The head mesodermal cell couples FMRFamide neuropeptide signaling with muscle contraction during a rhythmic behavior in *C. elegans*

Ukjin Choi, Mingxi Hu, Qixin Zhang, and Derek Sieburth

Derek Sieburth Email: <u>sieburth@usc.edu</u>

Supplementary Information:

Supplementary Figure 1 to Figure 8 Supplementary Table 1 to Table 2 Supplementary References



Supplementary Figure 1: Analysis of the expression patterns of *nmur-3* promoter fragments. a Schematic of the *nmur-3* promoter. The *nmur-3(3kb)* promoter fragment extends from -1bp to -2956bp relative to the ATG codon of *nmur-3*, and drives expression of GFP in AVL, DVB and hmc. The *Pnmur-3(1kb)* promoter fragment extends from -1bp to -1053 bp relative to the ATG codon of *nmur-3*, and drives GFP expression in AVL but not in hmc. The *Pnmur-3(Δ)* promoter fragment extends from -2026 bp to -2956 bp and drives GFP expression primarily in hmc but not in AVL. +++ indicates that 80-100% of animals exhibited fluorescence in the indicated cell, + indicates that <10% of animals exhibited fluorescence in the indicates that 0% of animals exhibited fluorescence in the indicated for each transgenic line. **b** Representative images of adults from the transgenic lines described in **a**. Scale bar, 40 μm.



Supplementary Figure 2: Phenotypic analysis of flp-22 and frpr-17 mutants. a Quantification of the number of aBocs per cycle in adult animals of the indicated genotypes. "AVL egl-3" denotes egl-3 cDNA expressed in AVL using the nmur-3(1kb) promoter. "hmc (Parg-1) frpr-17" denotes frpr-17 cDNA expressed in hmc using the arg-1 promoter. vjEx2548 is the GCaMP imaging strains used in this study. Data are presented as mean values \pm SEM. n = 6, 4, 3, 2, 2, 2, 5, 6, 5 independent animals. *** P<0.001 and * P<0.05 in one-way ANOVA with Bonferroni's correction for multiple comparisons; n.s., not significant. b Quantification of expulsion (Exp) frequency in the indicated genotypes. Data are presented as mean values ± SEM. n = 6, 3, 4, 5, 5 independent animals. *** P<0.001 in one-way ANOVA with Dunnett's correction for multiple comparisons; n.s., not significant. c Top, left: genomic organization of the flp-22 locus showing the location and lesion of vj229 allele. Top, right: genomic organization of the frpr-17 locus showing the locations and the lesions of the vj249 and vj265 alleles. vj249 is a glycine to glutamic acid substitution in exon 3. Bottom: diagram showing the predicted structure of the FRPR-17 protein and the position of the amino acid substitution in the extracellular domain in the vj249 mutant. d Quantification of cycle lengths in the indicated genotypes. Data are presented as mean values \pm SEM. n = 6, 3, 5, 5independent animals. One-way ANOVA with Dunnett's correction for multiple comparisons; n.s., not significant. e Locomotion, measured by body bends per minute, of young adult animals of the indicated genotypes. Data are presented as mean values ± SEM. n = 5 independent animals. *** P<0.001 in oneway ANOVA with Dunnett's correction for multiple comparisons; n.s., not significant. f Egg laying rates and total number of eggs laid in the indicated genotypes. Data are presented as mean values \pm SEM. n = 4, 4, 43, 4, 4, 4 independent animals. *** P<0.001 and ** P<0.01 one-way ANOVA with Dunnett's correction for multiple comparisons; n.s., not significant.



