

Supplementary Information

Supplementary Material and Methods

RNAi screen for RNA-binding proteins that might regulate the *die-1* 3'UTR:

RNAi by feeding was performed as described in (Ahringer, wormbook). A cherry-picked library of RNAi clones against 90% of all proteins with RNA-binding domains in the *C. elegans* genome was assembled from dsRNA-expressing clones from the Ahringer and Vidal libraries as well as a number of clones designed and built by us (see below for details on cloning). This library contains a total of 281 clones and was used for screening of two different strains, both in the *nre-1 lin15b* sensitized background, which has proven to be suitable for enhancing RNAi in neurons {Schmitz, 2007 #3117}. The first strain carried an integrated *cog-1* 3'UTR sensor that is under direct control of the miRNA *lisy-6* (ref DD?) and thus also under indirect control of *die-1*. In wild-type animals this sensor is expressed in ASER but repressed in ASEL, where *die-1* and *lisy-6* are expressed. We therefore speculated that factors affecting *die-1* asymmetry should result in symmetric repression of this GFP reporter as well. The second strain carries *otIs114* (*lim-6^{prom}::gfp*) to mark ASEL, and in addition, a hypomorphic allele of the miRNA *lisy-6* (*ot150*). This allele causes a ~20% loss of ASEL which we speculated could be suppressed, enhanced or completely reversed (i.e. causing conversion of ASER into ASEL) by reducing the levels of RNA-binding proteins (RBPs) affecting *die-1* asymmetry. In all cases we scored the F1 progeny of mothers plated onto each dsRNA clone. Specifically, 10-15 staged L1 hermaphrodites were placed onto plates seeded with dsRNA-expressing clones and incubated for 6 days at 22°C before scoring the F1 progeny as adults on a Zeiss axioplan2 compound microscope for the integrated *cog-1* 3'UTR sensor or Zeiss dissecting microscope for *otIs114*. In the case of P0 sterility or lethality, all P0s with a visible *gfp* signal were screened. In addition, for clones that resulted in sterility or lethality we also placed the P0s on the RNAi plates as staged L4 larvae. In some cases this resulted in a milder RNAi phenotype with regards to sterility and lethality and allowed us to score the F1.

Importantly, plating L4s resulted in an RNAi response against GFP or a number of other controls indistinguishable from that obtained by plating L1s. For every RNAi experiment we included empty vector and anti GFP controls to record the background reporter expression and confirm that the RNAi response was as expected, as well as a dsRNA clone against *fozi-1*, a zinc-finger domain-containing gene, which causes a two-ASEL phenotype.

RNAi clone generation:

To generate dsRNA-expressing clones against RBPs missing from the Ahringer and Vidal libraries we amplified exonic sequences of >100 bp either from genomic DNA or from cDNA when no exon was large enough. All primers contained linkers with sites for blunt-cutting restriction enzymes (EcoRV or SmaI). After digestion the amplified fragments were ligated into the double T7 promoter-containing vector, L4440 (ref Fire? Ahringer?), also linearized with EcoRV and treated with calf intestine alkaline phosphatase. All clones generated in this manner were sequenced and transformed into the strain typically used for feeding, HT115 (DE3).

Supplementary Figure Legends:

Supplemental Figure 1: *mir-273* family members match to phylogenetically conserved sites in the *die-1* 3'UTR. The phylogenetic conservation of the *mir-273* binding sites are shown as grey boxes in Fig.1C. All heteroduplexes are hand aligned and are not based on energetic criteria.

Supplemental Figure 2: Scanning deletion analysis across first 400bp of *die-1* 3'UTR fails to identify potential regulatory motif. 25bp deletion window were introduced across the first 400bp of the *die-1* 3'UTR without overlap. No single deletion resulted in a complete loss of regulation. The decrease in regulation of two constructs (#16 and #17) were due to one completely dysregulated line out of 2 or 3 lines, rather than a consistent decrease across lines, and were therefore not considered sequence motif candidates based on this analysis. Primary data is omitted for space reasons and only the symbol summary of the asymmetry indices (see legend to Fig.3 for more explanation is shown). All n values greater than or equal to 80.

Supplemental Figure 3: Double scanning deletion analysis. Scanning deletion analysis across the first 375bp for the *die-1* 3'UTR in the background of a 25bp deletion (375-400bp) reveals the presence of two additional regulatory sequence motifs. Primary data is omitted for space reasons and only the symbol summary of the asymmetry indices (see legend to Fig.3 for more explanation is shown). All n values greater than or equal to 80.

