Table S1. List of germline-expressed genes whose mRNAs affinity-purified with MBP::PUF-8.

Fold Change	**GENE ID**	**Expression pattern from NEXTDB**[1]	**Gene name**	**Chr. No.**	**Expression pattern from Reinke 2004**[2]	**Expression pattern from Kim 2001**[3]	**RNAi phenotype**[4]	**SAM rank in FBF target list**[5]	**Known or predicted biochemical function**[4]
5.35	W03C9.7	very strong in adult gonad	*mex-1*	II	intrinsic	Mount 7	emb stp	1239	CCCH-type zinc finger protein
4.43	F54C9.8	strong in the middle and proximal gonad	*puf-5*	II	intrinsic	Mount 7		1640	Member of PUF family of RNA-binding proteins
3.48	D1007.7		*nrd-1*	I	intrinsic	Mount 5	emb	3878	RNA polymerase II C-terminal domain-binding protein RA4, contains RPR and RRM domains
6.62	F52E1.1	very strong in adult gonad	*pos-1*	V	oogenesis-enriched	mount 7	emb	4590	CCCH-type zinc finger protein
4.86	ZC404.8	no expression	*spn-4*	V	oogenesis-enriched	mount 7	emb let ste	2127	RRM superfamily RNA-binding protein
3.02	F23B2.6		*aly-2*	IV	oogenesis-enriched	mount 7			Ref / ALY RNA export adaptor family member
3.85	Y18D10A.17		*car-1*	I	oogenesis-enriched	mount 11	emb	1983	Putative RNA-binding protein orthologous to budding yeast Scd6p fission yeast Sum2p Drosophila TRAL and human LSM14A and LSM14B
3.67	R03D7.7		*nos-1*	II	oogenesis-enriched	mount 7		1786	Member of the Nanos family RNA-binding protein
9.27	C27F2.5	no clear expression	*vps-22*	III		mount 2	let ste age	3039	*C. elegans* ortholog of the conserved vacuolar protein sorting protein EAP30/SNF8/VPS22

3.22	F57C2.2		*btb-19*	II		mount 2	ste emb	4436	BTB domain protein
3.21	T13B5.8	gonad expression	*sut-1*	II	mixed oogenesis + somatic	mount 5	ste	2154	RNA- and snRNP-binding protein (SUT-1/SL26p)
3.79	Y43E12A.1		*cyb-2.1*	IV	intrinsic		emb stp	906	Cyclin B and related kinase-activating proteins
3.30	H14E04.5		*cic-1*	III	mixed oogenesis + somatic	mount 11		2046	CDK8 kinase-activating protein cyclin C
4.10	C09H10.6	strong in gonad	*nasp-1*	II	oogenesis-enriched	mount 11		1859	Cell cycle-regulated histone H1-binding protein
3.92	Y44E3B.1a		*zip-4*	I	oogenesis-enriched	mount 11		3116	Basic region leucine zipper transcription factor
3.80	C38D4.6		*pal-1*	III	oogenesis-enriched	mount 7	gro emb	3584	Similar to the homeodomain protein Caudal
7.28	ZK632.9	faint in gonad		III		mount 2			DNA-binding nuclear protein p8
5.22	R11D1.10	no expression		V		mount 2		3205	
10.76	F22B5.1	gonad	*evl-20*	II	intrinsic	Mount 2	emb ste stp	1026	GTP-binding ADP-ribosylation factor-like protein ARL2
3.49	B0393.2		*rbg-3*	III	oogenesis-enriched	mount 7		1318	Ypt/Rab-specific GTPase-activating protein GYP6
3.69	K08F4.2			IV	oogenesis-enriched	mount 2 and 5	maternal sterile		RasGAP SH3 binding protein rasputin contains NTF2 and RRM domains
5.42	F36H1.4b	faint in gonad	*lin-3*	IV	oogenesis-enriched	mount 7 and 8	ste gro sick	17	Member of the EGF family of peptide growth factors
7.15	C14F5.1b	no expression	*dct-1*	X		mount 15			Similar to mammalian BNIP3 that ineract with Bcl-2
4.17	T21E3.1	no expression	*egg-4*	I	oogenesis-enriched	mount 7	ste emb let	727	Protein tyrosine phosphatase
4.58	R12E2.10		*egg-5*	I	oogenesis-enriched		emb ste	727	Protein tyrosine phosphatase

3.34	F44F4.2	strong posterior expression	*egg-3*	II	oogensis enriched	mount 7 and 6	emb ste	497	Protein tyrosine phosphatase
5.15	T12D8.8	strong in gonad	*hip-1*	III		mount 16			Hsp70-interacting protein Hip/Transient component of progesterone receptor complexes and an Hsp70-binding protein
7.48	T10B5.6	faint in gonad	*knl-3*	V	intrinsic	Mount 11	emb ste let sick	360	KNL-3 activity is essential for formation of a functional kinetochore
4.79	F54C8.2	no	*cpar-1*	III	intrinsic		emb ste let	1993	Homologous to inner kinetochore histone H3 variant CENP-A
3.64	F57B10.12		*mei-2*	I	oogenesis-enriched	mount 7	emb mei	679	
3.86	M01E11.6		*klp-15*	I	oogenesis-enriched	mount 7	emb him mei	38	Kinesin (KAR3 subfamily)
9.14	C50F4.7	whole gonad	*his-37*	V		mount 6	emb let ste		Histone H4
5.46	D2007.5	very faint in gonad	*atg-13*	III	herm sex enriched	Mount 2		2315	Divergent ortholog of the autophagic budding yeast protein Atg13p
9.07	T19E7.3	no expression	*bec-1*	IV		mount 11	let ste emb gro let	69	Beclin-like protein
5.19	ZK593.6	very strong in gonad + somatic tissue	*lgg-2*	IV		mount 18 and 15		104	Microtubule-associated anchor protein involved in autophagy and membrane trafficking
4.29	CD4.4	no expression	*vps-37*	V		mount 18	emb let ste	2265	Related to yeast Vacuolar Protein Sorting factor
9.48	B0334.4	no expression		II	intrinsic	Mount 7	let ste	1668	Protein similar to predicted member of the intramitochondrial sorting protein family
8.52	M03E7.5	very faint in gonad	*memb-2*	V	intrinsic	Mount 7	emb	3833	Golgi SNAP receptor complex member
8.46	ZK1098.5	no expression		III	intrinsic	Mount 2	emb ste		Transport protein particle (TRAPP) complex subunit
6.85	C10H11.10	very faint in	*kca-1*	I	intrinsic	Mount 7	emb lon	12	Kinesin Cargo Adaptor)

