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SUPPLEMENTARY INFORMATION

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Olfaction regulates organismal proteostasis and longevity via microRNA-dependent signalling

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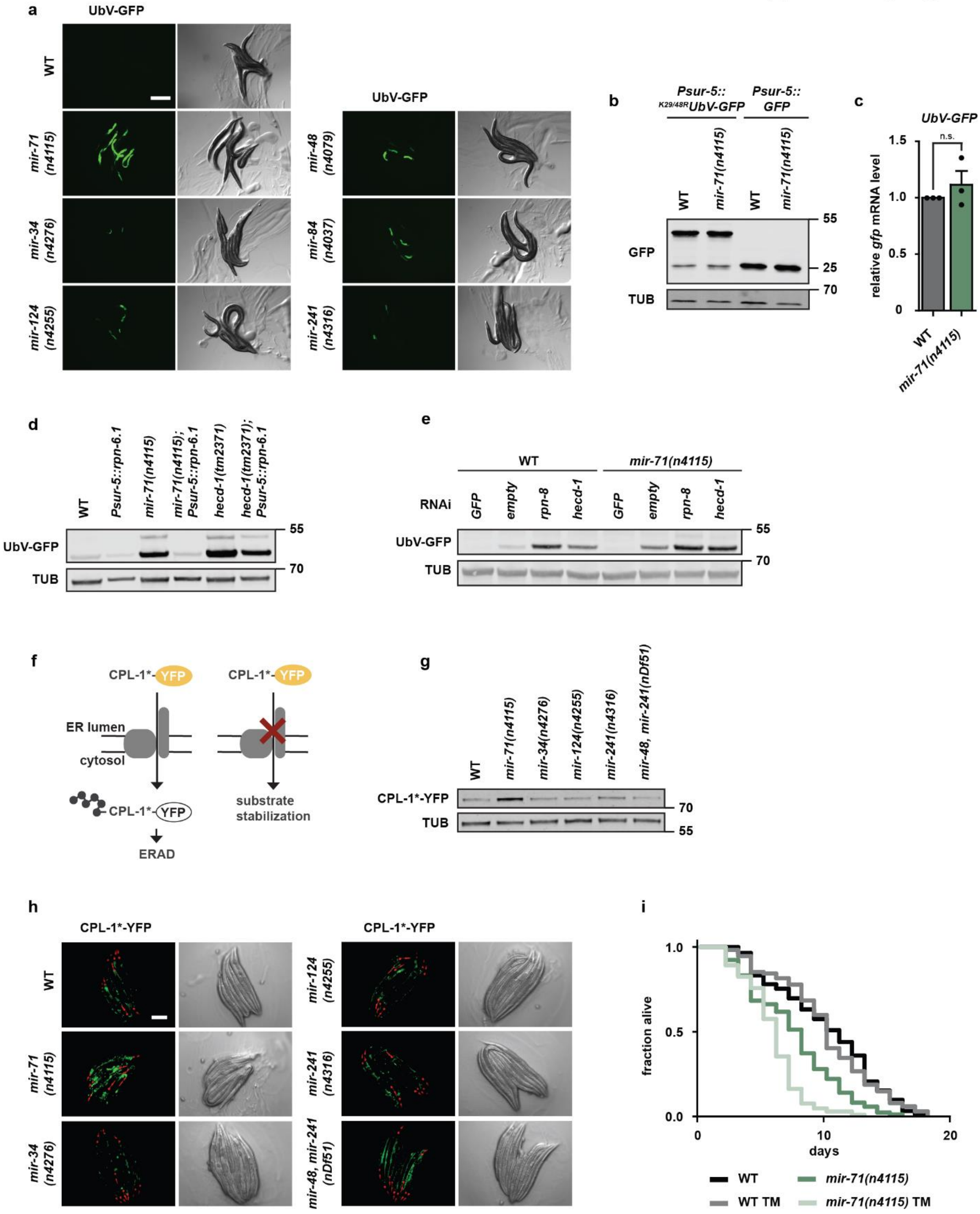
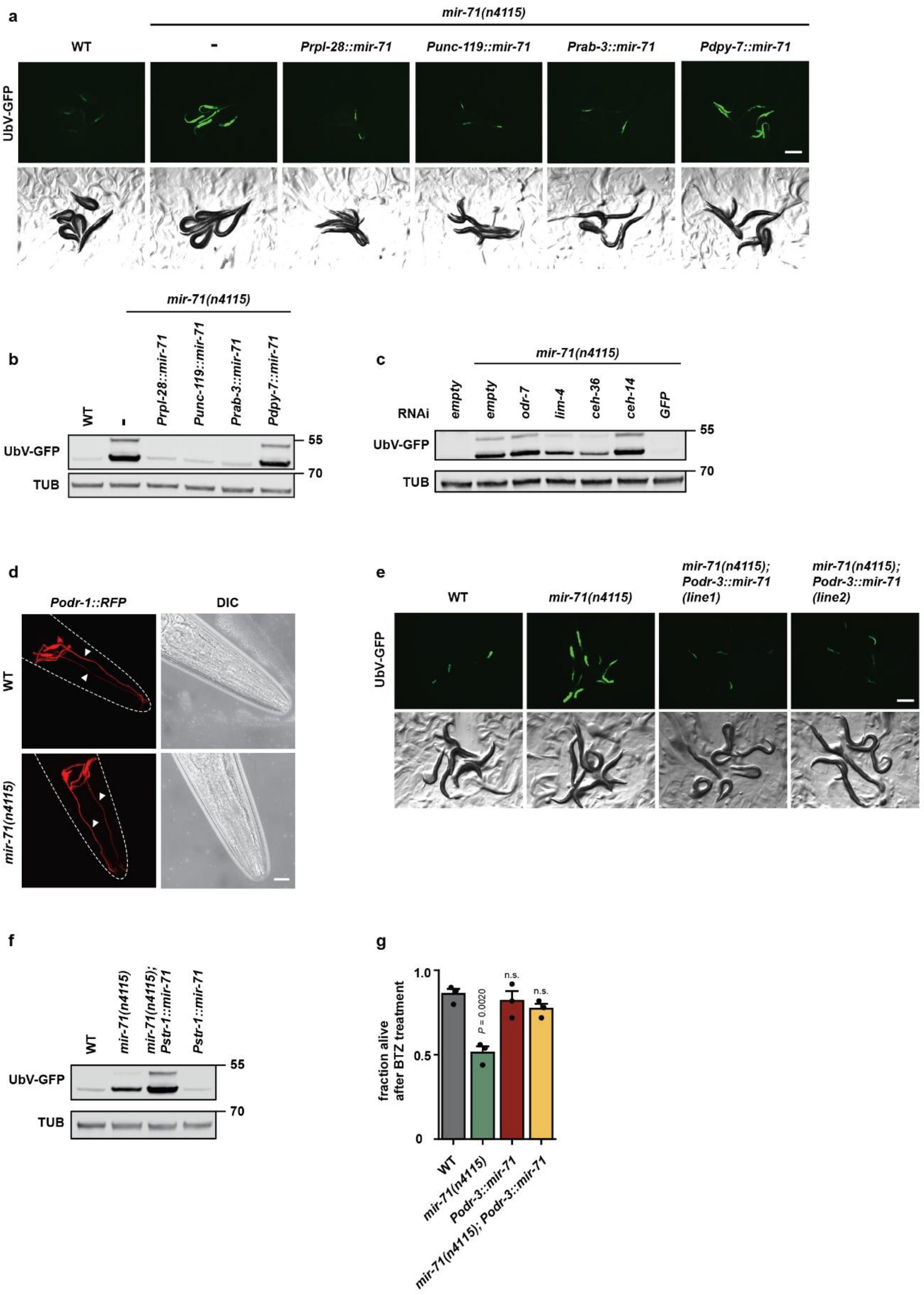
Supplementary Figure 1



Supplementary Figure 1 | Functional proteostasis requires the microRNA *mir-71*.

a, The *mir-71(n4115)* deletion allele exhibits stabilization of the UFD substrate. Fluorescent images of day 1 adult worms with indicated genotypes. Scale bar: 300 µm. **b**, Accumulation of the UFD substrate *Psur-5::UbV-GFP* in *mir-71(n4115)* is not a consequence of changes in gene expression. Western blot of worm lysates of indicated genotypes detect UbV-GFP, GFP, and tubulin (TUB). **c**, *UbV-GFP* mRNA levels are not increased in *mir-71(n4155)* mutant worms as tested by qRT-PCR. Data normalized to wild-type (WT). Bars show mean values ± SEM obtained from n=3 biological replicates with 3 technical replicates each (mean values represented by dots); statistics were determined by two-tailed paired Student's t-test; ns=not significant). **d**, *mir-71* affects UFD substrate degradation downstream of ubiquitylation. Western blot from worm lysates with indicated genotypes showing UbV-GFP and tubulin (TUB) levels. **e**, Inhibition of proteasomal degradation in *mir-71(n4115)* worms further elevates UFD substrate levels. Western blot depicting UbV-GFP and tubulin (TUB) in RNAi-depleted worms lacking *rpn-8* or *hecd-1*. **f**, The CPL-1*-YFP model substrate for studying ER-associated protein degradation (ERAD). **g**, The *mir-71(n4115)* deletion mutant accumulates the ERAD substrate. Western blot of worms imaged in (**h**) detecting CPL-1*-YFP and tubulin (TUB). **h**, Fluorescent images of day 1 adult worms expressing the ERAD substrate (CPL-1*-YFP); pharyngeal expression of *Pmyo-2::mCherry* served as transgenic marker. Scale bar: 250 µm. **i**, *mir-71(n4115)* exhibits increased sensitivity to ER stress induced by tunicamycin (TM) treatment (50 µg/µl). For statistics details see Supplementary Table 1. **a-b**, **d-e** and **g-h**, Representative data derived from at least 3 independent experiments with similar results. **b**, **d-e**, **g**, Molecular weights are shown in kilodalton (kDa).

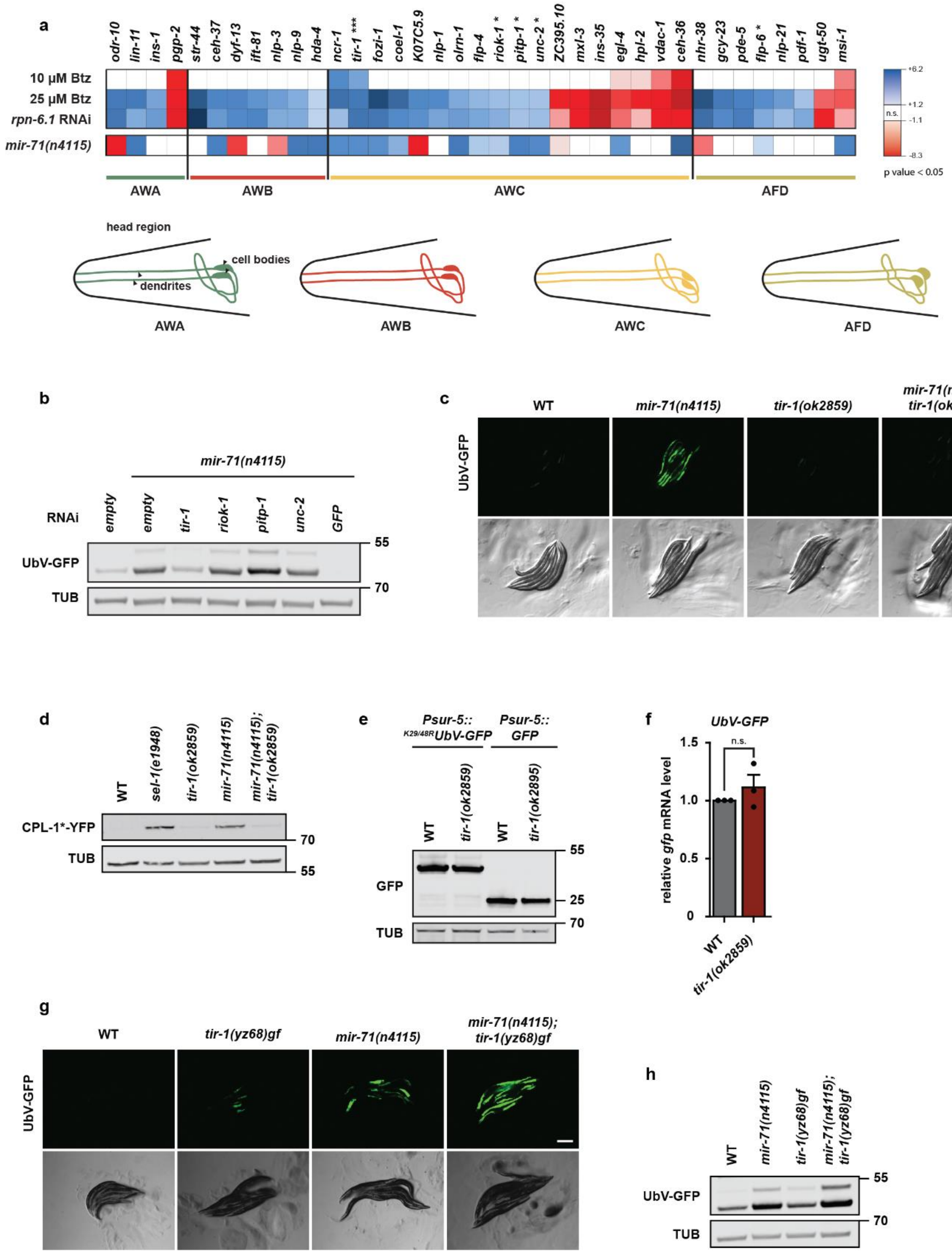
Supplementary Figure 2



Supplementary Figure 2 | Neuron-specific expression of *mir-71* modulates proteostasis.