FIRST SITE

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      A      U
site#2    5'-CA UC--UGU GUAUGGGUA-3'
          || || ||| |||||
mir-273   3'-GU GG GUG CAUGCCCGU-5'
          C CU U

      UU UC UC G
site#2    5'-UUC C AA U UUGUAUGGGUA-3'
          ||| | || | |||||
mir-55    3'-GAG G UU -G-AAUAUGCCCAU-5'
          UC UC U

      A CU U
site#2    5'-CUCA U- G UG-UAUGGGUA-3'
          |||| | | || |||||
mir-56    3'-GAGU G U GU AUGCCCAU-5'
          C CCU U A

      UUC C AUCU U G
site#2    5'-UUC U A G U UAUGGGUA-3'
          ||| | | | |||||
mir-54    3'-GAG A U C A-AUGCCCAU-5'
          CCU A ACUU U

      CU C      UG
site#2    5'- U U-CA-AUCUGU UAUGGGUA-3'
          | | | | || |||||
mir-51    3'- G A U U CG--AUGCCCAU-5'
          UU U CC A CCU

      U UC U U A
site#2    5'-CU C AA C-UG UGUAUGGGU -3'
          | | | | || |||||
mir-52    3'-UCG G UU G AU-ACAUGCCCA -5'
          U CC U U C

      U UC U U U A
site#2    5'-CU C AA C G UGUAUGGGU -3'
          | | | | || |||||
mir-53    3'-UCG G UU G U ACAUGCCCA -5'
          U CC U U U C

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SECOND SITE

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UC      A      CA
site#1  5'-C  CC GU UAG  ACGGGC-3'
          |  || || |||  |||||
mir-273 3'-G  GG UG GUC-  UGCCCC-5'
                                   UC  C  U      A

          U  CC      A CA      CC
site#1  5'-UUC- C-  AGUU G  ACGGG -3'
          |||  |  |||| |  |||||
mir-55  3'-GAG  G  UUGA U  -UGCCC -5'
          UC UCU      A A      AU

          UC CA UU      CC
site#1  5'-UUC  C  G  AGCA--ACGGG -3'
          |||  |  |  ||||  |||||
mir-56  3'-GAG  G  U--UUGU  UGCCC -5'
          UC CC      AA      AU

          UCCC GUU  CA      CC
site#1  5'-UUC-  A  AG-  ACGGG -3'
          |||  |  ||  |||||
mir-54  3'-GAG  U  UC  UGCCC -5'
          CCUAA ACU  UAA      AU

          U C CCC  UU  A      CC
site#1  5'-AA U U  -AG  AGC ACGGG -3'
          || | |  ||  ||| |||||
mir-51  3'-UU-G A  UC -UCG UGCCC -5'
          U CCUA  C  A      AU

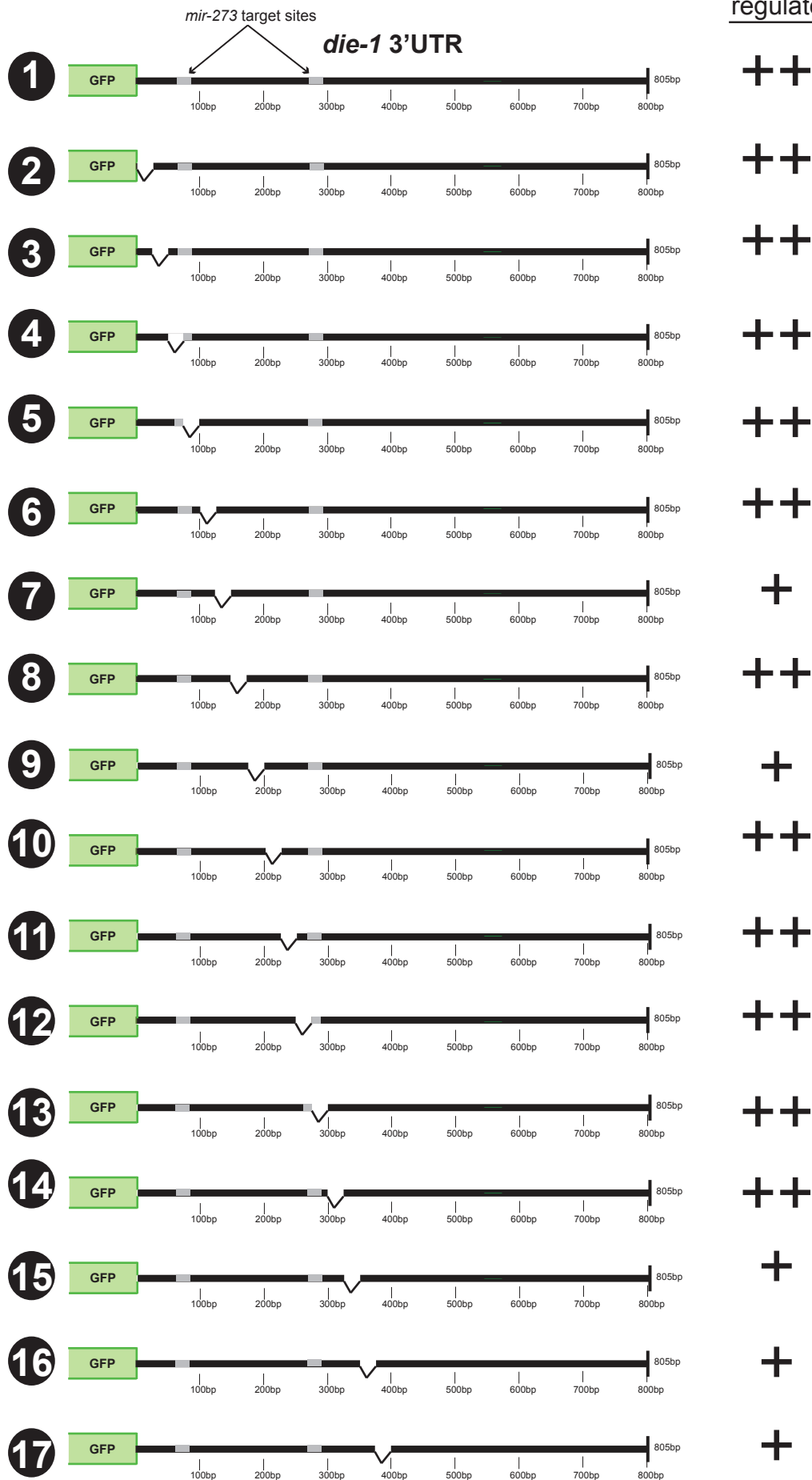
          UU U CC  U      CA      CC
site#1  5'-  C C  AG UA-G-  ACGGG -3'
          |  |  || |||  |||||
mir-52  3'-  G G  UU GU U  UGCCC -5'
          UC U CC  U  A ACA      CA