		gonad							
6.74	K08H10.9	no expression		V		mount 18		2260	Transport protein particle (TRAPP) complex subunit
6.03	C01G8.2	no expression	*cln-3.2*	I		mount 2		1964	Predicted small molecule transporter involved in cellular pH homeostasis
17.51	Y38F2AR.2	no expression	*trap-3*	IV		mount 20		2452	Translocon-associated complex TRAP gamma subunit
6.49	Y56A3A.21	no expression	*trap-4*	III		mount 20	unc prl		Translocon-associated complex TRAP delta subunit
3.29	F59B2.7		*rab-6.1*	III		mount 7	ste let	2498	Small monomeric Rab GTPase that is most closely related to the Drosophila and mammalian Rab6 GTPases
3.67	F57B10.5			I		mount 2			emp24/gp25L/p24 family of membrane trafficking proteins
3.85	Y47G6A.2		*inx-22*	I		mount 7	emb	85	INneXin
6.18	Y74C10AL.2	no expression		I		mount 2 and 34		1361	Predicted membrane protein
7.00	D1022.1	no expression	*ubc-6*	II	herm sex enriched	Mount 5		1205	Non-canonical ubiquitin conjugating enzyme 1 ubc-6 encodes an E2 ubiquitin-conjugating enzyme
14.31	T01C3.3	whole gonad		V	intrinsic	Mount 7		1150	Predicted E3 ubiquitin ligase
4.63	R01H2.6	germline expression	*ubc-18*	III	intrinsic	Mount 2	ste emb let	4217	Ubiquitin-protein ligase
4.24	C06A5.8	somatic + gonad		I	intrinsic	Mount 7		978	Predicted E3 ubiquitin ligase
5.73	ZK858.4	no expression	*mel-26*	I	oogenesis-enriched	mount 7	emb let ste	1359	MATH and BTB/POZ domain-containing protein that functions as substrate-specific adaptor of CUL-2-containing E3 ubiquitin ligase
7.68	Y54E5B.4	no expression	*ubc-16*	I		mount 2		2393	Ubiquitin conjugating enzyme
3.39	F46E10.8		*ubh-1*	V		mount 2			Ubiquitin C-terminal hydrolase UCHL1

4.42	F39B2.2	no expression	*uev-1*	I		mount 18		3832	Ubiquitin-conjugating enzyme E2
4.89	Y110A7A.14	no expression	*pas-3*	I		Mount 18 and 5	emb ste		20S proteasome regulatory subunit alpha type PSMA4/PRE9
3.64	C47B2.3a		*tba-2*	I		mount 20	emb let	2415	Alpha-tubulin
4.36	Y71F9AL.16	whole gonad	*arx-1*	I			emb	2682	Actin-related protein Arp2/3 complex subunit Arp3
3.46	Y79H2A.6	gonad expression	*arx-3*	III		mount 5	ste let	3728	Actin-related protein Arp2/3 complex subunit ARPC1/p41-ARC
5.75	C16A3.5	very faint in gonad		III	herm sex enriched	Mount 2	emb let		NADH:ubiquinone oxidoreductase NDUFB9/B22 subunit
7.04	F23B12.6	whole body + gonad	*fntb-1*	V	intrinsic			446	Beta subunit of Farnesyl Transferase
5.08	C36B1.7	gonad expression	*dhfr-1*	I	intrinsic	Mount 18	emb ste	1437	Dihydrofolate reductase
4.94	F30F8.3	proximal gonadl		I	intrinsic	Mount 7		2709	PDZ domain
3.85	C54G4.6		*dod-18*	I	intrinsic	Mount 2	age	2665	Maf-like protein, required for normal short lifespan
3.68	Y54E2A.3		*tac-1*	II	intrinsic	Mount 5	emb	164	Transforming acidic coiled-coil (TACC) protein family member
3.63	Y18D10A.20		*pfn-1*	I	intrinsic	Mount 2			Profilin
3.10	ZK970.3		*mdt-22*	II	intrinsic	Mount 2 and 7	emb	2257	Surfeit family protein 5
3.05	F33G12.4		*lrr-1*	II	intrinsic	Mount 2	ste let	2976	Leucine rich repeat
3.53	F43G9.9		*cpn-1*	I	intrinsic	mount 7		3763	Calponin homolog more closely related to calponin per se than to its paralogs transgelin (SM22 alpha) or neuronal protein NP25
10.09	F56A11.5	proximal gonad		IV	mixed oogenesis + somatic	Mount 20			Uncharacterized Fe-S protein
5.18	R11E3.8	strong in	*dpf-5*	IV	mixed	Mount 2		4602	Dipeptidyl aminopeptidase