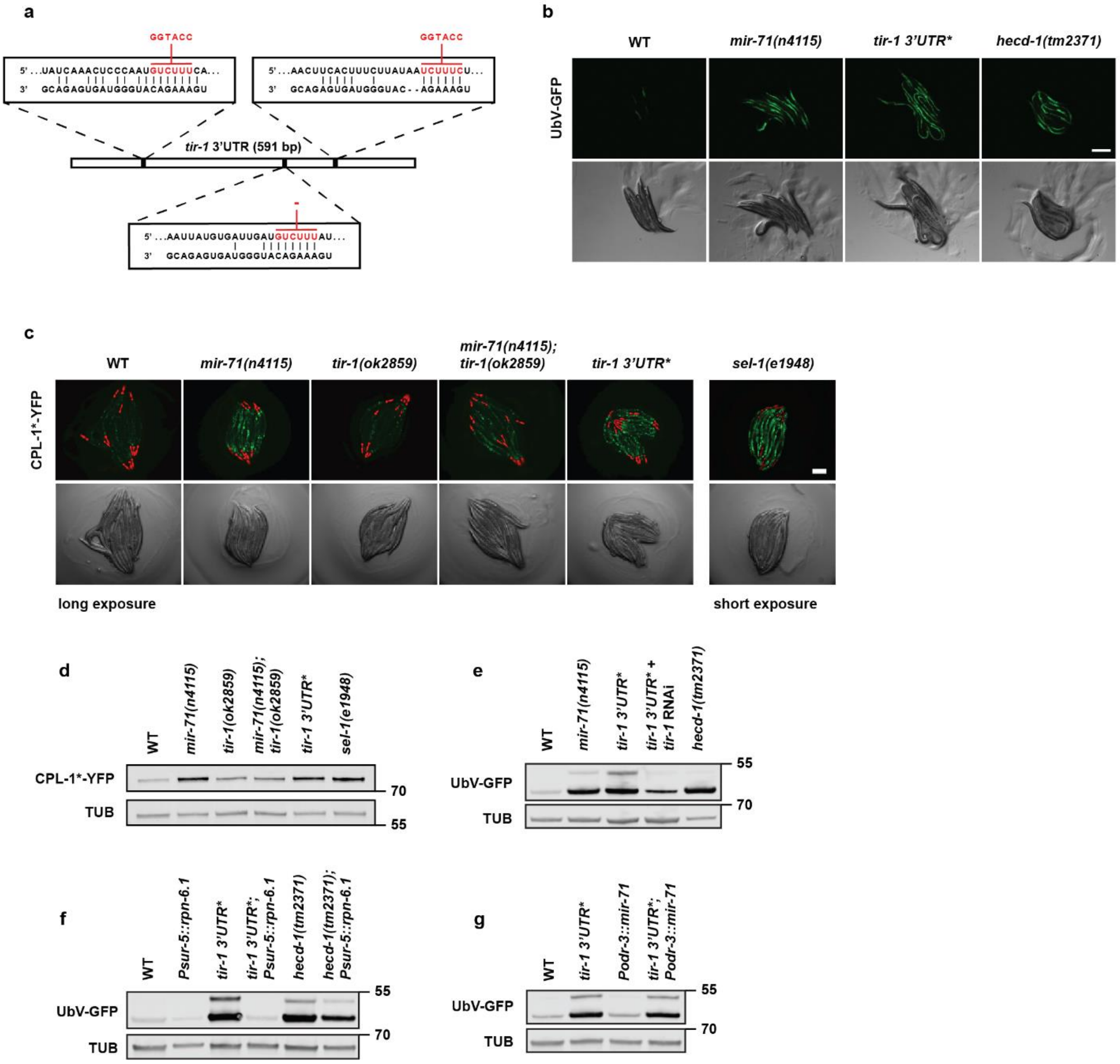
a, Neuronal expression of *mir-71* rescues protein degradation defects of *mir-71(n4115)*. Fluorescent images of day 1 adult *mir-71(n4115)* worms expressing the UFD substrate and the indicated tissue-specific rescue constructs *Prpl-28::mir-71* (ubiquitous), *Punc-119::mir-71* and *Prab-3::mir-71* (both pan-neuronal), *Pdpy7::mir-71* (hypodermal). Scale bar: 300 µm. **b**, Western blot of worms imaged in (**a**) detect UbV-GFP and tubulin (TUB). **c**, Inhibition of neuronal development ameliorates *mir-71(n4115)* proteolytic defects. Western blot of *mir-71(n4115)* worms treated with RNAi against the indicated transcription factors show UbV-GFP and tubulin (TUB) levels. **d**, Deletion of *mir-71* does not affect AWC neuron morphology. Confocal microscopy images show AWC neurons (*Podr-1::RFP*) and differential interference contrast images (DIC) of the *C. elegans* head region. Scale bar: 15 µm. **e**, AWC-specific rescue of the *mir-71(n4115)* deletion mutant (*mir-71(n4115); Podr-3::mir-71*) restores protein degradation. Fluorescent images of day 1 adult worms expressing the UFD substrate. Scale bar: 300 µm. **f**, AWB-specific expression of *mir-71* (*Pstr-1::mir-71*) does not rescue proteostasis defects of *mir-71(n4115)* animals. Representative western blot of worm lysates with the indicated genotypes show UbV-GFP and tubulin (TUB). **a-f**, Representative data derived from at least 3 independent experiments with similar results. **b**, **c**, **f**, Molecular weights are shown in kDa. **g**, AWC-specific expression of *mir-71* increases survival upon proteasome inhibition (BTZ). Bars show mean values ± SEM obtained from n=3 biological replicates using at least 50 worms (mean values represented by dots); statistics were determined by one-way ANOVA with post-hoc test; ns=not significant.

Supplementary Figure 3



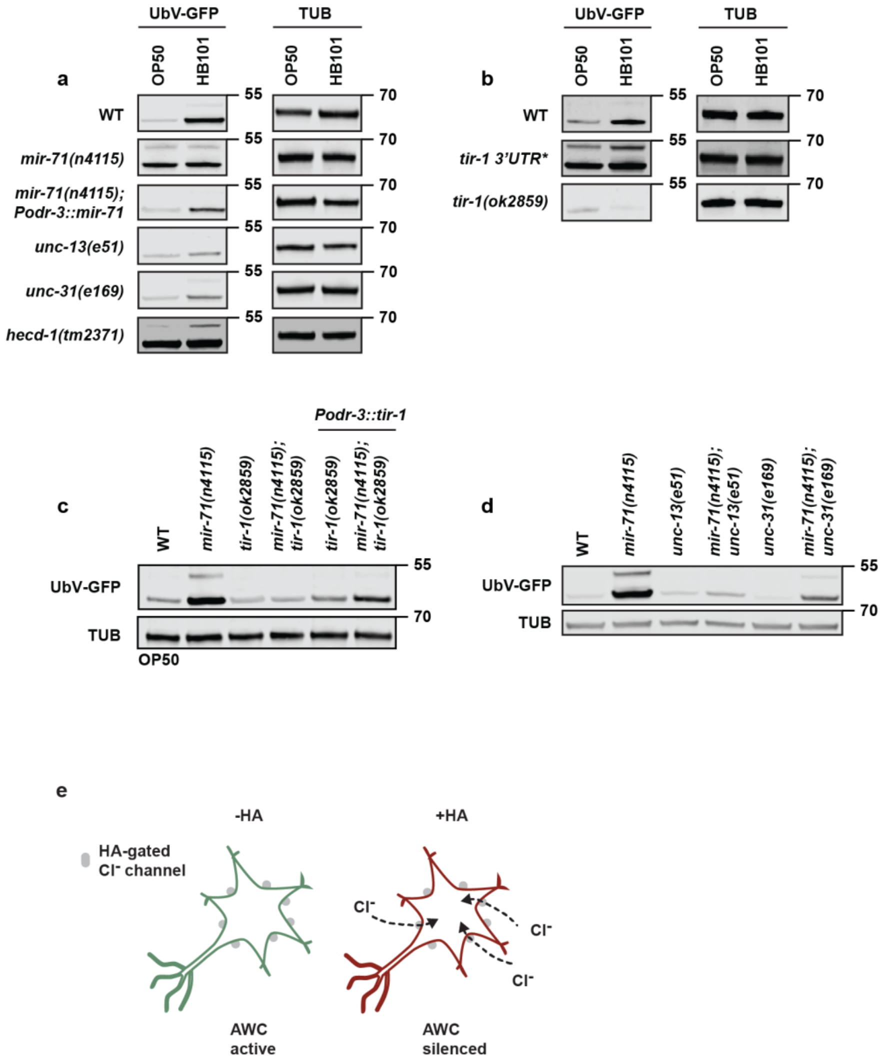
Supplementary Figure 3 | Genetic interaction between *mir-71* and *tir-1* affects proteostasis. a, *tir-1* mRNA levels are upregulated upon induction of proteotoxic stress and in *mir-71(n4115)*. Heat map of mRNA sequencing data for factors present in different chemosensory neurons. A schematic depiction of the investigated amphid sensillum neurons in the *C. elegans* head region is shown at the bottom. Olfactory neurons: AWA = Amphid wing A cell (green), AWB = Amphid wing B cells (red), AWC = Amphid wing C cells (yellow); thermosensory neuron: AFD = Amphid neurons with finger-like (AFD) ciliated endings (light green). mRNA level in wild-type (WT) worms with proteasomal inhibition (10 µM or 25 µM BTZ or *rpn-6.1* RNAi) and in *mir-71(n4115)* deletion mutants are compared to WT (untreated) worms. Asterisks (*) mark candidate transcripts that contain one (*) or up to three (***) potential *mir-71* binding sites; n.s.=not significant. Data derived from n=3 biological replicates **b**, *tir-1* depletion rescues *mir-71(n4115)* proteolytic defects. Western blot of *mir-71(n4115)* worm lysates treated with RNAi against the indicated factors show UbV-GFP and tubulin (TUB) levels. **c**, The *tir-1(ok2859)* deletion allele suppresses *mir-71(n4115)*-induced proteolytic defects. Fluorescent images of day 1 adult worms expressing the UFD substrate. Scale bar: 300 µm. **d**, *tir-1(ok2859)* deletion is able to suppress ERAD substrate (CPL-1*-YFP) stabilization in *mir-71(n4115)* worms. Western blot of worm lysates with indicated genotypes, detect CPL-1*-YFP and tubulin (TUB). **e**, UFD substrate stabilization in the *tir-1(ok2859)* deletion mutant is not caused by changes in gene expression. Western blots from worm lysates show UbV-GFP, GFP, and tubulin (TUB). **f**, *UbV-GFP* transcript levels are not altered by *mir-71* or *tir-1* deletions as detected by qRT-PCR. Data normalized to wild-type (WT). Bars show mean values ± SEM obtained from n=3 biological replicates with 3 technical replicates each (mean values represented by dots); statistics were determined by two-tailed paired Student's t-test; ns=not significant). **g-h**, The *tir-1* gain-of-function allele *tir-1(yz68)gf* leads to mild UPS defects. **g**, Fluorescent images of day 1 adult worms expressing the UFD substrate. Scale bar: 300 µm. **h**, Detection of the GFP signals shown in (**g**) via western blot, showing UbV-GFP and tubulin (TUB) level. **b-e** and **g-h**, Representative data derived from at least 3 independent experiments with similar results. **b**, **d**, **e**, **h**, Molecular weights are shown in kDa.

Supplementary Figure 4



Supplementary Figure 4 | Loss of *mir-71* binding sites in *tir-1* 3'UTR resembles proteolytic defects. **a**, Schematic overview of the *tir-1 3'UTR* sequence with indicated base pairs (bp). Mutated *mir-71* binding sites in *tir-1 3'UTR** are shown in red. **b**, The *tir-1 3'UTR** mutation induces proteolytic defects. Fluorescent images of day 1 adult worms expressing the UFD substrate. Scale bar: 300 µm. **c**, The *tir-1 3'UTR** mutant accumulates the ERAD substrate. Fluorescent images of day 1 adult worms expressing the ERAD substrate (CPL-1*-YFP); pharyngeal expression of *Pmyo-2::mCherry* served as transgenic marker. Scale bar: 250 µm. **d-g**, Western blots from worm lysates of indicated genotypes detect CPL-1*-YFP (**d**), UbV-GFP (**e-f**) and tubulin (TUB) protein level. Molecular weights are shown in kDa. **d**, The *tir-1 3'UTR** mutation affects ERAD. Detection of the fluorescent signals shown in (**c**). **e**, RNAi-mediated *tir-1* depletion rescues UFD substrate stabilization in the *tir-1 3'UTR** mutant. **f**, The *tir-1 3'UTR** mutant triggers proteostasis defects downstream of substrate ubiquitylation. **g**, AWC-specific expression of *mir-71* does not suppress proteostasis defects caused by the *tir-1 3'UTR** mutation. **b-g,** Representative data derived from at least 3 independent experiments with similar results.

Supplementary Figure 5

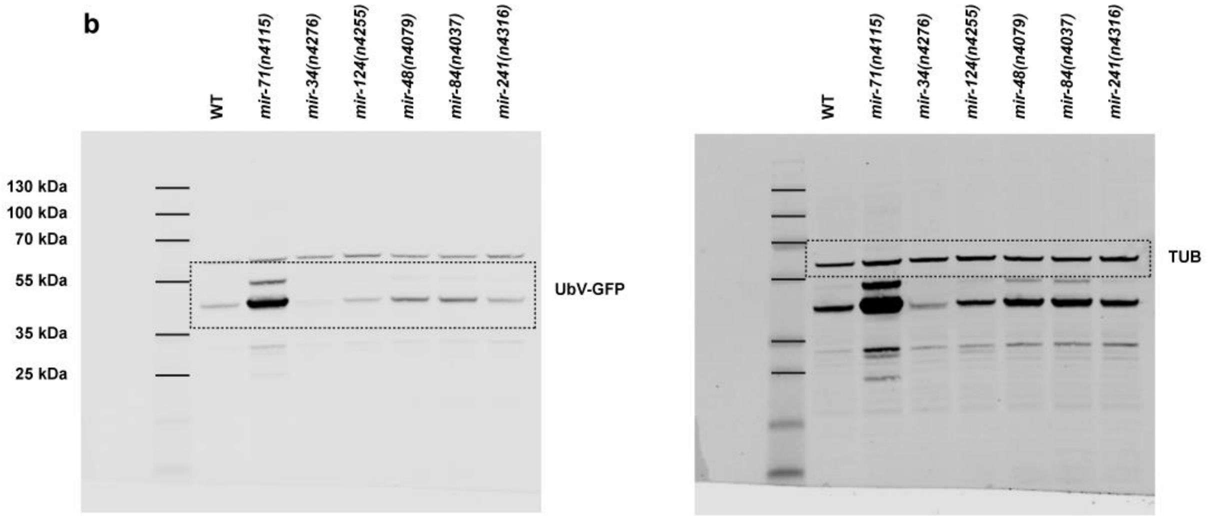


Supplementary Figure 5 | Neuronal signaling facilitates *mir-71/tir-1* regulation of proteostasis. a-b, Different food sources influence organismal protein degradation through *mir-71/tir-1* regulation. Animals were grown on indicated bacteria prior to lysis for western blotting. Western blots from day 1 adult worms of indicated genotypes show UbV-GFP and tubulin (TUB) level. **c**, AWC-specific *tir-1* expression is important for food perception and proteostasis. Animals were grown on OP50 bacteria prior to worm lysis. Western blot of worm lysates with the indicated genotypes detecting UbV-GFP and tubulin (TUB) level. **d**, Inhibition of neuronal signal transduction suppresses *mir-71(n4115)* proteolytic defects. Western blot from worm lysates with indicated genotypes show UbV-GFP and tubulin (TUB) protein levels. **a-d**, Representative data derived from at least 3 independent experiments with similar results. **e**, Shematic depiction of AWC silencing by histamine-gated chloride channel expression (*Pceh-36::HisCl*).