          U C CCC  U  CA      CC
site#1  5'-A U U  AGU AG-  ACGGG -3'
          |  |  ||| ||  |||||
mir-53  3'-U G G  UUG UU  UGCCC -5'
          C U CCU  U  ACA      AC

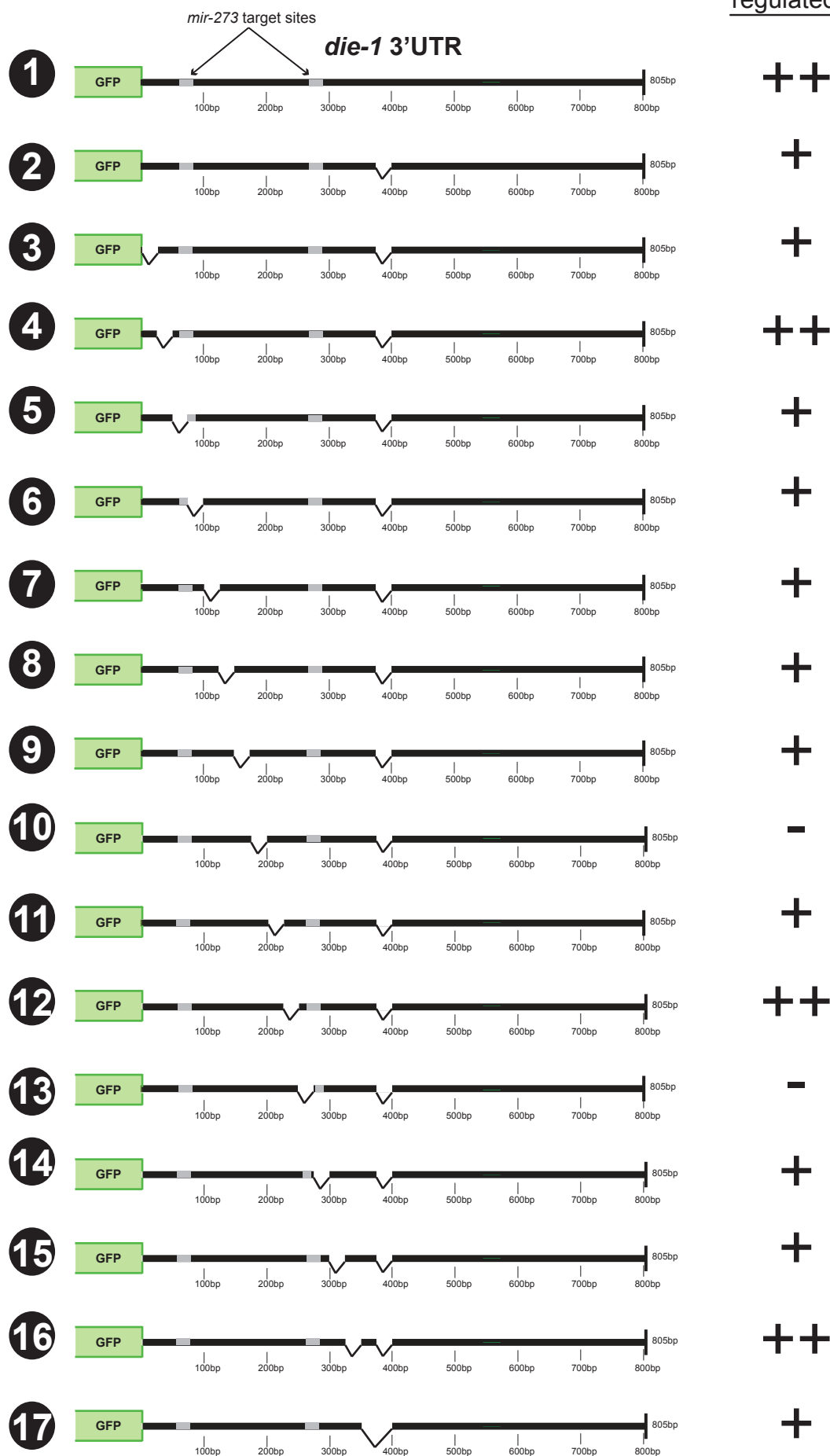
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Suppl. Fig.1