Supplementary Figure 3: Movement has minimal impact on GCaMP fluorescence intensity, aBoc can be detected using time lapse images, and muscles do not activate hmc. a Left: average traces of fluorescence intensity in AVL or hmc in animals co-expressing GCaMP and mCherry. Each trace is aligned to the calcium spike initiation time, and the solid lines indicate average fold change in fluorescence intensity and the shades indicate SEM. Right: quantification of the average peak amplitude of CGaMP and mCherry. Data are presented as mean values \pm SEM. n = 4 cycles from different animals. **b** Left: representative images from the live calcium imaging showing contractions of the neck muscle. Posterior is up and dorsal is to the left in these images. The lumen of the anterior intestine is outlined with a white dotted line. The lumen of the intestine begins to displace posteriorly at the initiation of aBoc (arrow) and reaches maximum displacement after about one second before beginning to relax. Similar expression patterns were observed in all 10 animals examined. Scale bar, 40 µm. Right: in wild-type animals, the duration of the maximal aBoc contraction is at least 500 ms (full aBoc). In the indicated mutants, the maximal displacement is not reached or it is less than 500 ms in about 30% of cycles (partial and no aBoc). ** P<0.01 and * P<0.05 in two-sided chi-square test with Bonferroni's correction for multiple comparisons; n.s., not significant. c Calcium spike frequency in AVL and hmc and aBoc frequency in unc-54/myosin mutants from time lapse imaging. "Weak aBoc" denotes a contraction with a very little movement to due to compromised muscle function. Wild-type: 33 cycles in 8 animals, unc-54: 10 cycles in 3 animals *** P<0.001 in two-sided Fisher's exact test. d Left: average traces of calcium dynamics in hmc in the indicated genotypes. Each trace is aligned to the calcium spike initiation time and the solid lines indicate average fold change in fluorescence intensity and the shades indicate SEM. Right: quantification of the average peak amplitude, rise time, and half-decay time of CGaMP. Data are presented as mean values ± SEM. n = 10, 5 cycles from different animals. ** P<0.01 and * P<0.05 in two-tailed Student's ttest; n.s., not significant.



Supplementary Figure 4: FLP-22 secreted from AVL can reach hmc. a Representative image of the proximal AVL axon of adults expressing FLP-22::pHluorin in AVL in the indicated genotypes. Arrowheads denote clusters of DCVs visible in the proximal axon containing unquenched FLP-22::pHluorin. Similar expression patterns were observed in all 25 animals examined for each genotype. Scale bar, 20 μm. b Representative images of adults co-expressing FLP-22::pHluorin in AVL and GBP::SAX-7 in hmc. Fluorescence is observed on the surface of hmc, indicating that FLP-22::pHluorin was secreted from AVL and is associated with hmc through interaction with the GFP binding domain of GBP::SAX-7. Similar expression patterns were observed in all 15 animals examined. Scale bar, 40 μm. **c** Representative images showing adults expressing only GBP::SAX-7 in hmc. Similar expression patterns were observed in all 15 animals examined. Scale bar, 40 μm.



Supplementary Figure 5: *flp-22* and *frpr-17* mutants do not alter calcium dynamics in AVL. a Violin plots of calcium spike initiation time in hmc after the end of intestinal calcium oscillation. Dashed line refers median and dotted lines refer quartiles. One-way ANOVA with Bonferroni's correction for multiple comparisons; n.s., not significant. **b** Quantification of the number of calcium spikes observed in AVL during DMP in adult animals of the indicated genotypes. *"hmc frpr-17"* denotes expressing *frpr-17* cDNA under the *nmur-3(* Δ) promoter. For a, b, and d, wild-type: 33 cycles in 8 animals, *flp-22*: 49 cycles in 9 animals, *frpr-17*: 56 cycles in 13 animals, *flp-22; frpr-17*: 43 cycles in 9 animals, *flp-22; frpr-17; hmc frpr-17*: 42 cycles in 9 animals, *flp-22; frpr-17; hmc frpr-17*: 42 cycles in 9 animals. **c** *Left:* traces of calcium dynamics in AVL aligned to the calcium spike initiation time. Solid lines indicate average fold change in GCaMP intensity and shades indicate SEM. *Right:* quantification of average peak amplitudes, rise times and decay times from the traces on the right. Data are presented as mean values ± SEM. *n* = 6, 5, 6, 5 cycles from different animals. One-way ANOVA with Bonferroni's correction for multiple comparisons; n.s., not significant. **d** Violin plots of calcium spike initiation time in hmc after the end of intestinal calcium oscillation. Dashed line refers median and dotted lines refer quartiles. *** P<0.001 in one-way ANOVA with Bonferroni's correction for multiple comparisons; n.s., not significant.