Supplementary Figure 6

uncropped blots related to Fig. 1:

b



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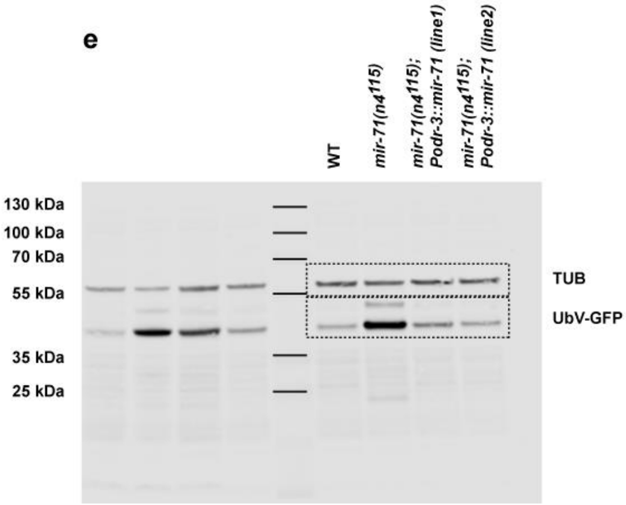

Supplementary Figure 6 (continued)

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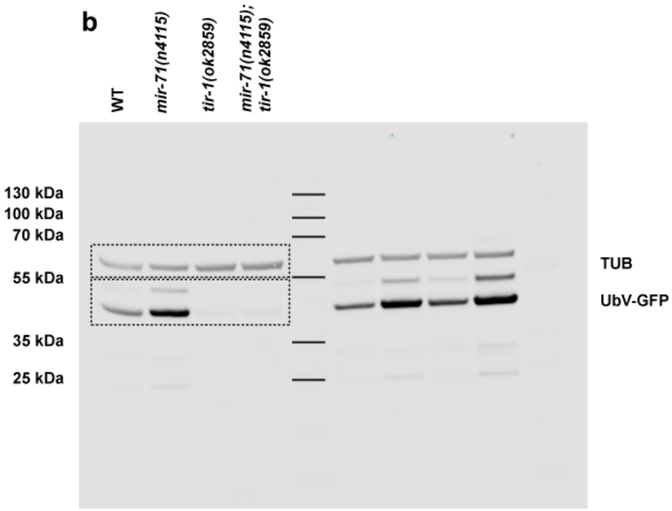

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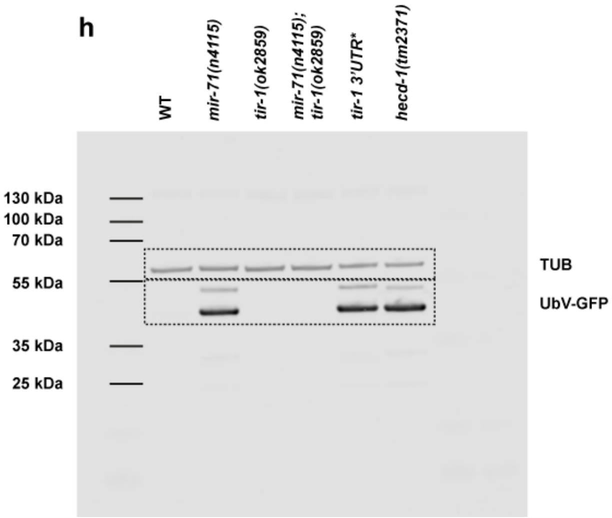

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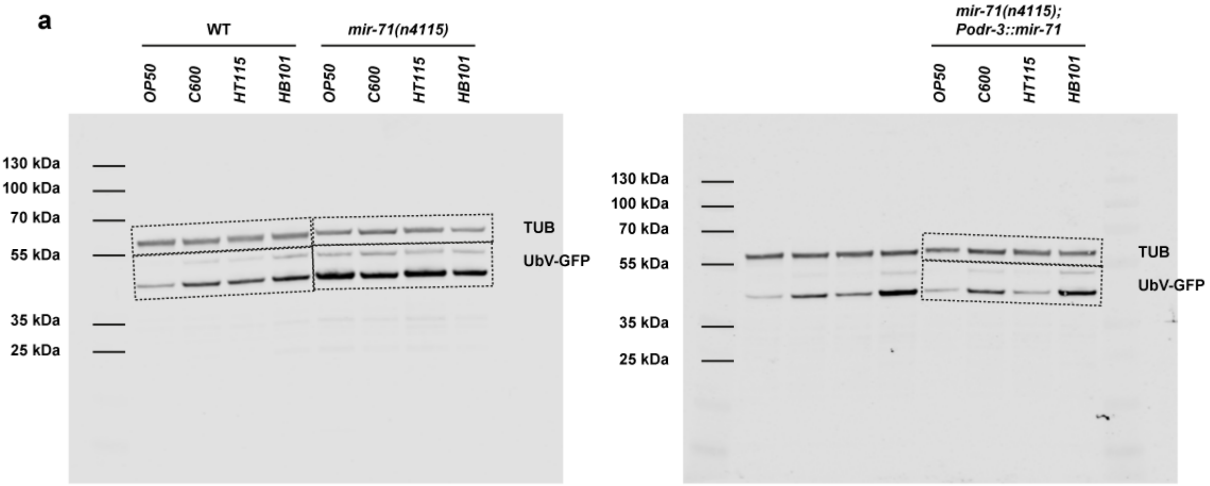

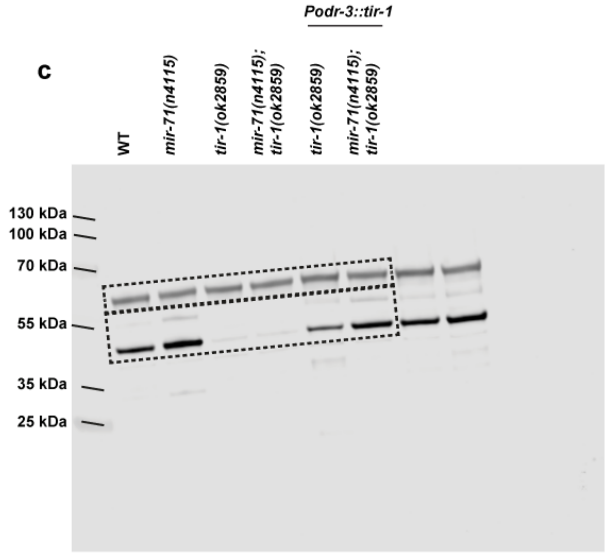

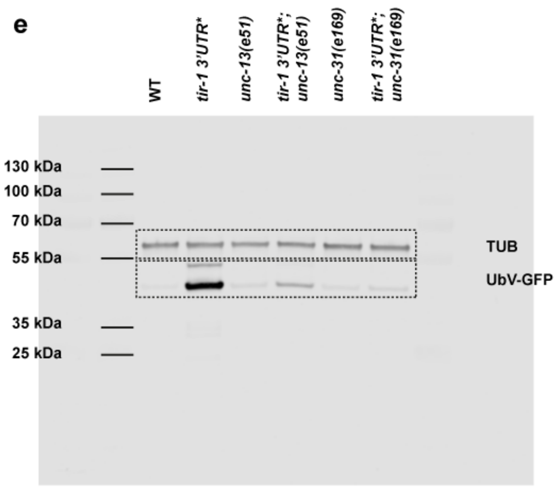

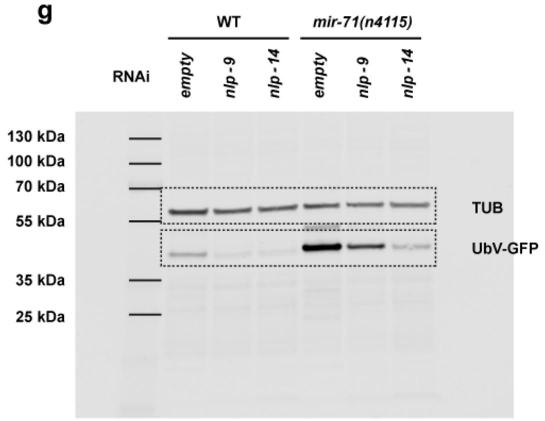

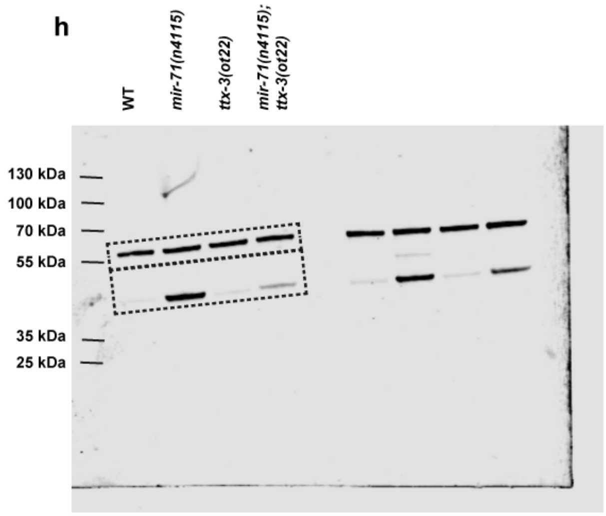

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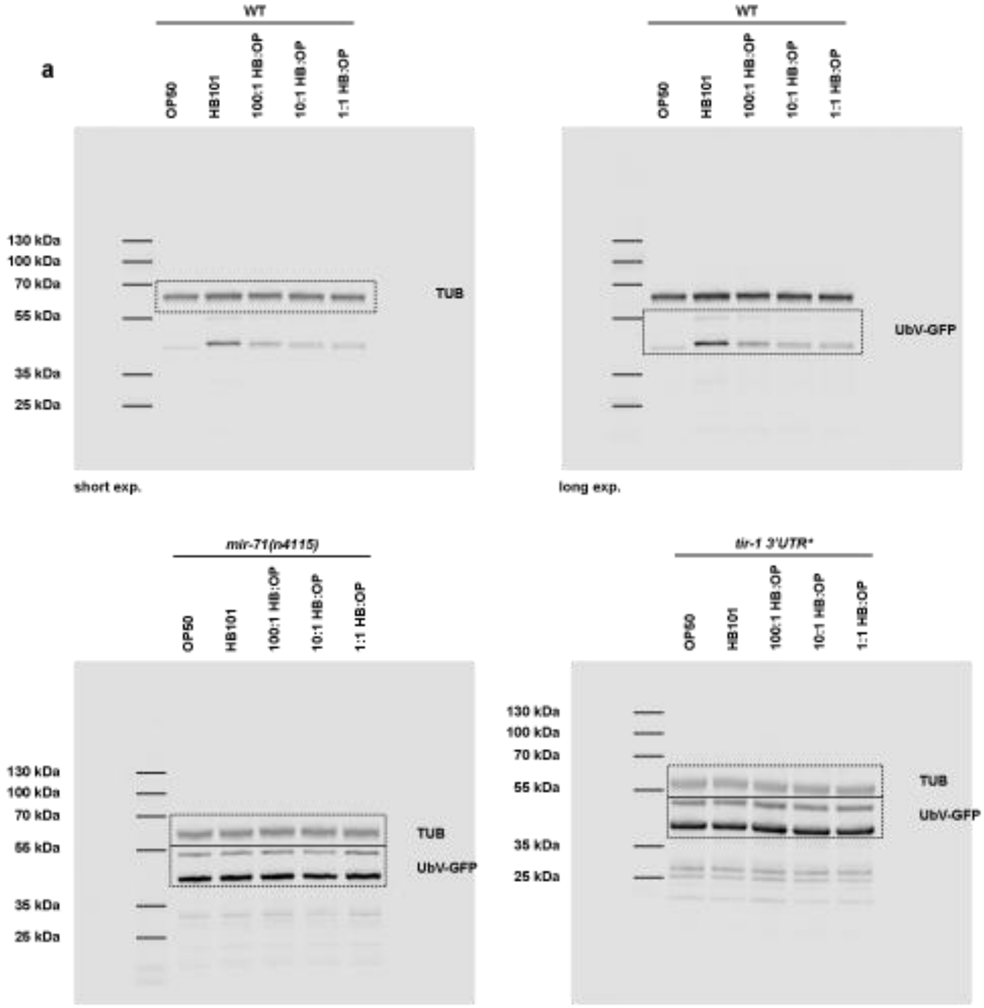

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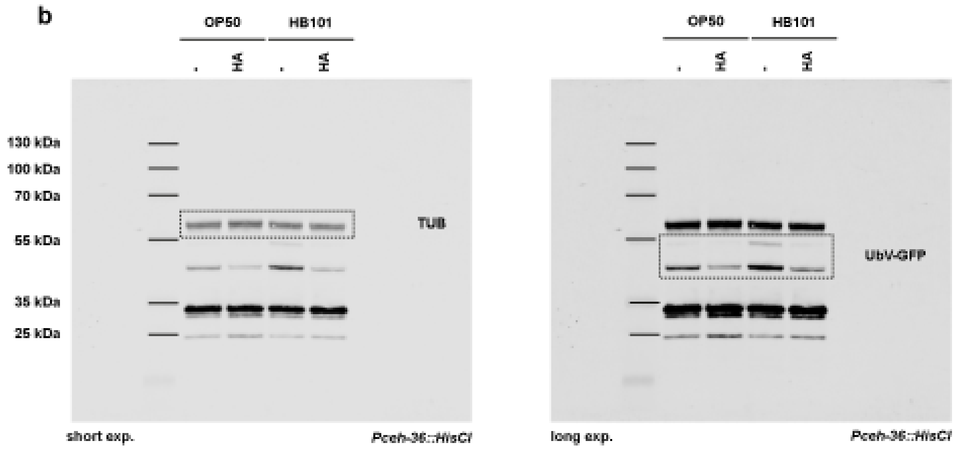

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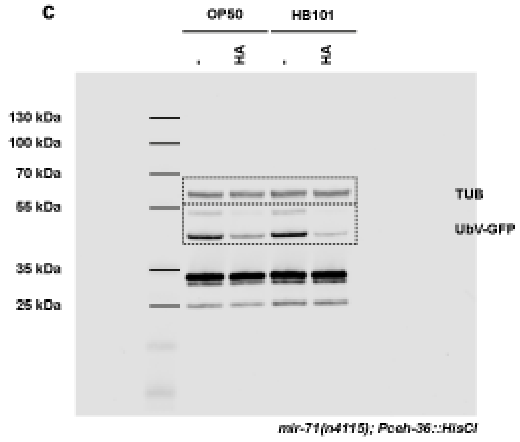