Asymmetrically regulated:



Asymmetrically
regulated:



Supplemental Table 1: Analysis of miRNA mutant strains. “Wildtype” indicates that animals are indistinguishable from wild-type animals in respect to the following marker: ¹ ASEL marker *lim-6::gfp*, ² ASER marker *gcy-5::gfp*, ³ *die-1* 3’UTR sensor. ⁴ this strain is lethal; dead embryos were scored and found to express ASER fate normally (gain of the ASEL inducer *die-1* in ASER is expected to result in loss of ASER fate). All other strains listed are viable. See Fig.1 for *mir-273* deletion allele and more detailed scoring data.

genotype	phenotype
<i>mir-273(n4438)II</i>	wildtype ^{1,2}
<i>mir-51(n4473)IV</i>	wildtype ¹
<i>mir-52(n4114)IV</i>	wildtype ¹
<i>mir-53(n4113)IV</i>	wildtype ¹
<i>mir-51,53(nDf67)IV</i>	wildtype ³
<i>mir-273(n4438); mir-54,55,56(nDf458)X</i>	wildtype ^{1,3}
<i>mir-273(n4438)II; mir-52(n4114)IV; mir-54,55,56(nDf458)X</i>	wildtype ²
<i>mir-273(n4438)II; mir-51,53(nDf67)IV; mir-54,55,56(nDf458)X</i>	wildtype ²
<i>mir-273(n4438)II; mir-54,55,56(nDf458)X; mir-52(n4114)mir-51,53(nDf67)IV</i>	wildtype ^{2,4}

Supplemental Table 2: Ectopic expression of *mir-273* family members in ASEL

induces ASER fate. ¹ Misexpression was achieved with the bilateral promoter of the *ceh-36* gene. ² Assessed using gain of the *gcy-5::gfp* (*ntls1*) ASER specific reporter in ASEL for all miRNAs, with the exception of *lsy-6*, for which the opposite phenotype is observed, i.e. gain of ASEL fate in ASER (assessed by loss of *gcy-5::gfp* in ASER; the *lsy-6* data is taken from Didiano and Hobert, 2008). Percentage ASE asymmetry phenotype is shown for multiple transgenic lines. *ceh-36p1::mir-X* constructs were injected as purified PCR fusion products at 25ng/ul with 100ng/ul *rol-6* into *ntls1* animals, with the exception of *lsy-6* which was injected at 40ng/ul; however, these transgenic lines were not stable and were lost over a few generations after injection. *ceh-36prom1::mir-X* constructs were injected as PCR fusion products to the microRNA locus, including the pri-microRNA precursor and approximately 10bp on either side of the precursor. This longer version of the *ceh-36* promoter utilized in all 3'UTR sensor experiments, is 5kb directly upstream of the *ceh-36* start codon.

Misexpressed miRNA ¹	Loss of asymmetry ²
<i>mir-273</i> family:	
<i>mir-273</i>	15% (n=41) 6% (n=53) 12% (n=51)
<i>mir-51</i>	11% (n=18) 0% (n=47) 0% (n=54)
<i>mir-52</i>	22% (n=54) 0% (n=68) 0% (n=62)
<i>mir-53</i>	18% (n=55) 52% (n=23) 0% (n=35)
<i>mir-54</i>	16% (n=50) 50% (n=56) 19% (n=31)
<i>mir-55</i>	16% (n=19) 20% (n=15) 22% (n=18)
<i>mir-56</i>	25% (n=24) 19% (n=43) 80% (n=20)
Controls:	
<i>lsy-6</i>	64% (n=30) 60% (n=40) 80% (n=44)
<i>mir-252</i>	0% (n=25) 0% (n=40)
<i>mir-253</i>	0% (n=40) 0% (n=40)

Supplemental Table 3: RNAi screen of RBP-encoding genes. List of all genes containing RBP domains in the *C. elegans* genome, with sequence identifier and type of RBP domain, shown in column 1, 2, and 3, respectively. Over 90% of this RNAi library has been screened twice in the *nre-1*; *lin-15b* RNAi sensitive genetic background with either an integrated *cog-1* 3'UTR sensor or an ASEL terminal cell-fate maker *lim-6::gfp*, shown in columns 4 and 5, respectively. A small number of clones was screened for one or the other marker only. The small fraction of clones which has not been screened at all is due to the failure to retrieve them from the respective libraries. We have also noted, in column 6, a number of different pleiotropies. See Supplementary Material and Methods for more information on the screen.