		gonad			oogenesis + somatic				
4.16	T23B12.6	very faint in gonad		V	mixed oogenesis + somatic	Mount 2		3380	SETA-binding protein SB1 and related proteins, contains BTB/POZ domain
3.06	C37C3.9			V	oogenesis-enriched	mount 7		1197	Uncharacterized protein, contains BTB/POZ domain
4.26	W06B4.1	no expression		II	oogenesis-enriched	mount 7		247	N-Acetylglucosamine kinase
11.65	Y75B12B.1			V	oogenesis-enriched	mount 7		1611	Probable transposase stabilized by GLD-1
9.56	B0280.5	very strong in adult gonad	*cpg-2*	III	oogenesis-enriched	mount 7		3373	Protein with six chitin-binding peritrophin-A domains and three mucin-like regions
8.75	C01G10.7	very faint in gonad		V	oogenesis-enriched	mount 7		3860	Citrate lyase beta subunit
8.44	C01G5.5	no expression		IV	oogenesis-enriched	mount 2			Aldo/keto reductase family proteins
8.11	W01A11.2	no expression		V	oogenesis-enriched	mount 7	emb sick	706	Acyl-CoA:diacylglycerol acyltransferase (DGAT)
5.37	M01E11.1			I	oogenesis-enriched	mount 2		2690	Farnesyl cysteine-carboxyl methyltransferase
5.08	C56C10.10	no expression		II	oogenesis-enriched	mount 2		28	Aryl-hydrocarbon receptor-interacting protein
8.57	K06B9.2	no expression		IV	oogenesis-enriched	mount 7	emb ste	1203	Putative UDP-N-acetylglucosamine pyrophosphorylase
4.27	R10D12.12	no expression		V	oogenesis-enriched	mount 18		1311	Predicted glycosyltransferase
4.12	T25E12.5	transition zone to oocytes in gonad	*gyg-2*	V	oogenesis-enriched	mount 7		429	Glycosyl transferase family 8 - glycogenin
4.12	F26D10.10	transition	*gln-5*	IV	oogenesis-	mount 7		1212	Glutamine synthetase

		zone to oocytes in gonad			enriched				
3.36	C17F4.5		*fbxc-50*	II	oogensis enriched	mount 7	small	895	Protein containing an F-box a motif predicted to mediate protein-protein interactions either with homologs of yeast Skp-1p or with other proteins.
14.66	Y40B10A.1	proximal gonad and oocytes	*lbp-9*	V		Mount 3			Fatty acid-binding protein FABP
3.59	Y60A3A.18	gonad	*skr-1*	V		mount 0	emb him		Homolog of yeast Skp1
6.60	C25B8.4	strong in distal gonad	*clec-266*	X		mount 12		636	C-type lectin
5.41	F57B10.10	no expression	*dad-1*	I		mount 18	emb let gro		Defender against cell death protein/oligosaccharyltransferase epsilon subunit
3.26	F25D7.1		*cup-2*	I		mount 18	sterile	3861	Predicted membrane protein
8.11	W01A11.1			V		mount 2			Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily)
5.49	F57C9.1b	no expression		I		mount 2		463	Pyridoxal/pyridoxine/pyridoxamine kinase
5.13	Y47D9A.1b	no		I		mount 2		1470	GDP-mannose pyrophosphorylase
5.07	C35D10.6	gonad		III		mount 2	gro unc	3867	Aldo/keto reductase family proteins
4.72	F23H11.9			III		mount 2	let ste		CDP-alcohol phosphatidyltransferase/Phosphatidylglycerol-phosphate synthase
4.59	H24K24.3a	gonad		V		mount 2		4549	Alcohol dehydrogenase class III
4.58	C52E4.2	expression not clear	*mif-2*	V		mount 2	emb		Macrophage migration inhibitory factor
4.59	H24K24.3b			V		mount 2		4549	Alcohol dehydrogenase class III
4.04	K11H3.1b		*gpdh-2*	III		mount 2		4054	Glycerol-3-phosphate dehydrogenase/dihydroxyacetone 3-phosphate

									reductase
3.12	F31C3.1		*cyn-5*	I		mount 2			Cyclophilin, similar to human cyclophilin B
3.01	C23G10.2b			III		mount 2			Putative translation initiation inhibitor UK114/IBM1
5.94	C52E4.1	gut	*cpr-1*	V		mount 2 and 8	age		Cysteine proteinase Cathepsin L
6.43	Y46G5A.5	very faint in gonad	*pisy-1*	II		mount 20	ste let	87	Phosphatidylinositol synthase
3.01	Y106G6D.4			I		mount 4			Glycogen synthase kinase-3
5.16	Y54E5A.7	very faint in gonad		I		mount 5			SPRY domain-containing proteins
3.22	C25A1.8		*clec-87*	I		mount 7		3750	Putative secreted C-type lectin p
3.19	Y47G6A.22a			I		mount 2		3915	Reductases with broad range of substrate specificities
3.56	F10D11.1		*sod-2*	I		mount 4			Manganese superoxide dismutase
3.30	K11H3.1a	no expression	*gpdh-2*	III		mount 2		4054	Glycerol-3-phosphate dehydrogenase/dihydroxyacetone 3-phosphate reductase
3.91	Y37H9A.6		*ndx-4*	I		mount 2			Diadenosine and diphosphoinositol polyphosphate phosphohydrolase
3.89	R01B10.4			V		mount 2		127	Predicted membrane protein
3.67	T02G5.8		*kat-1*	II		mount 20			Acetyl-CoA acetyltransferase
4.41	ZK829.9	loop region of gonad and oocytes		IV		mount 7		3612	Permease of the major facilitator superfamily
5.82	Y82E9BR.14	very faint in gonad		III				2970	Glycolipid transfer protein
4.60	Y105E8A.2	strong in gonad		I				4190	Protein OS-9
4.11	R06F6.9	gonad	*ech-4*	II		mount 20			Enoyl-CoA hydratase/isomerase

3.75	Y48G8AL.8b		*rpl-17*	I			let emb ste		60S ribosomal protein L22
3.15	T23B3.1		🟩	I	herm sex enriched	mount 7			
3.56	F52H3.4		🟩	II	inntrinsic	Mount 7		594	
15.46	Y54G9A.5	no clear expression	🟩	II	intrinsic	Mount 7		1735	
9.03	F32D1.7	proximal gonad and oocytes	🟩	V	intrinsic	Mount 7		131	
8.57	K03H1.7	no expression	🟩	III	intrinsic	Mount 7		372	
7.77	F31E3.6	just below pharynx	🟩	III	intrinsic	Mount 2			
7.49	C33F10.4	very faint in gonad	🟩	II	intrinsic	Mount 2			
5.19	F43G6.10	no	🟩	II	intrinsic	Mount 7		472	
3.97	F13A2.4		🟩	V	intrinsic	Mount 7			
3.95	C29A12.1		🟩	V	intrinsic	Mount 7		7	
3.84	W03C9.2		🟩	II	intrinsic	Mount 7		869	
3.20	ZK858.5		🟩	I	intrinsic	Mount 2	spn emb	1477	
25.09	F18A1.7	no expression	🟩	II	oogenesis-enriched	mount 7		1801	
14.53	Y37E11B.3	no expression	🟩	IV	oogenesis-enriched	mount 2		1240	
9.54	W03C9.5	no expression	🟩	II	oogenesis-enriched	mount 7 and 2			
9.46	T24D1.3	proximal gonad	🟩	I	oogenesis-enriched	mount 7	emb	154	
7.15	C17E7.4	very faint in gonad	🟩	V	oogenesis-enriched	mount 7		3037	
7.00	Y17G9B.9	no expression	🟩	IV	oogenesis-enriched	mount 7	emb	313	