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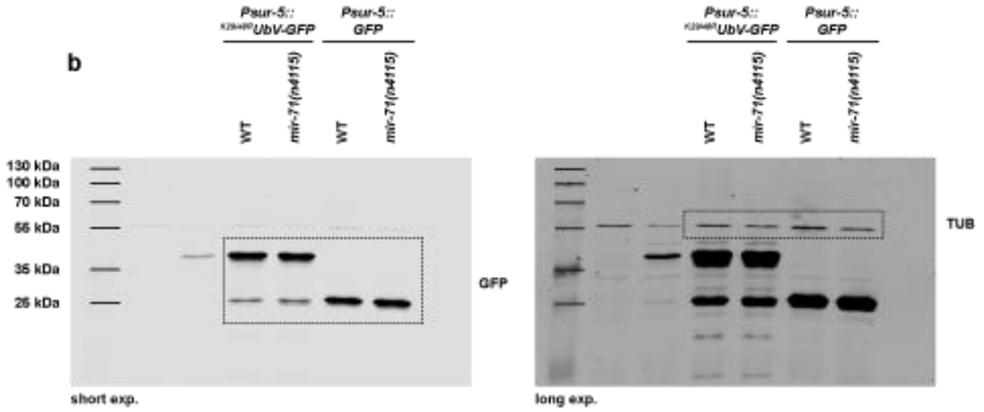

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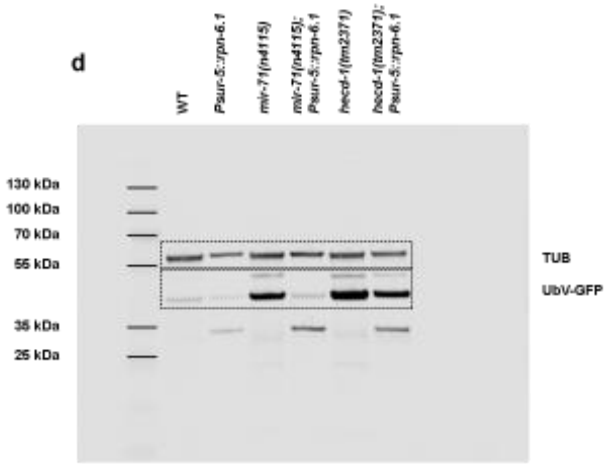

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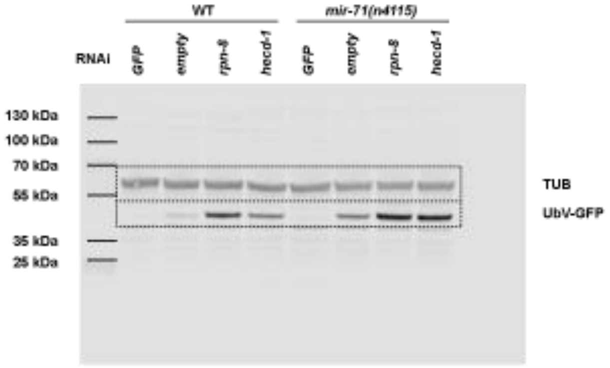

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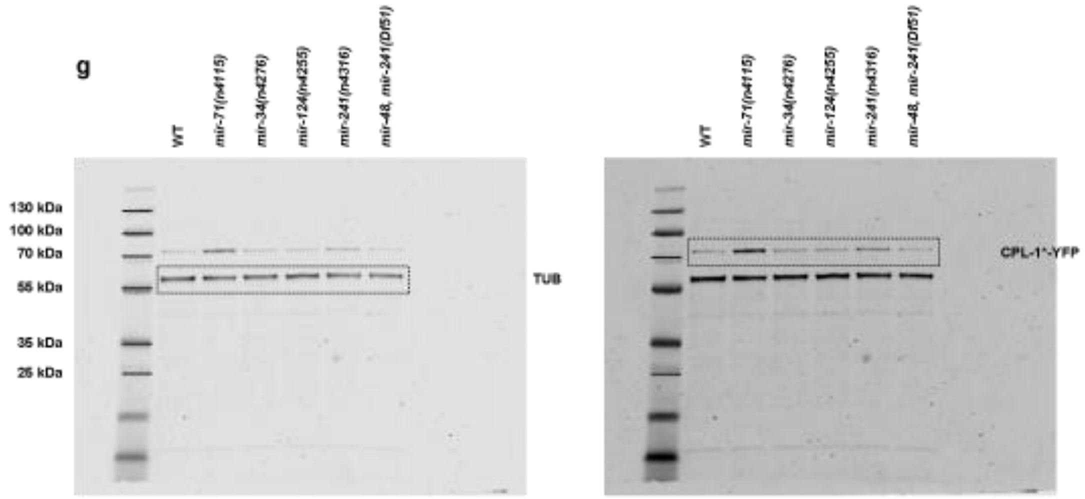

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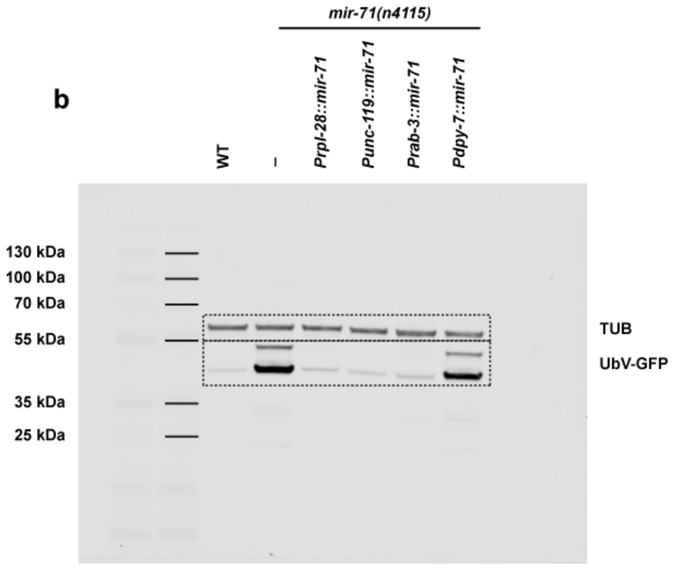

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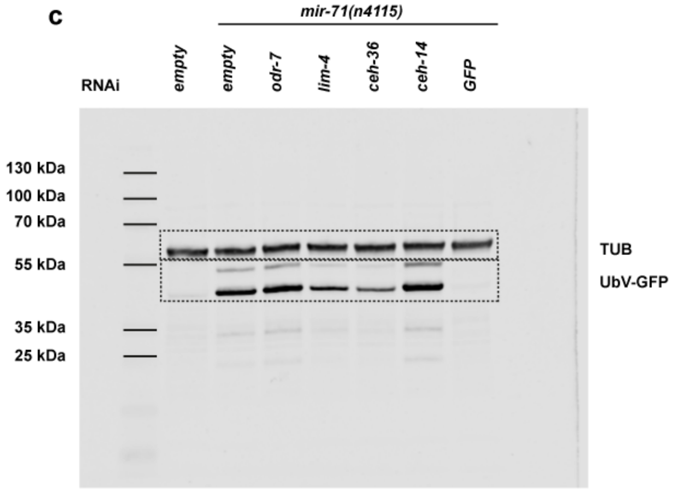

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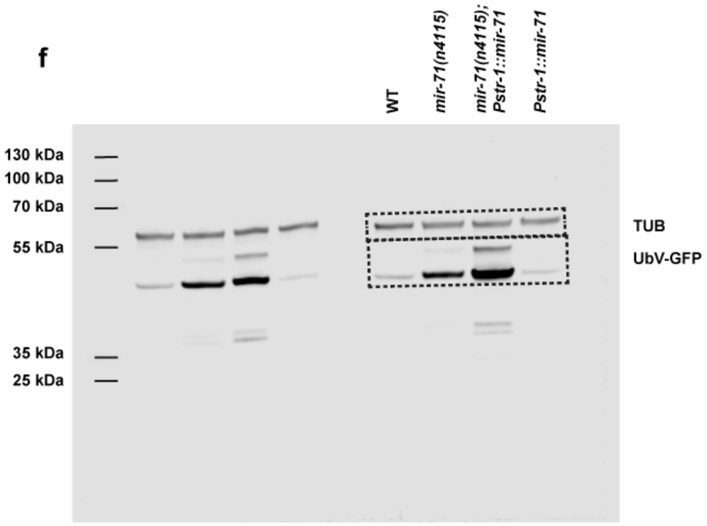

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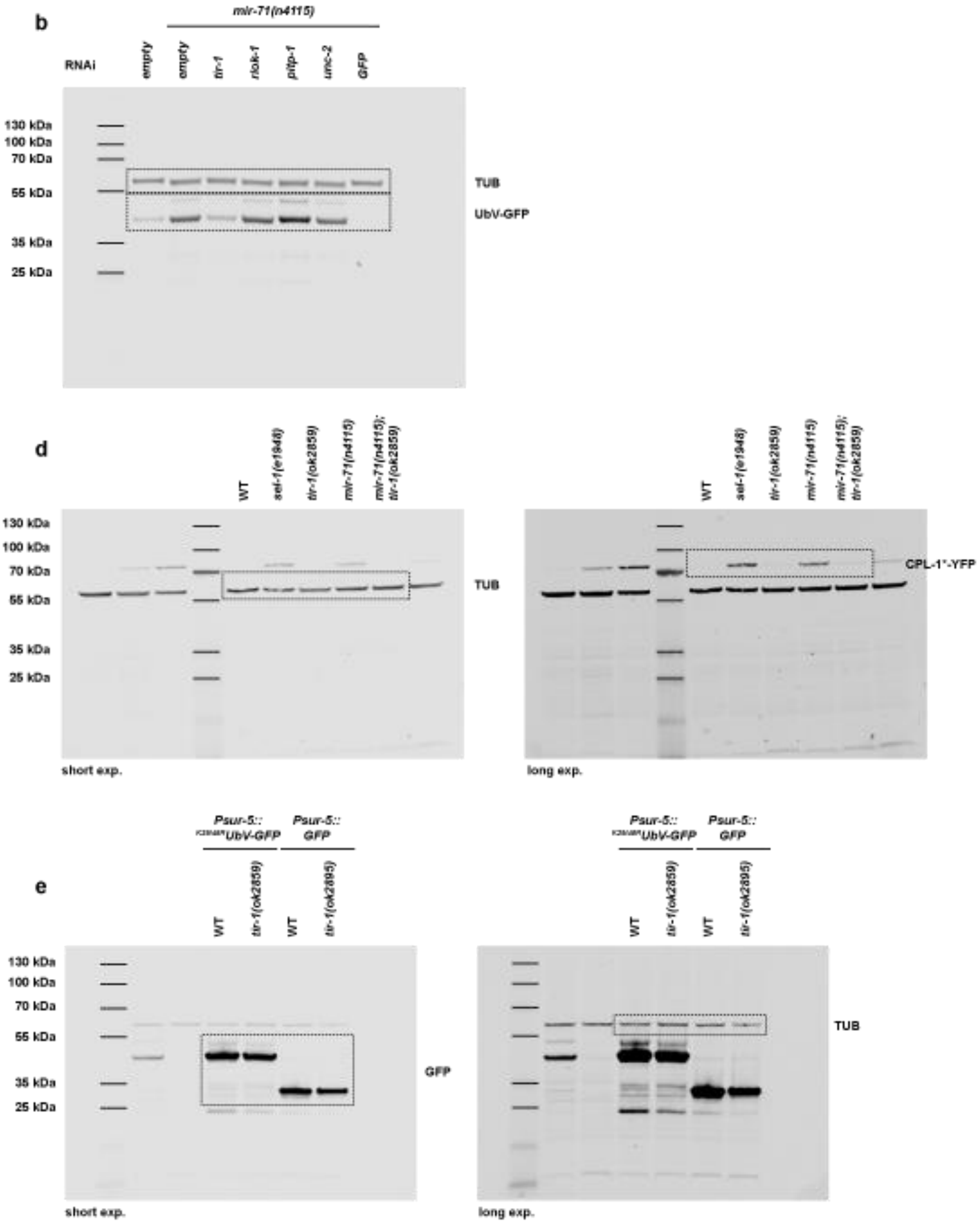

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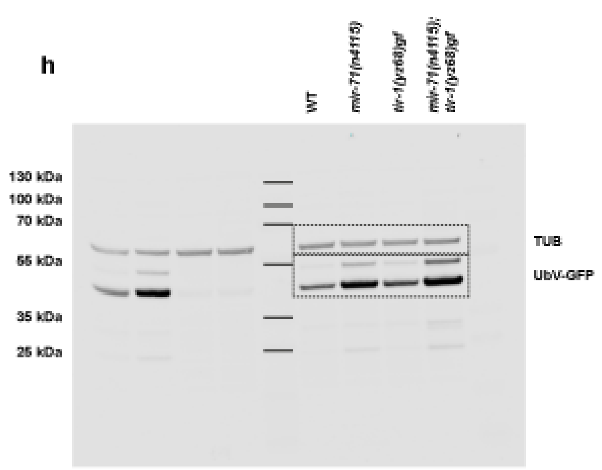

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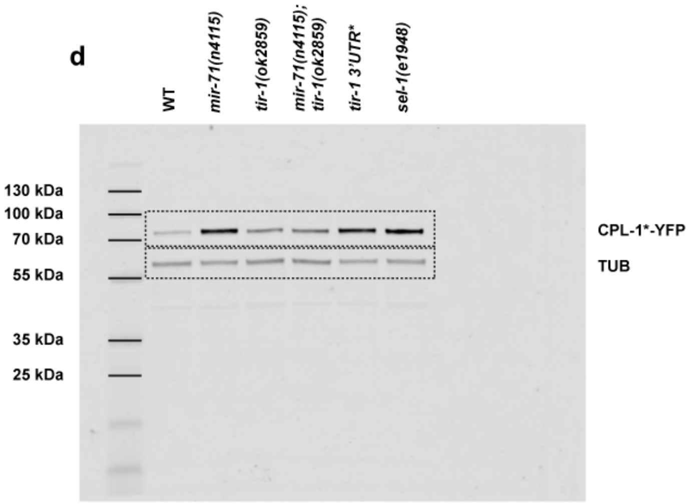