Gene	Sequence	Domain	Chromosome I		Pleiotropies
			<i>cog-1</i> 3'UTR	<i>lim-6::gfp</i> ; <i>ot150</i>	
<i>mex-3</i>	F53G12.5	KH	Yes	Yes	Emb
<i>rnp-8</i>	R119.7	RRM	Yes	Yes	
	D1037.1	dsRNA-BD	Yes	Yes	
<i>sago-2</i>	F56A6.1	PAZ	Yes	Yes	
<i>glh-4</i>	T12F5.3	DEAD/DEAH	Yes	Yes	
<i>glh-4</i>	T12F5.3	Zn knuckle	Yes	Yes	
<i>ppw-1</i>	C18E3.7	PAZ	Yes	Yes	
	C41D11.7	DEAD/DEAH	Yes	Yes	
<i>rps-10</i>	D1007.6	S1	Yes	Yes	Lva, Let
	D1007.7	RRM	Yes	Yes	
<i>ppw-2</i>	Y110A7A.18	PAZ	Yes	Yes	
	C44E4.4	RRM	Yes	Yes	Ste
	M01A10.1	KH	Yes	Yes	
<i>cey-3</i>	M01E11.5	Cold shock	Yes	Yes	
<i>cey-2</i>	F46F11.2	Cold shock	Yes	Yes	
	F55F8.2	DEAD/DEAH	Yes	Yes	Ste
<i>cpb-3</i>	F55A12.1	PAZ	Yes	Yes	
	B0414.5	RRM	Yes	Yes	Slow growing
	F33D11.10	DEAD/DEAH	Yes	Yes	
	Y65B4A.6	DEAD/DEAH	Yes	Yes	
	D2030.6	PAZ	Yes	Yes	
	F26B1.2	KH	Yes	Yes	
<i>gld-1</i>	F26A3.2	RRM	Yes	Yes	Lva
	T23G11.3	KH	Yes	Yes	
	R06C7.1	PAZ	Yes	Yes	
	E02D9.1	KH	Yes	Yes	
	F27D4.4	C-X8-C-X5-C-X3-H	Yes	Yes	
<i>adr-1</i>	H15N14.1	dsRNA-BD	Yes	Yes	Lva, Let
<i>drh-3</i>	D2005.5	DEAD/DEAH	Yes	Yes	
<i>glh-1</i>	T21G5.3	DEAD/DEAH	Yes	Yes	
<i>glh-1</i>	T21G5.3	Zn knuckle	Yes	Yes	

<i>star-2</i>	T21G5.5	KH	Yes	Yes	Lva
<i>glh-2</i>	C55B7.1	DEAD/DEAH	Yes	Yes	Lva, Let
<i>glh-2</i>	C55B7.1	Zn knuckle	Yes	Yes	
<i>ztf-4</i>	T10B11.3	RRM	Yes	Yes	
		C-X8-C-X5-C-X3-H	Yes	Yes	
<i>nuo-2</i>	C30F12.1				
	T10E9.7	KH	Yes	Yes	Ste
	R05D11.4	DEAD/DEAH	Yes	Yes	
		C-X8-C-X5-C-X3-H	Yes	Yes	
<i>gla-3</i>	T02E1.3				
	F52B5.3	DEAD/DEAH	Yes	Yes	
<i>drsh-1</i>	F26E4.10	dsRNA-BD	Yes	Yes	
<i>pabp-2</i>	C17E4.5	RRM	Yes	Yes	Ste, Let
<i>mec-8</i>	F46A9.6	RRM	Yes	Yes	
	C41G7.3	KH	Yes	Yes	
	T23D8.7	PAZ	Yes	Yes	
	F32B4.4	RRM	Yes	Yes	
<i>unc-75</i>	C17D12.2	RRM	No	No	
	Y106G6D.7	RRM	Yes	Yes	
	C25A1.4	RRM	Yes	Yes	
	B0511.6	DEAD/DEAH	Yes	Yes	Ste
	C34B2.6	S1	Yes	Yes	
<i>pab-1</i>	Y106G6H.2	RRM	Yes	Yes	Ste
	R09B3.2	RRM	Yes	Yes	
	R09B3.3	RRM	Yes	Yes	
	R06C1.4	RRM	Yes	Yes	
<i>snr-2</i>	W08E3.1	Sm/LSm	Yes	Yes	Lva, Let
	Y18D10A.8	KH	Yes	Yes	
	Y54E5A.6	dsRNA-BD	Yes	Yes	
	Y54E10BR.6	S1	Yes	Yes	Ste, Let
<i>rnp-6</i>	Y47G6A.20	RRM	Yes	Yes	Ste, Let
	Y65B4A.1	RRM	Yes	Yes	
<i>snr-7</i>	Y71F9B.4	Sm/LSm	Yes	Yes	Lva, Let
<i>lsm-6</i>	Y71G12B.14	Sm/LSm	Yes	Yes	Ste, Emb
<i>lin-28</i>	F02E9.2	Cold shock	Yes	No	
<i>lin-28</i>	F02E9.2	Zn knuckle	Yes	No	
<i>sig-7</i>	F39H2.2	RRM	Yes	No	Ste
<i>hrp-2</i>	F58D5.1	RRM	Yes	No	Ste
	H27M09.1	DEAD/DEAH	Yes	No	Ste, Emb
	W02D3.11	RRM	Yes	No	
	Y23H5B.6	DEAD/DEAH	Yes	No	Ste
<i>vbh-1</i>	Y54E10A.9	DEAD/DEAH	Yes	No	
	Y71A12B.3	PAZ	Yes	No	
	ZK973.1	S1	Yes	No	
	Y71A12B.2	PAZ	No	No	
	Y71G12B.8	DEAD/DEAH	No	No	
<i>glh-3</i>	B0414.6	DEAD/DEAH	Yes	No	
<i>glh-3</i>	B0414.6	Zn knuckle	Yes	No	
	K07A1.15	Sm/LSm	Yes	No	
	Y37E3.10	S1	Yes	No	Lva