Supplementary Figure 6: aBoc frequency of innexin mutants and calcium dynamics in *unc-9* mutants. a aBoc frequencies of the indicated genotypes. Data are presented as mean values \pm SEM. *n* = 6, 3, 3, 3, 3 independent animals. One-way ANOVA with Dunnett's correction for multiple comparisons; n.s., not significant. b *Left:* average traces of calcium dynamics in AVL or hmc aligned to the calcium spike initiation time in the indicated mutants. Solid lines indicate average fold change in GCaMP intensity and shades indicate SEM. *unc-9 (no aBoc)* refers to cycles with calcium spike followed by no aBoc and *unc-9 (aBoc)* refers to cycles with calcium spike followed by no eaverage peak amplitude, rise time, and half-decay time. Data are presented as mean values \pm SEM. *n* = 6, 5, 5 cycles from different animals. One-way ANOVA with Bonferroni's correction for multiple comparisons; n.s., not significant.



Supplementary Figure 7: aBoc frequency and calcium dynamics of receptors highly expressed in hmc. a Table of the GPCRs highly expressed in hmc and their relative abundance (adapted from [1]). b Quantification of the number of calcium spikes observed in hmc in each cycle in adult animals of the indicated genotypes. Wild-type: 33 cycles in 8 animals, nmur-3: 21 cycles in 7 animals srd-32: 25 cycles in 9 animals, npr-23: 23 cycles in 6 animals, T11F9.1: 20 cycles in 9 animals, frpr-17: 56 cycles in 13 animals, nmur-3 frpr-17: 49 cycles in 9 animals, srd-32; frpr-17: 47 cycles in 10 animals, npr-32; frpr-17: 27 cycles in 7 animals, T11F9.1; frpr-17: 49 cycles in 9 animals, frpr-4; frpr-17: 43 cycles in 9 animals. Two-sided chi-square test with Bonferroni's correction for multiple comparisons; n.s., not significant. c Above: average traces of calcium dynamics in hmc aligned to the calcium spike initiation time. Solid lines indicate average fold change in GCaMP intensity and shades indicate standard errors. Below: quantification of the average peak amplitude, rise time, and half-decay time. Data are presented as mean values ± SEM. n = 10, 9, 8, 5, 5, 6 cycles from different animals. * P<0.05 in one-way ANOVA with Dunnett's correction for multiple comparisons. d Quantification of the frequency of calcium spikes observed in AVL and hmc and aBocs from time lapse images of the indicated genotypes. Wild-type: 33 cycles in 8 animals, unc-25: 46 cycles in 7 animals unc-25; frpr-17: 40 cycles in 6 animals. Two-sided chisquare test with Bonferroni's correction for multiple comparisons; n.s., not significant.



Supplementary Figure 8: Calcium dynamics in flp-9 mutants and putative flp-9 GPCR mutants. a Quantification of the number of calcium spikes observed in AVL in each cycle in adult animals of the indicated genotypes. Wild-type: 33 cycles in 8 animals, frpr-21: 23 cycles in 9 animals, flp-9: 27 cycles in 8 animals, flp-9 (OE): 27 cycles in 5 animals. b Left: average traces of calcium dynamics in AVL aligned to the calcium spike initiation time in the indicated mutants. The solid lines indicate average fold change in GCaMP intensity and the shades indicate SEM. Right: quantification of the average peak amplitude, rise time, and half-decay time. Data are presented as mean values \pm SEM. n = 6, 6, 5, 4 cycles from different animals. * P<0.05 in one-way ANOVA with Bonferroni's correction for multiple comparisons; n.s., not significant. c Violin plots of calcium spike initiation time in hmc after the end of intestinal calcium oscillation. Dashed line refers median and dotted lines refer quartiles. *** P<0.001 and ** P<0.01 in oneway ANOVA with Dunnett's correction for multiple comparisons; n.s., not significant. d Quantification of the number of calcium spikes observed in hmc in each cycle in adult animals of the indicated genotypes. Wild-type: 33 cycles in 8 animals, dmsr-1: 30 cycles in 5 animals, dmsr-7: 36 cycles in 5 animals, egl-6: 34 cycles in 5 animals, frpr-8: 35 cycles in 6 animals, frpr-17: 56 cycles in 13 animals, dmsr-1; frpr-17: 41 cycles in 7 animals, dmsr-7; frpr-17: 47 cycles in 7 animals, egl-6 frpr-17: 40 cycles in 7 animals, frpr-8 frpr-17: 24 cycles in 7 animals. Two-sided chi-square test with Bonferroni's correction for multiple comparisons; n.s., not significant.