6.45	F10D11.2	probably in gonad		I	oogenesis-enriched	mount 7		4240	
6.39	W05F2.3	very strong in adult gonad		I	oogenesis-enriched	mount 7	ste let rbs	1825	
4.68	F42H10.2	no expression		III	oogenesis-enriched	mount 7		3942	
4.42	Y62E10A.14	no expression		IV	oogenesis-enriched	mount 7	emb	285	
4.22	C14B1.2	no expression		III	oogenesis-enriched	mount 7		2377	
4.06	K03B4.2	no expression		V	oogenesis-enriched	mount 2		582	
3.59	Y53C12A.6			II	oogenesis-enriched	mount 7	maternal sterile	302	
3.29	K09H9.2			I	oogenesis-enriched	mount 7	emb maternal sterile		
3.14	C28C12.2	medial gonad	*mesp-1*	IV	oogenesis-enriched	mount 7	ste let	763	
4.03	F54D10.5	somatic expression		II	oogenesis-enriched	mount 7		1004	
3.76	C17E4.10			I	oogenesis-enriched	mount 2		386	
3.06	F52A8.1			I		mount 18 and 1		3572	
11.91	R166.3	no expression		II		mount 2		26	orthologous to the human Alport syndrome mental retardation midface hypoplasia and elliptocytosis chromosomal region gene 1
6.51	C17E7.9b	no expression		V		mount 2		3547	
3.34	F35H10.5			IV		mount 2			
8.98	F15A4.10	no		II		mount 7		4375	

4.38	Y57E12AL.6	no	🟫	V		mount 18	ste emb		
3.68	F48C1.6		🟫	I		mount 20		442	
3.77	F40F11.3		🟫	IV		mount 7	gro		
6.26	Y20F4.4	very strong in adult pro gonad	🟫	I				1483	
6.04	Y73E7A.1	faint in gonad	🟫	I					
4.28	T24H7.3	gonad expression	🟫	II				2289	
4.20	Y73B6BL.27	strong in gonad + somatic (not strong)	🟫	IV					

Key for the color codes used:

🟨 RNA-binding proteins
🟪 Cell cycle
🟦 Transcription factors / DNA-binding proteins
🟦 Protein tyrosine phosphatase
🟧 Kinetochore and chromosomal
🟥 Transporters / membrane
🟩 Proteosomal

🟦 Cytoskeletal
🟩 Autophagy
🟧 Metabolic pathways
🟩 Signalling
🟫 Ribosomal protein
🟪 Heat-shock response
🟫 Unknown molecular function

Fold change indicates ratio of hybridization intensities obtained with affinity-purified mRNA (Test) to total mRNA. [1]Expression pattern information from the Nematode Expression Pattern DataBase (NEXTDB) (http://nematode.lab.nig.ac.jp/db2/index.php). [2]Expression pattern information from Reinke et al.(Reinke et al., 2004). [3]Expression pattern information from Kim et al (Kim et al., 2001). [4]These informations are annotations found at www.wormbase.org. [5]The FBF SAM ranks are from Kershner and Kimble (Kershner and Kimble, 2010). Blank fields indicate that the corresponding gene has not been ranked on the list of potential FBF targets. Age – life span abnormal; emb – embryonic lethal; gro – slow growth; him – more number of males among progeny than wild-type; let – larval lethal; lon – longer than wild-type; mei – defective meiosis; prl - paralyzed; rbs – reduced brood size; spn – defective spindle orientation; ste - sterile; stp – sterile progeny; and unc – uncoordinated locomotion.

Table S2. Sequences of primers used in this study: 1. General primers

Name	Sequence	Description
KS1448	TCTGTCGACGCCACAGGCATATTTTCAAAT	Forward and reverse primers, respectively for amplifying PUF domain of PUF-8 for cloning in pMAL-c4E to express MBP::PUF-8 fusion protein in *E. coli*
KS1449	TCTGCGGCCGCCTAGTGAGATCCCTGCATATC	
KS1461	TGTGTGTGTGCTATGTACATGTGTGTGTGCCCTATAGTGAGTCGTATTAAGA	Template for in vitro transcription of NRE-containing RNA. Reverse complementary sequence of T7 promoter is at the 3’ end.
KS2096	GCATTAGCGGCCGCGAAATTAATACGACTCACTATAGGGAGA$(T)_{21}$V	Primer for first strand cDNA synthesis to incorporate T7 promoter sequence
KS2496	ACTCTAATACGACTCACTATAG	Sequence of T7 promoter
KS2952	GTTAATCTCATCAATTTCTGCTG	Reverse PCR primer at 506 bp downstream of *pal-1* STOP codon
KS2983	AACGTCGTCGGCAGAGATTC	Forward PCR primer at 350 bp upstream of *pal-1* STOP codon
KS2995	TCTGGGCCCGTGACAAACAGAAGATTCGGC	Forward PCR primer at 20 bp upstream of *pal-1* STOP codon
KS2997	TCTGGGCCCGTTAATCTCATCAATTTCTGCTG	Same as KS2952, but contains Bsp 120I site

Table S3. Sequences of primers used in this study: 2. Primers for testing translational activity of 3’UTRs