<i>fog-1</i>	Y48G1C.9 Y54E10A.4	Sm/LSm RRM	No No	No No	
Chromosome II					
Gene	Sequence	Domain	<i>cog-1</i> 3'UTR	<i>lim-6::gfp;</i> <i>ot150</i>	Pleiotropies
	C23H3.3	KH	No	No	
	C50D2.5	RRM	Yes	Yes	
<i>alg-2</i>	T07D3.7	PAZ	Yes	Yes	Ste, Let
<i>etr-1</i>	T01D1.2	RRM	Yes	Yes	Let
	C24H12.4	DEAD/DEAH	Yes	Yes	
	F07E5.5	Zn knuckle	Yes	Yes	
	K02F6.1	Zn knuckle	Yes	Yes	
	F39E9.7	dsRNA-BD	Yes	Yes	
<i>fbf-1</i>	H12I13.4	PUF	Yes	Yes	
<i>fbf-2</i>	F21H12.5	PUF	Yes	Yes	
	EEED8.4	RRM	Yes	Yes	
<i>mog-5</i>	EEED8.5	S1	Yes	Yes	Lva
<i>rsp-4</i>	EEED8.7	RRM	Yes	Yes	
	C18A3.5	RRM	Yes	Yes	
	C30B5.4	RRM	Yes	Yes	
	EEED8.10	RRM	Yes	Yes	
	EEED8.12	RRM	Yes	Yes	
<i>daz-1</i>	F56D1.7	RRM	Yes	Yes	Ste
	ZK1248.9	PAZ	Yes	Yes	
	C44B7.2	RRM	Yes	Yes	
<i>rsp-5</i>	T28D9.2	RRM	Yes	Yes	
<i>snr-3</i>	T28D9.10	Sm/LSm	Yes	Yes	Lva
<i>lsm-4</i>	F32A5.7	Sm/LSm	Yes	Yes	Ste
<i>wrn-1</i>	F18C5.2	DEAD/DEAH	Yes	Yes	
<i>puf-8</i>	C30G12.7	PUF	Yes	Yes	
<i>nos-2</i>	ZK1127.1	Nanos RBD	Yes	Yes	
	T02G5.11	Nanos RBD	Yes	Yes	
<i>sap-49</i>	C08B11.5	RRM	Yes	Yes	Lva, Let
	C27H5.3	RRM	Yes	Yes	
<i>puf-5</i>	F54C9.8	PUF	Yes	Yes	
<i>tag-169</i>	F44G4.4	RRM	Yes	Yes	
		C-X8-C-X5-C-	Yes	Yes	
<i>mex-6</i>	AH6.5	X3-H			
<i>exc-7</i>	F35H8.5	RRM	Yes	Yes	
<i>hel-1</i>	C26D10.2	DEAD/DEAH	Yes	Yes	Lva, Let
<i>sym-2</i>	ZK1067.6	RRM	No	No	
<i>eif-3.G</i>	F22B5.2	RRM	Yes	Yes	Lva, Let
<i>rha-1</i>	T07D4.3	DEAD/DEAH	Yes	Yes	
<i>rha-1</i>	T07D4.3	dsRNA-BD	Yes	Yes	
	T07D4.4	DEAD/DEAH	Yes	Yes	
	Y53C12B.2	KH	Yes	Yes	Ste
<i>nos-3</i>	Y53C12B.3	Nanos RBD	Yes	Yes	
	C08H9.2	KH	Yes	Yes	Ste
<i>npp-19</i>	R06F6.5	RRM	Yes	Yes	Ste
<i>rsp-2</i>	W02B12.2	RRM	Yes	Yes	

<i>rsp-1</i>	W02B12.3	RRM	No	No	
<i>nos-1</i>	R03D7.7	Nanos RBD	Yes	Yes	
<i>cey-1</i>	F33A8.3	Cold shock	Yes	Yes	
<i>din-1</i>	F07A11.6	RRM	Yes	Yes	Lva
<i>lsm-1</i>	F40F8.9	Sm/LSm	Yes	Yes	
<i>rsp-7</i>	D2089.1	RRM	Yes	Yes	Lva
	F58G1.1	PAZ	No	No	
<i>puf-6</i>	F18A11.1	PUF	Yes	Yes	
		C-X8-C-X5-C-X3-H	Yes	Yes	
<i>moe-3</i>	F32A11.6				
	Y54E2A.6	DEAD/DEAH	Yes	Yes	
	R05H10.2	RRM	Yes	Yes	Ste
	Y46G5A.6	DEAD/DEAH	Yes	Yes	Lva
<i>ptb-1</i>	D2089.4	RRM	Yes	No	
	H20J04.4	DEAD/DEAH	Yes	No	
	Y46G5A.13	RRM	Yes	No	
	Y46G5A.4	DEAD/DEAH	Yes	No	
	Y49F6A.1	PAZ	Yes	No	
	Y54G11A.3	DEAD/DEAH	Yes	No	
<i>gld-3</i>	T07F8.3	KH	Yes	Yes	
			Yes	No	Lva
		C-X8-C-X5-C-X3-H			
<i>mex-1</i>	W03C9.7				
<i>puf-12</i>	ZK945.3	PUF	Yes	Yes	Ste