Strain	Genotype	Figures	Source
N2	Wild-type Bristol strain	Fig. 1, Fig.	
		S2a, b, d, e,	
		f, Fig. 3a,	
		Fig. 4b, Fig.	
		S5A, Fig. 5A,	
		D	
OJ794	nlp-40(tm4085) I	Fig. 1b	[2]
OJ6846	aex-2(vj304) X	Fig. 1b	This paper
OJ3271	flp-22(vj229) I	Fig. 1c, Fig.	This paper
		S2b, d, e, f	
		Fig. 5a	
OJ6057	frpr-17(vj265) X	Fig. 1c, Fig.	This paper
		S2b, d, e, f	
	flp-22(vj229) I; frpr-17(vj265) X	Fig. 1c	This paper
OJ6754	hlh-8(nr2061) X	Fig. 1d	This paper
OJ7173	flp-22(vj229) I; hlh-8(nr2061) X	Fig. 1d	This paper
OJ1218	unc-25(e156) III	Fig. S2a	This paper
OJ2424	egl-3(nr2090) V	Fig. S2a, b,	This paper
		e, f	
OJ5308	frpr-17(vj249) X	Fig. S2a	This paper
OJ3584	egl-30(ad806)	Fig. 3a	This paper
018203	unc-9(e101) X	Fig. 4b	This paper
OJ2451	Inx-10(ok2/14) V	Fig. S6a	This paper
OJ4154	INX-11(0K2783) V	Fig. S5a	I his paper
019407	INX-7(0K2319) IV	Fig. S5a	I his paper
012650	INX-1(IM3524) X	Fig. Soa	[J] This paper
0123020	$\frac{1}{100}$	Fig. 55a	This paper
037399	11p1-21((114009) 11	520 f	This paper
0.16524	fln-22(vi229) 1: frnr-21(tm4669) 11	Fig. 5a	This naner
0.13844	flp-9(vn.36) IV	Fig. 5e. Fig.	This paper
		S2e f	
OJ7009	viEx2445 [pMH569 (Pnmur-3(1kb)::ICE). 10 na/uL1	Fig. 1b	This paper
OJ1626	nlp-40(tm4085) I; viEx368 [pHW61 (Pges-1::nlp-40 cDNA),	Fig. 1b	[2]
	25 ng/µL]	Ű	
OJ9177	aex-2(vj304) X; vjEx3004 [pDS728 (Pnmur-3(1kb)::aex-2	Fig. 1b	This paper
	cDNA), 10 ng/µL]		
OJ7011	vjEx2447 [pDS729 (Pnmur-3(1kb)::TeTx), 10 ng/µL]	Fig. 1b	This paper
OJ9314	flp-22(vj229) I; vjEx1837 [pHM363 (Punc-47::flp-22 cDNA),	Fig. 1c	This paper
	25 ng/µL]		
OJ5082	flp-22(vj229) I; vjEx1534 [pHM184 (Punc-129::flp-22 cDNA),	Fig. 1c	This paper
	25 ng/µL]		
OJ7439	flp-22(vj229)	Fig. 1c	This paper
	cDNA), 10 ng/µL]		
OJ9395	frpr-17(vj249) X; vjEx1596 [pDS573 (Prab-3::frpr-17 cDNA),	Fig. 1c	This paper
	5 ng/µL]		
OJ5372	frpr-17(vj249) X; vjEx1580 [pDS567 (Pmyo-3::frpr-17 cDNA)	Fig. 1c	This paper
	10 ng/µL]		
OJ9396	frpr-17(vj265) X; vjEx2830 [pUC259 (Pnmur-3(Δ)::frpr-17	Fig. 1c	This paper
	cDNA) 25 ng/µL]		

Supplementary Table 1: Strains, transgenic lines, and plasmids used in this study