Name	Sequence	Description
KS2745	TCTGGGCCCTTGGAAACCAGAGCCGCTTG	Forward PCR primer for C06A5.8*i*
KS2746	TCTGGGCCCACAAATACACTGGGCGGTCC	Reverse PCR primer for C06A5.8
KS2747	TCTGGGCCCCAAAAGACGGTTCCGAGTTG	Forward PCR primer for D1022.1
KS2748	TCTGGGCCCCAACAGGTTTCTCGAAGATA	Reverse PCR primer for D1022.1
KS2749	TCTGGGCCCATTGCAGCAACCGGCAGAGG	Forward PCR primer for F39B2.2
KS2750	TCTGGGCCCTTGTGGCTGGTGCTGATGGT	Reverse PCR primer for F39B2.2
KS2753	TCTGGGCCCGCGCCAAGAGCTCAGATCTA	Forward PCR primer for R01H2.6
KS2754	TCTGGGCCCCCAACTAAGCCAGTTCCTCC	Reverse PCR primer for R01H2.6
KS2755	TCTGGGCCCCTGCTCCCATTTCTACATTG	Forward PCR primer for T01C3.3
KS2756	TCTGGGCCCCGCTGTGAGGAAAGAAGTGA	Reverse PCR primer for T01C3.3
KS2759	TCTGGGCCCAGGACCCCTCCAATCTTCTT	Forward PCR primer for *ubc-16*
KS2760	TCTGGGCCCTCAAATGTGGGTACTGTAGC	Reverse PCR primer for *ubc-16*
KS2650	TCTGGGCCCGTTTCGACGAATGCATGCTG	Forward PCR primer for *kca-1*
KS2651	TCTGGGCCCGAACGAACAAGTCTTCCAGC	Reverse PCR primer for *kca-1*
KS2652	TCTGGGCCCGTTGGAACTCCCCAAGTCAC	Forward PCR primer for F30F8.3
KS2653	TCTGGGCCCGAGAGCATGTCAAGATCTC	Reverse PCR primer for F30F8.3

KS2654	TCTGGGCCCCCGGAGCCAGATCTTGACTA	Forward PCR primer for *hip-1*
KS2655	TCTGGGCCCGACTCCGCCCAATTCTTGGCC	Reverse PCR primer for *hip-1*
KS2656	TCTGGGCCCGGCTCACGAGCGGCCAGATC	Forward PCR primer for Y54E5A.7
KS2657	TCTGGGCCCCTGTAGTAGTACTGTAGAGG	Reverse PCR primer for Y54E5A.7
KS2658	TCTGGGCCCGGCTGACTCTCGTGTCACTT	Forward PCR primer for C56C10.10
KS2659	TCTGGGCCCCTCCAGATGTTCTTCCATG	Reverse PCR primer for C56C10.10
KS3092	TCTGGGCCCGACAACCAAGGCAATACTGC	Forward PCR primer for *car-1*
KS3093	TCTGGGCCCGGTTACTGTTGGAAAGGCTG	Reverse PCR primer for *car-1*
KS3094	TCTGGGCCCTAATCTGGATTCCTCCGTCC	Forward PCR primer for *mex-1*
KS3095	TCTGGGCCCCTCATGATCTCATGGTCCCG	Reverse PCR primer for *mex-1*

Table S4. Sequences of primers used in this study: 3. Primers for mutation analysis of *pal-1* 3'UTR

Name	Sequence	Description
KS2984	TCTGAAGACCTGTGTGTGTGTCTTTGTAAGTAGATGAGTACT	Reverse primer for the upstream fragment for PRE 1 mutation
KS2985	TCTGAAGACCTACACACACACCTGGGAATTTTCATATTTTTCTAG	Forward primer for the downstream fragment for PRE 1 mutation
KS2986	TCTGAAGACCTGTGTGTGTGTTCTAGAAAAATATGAAAATTCCC	Reverse primer for the upstream fragment for PRE 2 mutation
KS2987	TCTGAAGACCTACACACACACTTATATTTTTACATTTCTCTCGC	Forward primer for the downstream fragment for PRE 2 mutation
KS2988	TCTGAAGACCTGTGTGTGTGGAAGAAATTATATAAAAGTGTG	Reverse primer for the upstream fragment for PRE 3 mutation
KS2989	TCTGAAGACCTACACACACCATTCTCTCACATCAGAATATTC	Forward primer for the downstream fragment for PRE 3 mutation
KS3069	TCTGAAGACCTGTGTGTGTGTGTGTGTGTGCAGAAGGAATGATCGGAAAG	Reverse primer for the upstream fragment for PRE 4 mutation
KS3070	TCTGAAGACCTACACCATTCTCTAATGAATTATTCCCT	Forward primer for the downstream fragment for PRE 4 mutation
KS3355	TTCCCAGAATTTTTGTACATTTTCTTTGTTTCTCCCTATAGTGAGTCGTATTA	T7 promoter-containing template for in vitro transcription of the 29-nt PRE 1 RNA with wild-type PRE 1 sequence
KS3356	TTCCCAGAATTGTAGATGTTTTTCTTTGTTTCTCCCTATAGTGAGTCGTATTA	Same as KS3355, but with mutant PRE 1 sequence
KS3357	GAGAATGGGAGATGGGACAGGAAGAAATTTTCTCCCTATAGTGAGTCGTATTA	T7 promoter-containing template for in vitro transcription of the 29-nt PRE 3 RNA with wild-type PRE 3 sequence

Table S5. Sequences of primers used in this study: 4. Primers used in RT-PCR validation of microarray results.