Chromosome III

Gene	Sequence	Domain	<i>cog-1</i> 3'UTR	<i>lim-6::gfp; ot150</i>	Pleiotropies
	K02F3.12	DEAD/DEAH	Yes	Yes	
<i>rnp-5</i>	K02F3.11	RRM	Yes	Yes	
	C46F11.4	DEAD/DEAH	Yes	Yes	
<i>msi-1</i>	R10E9.1	RRM	Yes	Yes	
<i>rnp-4</i>	R07E5.14	RRM	Yes	Yes	Ste
<i>rcq-5</i>	E03A3.2	DEAD/DEAH	Yes	Yes	
	M88.5	KH	No	No	
	C16C10.3	PAZ	Yes	Yes	Ste
<i>asd-1</i>	R74.5	RRM	Yes	Yes	
<i>set-2</i>	C26E6.9	RRM	Yes	Yes	
<i>tag-310</i>	R10E4.2	RRM	Yes	Yes	
	T04A8.6	RRM	Yes	Yes	Ste
<i>emb-5</i>	T04A8.14	S1	Yes	Yes	
		C-X8-C-X5-C-X3-H	Yes	Yes	Ste
	B0336.3				
	ZK418.8	KH	Yes	Yes	
	ZK418.9	KH	Yes	Yes	
<i>rps-3</i>	C23G10.3	KH	Yes	Yes	Lva
<i>polq-1</i>	W03A3.2	DEAD/DEAH	Yes	Yes	
	F01F1.7	DEAD/DEAH	Yes	Yes	Lva
	C56G2.1	KH	Yes	Yes	
	C28H8.3	DEAD/DEAH	Yes	Yes	
<i>adr-2</i>	T20H4.4	dsRNA-BD	Yes	Yes	
<i>rps-13</i>	C16A3.9	S1	Yes	Yes	Lva

<i>cgh-1</i>	C07H6.4	RRM	Yes	Yes	
	C07H6.5	DEAD/DEAH	Yes	Yes	Let, Ste
	F44E2.2	Zn knuckle	Yes	Yes	
<i>dcr-1</i>	K12H4.8	DEAD/DEAH	Yes	Yes	
<i>dcr-1</i>	K12H4.8	dsRNA-BD	Yes	Yes	
<i>dcr-1</i>	K12H4.8	PAZ	Yes	Yes	
		C-X8-C-X5-C-X3-H	Yes	Yes	
	C50C3.1				
	ZK686.2	DEAD/DEAH	Yes	Yes	Ste
<i>snr-5</i>	ZK652.1	Sm/LSm	Yes	Yes	Lva, Let
	R05D3.8	RRM	Yes	Yes	
<i>cpb-1</i>	C40H1.1	RRM	Yes	Yes	
<i>rde-4</i>	T20G5.11	dsRNA-BD	Yes	Yes	
	ZK632.2	dsRNA-BD	Yes	Yes	Ste, Let
	T26G10.1	DEAD/DEAH	Yes	Yes	Ste, Let
<i>cey-4</i>	Y39A1C.3	Cold shock	Yes	Yes	
<i>tag-76</i>	ZK757.3	PAZ	Yes	Yes	
<i>drr-2</i>	T12D8.2	RRM	Yes	Yes	
		C-X8-C-X5-C-X3-H	Yes	Yes	Ste, Emb
<i>pie-1</i>	Y49E10.14				
<i>snr-6</i>	Y49E10.15	Sm/LSm	Yes	Yes	Lva
<i>rsp-8</i>	C18D11.4	RRM	Yes	Yes	Ste
<i>rsp-3</i>	Y111B2A.18	RRM	Yes	Yes	Ste
	Y75B8A.4	S1	Yes	Yes	
	Y37D8A.21	RRM	Yes	Yes	
		C-X8-C-X5-C-X3-H	Yes	Yes	
	Y53G8AR.9				
	BE0003N10.1	KH	Yes	Yes	
<i>cpf-2</i>	F56A8.6	RRM	Yes	Yes	Ste, Let
	Y55B1AL.3	DEAD/DEAH	Yes	Yes	
	Y71H2AM.19	DEAD/DEAH	Yes	Yes	Lva, Ste, Let
	B0280.17	KH	No	Yes	Let, Ste
	C06G4.1	KH	No	Yes	
	F25B5.7	RRM	No	Yes	Let, Ste
	F57B9.3	DEAD/DEAH	No	No	
<i>inf-1</i>	F57B9.6	DEAD/DEAH	No	No	
		C-X8-C-X5-C-X3-H	No	No	
<i>rnf-113</i>	K01G5.1				
<i>rnp-7</i>	K04G7.10	RRM	No	Yes	Let, Ste
<i>pes-4</i>	Y119D3B.17	KH	No	Yes	
<i>tag-262</i>	Y54H5A.3	RRM	No	Yes	Let, Ste
<i>uaf-1</i>	Y92C3B.2	RRM	No	Yes	Let, Ste
	ZK512.2	DEAD/DEAH	No	Yes	Ste

