATGGGCATGAAAGCGGCATCAAATAGTG	
	1031	TCTCTCGAGCTAATAGTGTCCTCTTAGTCCG	
oma-1	1539	TCTGAATTCATGAACGTTAACGGTGAAAAC	
	1540	TCTGAATTCTTCTAAAGGATGCTGAATGGC	
oma-2	1541	TCTGAATTCCATTCGATGCAAATGAGAGC	
	1542	TCTGAATTCGAGTGGAGACGAATCACTAT	
pal-1	1178	TCTTCTAGATGTCGGTCGATGTCAAGTC	3.8
	1179	TCTTCTAGAGCCGAATCTTCTGTTTGT	
pgl-1	2669	GGAGCTTCCAAAGACGCTCC	
	2670	CTTGGATGATGTGATTGCCG	
pie-1	1034	TCTCCATGGCTCAAACAAAGCCGATT	
	1035	TCTCTCGAGTTAGGAAATAATAGTTGGTGG	

pos-1	1028	TCTCCATGGCTGACAACGATTTCCT	6.62
	1029	TCTCTCGAGCTAGTGATGATGGGAGGAGA	
puf-5	2675	GATCTCAGCATTTTCAACGG	4.43
	2676	TTCTGGATCGACATCTGCAC	
rme-2	2695	CGGCATCATTCAATGGCTTC	
	2696	TTCGGCGTCGTCAGAAATCG	
spn-4	1088	TCTCCATGGGCATGCAAAACACACAGATATTTACTAAC	4.86
	1089	TCTCTCGAGTTACTGGCTTGACGATTCTTTTG	
cyb-2.1 pre-mRNA	2241	ATGTTGCGAGTTACTACAAGC	
	3546	GAGGCAACGAACCTGAAATC	
egg-5 pre-mRNA	3157	TCTCCCGGGGAATTCGAAGACGCTCTTCGC	
	3548	CCAACTTACAAGGTTTGTATCAG	
pal-1 pre-mRNA	3545	CTGACCAGCTCGCAGAGATA	
	1179	TCTTCTAGAGCCGAATCTTCTGTTTGT	
pos-1 pre-mRNA	1028	TCTCCATGGCTGACAACGATTTCC	
	2700	CGAGGCTGAAAATTCCAGTC	
spn-4 pre-mRNA	2839	CAGGTAAATTTGTCGTGCCG	
	1089	TCTCTCGAGTTACTGGCTTGACGATTCTTTTG	

*Fold enrichment values are given only for the mRNAs that showed significant enrichment (Mainpal et al., 2011).

Table S4. DNA-binding domain fusions tested in the yeast two-hybrid assay

Name	Part of PUF-8 sequence cloned in pGBDU-C2	PCR primers	
PUF8-BD	Amino acids 1-535 (full-length)	KS3022	Table S2
		KS3024	TCTAGATCTCTAGTGAGATCCCTGCATAT
Partial PUF8-BD	Amino acids 143-535 (Δ1-143 aa)	KS3023	TCTAGATCTCTATGCACCAAGCGCATTCTCA
		KS3024	TCTAGATCTCTAGTGAGATCCCTGCATAT
N1-BD	Amino acids 1-173 (Δ174-535 aa)	KS3022	Table S2
		KS3181	TCTGGATCCGGTGGTTGTTGGTTCCCTGT
N16-BD	Amino acids 1-50 and 101-535 (Δ51-100 aa)	KS3022 and KS3551 for 1-50aa, and KS3609 and KS3320 for 101-535aa; all four sequences are given Table S2	
N18-BD	Amino acids 1-110 and 144-535 (Δ111-143 aa)	KS3022 and KS3612 for 1-110aa, and KS3304 and KS3320 for 144-535aa; all four sequences are given Table S2	
N20-BD	Amino acids 51-535 (Δ1-50 aa)	KS3645	TCTGCACCCGGGCAATCCAAAAAATGAACGCC
		KS3646	TCTGCACCCGGGCTAGTGAGATCCCTGCATAT

Table S5. Proteins tested for interaction with PUF-8 and TCER-1 in the yeast two-hybrid assay

Name	Yeast homologue*	Mammalian homologue*	Functional description[#]
PHI-11	HSH155	SF3B1	Splicing factor 3b subunit 1
PRP-21	PRP21	SF3A1	Splicing factor 3a subunit 1
UAF-1	MRD1	U2AF2	Large subunit of the splicing factor U2AF
LSM-4	LSM4	LSM4	Small nuclear ribonucleoprotein (snRNP)
LSM-8	LSM1	NAA38	snRNP
SNR-3	Sm D1	SNRPD1	Sm D1 is a part of heteroheptameric complex that is part of the spliceosomal U1, U2, U4 and U5 snRNPs[‡]
THOC-1		THOC1	THOC complex component; THOC complex links transcription elongation and mRNA export machinery
THOC-2	THO2	THOC2	Same as above
THOC-3	TEX1	THOC3	TEX1 is a component of the transcription export (TREX) complex required for nuclear mRNA export[‡]
DDX-19	DBP5	DDX19	DEAD-box helicase involved in mRNA export from the nucleus[‡]
NXF-1	MEX67	NXF1	Shuttling transport receptor for nuclear export of mRNA
RSP-3	NPL3	SRSF1	Required for splicing; influences alternative splicing
HEL-1	SUB2	DDX39	Component of the TREX complex
ALY-1	YRA1	ALYREF	RRM motif protein; required for export of TRA-1/tra-2 mRNA complexes
ALY-2	YRA1	ALYREF	RRM motif protein; required for export of TRA-1/tra-2 mRNA complexes
ALY-3		ALYREF	RRM motif protein; thought to promote recruitment of mRNA export factors to mRNAs
NXT-1	NTF2	NXT1	RNA export factor
C27F2.10	THP1	PCID2	Nuclear pore-associated protein; component of the TREX-2 complex[‡]
IFE-1	CDC33	EIF4E	eIF4E homolog
IFE-5	CDC33	EIF4E	Same as above
IFG-1	TIF4631	EIF4G	eIF4G
PAB-1	PAB1	PABPC	Polyadenylate-binding protein
NCBP-2	CBC2	NCBP2	*C. elegans* ortholog of the CBP20 subunit of the nuclear cap binding protein complex
NPP-1	Nup57	NUP54	Nuclear pore complex component; Central FG Nup[§,¶]
NPP-4	Nup49	NUP62	Same as above
NPP-7	Nup60	NUP153	Nuclear pore complex component; Nuclear FG Nup[§,¶]
NPP-10	Nup145N	NUP98-	Nuclear pore complex component; Central FG Nup[§,¶]

		NUP96	
NPP-11	Nsp1	NUP62	Same as above
NPP-14	Nup159	NUP214	Nuclear pore complex component; Cytoplasmic FG Nup[§,¶]
RAE-1	Gle2	RAE1	Nuclear pore complex component; Required for mRNA export[§,**]
NPP-21	MLP1	TPR	Myosin-like protein associated with the nuclear envelope, connects the nuclear pore complex with the nuclear interior[‡]

Protein names shown in bold were positive for interaction with PUF-8 in the yeast two-hybrid assay (see Fig. 4A).

Protein names underlined were positive for interaction with TCER-1 in the yeast two-hybrid assay (see Fig. 4A).

*For convenience, the corresponding more familiar yeast and mammalian homologues are also listed.

[#] Unless an additional reference is provided the functional description is from www.wormbase.org.

[‡] www.yeastgenome.org.

[§] (Galy et al., 2003).

[¶] (Strambio-De-Castillia et al., 2010).

**(Rodriguez et al., 2004).