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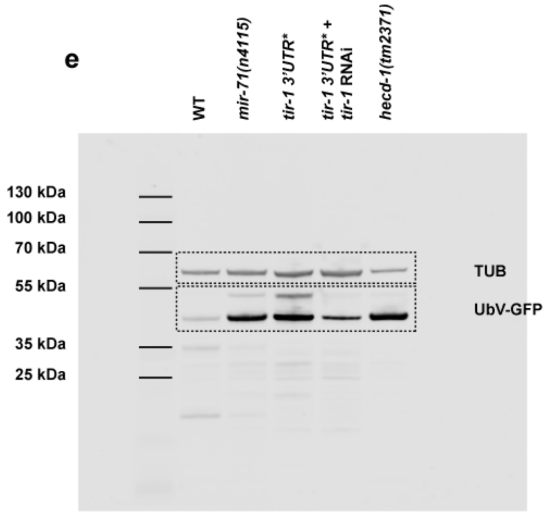

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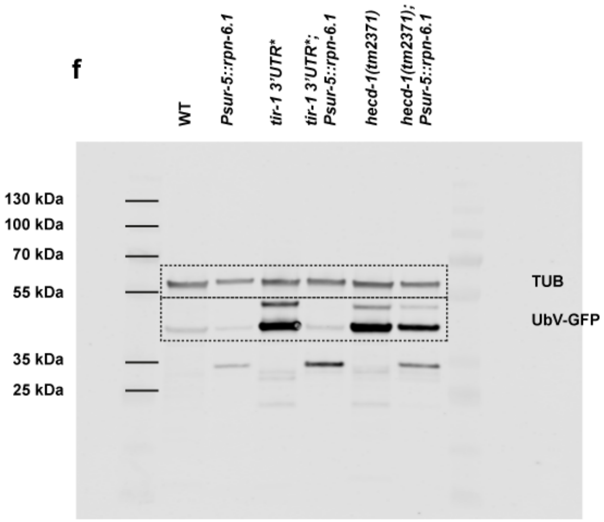

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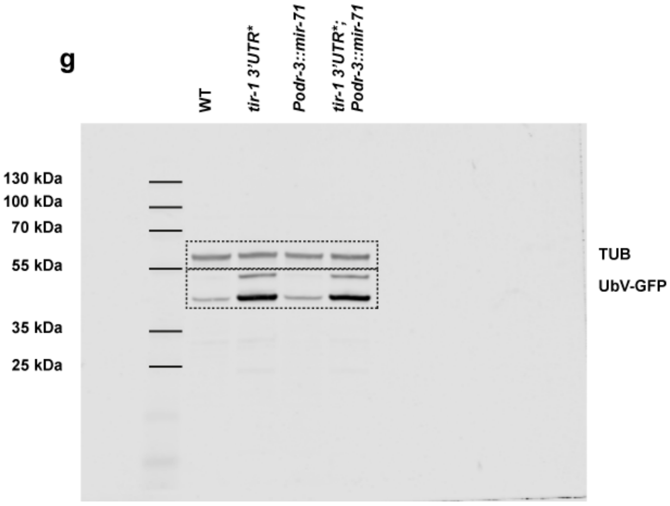

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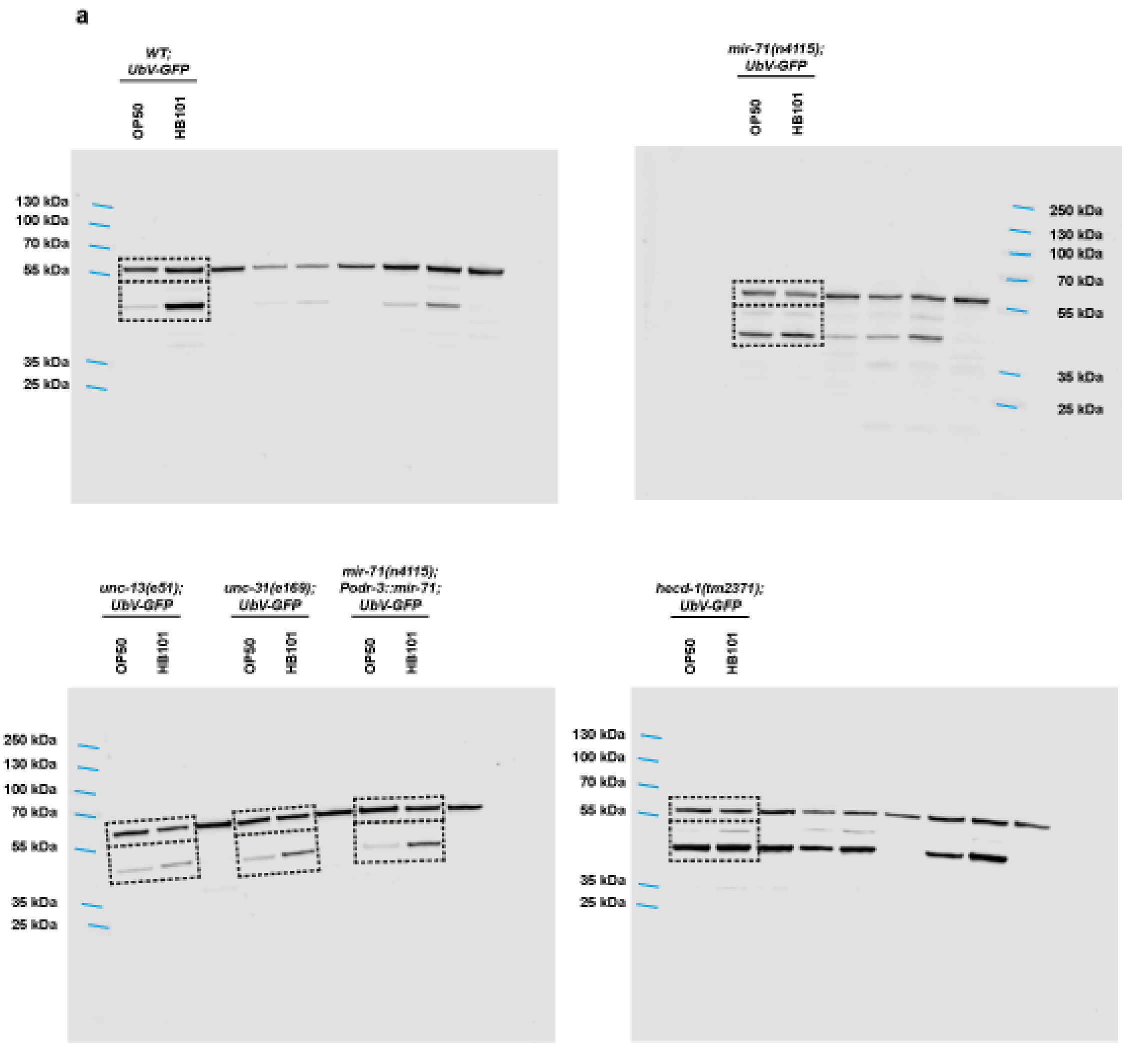

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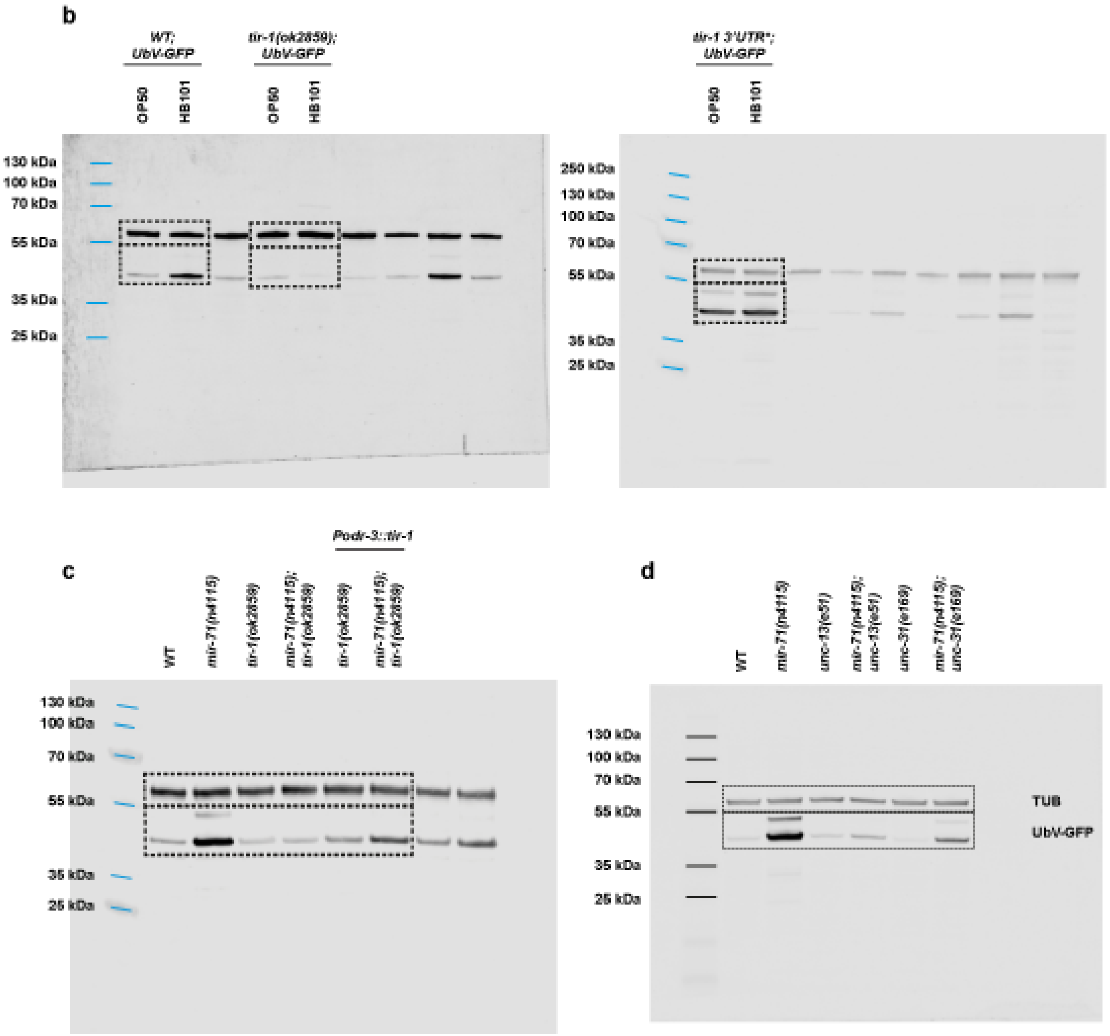

Supplementary Table 1

Summary of lifespan experiments

Statistics were determined by using a two-sided Log-rank (Mantel-Cox) test

20°C	Genotype	Median Lifespan (Days)	% increase median lifespan	Log Rank P Value	Total Animals Died/Total	% increase median lifespan compared to *mir-71(n4115)* mutant	Log Rank P Value compared to *mir-71(n4115)* mutant	% increase median lifespan compared to *mir-71(n4115); odr-3p::mir-71* mutant	Log Rank P Value compared to *mir-71(n4115); odr-3p::mir-71* mutant
(exp. 1)	WT	17			95/102				
	mir-71(n4115)	10,00	-41,18	< 0,0001	92/100				
	mir-71(n4115); odr-3p::mir-71	22,00	29,41	< 0,0001	94/100	120,00	< 0,0001		
	Podr-3::mir-71	22,00	29,41	< 0,0001	91/100			0,00	0,2132
(exp. 2)	WT	16,5			95/100				
	mir-71(n4115)	9,00	-45,45	< 0,0001	86/98				
	mir-71(n4115); odr-3p::mir-71	21,00	27,27	< 0,0001	94/101	133,33	< 0,0001		
	Podr-3::mir-71	22,00	33,33	< 0,0001	88/99			4,76	0,2923

20°C	Genotype	Median Lifespan (Days)	% increase median lifespan	Log Rank P Value	Total Animals Died/Total
(exp. 1)	WT	11,00			90/102
	WT TM	10,00	-9,09	0,7964	92/105
	mir-71(n4115)	8,00	-20,00	0,0001	72/90
	mir-71(n4115) TM	6,00	-25,00	< 0,0001	98/105
(exp. 2)	WT	12,00			89/111
	WT TM	11,00	-8,33	0,0076	102/111
	mir-71(n4115)	9,00	-18,18	0,0002	65/104
	mir-71(n4115) TM	7,00	-22,22	< 0,0001	94/117

20°C, 25uM FuDR	Genotype	Median Lifespan (Days)	% increase median lifespan	Log Rank P Value	Total Animals Died/Total	% increase median lifespan compared to *mir-71(n4115)* mutant	Log Rank P Value compared to *mir-71(n4115)* mutant	% increase median lifespan compared to *tir-1(ok2859)* mutant	Log Rank P Value compared to *tir-1(ok2859)* mutant
(exp. 1)	WT	20,00			88/100				
	mir-71(n4115)	11,00	-45,00	< 0,0001	93/100				
	tir-1(ok2859)	17,00	-15,00	< 0,0001	91/99				
	mir-71(n4115); tir-1(ok2859)	15,00	-25,00	< 0,0001	95/102	36,36	< 0,0001	-11,76	0,0001
(exp. 2)	WT	20,00			93/99				
	mir-71(n4115)	12,00	-40,00	< 0,0001	91/99				
	tir-1(ok2859)	17,00	-15,00	0,0003	92/102				
	mir-71(n4115); tir-1(ok2859)	14,00	-30,00	< 0,0001	96/101	16,67	< 0,0001	-17,65	< 0,0001

20°C	Genotype	Median Lifespan (Days)	% increase median lifespan	Log Rank P Value	Total Animals Died/Total	% increase median lifespan compared to *tir-1 3'UTR**) mutant	Log Rank P Value compared to *tir-1 3'UTR**) mutant
(exp. 1)	WT	19,00			96/99		
	*tir-1 3'UTR**	12,00	-36,84	< 0,0001	91/99		
	*tir-1 3'UTR** + *tir-1* RNAi	17,00	-10,53	0,0009	97/100	41,67	< 0,0001
(exp. 2)	WT	19,00			95/100		
	*tir-1 3'UTR**	12,00	-36,84	< 0,0001	95/98		
	*tir-1 3'UTR** + *tir-1* RNAi	17,00	-10,53	0,0006	94/100	41,67	< 0,0001

Supplementary Table 2

mRNAs regulated in amphid sensory neurons upon proteasomal stress and *mir-71(n4415)* deletion