OJ6607	vjEx2174 [pUC168 (Pnmur-3::GFP) 50 ng/µL]	Fig. 1d, Fig.	This paper
		S1	
OJ7659	vjEx2653 [pUC249 (Pnmur-3(Δ)::ICE), 25 ng/μL]	Fig. 1d	This paper
OJ7716	frpr-17(vj265) X; vjEx2653 [pUC249 (Pnmur-3(Δ)::ICE), 25	Fig. 1d	This paper
	ng/uL]	0	
OJ7656	viEx2651 [pUC246 (Pnmur-3(Δ)::PH	Fia. 1d	This paper
	domain::miniSOG::SL2::mCherry), 25 ng/uL1	5	
0.16889	otls348 viEx2349 InUC214 (Pnmur-3(1kb)) GEP) 2 na/ul 1	Fig. S1	This paper
OJ7018	viEx2454 [pUC218 (Pnmur-3(A)::GFP) 50 na/uL1	Fig. S1	This paper
OJ7149	eal-3(nr2090) V: viEx2535 [pMH576 (Pnmur-3(1kb)::eal-	Fig. S2a	This paper
	3Venus) 5 na/ul 1		
0.16220	frpr-17(vi265): viEx1926 InUC163 (Para-1::Peal-18::frpr-17	Fig. S2a	This paper
	cDNA::mCherry) 50 ng/ul 1	1 19. 024	The paper
0.18149	lite-1(ce314) gur-3(ok2245) X: viEx2548 [nUC191 (Pnmur-	Fig 2 Fig	This paper
000140	3(3kb)::CC=MP6) 12 na/ul + nHW107 (Pnln-40::CC=MP3)	S2h d Fia	
	3(3Kb)GCalvir 6) 12 hg/µE + privir67 (Fhip-40GCalvir 3)	SZD, U, TIY. SZD d Eig	
	Το hg/μLj	SSD-U, FIG.	
		55, FIG. 30-	
		e, Fig. 4d-1,	
		FIG. S6D, FIG.	
		5b, c, f, Fig.	
		S7b-d, Fig.	
		S8	
OJ9089	lite-1(ce314) gur-3(ok2245) X; vjEx2548; vjEx2957 [pMH569	Fig. 2d	This paper
	(Pnmur-3(1kb)::ICE) 10 ng/µL]		
OJ9397	lite-1(ce314) gur-3(ok2245) aex-2(vj302) X; vjEx2548	Fig. 2d, e	This paper
OJ9398	lite-1(ce314) gur-3(ok2245) aex-2(vj302) X; vjEx2548;	Fig. 2d, e	This paper
	vjEx2985 [pDS728 (Pnmur-3(1kb)::aex-2 cDNA) 7 ng/µL]		
OJ8231	flp-22(vj229)	Fig. 2f, g,	This paper
		Fig. S3b, Fig.	
		S5	
OJ9634	flp-22(vj229)	Fig. 2f	This paper
	vjEx3125 [pDS747 (Pnmur-3(1kb)::flp-22 cDNA) 10 ng/µL]		
OJ8229	lite-1(ce314) gur-3(ok2245) frpr-17(vj265) X; vjEx2548	Fig. 2f, g,	This paper
		Fig. S3b, Fig.	
		S5, Fig. 3b,	
		c, e, Fig. 5b,	
		c, Fig. S7b,	
		d, Fig. S8c, d	
OJ9399	flp-22(vj229) I; lite-1(ce314) gur-3(ok2245) frpr-17(vj265) X;	Fig. 2f, Fig.	This paper
	vjEx2548	S3b, Fig.	
		S5b	
OJ8725	lite-1(ce314) gur-3(ok2245) frpr-17(vj265) X; vjEx2548;	Fig. 2f, Fig.	This paper
	vjEx2830 [pUC259 (Pnmur-3(Δ)::frpr-17 cDNA) 25 ng/μL]	S5b	
OJ8783	flp-22(vj229) I; lite-1(ce314) gur-3(ok2245) frpr-17(vj265) X;	Fig. 2f, Fig.	This paper
	vjEx2548; vjEx2830 [pUC259 (Pnmur-3(Δ)::frpr-17 cDNA)	S5b	
	25 ng/µL]		
OJ9721	lite-1(ce314) gur-3(ok2245) X; vjEx3153 [pUC297 (Pnmur-	Fig. S3a	This paper
	3(Δ)::GCaMP6::SL2::mCherry) 12 ng/μL]		
OJ9711	unc-54(e1108) l; vjEx2548	Fig. S3c, d	This paper
OJ7370	vjEx2589 [pDS788 (Pnmur-3(1kb)::flp-22::pHluorin::flp-22)	Fig. S4a	This paper
OJ8077	unc-32(e189)	Fig. S4a	This paper
	22::pHluorin::flp-22)		
OJ9320	vjEx2589 [pDS788 (Pnmur-3(1kb)::flp-22::pHluorin::flp-22) 5	Fig. S4b, c	This paper
	ng/μL]; vjEx3038 [pDS834 (Pnmur-3(Δ)::GBP::sax-7) 20		
	ng/µL]		
OJ8127	vjEx2749 [pUC247 (Pnmur-3(Δ)::kin-2a(G310D)) 50 ng/μL]	Fig. 4a	This paper