Name	Sequence	Gene ID	Gene name	Fold enrichment with MBP::PUF-8
KS2363	GAGACGGAGAGAAAGTTGGC	T01C3.3		14.3
KS2364	GATTGCAAGGGCGATCCTCG			
KS2365	ATTCTCCGTAAGCAACGTGC	F22B5.1	*evl-20*	10.8
KS2366	TTGGACCAGTCGATCACCAG			
KS2367	ATGCCCGTCATCAAAGTGCA	F13G3.9	*mif-3*	10.1
KS2368	GCAAGAAACGCAATGCCTAG			
KS2369	ATCTGGAGAGGCTTCTGGTG	B0280.5	*cpg-2*	9.6
KS2370	ATGGCATTGAAGCAGGGTCG			
KS2371	ATCTGCACGAGCTCTTCTGG	C01G10.7		8.8
KS2372	TGAACTCTCTCCACGAGCTG			
KS2373	CGACTGGAATCACAACTGGG	M03E7.5	*gosr-2.2*	8.5
KS2374	GCAGAACATGAATATCAGGC			
KS2375	CTGGCAGTCCAGATACTGTG	C33F10.4		7.5
KS2376	TCAGTTGAATGCCGCAAGCA			
KS2377	ATGACTCGACGCAACTGGAG	T10B5.6	*knl-3*	7.5
KS2378	AGCATCGATTCGCTCGAAGC			
KS2379	CTCCAAAATCCAATGCTGCC	C17E7.4		7.1
KS2380	AGTATTGGAAGCCTGTGGGC			
KS2381	CGTCTTGCTGATATGGAAGG	F23B12.6	*fntb-1*	7.0
KS2382	GAAGTGAAGAACTCCTTGGC			
KS2383	CTACCAGCTGGCCTATGTCG	C10H11.10	*kca-1*	6.8
KS2384	AACTTCCGACATCGGATTCC			
KS2385	CATCAAGATCAGGGTCCAAC	F10D11.2		6.4
KS2386	CGCAGAGTATCGCTCAGATG			
KS2387	ATTCAGAACACCCACGTACC	W05F2.3		6.4
KS2388	GATATCCTCGTCGCTGTTCG			
KS2389	CGCTGAGCCATAGACAGAAG	C16A3.5		5.8
KS2390	TTGGAAACAGTTGGGGCAGC			
KS2391	TCCCGAGAAGCTGCTCCTAG	D2007.5	*atg-13*	5.5
KS2392	CATCGGAGAACGAATTGACG			
KS2393	TGCGTGTTGCTCAAGCAGAG	F35A5.8b	*erp-1*	5.4
KS2394	GCTGACAGGCAATTTTCCGC			
KS2395	GATCAGGCCGACTATGAAGC	W03C9.7	*mex-1*	5.4
KS2396	TCTTCGTGAGCATCGTCGTC			
KS2397	CGCAGTTCTCACCGTCTTGG	R11E3.8	*dpf-5*	5.2

KS2398	TTGCATAGTCGGCCTCAACG			
KS2399	CATGCAGTATTTCGCGTCTG	C36B1.7	*dhfr-1*	5.1
KS2400	GTGGTTCTCGACAACCTTCC			
KS2401	GCTGATCGCTGCGGGATAAC	F30F8.3		4.9
KS2402	CTAGAGACGCGTGACTTGGG			
KS2403	CGACACGGCGTCTTCAGAAG	R01H2.6	*ubc-18*	4.6
KS2404	GCGTGCTTTCGAGTGTGCTC			
KS2405	AGTGGCACGCAACTGCTTCC	F54C9.8	*puf-5*	4.4
KS2406	GCACTGATGTCCATGAGTGG			
KS2407	CCAACGTCAACACTACCACG	C25B8.4	*clec-266*	6.6
KS2408	TCCGTTTCTCTCGCAGATCG			
KS2409	TCAGAAGGCCGATATCGAGC	T12D8.8		5.2
KS2410	TGTTGTGGGACAGAAGCTCC			
KS2411	ATGAGCGGAAATCGGGGAGG	ZK593.6	*lgg-2*	5.2
KS2412	TCCAAATGCTGGTTGAGACG			
KS2413	ATGTCGTCGACTGCTGAAGA	ZK632.9		7.3
KS2414	TTTGCCTCTCCGTTGCTGGC			
KS2415	TTGCTCATTCACTGGCCTGG	C35D10.6		5.1
KS2416	AAACCACTACGCGAGGATCC			
KS2417	CTCGGTGCAGTCGGATTGGC	H24K24.3a		4.6
KS2418	CGCAGACTCTCTCCCTTGTG			
KS2419	GGCGCTCTGCAAGTTCTACC	Y46G5A.5	*pisy-1*	6.4
KS2420	CATTGGGCCTTCTGAGCAGC			
KS2421	GGGAATATTGCTCCAGAAGC	Y54E5A.7		5.2
KS2422	CGCTGCTGACGAATAATCTC			
KS2423	ATGTCTGGACGTGGAAAGGG	C50F4.7	*his-37*	9.1
KS2424	TATCCACCGAATCCGTAGAG			
KS2425	GGAGGAGGAGATGAGTAGTC	Y73E7A.1		6.0
KS2426	GAGCCAGAAGACGAGCGTTG			
KS2427	GTTCAGCCTCGTTCGGAAGG	Y82E9BR.14		5.8
KS2428	CATCCGGCGTATCGAGCTTC			
KS2429	ATCCGATCCCAAAGTCGTCC	T01C8.1b	*aak-2*	4.4
KS2430	GCCAGTGTTCCAATCAATGC			
KS2431	CTTTCGGACAACATCTCGTG	Y110A7A.14	*pas-3*	4.9
KS2432	TCTCAGCAGTCTCAGCTTCC			
KS2433	ATCAATGGCCCAGCCGTAGG	R06F6.9	*ech-4*	4.1
KS2434	CAATCGCTTGGTGACACTCC			
KS2435	CTTCATCTTCAGCATCATGG	Y73B6BL.27		4.2
KS2436	GATTTTCCCATGATTGAGCC			