			RNA sequencing						microarray	
Ensembl ID	**gene symbol**	**neuron type**	**fold change 10µM Btz vs. WT**	**p-value**	**fold change 25µM Btz vs. WT**	**p-value**	**fold change *rpn-6.1* RNAi vs. WT**	**p-value**	**fold change *mir-71(n4115)* vs. WT**	**p-value**
WBGene00003856	***odr-10***	**AWA**	n.s.	n.s.	2,77	0,001685	2,98	0,000786	-2,32	0,00243081
WBGene00003000	***lin-11***	**AWA**	n.s.	n.s.	2,76	0	1,51	0,041323	2,73	0,00176989
WBGene00002084	***ins-1***	**AWA**	n.s.	n.s.	1,57	0,016922	1,64	0,009464	n.s.	n.s.
WBGene00003996	***pgp-2***	**AWA**	-1,78	0	-3,47	0	-4,17	0	n.s.	n.s.
WBGene00006109	***str-44***	**AWB**	n.s.	n.s.	4,58	0,015927	6,19	0,001763	n.s.	n.s.
WBGene00000458	***ceh-37***	**AWB**	n.s.	n.s.	2,22	0,006025	1,66	0,007874	2,39	0,00534378
WBGene00001129	***dyf-13***	**AWB**	n.s.	n.s.	2,18	0,010645	1,95	0,03587	-1,62	0,00542693
WBGene00017973	***ift-81***	**AWB**	n.s.	n.s.	1,70	0,019075	2,23	0,000342	n.s.	n.s.
WBGene00003741	***nlp-3***	**AWB**	n.s.	n.s.	1,62	0,000242	1,51	0,001688	-1,38	0,0178225
WBGene00003747	***nlp-9***	**AWB**	n.s.	n.s.	1,50	0,000468	1,51	0,001966	2,92	0,000274251
WBGene00001837	***hda-4***	**AWB**	n.s.	n.s.	1,21	0,013735	1,20	0,012942	2,91	0,00482287
WBGene00003561	***ncr-1***	**AWC**	1,86	0,000139	3,35	0	1,37	0,039385	1,79	0,0137333
WBGene00006575	***tir-1***	**AWC**	1,57	0,00001	2,91	0	3,10	0	1,77	0,000123714
WBGene00010453	***fozi-1***	**AWC**	n.s.	n.s.	5,23	0	3,00	0,000054	1,74	0,0204151
WBGene00016866	***coel-1***	**AWC**	n.s.	n.s.	3,81	0	1,89	0	1,48	0,00406593
WBGene00010632	***K07C5.9***	**AWC**	n.s.	n.s.	2,01	0,001793	1,72	0,014334	-2,14	0,00228023
WBGene00003739	***nlp-1***	**AWC**	n.s.	n.s.	1,95	0,000355	1,55	0,0243	n.s.	n.s.
WBGene00007260	***olrn-1***	**AWC**	n.s.	n.s.	1,52	0,000933	1,63	0,000119	2,76	0,000826669
WBGene00001447	***flp-4***	**AWC**	n.s.	n.s.	1,43	0,018755	1,54	0,012192	1,27	0,0390078
WBGene00019698	***riok-1***	**AWC**	n.s.	n.s.	1,36	0	1,49	0	1,25	0,0391208
WBGene00010813	***pitp-1***	**AWC**	n.s.	n.s.	1,33	0,046276	1,32	0,037686	2,53	0,00347053
WBGene00006742	***unc-2***	**AWC**	n.s.	n.s.	1,32	0,041702	1,36	0,022473	1,93	8,46742E-06
WBGene00022599	***ZC395.10***	**AWC**	n.s.	n.s.	-1,92	0	-1,31	0,000215	-1,11	0,0478619
WBGene00003511	***mxl-3***	**AWC**	n.s.	n.s.	-2,53	0,0001	-3,46	0	n.s.	n.s.
WBGene00002118	***ins-35***	**AWC**	n.s.	n.s.	-8,32	0,002031	-7,84	0,001585	n.s.	n.s.
WBGene00001173	***egl-4***	**AWC**	-1,15	0,000524	-1,62	0	-1,46	0	1,68	0,00804379
WBGene00001996	***hpl-2***	**AWC**	-1,14	0,04841	-1,82	0	-1,23	0,004517	n.s.	n.s.
WBGene00019900	***vdac-1***	**AWC**	-1,42	0	-2,82	0	-2,04	0	n.s.	n.s.
WBGene00000457	***ceh-36***	**AWC**	-5,08	0,000454	-8,12	0,000291	-2,63	0,037317	3,90	0,00266951
WBGene00003629	***nhr-38***	**AFD**	n.s.	n.s.	4,79	0,006025	3,52	0,048148	-1,44	0,0436177
WBGene00001548	***gcy-23***	**AFD**	n.s.	n.s.	2,91	0,000241	1,93	0,025811	n.s.	n.s.
WBGene00016328	***pde-5***	**AFD**	n.s.	n.s.	2,50	0,028109	2,66	0,029989	n.s.	n.s.
WBGene00001449	***flp-6***	**AFD**	n.s.	n.s.	1,77	0	1,51	0	1,15	0,00893673
WBGene00003759	***nlp-21***	**AFD**	n.s.	n.s.	1,64	0,00003	1,37	0,019334	n.s.	n.s.
WBGene00020317	***pdf-1***	**AFD**	n.s.	n.s.	1,32	0,000291	1,52	0	n.s.	n.s.
WBGene00011564	***ugt-50***	**AFD**	n.s.	n.s.	-1,49	0,0062	-1,88	0,000026	n.s.	n.s.
WBGene00003423	***msi-1***	**AFD**	-1,40	0,000342	-1,54	0,000005	-1,28	0,010516	2,23	0,000769833

Supplementary Table 3

RNA-sequencing/Microarray data for potential *mir-71* targets upon proteostoxic stress

			RNA sequencing												microarray	
Ensembl ID	**gene symbol**	**neuron type**	**fold change 25µM Cadmium vs. WT**	**p-value**	**fold change 200µM Cantharidin vs. WT**	**p-value**	**fold change 200µM Fluphenazine vs. WT**	**p-value**	**fold change 10µM Btz vs. WT**	**p-value**	**fold change 25µM Btz vs. WT**	**p-value**	**fold change *rpn-6.1* RNAi vs. WT**	**p-value**	**fold change *mir-71(n4115)* vs. WT**	**p-value**
WBGene00006575	***tir-1***	AWC	1,59	0	3,56	0	2,33	0	1,57	0,00001	2,91	0	3,10	0	1,77	0,000123714
WBGene00019698	***riok-1***	AWC	-1,21	0,024451	n.s.	n.s.	n.s.	n.s.	n.s.	n.s.	1,36	0	1,49	0	1,25	0,0391208
WBGene00010813	***pitp-1***	AWC	n.s.	n.s.	n.s.	n.s.	n.s.	n.s.	n.s.	n.s.	1,33	0,046276	1,32	0,037686	2,53	0,00347053
WBGene00006742	***unc-2***	AWC	n.s.	n.s.	1,41	0,019391	1,47	0,027061	n.s.	n.s.	1,32	0,041702	1,36	0,022473	1,93	8,46742E-06

Supplementary Table 4

Neuropeptide mRNAs regulated upon *mir-71(n4115)* deletion

insulin-like peptides

gene symbol	fold change(*mir-71(n4115)* vs. WT)	p-value
ins-2	-2,2646	0,004975
ins-5	1,8976	0,001525
ins-10	-2,2401	0,005381
ins-12	-3,1031	0,000113
ins-24	2,0026	0,000179
ins-31	-4,6013	0,003063
ins-33	-2,0609	0,002678
ins-34	-2,8311	0,000204

FRMF-like peptides

gene symbol	fold change(*mir-71(n4115)* vs. WT)	p-value
flp-3	1,5704	0,000391
flp-8	-1,6706	0,007151
flp-12	-1,8135	0,003158
flp-15	-2,0221	0,003966
flp-16	1,6139	0,002402
flp-17	-2,0482	0,002479
flp-22	-2,2135	0,003794
flp-24	-2,0124	0,006178

neuropeptide-like proteins

gene symbol	fold change(*mir-71(n4115)* vs. WT)	p-value
nlp-4	-1,9161	0,000829
nlp-5	-2,9974	0,000056
nlp-9	2,9161	0,000274
nlp-13	1,7180	0,001724
nlp-14	2,3555	0,000402
nlp-17	-1,8117	0,001413
nlp-20	-1,8869	0,009217
nlp-25	-4,4854	0,000144
nlp-26	-1,5791	0,006250
nlp-27	-2,3196	0,001470
nlp-28	-3,0186	0,000266
nlp-29	-4,5787	0,002695
nlp-30	-5,2101	0,006844
nlp-33	-1,7984	0,000068
nlp-34	-2,5120	0,006185
nlp-40	-1,6439	0,000759

Affymetrix EleGene-1_0-st-v1.na34.ce6

≥ 1.5 fold change, p-value ≤ 0,01

Supplementary Table 5

Summary of chemotaxis experiments (part 1)
Statistical analysis was done via one-way ANOVA with post-hoc test for multiple comparison

	Genotype	excluded	# animals LB medium (control)	# animals OP50 (test)	# total animals	Chemotaxis Index (CI)
(exp. 1)	WT	8	26	56	90	0,333
	mir-71(n4115)	4	57	65	126	0,063
	mir-71(n4115); Podr-3::mir-71	21	19	64	104	0,433
	mir-71(n4115); Pstr-1::mir-71	12	87	114	213	0,127
	*tir-1 3'UTR**	21	62	91	174	0,167
	odr-3(n1605)	30	19	17	66	-0,030
(exp. 2)	WT	8	62	88	158	0,165
	mir-71(n4115)	3	49	53	105	0,038
	mir-71(n4115); Podr-3::mir-71	8	77	134	219	0,110
	mir-71(n4115); Pstr-1::mir-71	9	85	109	203	0,118
	*tir-1 3'UTR**	58	101	107	266	0,023
	odr-3(n1605)	45	21	18	84	-0,036
(exp. 3)	WT	23	49	75	147	0,177
	mir-71(n4115)	7	78	93	178	0,084
	mir-71(n4115); Podr-3::mir-71	23	98	165	286	0,234
	mir-71(n4115); Pstr-1::mir-71	9	95	148	252	0,210
	*tir-1 3'UTR**	16	35	58	109	0,211
	odr-3(n1605)	38	27	22	87	-0,057
(exp. 4)	WT	37	57	113	207	0,271
	mir-71(n4115)	64	123	136	323	0,040
	mir-71(n4115); Podr-3::mir-71	29	103	155	287	0,181
	mir-71(n4115); Pstr-1::mir-71	63	82	91	236	0,038
	*tir-1 3'UTR**	58	202	174	434	-0,065
	odr-3(n1605)	97	28	15	140	-0,093
(exp. 5)	WT	42	53	101	196	0,245
	mir-71(n4115)	28	76	96	200	0,100
	mir-71(n4115); Podr-3::mir-71	32	73	146	251	0,291
	mir-71(n4115); Pstr-1::mir-71	44	93	107	244	0,057
	*tir-1 3'UTR**	93	162	199	454	0,081
	odr-3(n1605)	144	16	11	171	-0,029
(exp. 6)	WT	46	46	96	188	0,266
	mir-71(n4115)	57	89	109	255	0,078
	mir-71(n4115); Podr-3::mir-71	35	52	93	180	0,228
	mir-71(n4115); Pstr-1::mir-71	51	68	72	191	0,021
	*tir-1 3'UTR**	108	216	265	589	0,083
	odr-3(n1605)	168	16	16	200	0,000
(exp. 7)	WT	11	110	158	279	0,172
	mir-71(n4115)	9	94	121	224	0,121
	mir-71(n4115); Podr-3::mir-71	9	87	120	216	0,153
	mir-71(n4115); Pstr-1::mir-71	31	87	112	230	0,109
	*tir-1 3'UTR**	15	95	151	261	0,215
	odr-3(n1605)	59	66	80	205	0,068
(exp. 8)	WT	14	74	128	216	0,250
	mir-71(n4115)	12	150	162	324	0,037
	mir-71(n4115); Podr-3::mir-71	18	103	162	283	0,208
	mir-71(n4115); Pstr-1::mir-71	35	145	192	372	0,126
	*tir-1 3'UTR**	31	111	153	295	0,142
	odr-3(n1605)	45	52	49	146	-0,021
(exp. 9)	WT	19	90	171	280	0,289
	mir-71(n4115)	11	127	170	308	0,140
	mir-71(n4115); Podr-3::mir-71	3	70	96	169	0,154
	mir-71(n4115); Pstr-1::mir-71	26	121	146	293	0,085
	*tir-1 3'UTR**	22	118	139	279	0,075
	odr-3(n1605)	62	76	41	179	-0,196

	Genotype	mean Chemotaxis Index	± Standard deviation (SD)	± Standard error (SEM)	p Value compared to WT
	WT	0,241	0,058	0,019	
	mir-71(n4115)	0,078	0,037	0,012	0,0001
	mir-71(n4115); Podr-3::mir-71	0,221	0,096	0,032	0,9999
	mir-71(n4115); Pstr-1::mir-71	0,099	0,057	0,019	0,0004
	*tir-1 3'UTR**	0,104	0,091	0,030	0,0006
	odr-3(n1605)	-0,044	0,072	0,024	0,0001

Supplementary Table 5

Summary of chemotaxis experiments (part 2)

Statistical analysis was done via one-way ANOVA with post-hoc test for multiple comparison

	Genotype	excluded	# animals LB medium (control)	# animals OP50 (test)	# total animals	Chemotaxis Index (CI)
(exp. 1)	WT	42	101	118	261	0,065
	tir-1(ok2859)	52	66	54	172	-0,070
	tir-1(ok2859); Podr-3::tir-1	80	46	65	191	0,099
	tir-1(ok2859); Pnhx-2::tir-1	43	24	20	87	-0,046
(exp. 2)	WT	50	121	147	318	0,082
	tir-1(ok2859)	49	91	93	233	0,009
	tir-1(ok2859); Podr-3::tir-1	64	41	52	157	0,070
	tir-1(ok2859); Pnhx-2::tir-1	38	26	28	92	0,022
(exp. 3)	WT	65	98	128	291	0,103
	tir-1(ok2859)	34	77	69	180	-0,044
	tir-1(ok2859); Podr-3::tir-1	79	26	45	150	0,127
	tir-1(ok2859); Pnhx-2::tir-1	39	24	17	80	-0,088
(exp. 4)	WT	66	104	153	323	0,152
	tir-1(ok2859)	32	61	57	150	-0,027
	tir-1(ok2859); Podr-3::tir-1	95	22	40	157	0,115
	tir-1(ok2859); Pnhx-2::tir-1	35	25	29	89	0,045
(exp. 5)	WT	67	92	145	304	0,174
	tir-1(ok2859)	32	72	66	170	-0,035
	tir-1(ok2859); Podr-3::tir-1	82	37	43	162	0,037
	tir-1(ok2859); Pnhx-2::tir-1	65	19	21	105	0,019
(exp. 6)	WT	52	96	122	270	0,096
	tir-1(ok2859)	34	60	46	140	-0,100
	tir-1(ok2859); Podr-3::tir-1	103	37	49	189	0,063
	tir-1(ok2859); Pnhx-2::tir-1	63	24	23	110	-0,009
(exp. 7)	WT	10	84	112	206	0,136
	tir-1(ok2859)	50	124	129	303	0,017
	tir-1(ok2859); Podr-3::tir-1	73	42	62	177	0,113
	tir-1(ok2859); Pnhx-2::tir-1	100	38	41	179	0,017
(exp. 8)	WT	17	83	119	219	0,164
	tir-1(ok2859)	29	149	141	319	-0,025
	tir-1(ok2859); Podr-3::tir-1	64	48	79	191	0,162
	tir-1(ok2859); Pnhx-2::tir-1	92	42	39	173	-0,017
(exp. 9)	WT	27	106	163	296	0,193
	tir-1(ok2859)	41	144	154	339	0,029
	tir-1(ok2859); Podr-3::tir-1	64	57	78	199	0,106
	tir-1(ok2859); Pnhx-2::tir-1	71	46	51	168	0,030