OJ9150	lite-1(ce314) gur-3(ok2245) X; vjEx2548; vjEx2987 [pUC247	Fig. 3b-e	This paper
	(Pnmur-3(Δ)::kin-2a(G310D)) 50 ng/μL]		
OJ8824	lite-1(ce314) gur-3(ok2245) frpr-17(vj265) X; vjEx2548;	Fig. 3b-e	This paper
	vjEx2871 [pUC273 (Pnmur-3(Δ)::kin-1a(H96Q,W205R)) 25		
	ng/µL]		
OJ9714	unc-9(e101) X; vjEx3150 [pUC291 (Pnmur-3(Δ)::unc-9	Fig. 4b	This paper
	cDNA::mTurquoise2) 25 ng/µL]	-	
OJ9148	unc-9(e101) X; vjEx3000 [pUC258 (Pmyo-3::unc-9 cDNA)	Fig. 4b	This paper
	10 ng/µL]	-	
OJ9356	vjEx3049 [pUC265 (Pnmur-3(Δ)::frpr-17 cDNA::Venus) 20	Fig. 4c	This paper
	$ng/\mu L + pUC291$ (Pnmur-3(Δ)::unc-9	-	
	cDNA::linker::mTurquoise2) 20 ng/µL + pDS833 (Pnmur-		
	3(Δ)::wdr-23b NLS::mCherry) 20 ng/μL]		
OJ8578	lite-1(ce314) gur-3(ok2245) unc-9(e101) X; vjEx2548	Fig. 4d-f, Fig.	This paper
		S6b	
OJ8615	frpr-21(tm4669) II; lite-1(ce314) gur-3(ok2245) X; vjEx2548	Fig. 5b, c,	This paper
		Fig. S8a-c	
OJ8635	frpr-21(tm4669) II; lite-1(ce314) gur-3(ok2245) frpr-17(vj265)	Fig. 5b, c,	This paper
	X; vjEx2548	Fig. S8c	
OJ8740	frpr-21(tm4669) II; lite-1(ce314) gur-3(ok2245) frpr-17(vj265)	Fig. 5b	This paper
	X; vjEx2548; vjEx2838 [pUC276 (Pnmur-3(Δ)::frpr-21 cDNA)	-	
	25 ng/µL]		
OJ8976	flp-9(yn36) IV; lite-1(ce314) gur-3(ok2245) frpr-17(vj265) X;	Fig. 5b, c,	This paper
	vjEx2548	Fig. S8c	
OJ9653	flp-9(yn36) IV; lite-1(ce314) gur-3(ok2245) frpr-17(vj265) X;	Fig. 5b	This paper
	vjEx2548; vjEx3128 [pMH189 (Pflp-9::flp-9 cDNA) 25 ng/µL]		
OJ9652	flp-9(yn36) IV; lite-1(ce314) gur-3(ok2245) frpr-17(vj265) X;	Fig. 5b	This paper
	vjEx2548; vjEx2867 [pMH351 (Punc-47::flp-9 cDNA) 25		
	ng/µL]		
OJ8977	frpr-21(tm4669) II; flp-9(yn36) IV; lite-1(ce314) gur-	Fig. 5b, Fig.	This paper
	3(ok2245) frpr-17(vj265) X; vjEx2548	S8c	
OJ8875	vjEx2899 [pUC281 (Pnmur-3(Δ)::frpr-21 cDNA::GFP) 25	Fig. 5d	This paper
	ng/µL]		
OJ5929	vjEx1785 [pMH351 (Punc-47::flp-9 cDNA) 25 ng/µL]	Fig. 5e	This paper
OJ6572	frpr-21(tm4669) II; vjEx1785 [pMH351 (Punc-47::flp-9	Fig. 5e	This paper
0.10075	cDNA) 25 ng/µL]		
018975	flp-9(yn36) IV; lite-1(ce314) gur-3(ok2245) X; vjEx2548	Fig. 5C, f,	This paper
0.10050		Fig. S8a-c	
OJ8856	lite-1(ce314) gur-3(ok2245) X; vjEx2548; vjEx2867 [pMH351	Fig. 5f, Fig.	This paper
0.10057	(PUNC-47::fip-9 CDNA) 25 ng/µLj	S8a, D	T his man an
018821	trpr-21(tm4669) II; lite-1(ce314) gur-3(0k2245) X; VJEX2548;	Fig. 51	i nis paper
0.10.400	VJEX2807 [plvIH351 (Punc-4711p-9 cDNA) 25 flg/µL]	Fig. Ef	This non or
039400	IIIE-1(CE314) GUI-3(OK2243) X, VJEX2340, VJEX2030 [DUC270	FIG. DI	This paper
0.0017	(Phillul-3(Δ)IIpI-21 CDNA) 25 Hg/μL] from 21(tm 4660) II: lite 1(20214) gur 2(2(2245) X: μiEx2548;	Fig. 5f	This paper
039017	11p1-21(1114009) 11, 11e-1(ce314) gui-3(0k2243) A, VJEX2340,	FIQ. 51	This paper
0 18202	vj=x2636 [p0C276 (P111101-3(Д)11p1-21 cDNA) 25 lig/µLj	Fig S7h c	This paper
018570	$lite_1(ce314)$ gur-3(ok2245) nmur-3(vi353) A, VjEX2546	Fig. 57b, c	This paper
000019	viEx2548	1 19. 07.0	This paper
0,18617	srd-32(vi308) V: lite-1(ce314) gur-3(ok2245) X: viEv2548	Fig S7b c	This naper
0,19403	srd-32(vi308) V: lite-1(ce314) aur-3(ok2245) fror-17(vi265)	Fig. S7b, 0	This paper
	X: viEx2548		
OJ8618	npr-23(vi298) [; lite-1(ce314) aur-3(ok2245) X ⁻ viFx2548	Fig. S7b. c	This paper
OJ8637	npr-23(vj298) I; lite-1(ce314) gur-3(ok2245) frpr-17(vi265) X:	Fig. S7b	This paper
	viEx2548		1 6
OJ8616	T11F9.1(ok2284) V; lite-1(ce314) gur-3(ok2245) X;	Fig. S7b, c	This paper
	viEx2548		