KS2437	AGCCGAGCAGAGCTATGAGG	Y71F9AL.16	*arx-1*	4.4
KS2438	ATCGGCTTCGGCTTCAACCG			
KS2439	ATGCCTCTGTGAGCGAGACG	T24H7.3		4.3
KS2440	CATCGGAATCGCTTCTTTCC			
KS2441	ATGGAGTCGTGTCTCAACCC	F18A1.7		25.1
KS2442	GCCTTGAAATCGCCGTTGCG			
KS2443	AATCATGGCTTGCAAGTGTG	K11G9.6	*mtl-1*	24.6
KS2444	AATGAGCCGCAGCAGTTCCC			
KS2445	CGAATTGTAGCGTAGCAGCC	Y54G9A.5		15.5
KS2446	CGCAGAAGGTCGAGCGATTC			
KS2447	TGTCCGCCCAACTGCAGAAG	F15A4.10		9.0
KS2448	GGTCATCATCGGAAGAGTCG			
KS2449	AATATGGGCACCCGCCTTGC	ZK1098.5		8.5
KS2450	ATCTTCACCGGCAGGTAGGC			
KS2451	CATGCGCAATTGTCATTGGC	W01A11.2		8.1
KS2452	TCACTGGAAGATGAGATGAG			
KS2453	AAGAGCGCCAGCGTTTAGCC	D1022.1	*ubc-6*	7.0
KS2454	TCGACAAGGAAGCGACGAGC			
KS2455	AAACTCATCATCGCCTTCGC	F41F3.3		6.3
KS2456	TTTCTTCCGGCGTAAGCTCC			
KS2457	ACGCTCAGTACAGTGACTCG	R102.5a		6.1
KS2458	AGCTCGAGAAGTCTTCCAGC			
KS2459	TGTTCTGGCTGCTCGATCTC	ZK858.4	*mel-26*	5.7
KS2460	CAGATGGAGGTGGTACAATG			
KS2461	CGAATTCGTCTTCACAGCAC	M01E11.1		5.4
KS2462	CATGGTCTTTGATACCCACG			
KS2463	GAAGAGGAGATGAAGCTTCC	R07E5.7		5.3
KS2464	GCTCTGAGTTTGTCTTCGGC			
KS2465	TCATCCCACTTGTCCAGAGC	R11.4		5.3
KS2466	TCAGCAAAGTTTCATGGCTC			
KS2467	ATGGGCGGATGCTTTTCCCG	F43G6.10		5.2
KS2468	CTACTGTTGATGATCCAACTG			
KS2469	ATGTCTCGCCTTGCTATCCT	Y5F2A.2	*ttr-17*	5.1
KS2470	TTGCAGATGGTCTTCTCTCC			
KS2471	GAAGCCATTGATGCGTATCG	C56C10.10		5.1
KS2472	TAAGTGACACGAGAGTCAGC			
KS2473	CTTGTCGATTACTCCCACGG	F54C8.2	*cpar-1*	4.8
KS2474	CACGTCTGTAGTCGTCAGTG			
KS2475	ATTCGGAGCTTGGAGCCGAG	K06B9.2		4.7

KS2476	ATGATCGGATTCCAAGGCAC			
KS2477	AGTTGTGAGAATGAGCGTCG	F42H10.2		4.7
KS2478	TATCATTGTCACCGGTACCG			
KS2479	ATAAGCATCGTCTGGCGCTG	W06B4.1		4.3
KS2480	AGCAGAATGCGACACGATCG			
KS2481	TCTCTGCCGCTGCCGATATC	T25E12.5	*gyg-2*	4.1
KS2482	GCCATGCTCTCGTCAAGTGC			

In all cases, the first and the second sequences represent the forward and reverse PCR primers, respectively.

Table S6. Potential common targets of PUF-8 and FBF

Gene name	PRE	FBE	Fold enrichment with MBP::PUF-8	SAM rank in FBF target list
C29A12.1	None	uguaccau	9.5	7
C10H11.10	uguaaaau ugucaaau	uguaaaau uguacuau	3.7	12
F36H1.4b	uguauaau	ugugcuau uguuuuau uguucuau uguauaau	5.4	17
R166.3	uguaaaau uguauaau uguaaaaa	uguaaaau uguauuau uguauaau	5.5	26
C56C10.10	uguacauu	uguacuau	9.0	28
M01E11.6	uguaaaau	uguaaaau	4.0	38
U19E7.3	uguaaaua	uguaccau	3.7	69
Y47G6A.2	None	uguucuau	3.6	85
Y46G5A.5	uguaaaau	uguaaaau	4.7	87
ZK593.6	uguaaaau uguaaaua uguaugua	uguaaaau uguuccau	4.9	104
R01B10.4	uguacgau	uguuuuau ugugcaau uguuccau	3.6	127
F32D1.7	uguauaua	ugugcuau	3.4	131
U24D1.3	uguaaauu uguaaaau uguauaua	ugugccau uguaaaau	6.4	154
Y54E2A.3	uguaaaau	uguaaaau	10.7	164
W06B4.1	uguauauu	ugugucau	3.4	247
Y62E10A.14	uguacaua uguauaua uguauauu	uguauuau	5.2	285
Y53C12A.6	ugucaaau	uguauuau uguguaau	4.3	302
Y17G9B.9	uguauaua uguauauu	uguauuau uguuuuau	6.3	313

PRE – UGUMHRDW, where M is A or C, H is A, U, or C, R is A or G, D is A, U, or G, and W is A or T (Opperman et al., 2005); FBE – UGUDHHAU, where D is A, U, or G and H is A, U, or C (Bernstein et al., 2005; Kershner and Kimble, 2010). Highlighted sequences match both PRE and FBE.