	Genotype	mean Chemotaxis Index	± Standard deviation (SD)	± Standard error (SEM)	p Value compared to WT
	WT	0,129	0,045	0,015	
	tir-1(ok2859)	-0,027	0,042	0,014	0,0001
	tir-1(ok2859); Podr-3::tir-1	0,099	0,037	0,012	0,2981
	tir-1(ok2859); Pnhx-2::tir-1	-0,003	0,042	0,014	0,0001

Supplementary Table 6

C. elegans strains used in this study

Strain name	**Origin**	**Resource**
C. elegans: Bristol (N2) strain as wild-type (WT)	CGC	Wormbase ID: N2
C. elegans: *unc-119(ed4)III; hhIs64[unc-119(+); Psur-5::UbV-GFP]III*	Segref et al., 2011	N/A
C. elegans: *hhIs113[Pnhx-2::cpl-1*^{W32AW35A}*::yfp; Pmyo-2::mCherry]I*	Hoppe Lab	N/A
C. elegans: *hsf-1(sy441)I*	CGC	Wormbase ID: WBVar00248994
C. elegans: *hhIs111[Pnhx-2::cpl-1*^{W32AW35A}*::gfp]II; sqt-3(sc8) sel-1(e1948)V*	Hoppe Lab	N/A
C. elegans: *hhIs64[unc-119(+); Psur-5::UbV-GFP]III; hecd-1(tm2371)IV*	Segref et al. , 2011	N/A
C. elegans: *hhIs64[unc-119(+); Psur-5::UbV-GFP]III; mir-84(n4037)X*	This study	N/A
C. elegans: *hhIs64[unc-119(+); Psur-5::UbV-GFP]III; mir-124(n4255)IV*	This study	N/A
C. elegans: *hhIs64[unc-119(+); Psur-5::UbV-GFP]III; mir-34(n4276)X*	This study	N/A
C. elegans: *hhIs64[unc-119(+);Psur-5::UbV-GFP]III; mir-241(n4316)V*	This study	N/A
C. elegans: *hhIs64[unc-119(+);Psur-5::UbV-GFP]III; mir-71(n4115)I*	This study	N/A
C. elegans: *hhIs64[unc-119(+);Psur-5::UbV-GFP]III; mir-48(n4097)V*	This study	N/A
C. elegans: *hhIs113[Pnhx-2::cpl-1*^{W32AW35A}*::yfp; Pmyo-2::mCherry]I; mir-241(n4316)V*	This study	N/A
C. elegans: *hhIs113[Pnhx-2::cpl-1*^{W32AW35A}*::yfp; Pmyo-2::mCherry]I; mir-124(n4255)IV*	This study	N/A
C. elegans: *hhIs113[Pnhx-2::cpl-1*^{W32AW35A}*::yfp; Pmyo-2::mCherry]I; mir-34(n4276)X*	This study	N/A
C. elegans: *hhIs113[Pnhx-2::cpl-1*^{W32AW35A}*::yfp; Pmyo-2::mCherry]I; mir-71(n4115)I*	This study	N/A

Strain name	**Origin**	**Resource**
C. elegans: *hhIs113[Pnhx-2::cpl-1*^{W32AW35A}*::yfp; Pmyo-2::mCherry]I; lin-58&mir-241(nDf51)V*	This study	N/A
C. elegans: *mir-71(n4115)I*	CGC	Wormbase ID: WBVar00090803
C. elegans: *unc-119(ed4)III; hhIs64[unc-119(+); Psur-5::UbV-GFP]III; uthEx556[Psur-5::rpn-6.1; Pmyo-3::GFP]*	Hoppe lab	N/A
C. elegans: *mir-71(n4115)I; uthEx556[Psur-5::rpn-6.1; Pmyo-3::GFP]; hhIs64 [unc-119(+); Psur-5::UbV-GFP]III*	This study	N/A
C. elegans: *hecd-1(tm2371)IV; uthEx556[Psur-5::rpn-6.1; Pmyo-3::GFP]; hhIs64 [unc-119(+); Psur-5::UbV-GFP]III*	This study	N/A
C. elegans: *hhIs53[unc-119(+); Psur-5::K29/48R-UbV-GFP]*	Segref et al., 2011	N/A
C. elegans: *mir-71(n4115)I; hhIs53 [unc-119(+); Psur-5::K29/48R-UbV-GFP]III*	This study	N/A
C. elegans: *hhIs57[unc-119(+); Psur-5::GFP]III*	Segref et al., 2011	N/A
C. elegans: *mir-71(n4115)I; hhIs57 [unc-119(+); Psur-5::GFP]III*	This study	N/A
C. elegans: *mir-71(n4115)I; hhIs64[unc-119(+); Psur-5::UbV-GFP]III; nEx1802[Prpl-28::mir-71 + pRF4]*	This study	N/A
C. elegans: *mir-71(n4115)I; hhIs64 [unc-119(+); Psur-5::UbV-GFP]III; nEx1823[Punc-119::mir-71 + pRF4]*	This study	N/A
C. elegans: *mir-71(n4115)I; hhIs64 [unc-119(+); Psur-5::UbV-GFP]III; nEx1825[Prab-3::mir-71 + pRF4]*	This study	N/A
C. elegans: *mir-71(n4115)I; hhIs64 [unc-119(+); Psur-5::UbV-GFP]III; nEx1805[Pdpy-7::mir-71 + pRF4]*	This study	N/A
C. elegans: *unc-13(e51)I; hhIs64[unc-119(+); Psur-5::UbV-GFP]III*	This study	N/A
C. elegans: *mir-71(n4115)I; unc-13(e51)I; hhIs64[unc-119(+); Psur-5::UbV-GFP]III*	This study	
C. elegans: *unc-31(e169)IV; hhIs64[unc-119(+); Psur-5::UbV-GFP]III*	This study	N/A
C. elegans: *mir-71(n4115)I; unc-31(e169)IV; hhIs64[unc-119(+); Psur-5::UbV-GFP]III*	This study	

Strain name	**Origin**	**Resource**
C. elegans: oyIs44[odr-1::RFP]V	CGC	Wormbase ID: PY2417
C. elegans: *oyIs44[odr-1::RFP]V; maIs352[unc-119(+) + Pmir-71::GFP]*	This study	N/A
C. elegans: luc51[tir-1::gfp]; oyIs44[odr-1::RFP]V	This study	N/A
C. elegans: mir-71(n4115)I; oyIs44[odr-1::RFP]V	This study	
C. elegans: *mir-71(n4115)I; hhIs64[unc-119(+); Psur-5::UbV-GFP]III; hhIs172[Podr-3::mir-71; Pofm-1::DsRed]*	This study	N/A
C. elegans: *mir-71(n4115)I; hhIs64[unc-119(+); Psur-5::UbV-GFP]III; hhIs173[Podr-3::mir-71; Pofm-1::DsRed]*	This study	N/A
C. elegans: *hhIs64[unc-119(+);Psur-5::UbV-GFP]III; hhIs172[Podr-3::mir-71; Pofm-1::DsRed]*	This study	N/A
C. elegans: *tir-1(ok2859)III; hhIs64[unc-119(+); Psur-5::UbV-GFP]III*	This study	N/A
C. elegans: *mir-71(n4115)I; tir-1(ok2859)III; hhIs64[unc-119(+); Psur-5::UbV-GFP]III*	This study	N/A
C. elegans: *hhIs113 [Pnhx-2::cpl-1*^{W32AW35A}*::yfp; Pmyo-2::mCherry]I; tir-1(ok2859)III*	This study	N/A
C. elegans: *mir-71(n4115)I; hhIs113[Pnhx-2::cpl-1*^{W32AW35A}*::yfp; Pmyo-2::mCherry]I; tir-1(ok2859)III*	This study	N/A
C. elegans: *tir-1(ok2859)III*	CGC	Wormbase ID: WBVar00093954
C. elegans: *mir-71(n4115)I; tir-1(ok2859)III*	This study	N/A
C. elegans: *tir-1(ok2859)III; hhIs53[unc-119(+); Psur-5::K29/48R-UbV-GFP]*	This study	N/A
C. elegans: *tir-1(ok2859)III; unc-119(ed4)III; hhIs57[unc-119(+); Psur-5::GFP]*	This study	N/A
C. elegans: *hhIs64[unc-119(+); Psur-5::UbV-GFP]III; tir-1(yz68)III*	This study	N/A
C. elegans: *mir-71(n4115)I; hhIs64[unc-119(+); Psur-5::UbV-GFP]III; tir-1(yz68)III*	This study	N/A
C. elegans: *luc56[tir-1-3UTRmod]III*	This study	MLC878
C. elegans: *luc56[tir-1-3UTRmod]III; hhIs64 [unc-119(+); Psur-5::UbV-GFP]III*	This study	N/A

Strain name	**Origin**	**Resource**
C. elegans: hhIs113 [Pnhx-2::cpl-1W32AW35A::yfp; Pmyo-2::mCherry]I; luc56[tir-1-3UTRmod]III	This study	N/A
C. elegans: luc56[tir-1-3UTRmod]III; hhIs64 [unc-119(+); Psur-5::UbV-GFP]III ; uthEx556[Psur-5::rpn-6.1; Pmyo-3::GFP]	This study	N/A
C. elegans: unc-13(e51)I; luc56[tir-1-3UTRmod]III; hhIs64 [unc-119(+); Psur-5::UbV-GFP]III	This study	N/A
C. elegans: luc56[tir-1-3UTRmod]III; hhIs64 [unc-119(+); Psur-5::UbV-GFP]III; unc-31(e169)IV	This study	N/A
C. elegans: luc56[tir-1-3UTRmod]III; hhIs64 [unc-119(+); Psur-5::UbV-GFP]III; hhIs172[Podr-3::mir-71; Pofm-1::DsRed]	This study	N/A
C. elegans: tir-1(ok2859)III; hhIs64 [unc-119(+); Psur-5::UbV-GFP]III; hhIs198[Podr-3::tir-1; Prps-0::hygR::mCherry]	This study	N/A
C. elegans: mir-71(n4115)I; tir-1(ok2859)III; hhIs64 [unc-119(+); Psur-5::UbV-GFP]III; hhIs198[Podr-3::tir-1; Prps-0::hygR::mCherry]	This study	N/A
C. elegans: mir-71(n4115)I; tir-1(ok2859)III; hhIs64 [unc-119(+); Psur-5::UbV-GFP]III; hhIs199[Pnhx-2::tir-1; Prps-0::hygR::mCherry]	CGC	Wormbase ID: WBVar00090219
C. elegans: hhIs64 [unc-119(+); Psur-5::UbV-GFP]III; hhIs203[Pstr-1::mir-71; Prps-0::hygR::mCherry]	This study	N/A
C. elegans: mir-71(n4115)I; hhIs64 [unc-119(+); sur-5::UbiV-GFP]III; hhIs203[Pstr-1::mir-71; Prps-0::hygR::mCherry]	This study	N/A
C. elegans: hhIs64 [unc-119(+); Psur-5::UbV-GFP]III; ttx-3(ot22)X	Hoppe lab	N/A
C. elegans: mir-71(n4115)I; hhIs64 [unc-119(+); Psur-5::UbV-GFP]III; ttx-3(ot22)X	This study	N/A
C. elegans: hhIs64 [unc-119(+); sur-5::UbiV-GFP]III; ceh-36(ks86)X	This study	N/A
hhIs64 [unc-119(+); sur-5::UbiV-GFP]III; Ex[pceh-36::HisCl; pmyo-3::gfp]	This study	N/A

Strain name	**Origin**	**Resource**
mir-71(n4115)I; hhIs64 [unc-119(+); sur-5::UbiV-GFP]III; Ex[pceh-36::HisCl; pmyo-3::gfp]	This study	N/A

Supplementary Table 7

Oligonucleotides used in this study

Name	5‘-3‘ sequence	Source
Genotyping primer		
gfp genotyping	CTACCTGTTCCATGGGTAAG	This study
gfp genotyping	CTTCCATCTTCAATGTTGTGTC	This study
hecd-1(tm2371) genotyping	GTCTCGATAAATCAGCTGCC	This study
hecd-1(tm2371) genotyping	TTCAGAAGATTTGGAGGACC	This study
hecd-1(tm2371) genotyping	GGACTATCGTATAAATGCTGTGGG	This study
mir-241(n4316) genotyping	GAGCTGGCAAATAAACTGAAAC	This study
mir-241(n4316) genotyping	CGGTGACATTCAATCCCTTC	This study
mir-241(n4316) genotyping	TCGGCATCCATATAGTAATCGT	This study
mir-48(n4079) genotyping	CTTGAAACTTGGCTTTAACCTG	This study
mir-48(n4079) genotyping	CTTGAAACTTGGCTTTAACCTG	This study
nDf51 genotyping	GACTTGGCGAACTGAAGAAACTG	This study
nDf51 genotyping	TTTGGAACGTTTCGGAATGAGAG	This study
nDf51 genotyping	AAATGGTCTAAAGAATGGTCCGTG	This study
mir-71(n4115) genotyping	CTTACAAGTTTACAGCTTCCAG	This study
mir-71(n4115) genotyping	TGACGTTAGGTTAAGCTTCAG	This study
mir-124(n4255) genotyping	CACAGGAGGCATGTAATCTC	This study
mir-124(n4255) genotyping	GCTCAACTGTCCAGTTTCTC	This study
mir-84(n4037) genotyping	ATCAAGTATAGGAGGAACGGG	This study
mir-84(n4037) genotyping	ATGCCTGACTCAGACTTCTC	This study
mir-84(n4037) genotyping	GAATGCGACATCACTGTCTG	This study
mir-34(n4276) genotyping	GACAGAAGTGCATTGTAGCA	This study
mir-34(n4276) genotyping	CTGGGTGGCTATACATTTCTC	This study
mir-34(n4276) genotyping	GTTAGCTGGTTGCATATTTCC	This study
tir-1(ok2859) genotyping	CTTCCATCTTCAATGTTGTGTC	This study
tir-1(ok2859) genotyping	TTTCCTCATTCTTGCTCAGTACAG	This study