OJ8636	T11F9.1(ok2284) V; lite-1(ce314) gur-3(ok2245) frpr-17(vj265)	Fig. S7b	This paper
	X; vjEx2548		
OJ8638	frpr-4(ok2376) II; lite-1(ce314) gur-3(ok2245) X; vjEx2548	Fig. S7b, c	This paper
OJ8639	frpr-4(ok2376) II; lite-1(ce314) gur-3(ok2245) frpr-17(vj265) X;	Fig. S7b	This paper
	vjEx2548		
OJ9615	unc-25(e156)	Fig. S7d	This paper
OJ9616	unc-25(e156) III; lite-1(ce314) gur-3(ok2245) frpr-17(vj265) X;	Fig. S7d	This paper
	vjEx2548		
OJ9617	dmsr-1(sy1522) V; lite-1(ce314) gur-3(ok2245) X; vjEx2548	Fig. S8d	This paper
OJ9618	dmsr-1(sy1522) V; lite-1(ce314) gur-3(ok2245) frpr-17(vj265)	Fig. S8d	This paper
	X; vjEx2548		
OJ9619	dmsr-7(sy1539) V; lite-1(ce314) gur-3(ok2245) X; vjEx2548	Fig. S8d	This paper
OJ9620	dmsr-7(sy1539) V; lite-1(ce314) gur-3(ok2245) frpr-17(vj265)	Fig. S8d	This paper
	X; vjEx2548		
OJ9586	egl-6(n4537) X; vjEx2548	Fig. S8d	This paper
OJ9592	egl-6(n4537) frpr-17(vj265) X; vjEx2548	Fig. S8d	This paper
OJ9622	frpr-8(sy1362) X; vjEx2548	Fig. S8d	This paper
OJ9629	frpr-8(sy1362) frpr-17(vj265) X; vjEx2548	Fig. S8d	This paper