Table S7. *C. elegans* strains used in this study

3'UTR fusions

Fusions	**Strain**	**Transgene**	**Genotype**	**Lines**	**Reference**
hip-1	IT258	*pie-1 prom:gfp:H2B:hip-1 3'utr*	*unc-119(ed3) III; kpIs(pPA1)*	3	This study
mex-1	IT258	*pie-1 prom:gfp:H2B:mex-1 3'utr*	*unc-119(ed3) III; kpIs(pPA2)*	3	This study
pal-1	JH2236	*pie-1 prom:gfp:H2B:pal-1 3'utr*	*unc-119(ed3) III; axIs1624*	-	(Merritt et al., 2008)
spn-4	JH2311	*pie-1 prom:gfp:H2B:spn-4 3'utr*	*unc-119(ed3) III; axIs1668*	-	(Merritt et al., 2008)
puf-5	JH2418	*pie-1 prom:gfp:H2B:puf-5 3'utr*	*unc-119(ed3) III; axIs1721*	-	(Merritt et al., 2008)
pos-1	JH2427	*pie-1 prom:gfp:H2B:pos-1 3'utr*	*unc-119(ed3) III; axIs1751*	-	(Merritt et al., 2008)
ubc-6	IT258	*pie-1 prom:gfp:H2B:ubc-6 3'utr*	*unc-119(ed3) III; kpIs(pPA3)*	3	This study
ubc-16	IT258	*pie-1 prom:gfp:H2B:ubc-16 3'utr*	*unc-119(ed3) III; kpIs(pMP20)*	3	This study
D1022.1	IT260	*pie-1 prom:gfp:H2B:D1022.1 3'utr*	*unc-119(ed3) III; kpIs(pMP21)*	4	This study
F30F8.3	IT258	*pie-1 prom:gfp:H2B:F30F8.3 3'utr*	*unc-119(ed3) III; kpIs(pPA4)*	3	This study
F39B2.2	IT261	*pie-1 prom:gfp:H2B:F39B2.2 3'utr*	*unc-119(ed3) III; kpIs(pMP22)*	3	This study
R01H2.6	IT262	*pie-1 prom:gfp:H2B:R01H2.6 3'utr*	*unc-119(ed3) III; kpIs(pMP23)*	2	This study
T01C3.3	IT264	*pie-1 prom:gfp:H2B:T01C3.3 3'utr*	*unc-119(ed3) III; kpIs(pMP24)*	4	This study
C06A5.8	IT266	*pie-1 prom:gfp:H2B:C06A5.8 3'utr*	*unc-119(ed3) III; kpIs(pMP25)*	5	This study
pal-1 PRE-1	IT314	*pie-1 prom:gfp:H2B:pal-1 PRE-1 3'utr*	*unc-119(ed3) III; kpIs(pMP27)*	3	This study
pal-1 PRE-2	IT316	*pie-1 prom:gfp:H2B:pal-1 PRE-2 3'utr*	*unc-119(ed3) III; kpIs(pMP28)*	4	This study
pal-1 PRE-3	IT318	*pie-1 prom:gfp:H2B:pal-1 PRE-3 3'utr*	*unc-119(ed3) III; kpIs(pMP29)*	3	This study
pal-1 PRE-4	IT300	*pie-1 prom:gfp:H2B:pal-1 PRE-4 3'utr*	*unc-119(ed3) III; kpIs(pMP26)*	4	This study

ORF fusions

Fusions	**Strain**	**Transgene**	**Genotype**	**Lines**	**Reference**
pal-1	JH2013	*pie-1 prom:gfp:pal-1 ORF:pal-13'utr*	*unc-119(ed3) III; axIs1460*	-	(Merritt et al., 2008)
ify-1	IT233	*pie-1 prom:gfp:ify-1 ORF:ify-1 3'utr*	*unc-119(ed3) III; kpIs(pMP16)*	2	This study

Promoter fusions

Fusions	**Strain**	**Transgene**	**Genotype**	**Reference**
hlh-1	RW10097	*hlh-1(3.3kb)::HIS-24::mCherry*	*unc-119(ed3) III; zuIs178V;stIs10088*	Murray et al., 2008
hlh-1	RW10112	*hlh-1(3.3kb)::HIS-24::mCherry*	*unc-119(ed3) III; stIs10026; st10089*	Murray et al., 2008
unc-119	DP132	*unc-119::GFP*	*edIs6 IV*	Ciosk et al., 2006

Other strains

Strain	**Genotype**	**References**
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
IT273	*puf-8(ok302) unc-4(e120)/mnC1* II; *axIs1624(gfp:h2b:pal-1 3'utr)*	This study
IT274	*puf-8(ok302) unc-4(e120)/mnC1* II; *axIs1460(gfp:pal-1ORF:pal-1 3'utr)*	This study

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  1   GUGACAAACA  GAAGAUUCGG  CUAUAAGUAC  UCAUCUACUU  ACAAAGAAAA
 51   UGUACAAAAA  UUCUGGGAAU  UUUCAUAUUU  UUCUAGAAUA  UUGUACACAU
101   UUAUUAUAUU  UUUACAUUUC  UCUCGCUUGA  AUACGGUUAA  AUUCACACUU
151   UUAUAUAAUU  UCUUCCUGUC  CCAUCUCCCA  UUCUCUCACA  UCAGAAUAUU
201   CUAAUCAUCA  CUGCCCUUAA  CAUAUAUAUA  UAUAUAUUUA  UAACUUUCCG
251   AUCAUUCCUU  CUGCUUUGUA  AACUAAUCCA  AUCAUUCUCU  AAUGAAUUAU
301   UCCCUAAUAU  AGAGCUUCUU  UAUUUAUUGU  GAUUUCUUGU  UUCUUACCCU
351   UCUCAAGGUU  UAGGAAAAAG  UUUAGGUCCC  CAUUUGUUAU  GUAUUUACUU
401   CCCACUCUGA  ACGGAUCCAU  UUUGAACAUG  UUUUCUAUUU  UUUGGAAAAG
451   UUUAGAGAAU  UCUUUGCUUU  UCUCACAUAU  CUUGAUUGCA  UAUUUUUUAU
501   AACAAAACAA  UGAAACAAUU  UUGAAGAAUU  UACAGCAGAA  AUUGAUGAGA
551   UUAAC
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Fig. S1. Sequences downstream of PAL-1 coding region. The 3' UTR region (GenBank accession#NM_001026039) is underlined. PAL-1 stop codon is shown in red; highlighted regions are: blue – the four PUF-8 recognition elements; yellow – GLD-1 recognition element; green – MEX-3 recognition elements (Mootz et al., 2004; Pagano et al., 2009). Bases 1-279 and 278-555 correspond to Region 1 and Region 2 RNAs, respectively, used in gel shift assays described in Fig. 5.

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