Name	**5‘-3‘ sequence**	**Source**
tir-1(yz68) genotyping	AAACTCTTTGACACTGACGATTGGGT	This study
tir-1(yz68) genotyping	GAGATACTATGCATGTATCGCGGTTTG	This study
tir-1(yz68) genotyping	TTTTTAAATTCCAATTCCACCAACCTTT	This study
tir-1(yz68) genotyping	CTAATCGAGACTGACGTGATTGACCATA	This study
ttx-3(ot22) genotyping	TACCAAGTGTAGATTATTGATTGTTACCTGGCGGACATCATTTAAACATCGCC	This study
ttx-3(ot22) genotyping	GCGGACATCATTTAAACATCCCT	This study
ttx-3(ot22) genotyping	GATGATGAAGAAGAGAGTGG	This study
*tir-1 3’UTR** genotyping	GAACCTCCTACGCCAACGT	This study
*tir-1 3’UTR** genotying	GTTGAATCTGAAGGACTATGCTGC	This study
*tir-1 3’UTR** _CrispR_fwd	GAACCTCCTACGCCAACGTG	This study
*tir-1 3’UTR** _CrispR_rev	GCAGCATAGTCCTTCAGATTCAAC	This study
tir-1::gfp _CrispR_fwd	TATCAGGATGCATGTATGGCAAAAG	This study
tir-1::gfp _CrispR_rev	GTCAGTGGAGAGGGTGAAGGTGA	This study
qRT-PCR primer		
cdc-42 qRT-PCR	CTGCTGGACAGGAAGATTACG	This study
cdc-42 qRT-PCR	CTCGGACATTCTCGAATGAAG	This study
pmp-3 qRT-PCR	GTTCCCGTGTTCATCACTCAT	This study
pmp-3 qRT-PCR	ACACCGTCGAGAAGCTGTAGA	This study
tir-1 qRT-PCR	ATGATGATAACTGTGAGGATTGGG	This study
tir-1 qRT-PCR	ATAGAAGGCATTTCTTTGGTGG	This study
gfp qRT-PCR	ATGAGTAAAGGAGAAGAACTTTTC	This study
gfp qRT-PCR	CCTTCAAACTTGACTTCAGC	This study
Cloning primer		
IR101_*tir-1*_fwd	ATGGGAGAGGAAATACTAACGGAACGAAATCAAC	This study
IR101_*tir-1*_rev	CGCACCTATAAAGGTACATGCTCTAGAGAG	This study
IR101_*tir-1*_*Podr-3*_fwd	TAGAGCATGTACCTTTATAGGTGCGAGCAACTCGCTCCTTTCATTG	This study
IR101_*tir-1*_*Podr-3*_rev	GTTCCGTTAGTATTTCCTCTCCCATATCTAAAAAAACAATGATCTATGAGTAATTGATTTG	This study
IR101_*Pnhx-2*_fwd	CATGTACCTTTATAGGTGCGTCTGACACGCAAGACTTTTTC	This study
IR101 _rev	CGCACCTATAAAGGTACATG	This study
*Pnhx-2*_*tir-1*_fwd	GGCTAGCAGAATGGGAGAGGAAATACTAAC	This study
*tir-1*_*Pnhx-2*_rev	CCTCTCCCATTCTGCTAGCCAAGGGTCC	This study
IR101_fwd	TAAAGCAATGATAAGATATGTTAAG	This study
*tir-1*_IR101_rev	CATATCTTATCATTGCTTTATCCGAAACATTCATTAGG	This study

Name	**5‘-3‘ sequence**	**Source**
*Pstr-1*_fwd	CAGAGCAGACTAGTCAAATGATATGAAGTTTGTGTTAAGAATTTAGAAAATCTCAAAA	This study
Pstr-1_rev	GTCACTATGGTCGACCTGCATGCTTTATTATGGTATTTGGATATTTTGTAACACGG	This study
Pstr-1_mir-71_fwd	ACATATCCAGTCACTATGGCTTCCAGGTCACGATCCC	This study
Pstr-1_mir-71_rev	CATTTGACTAGTCTGCTCTGAACGATGAAAGACAT	This study

Supplementary Table 8

Oligonucleotides and repair templates used for CrispR/Cas9-mediated gene editing

Oligonucleotides to clone sgRNAs into pIKIII		
tir-1 3’UTR*_tir-1::gfp_sgRNA1_fwd	AATTGCAAATCTAAATGTTTggaagagacttaattccgatGTTTTAGAGCTAGAAATAGC	This study
tir-1 3’UTR*_tir-1::gfp_sgRNA1_rev	GCTATTTCTAGCTCTAAAACatcggaattaagtctcttccAAACATTTAGATTTGCAATT	This study
tir-1 3’UTR*_tir-1::gfp_sgRNA2_fwd	AATTGCAAATCTAAATGTTTggcagggcattgggtaaatgGTTTTAGAGCTAGAAATAGC	This study
tir-1 3'UTR*_tir-1::gfp_sgRNA2_rev	GCTATTTCTAGCTCTAAAACcatttacccaatgccctgccAAACATTTAGATTTGCAATT	This study
sgRNAs		
tir-1 3’UTR*_tir-1:gfp_sgRNA1	ATCGGAATTAAGTCTCTTCT	This study
tir-1 3’UTR*_tir-1:gfp_sgRNA2	CATTTACCCAATGCCCTGCC	This study

CrispR/Cas9 repair templates:

tir-1 3’UTR mutant:

TTCACAAAATATTATATTGCACGAGCACAAAAATTTGAGAATACGTAATGGTAACAAAGAAAACTACAGTACCT
CCTTTAGTGACTACTATAGCTCTTTATGTGCTCGATTTTCGAAGGTTTTATCAATTATATCTTTTATTTTCAGATG
CCTTCTATCTCCCGAAAAACTACCCAACAACGGTGGCAGACCACAAATACAGTAAGCCGTACTGGGCCATCCA
GAAGCATCGGTGGACCAAGAATGGAACCTCCTACGCCAACGTGTAAGTTGTTGAAACATCGTCACTTGGTATA
TTATTTAATTTTTTTAGTCTTTTCAGTTACACCAACTGGATCACAAGAACGTGCAACATCGACGAGAAGGAAAA
TTCAGCCTTCTGCATCCACAACTTCTGATCGGAATTAAGTCTCTTCTTTAATCAATACATCAAGTGCCGGTTCATT
TTATCCATTTTCCAACAAAAAACCAATTTTCTTCAACCATCCCAATATCAAATATCAAACTCCCAATGGTACCATC
ATCCCACACGAAAGTTTTAATGTATTTGACCCTCATTTTAAATCAGTCAAAACCTCAAAAAAAGTGTTCCACAAA
AAACTGGAAATTCAAAGCGTAGAATCTATGATTTCAACTGTCTCTCTCTCTTCGTCATTTACCCAATGCCCTGCC
GTTTTCTGCAAATAATAATAATAATTGTAATAATCTCTATAAATTATGTGATTGATATGAAACCAAAAAGAAAAC
TCTGAAACTTCACTTTCTTATAAGGTACCTGTTTATATATTCCGATCTCCATCTGTTTCATTCGTTTCACTTTTTCT
GTTTTATTTCGTGCAACGTGTAATAGTCGATCAACGCCCAACTCAGGAACCCATCAAATTCGAACCCTTTAACTC
CCTCTTTAAATTGAACTTTTTATCTTAACAATTACCGGGTCTAACACCCTTCCAGATTTCTAATGTTATACCTAAT
GAATGTTTCGGATTATTGGGGATCCTCTAGAGTCGACCTGCAGGCATGCAAGCTTGGCGTAATCATGGTCATA
GCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAACATACGAGCCGGAAGCATAAAGTGTAAAG

CCTGGGGTGCCTAATGAGTGAGCTAACTCACATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAAC
CTGTCGTGCCAGCTGCATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCG
CTTCCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGT
AATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCA
GGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCG
ACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTC
GTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTT
TCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACC
CCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTAT
CGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGA
AGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTC
GGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAGC
AGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTG
GAACGAAAACTCACGTTAAGGGATTTTGGTCATGAGATTATCAAAAAGGATCTTCACCTAGATCCTTTTAAATT
AAAAATGAAGTTTTAAATCAATCTAAAGTATATATGAGTAAACTTGGTCTGACAGTTACCAATGCTTAATCAGT
GAGGCACCTATCTCAGCGATCTGTCTATTTCGTTCATCCATAGTTGCCTGACTCCCCGTCGTGTAGATAACTACG
ATACGGGAGGGCTTACCATCTGGCCCCAGTGCTGCAATGATACCGCGAGACCCACGCTCACCGGCTCCAGATT
TATCAGCAATAAACCAGCCAGCCGGAAGGGCCGAGCGCAGAAGTGGTCCTGCAACTTTATCCGCCTCCATCCA
GTCTATTAATTGTTGCCGGGAAGCTAGAGTAAGTAGTTCGCCAGTTAATAGTTTGCGCAACGTTGTTGCCATTG
CTACAGGCATCGTGGTGTCACGCTCGTCGTTTGGTATGGCTTCATTCAGCTCCGGTTCCCAACGATCAAGGCGA
GTTACATGATCCCCCATGTTGTGCAAAAAAGCGGTTAGCTCCTTCGGTCCTCCGATCGTTGTCAGAAGTAAGTT
GGCCGCAGTGTTATCACTCATGGTTATGGCAGCACTGCATAATTCTCTTACTGTCATGCCATCCGTAAGATGCTT
TTCTGTGACTGGTGAGTACTCAACCAAGTCATTCTGAGAATAGTGTATGCGGCGACCGAGTTGCTCTTGCCCGG
CGTCAATACGGGATAATACCGCGCCACATAGCAGAACTTTAAAAGTGCTCATCATTGGAAAACGTTCTTCGGG
GCGAAAACTCTCAAGGATCTTACCGCTGTTGAGATCCAGTTCGATGTAACCCACTCGTGCACCCAACTGATCTT
CAGCATCTTTTACTTTCACCAGCGTTTCTGGGTGAGCAAAAACAGGAAGGCAAAATGCCGCAAAAAAGGGAAT
AAGGGCGACACGGAAATGTTGAATACTCATACTCTTCCTTTTTCAATATTATTGAAGCATTTATCAGGGTTATTG
TCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAGGGGTTCCGCGCACATTTCCCCGAA
AAGTGCCACCTGACGTCTAAGAAACCATTATTATCATGACATTAACCTATAAAAATAGGCGTATCACGAGGCCC
TTTCGTC

tir-1::gfp:

TCACAAAATATTATATTGCACGAGCACAAAAATTTGAGAATACGTAATGGTAACAAAGAAAACTACAGTACCTC
CTTTAGTGACTACTATAGCTCTTTATGTGCTCGATTTTCGAAGGTTTTATCAATTATATCTTTTATTTTCAGATGC
CTTCTATCTCCCGAAAAACTACCCAACAACGGTGGCAGACCACAAATACAGTAAGCCGTACTGGGCCATCCAG
AAGCATCGGTGGACCAAGAATGGAACCTCCTACGCCAACGTGTAAGTTGTTGAAACATCGTCACTTGGTATAT
TATTTAATTTTTTTAGTCTTTTCAGTTACACCAACTGGATCACAAGAACGTGCAACATCGACGAGAAGGAAAAT
TCAGCCTTCTGCATCCACAACTTCTGATCGGAATATGAGTAAAGGAGAAGAACTTTTCACTGGAGTTGTCCCAA
TTCTTGTTGAATTAGATGGTGATGTTAATGGGCACAAATTTTCTGTCAGTGGAGAGGGTGAAGGTGATGCAAC
ATACGGAAAACTTACCCTTAAATTTATTTGCACTACTGGAAAACTACCTGTTCCATGGGTAAGTTTAAACATATA
TATACTAACTAACCCTGATTATTTAAATTTTCAGCCAACACTTGTCACTACTTTCTGTTATGGTGTTCAATGCTTC
TCGAGATACCCAGATCATATGAAACGGCATGACTTTTTCAAGAGTGCCATGCCCGAAGGTTATGTACAGGAAA
GAACTATATTTTTCAAAGATGACGGGAACTACAAGACACGTAAGTTTAAACAGTTCGGTACTAACTAACCATAC
ATATTTAAATTTTCAGGTGCTGAAGTCAAGTTTGAAGGTGATACCCTTGTTAATAGAATCGAGTTAAAAGGTAT
TGATTTTAAAGAAGATGGAAACATTCTTGGACACAAATTGGAATACAACTATAACTCACACAATGTATACATCA
TGGCAGACAAACAAAAGAATGGAATCAAAGTTGTAAGTTTAAACATGATTTTACTAACTAACTAATCTGATTTA
AATTTTCAGAACTTCAAAATTAGACACAACATTGAAGATGGAAGCGTTCAACTAGCAGACCATTATCAACAAAA
TACTCCAATTGGCGATGGCCCTGTCCTTTTACCAGACAACCATTACCTGTCCACACAATCTGCCCTTTCGAAAGA
TCCCAACGAAAAGAGAGACCACATGGTCCTTCTTGAGTTTGTAACAGCTGCTGGGATTACACATGGCATGGAT
GAACTATACAAATAGGTCTCTTCTTTAATCAATACATCAAGTGCCGGTTCATTTTATCCATTTTCCAACAAAAAA
CCAATTTTCTTCAACCATCCCAATATCAAATATCAAACTCCCAATGTCTTTCAATCATCCCACACGAAAGTTTTAA
TGTATTTGACCCTCATTTTAAATCAGTCAAAACCTCAAAAAAAGTGTTCCACAAAAAACTGGAAATTCAAAGCG
TAGAATCTATGATTTCAACTGTCTCTCTCTCTTCCTCATTTACCCAATGCCCTGCCGTTTTCTGCAAATAATAATA
ATAATTGTAATAATCTCTATAAATTATGTGATTGATGTCTTTATGAAACCAAAAAGAAAACTCTGAAACTTCACT
TTCTTATAATCTTTCTGTTTATATATTCCGATCTCCATCTGTTTCATTCGTTTCACTTTTTCTGTTTTATTTCCTGCA
ACGTGTAATAGTCGATCAACCCCCAACTCAGGAACCCATCAAATTCGAACCCTTTAACTCCCTCTTTAAATTGAA
CTTTTTATCTTAACAATTACCGGGTCTAACACCCTTCCAGATTTCTAATGTTATACCTAATGAATGTTTCGGATTA
TT