Supplementary Table 2: Oligonucleotides used in this study

Sequence		Oligos	Source
nmur-3(3kb) promoter	forward	ccccccGCATGCctgtttcaagattcgggaca	[3]
	reverse	cccccCCCGGGATCCggcttcaattagttgtgtca	1
nmur-3(1kb) promoter	forward	cccccGCATGCgcgtgagcaaaatctatgttg	This paper
	reverse	cccccCCCGGGATCCggcttcaattagttgtgtca	1
<i>nmur-3(Δ)</i> promoter	forward	cccccGCATGCctgtttcaagattcgggaca	This paper
	reverse	cccccCCCGGGATCCcaacgagttgaacgtgtgtt	
arg-1 promoter	forward	ccccGCATGCaagagtttaagacgtcgca	This paper
	reverse	ccccGGATCCctttaatgatgtctagtag	
egl-18 basal promoter	forward	cccccGGATCCctccatagtagtacattttaaggt	[3]
	reverse	cccccCCCGGGatagactgtgtggagacac	
flp-9 promoter	forward	cccccGCATGCgcatgatgagaacgaatttaatc	This paper
	reverse	cccccGGATCCttttttcttctttgaaacaaaaatg	
ICE	forward	CCCCCCgctagcAAAAatggccgacaaggtcctg	This paper
	reverse	CCCCCCggtaccttaatgtcctgggaagaggtag	
ТеТх	forward	CCCCCCGCTAGCAAAAatgccgatcaccatcaacaac	This paper
	reverse	cccccGCGGCCGCttaagcggtacggttgtacagg	
flp-22 cDNA	forward	CCCCCCgctagcAAAAATGAACCGTTCCATGATTG	This paper
	reverse	CCCCGGTACCttaATAATCCTGTTCAGAAACTG	
frpr-17 cDNA	forward	ccccgctagcaaaaATGGATGATTCCGTGGATATTTATG	This paper
	reverse	CCCCggtaccTCAAATAAGTACCTCTGGTTG	
PH domain::miniSOG	forward	cccccgctagcaaaaATGGACTCGGGTAGGGACTTCC	This paper
	reverse	cccccGCGGCCGCttatccggaagatcctccatc	
SL2::mCherry	forward	CCCCCCgcggccgcGCTGTCTCATCCTACTTTCAC	This paper
	reverse	CCCCCggtaccTTACTTGTACAGCTCGTCCA	
frpr-21 cDNA	forward	CCCCGCTAGCaaaaATGGATCAAATAACAAGCAC	This paper
	reverse	CCCCGGTACCTTACGAGCTGTTCGTCTCG	
flp-9 cDNA	forward	CCCCGCTAGCaaaaATGAATCAATTTTATGC	This paper
-	reverse	CCCCGGTACCCtaCTTTCTTCCAAATCGAAC	
For 3' terminal			
fusion with Venus,			
GFP, mCherry, or			
linker::mTurquoise2	6		
War-230 NLS	forward	CTAGCAAAAatgeettacaaaagaeatteetetteaaatetga	I his paper
		aaaggA	4
	reverse		
	6	tTTTTG	
IIPT-IT CUNA	Torward		1 ms paper
	forward		This near
	lorward	CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	ms paper
	reverse	CCCCCCaccggtCACGTCGTGCATTTTTCCTTC	
frpr-21 cDNA	forward	CCCCGCTAGCaaaaATGGATCAAATAACAAGCAC	This paper
	reverse	CCCCACCGGTCGAGCTGTTCGTCTCGATG	
For flp-22			
cDNA::pHluorin::flp-			
22 cDNA			
flp-22 5' fragment	forward	CCCCCCgctagcAAAAATGAACCGTTCCATGATTG	This paper
	reverse	GACGGGGAcctaggcttACCGGTACCGAATCGCATCCATTTGG	
flp-22 3' fragment	forward	GATTCGGTACCGGTaagcctaggTCCCCGTCAGCCAAATGG	This paper
	reverse	CCCCGGTACCttaATAATCCTGTTCAGAAACTG	
pHluorin	forward	CCCCCACCGGTAGTAAAGGAGAAGAACTTTTC	This paper
	reverse	CCCCCCcctaggTTTGTATAGTTCATCCATGCC	

Supplementary References

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