Chromosome IV

Gene	Sequence	Domain	<i>cog-1</i> 3'UTR	<i>lim-6::gfp; ot150</i>	Pleiotropies
	F29C4.7	RRM	Yes	Yes	
<i>hrp-1</i>	F42A6.7	RRM	Yes	Yes	Ste, Let
	K08D12.3	Zn knuckle	Yes	Yes	Lva
	Y55F3BR.1	DEAD/DEAH	Yes	Yes	Ste
	Y37E11B.5	C-X8-C-X5-C-	Yes	Yes	

		X3-H			
<i>rnp-3</i>	K08D10.3	RRM	Yes	No	
<i>rnp-2</i>	K08D10.4	RRM	Yes	Yes	
<i>puf-7</i>	B0273.2	PUF	Yes	Yes	
	C02B10.4	RRM	Yes	No	
<i>drh-1</i>	F15B10.2	DEAD/DEAH	Yes	Yes	
<i>pgl-1</i>	ZK381.4	RGG box	Yes	Yes	
<i>tag-292</i>	C01G5.2	PAZ	Yes	Yes	
<i>rsp-6</i>	C33H5.12	RRM	Yes	Yes	
		C-X8-C-X5-C-	Yes	Yes	
	C33H5.17	X3-H			
	C49H3.4	Sm/LSm	Yes	Yes	
<i>ntl-4</i>	C49H3.5	RRM	Yes	Yes	
<i>csr-1</i>	F20D12.1	PAZ	Yes	Yes	Emb
		C-X8-C-X5-C-	Yes	Yes	Lva, Ste
	T26A8.4	X3-H			
		C-X8-C-X5-C-	Yes	Yes	
<i>oma-1</i>	C09G9.6	X3-H			
	C27B7.5	Zn knuckle	Yes	Yes	
		C-X8-C-X5-C-	Yes	Yes	
	Y55F3AM.6	X3-H			
	K07H8.9	KH	Yes	Yes	
	K07H8.10	RRM	Yes	Yes	
	R11A8.7	KH	Yes	Yes	
<i>lsm-7</i>	ZK593.7	Sm/LSm	Yes	Yes	Lva, Ste
	K08F4.2	RRM	Yes	Yes	
	W08D2.7	DEAD/DEAH	Yes	Yes	Lva
<i>bcc-1</i>	M7.3	KH	Yes	Yes	
	F01G4.3	DEAD/DEAH	Yes	Yes	
	ZK792.5	PUF	Yes	Yes	
	T22B3.2	PAZ	Yes	Yes	Ste
<i>rbd-1</i>	T23F6.4	RRM	Yes	Yes	Ste
	B0035.12	RRM	Yes	Yes	Ste
<i>him-6</i>	T04A11.6	DEAD/DEAH	Yes	Yes	
		C-X8-C-X5-C-	Yes	Yes	Ste
<i>tag-287</i>	F11A10.8	X3-H			
	Y57G11A.5	RRM	Yes	Yes	
		C-X8-C-X5-C-	Yes	Yes	Ste
<i>mex-5</i>	W02A2.7	X3-H			
<i>lsm-3</i>	Y62E10A.12	Sm/LSm	Yes	Yes	
<i>lst-1</i>	Y37A1B.1	Cold shock	Yes	Yes	
		C-X8-C-X5-C-	Yes	Yes	
	F38C2.5	X3-H			
		C-X8-C-X5-C-	Yes	Yes	
	F38C2.7	X3-H			
		C-X8-C-X5-C-	Yes	Yes	
	Y57G11C.25	X3-H			
	C35D6.3	PAZ	Yes	Yes	
		C-X8-C-X5-C-	Yes	Yes	
	C35D6.4	X3-H			
	Y59E9AL.4	RRM	Yes	Yes	
<i>mel-46</i>	T06A10.1	DEAD/DEAH	Yes	Yes	Ste

		C-X8-C-X5-C-X3-H	Yes	Yes	
	Y116A8C.17	C-X8-C-X5-C-X3-H	Yes	Yes	
	Y116A8C.19	C-X8-C-X5-C-X3-H	Yes	Yes	
	Y116A8C.20	C-X8-C-X5-C-X3-H	Yes	Yes	
<i>sfa-1</i>	Y116A8C.32	Zn knuckle	Yes	Yes	Ste
		C-X8-C-X5-C-X3-H	Yes	Yes	Lva
<i>uaf-2</i>	Y116A8C.35	X3-H			
<i>snr-1</i>	Y116A8C.42	Sm/LSm	Yes	Yes	Lva
	Y69A2AR.32	KH	Yes	Yes	
	Y55F3AM.3	RRM	Yes	Yes	Ste
	F11A10.7	RRM	No	No	
	F49F1.8	Zn knuckle	Yes	Yes	
	F53H1.1	DEAD/DEAH	Yes	Yes	Ste
<i>puf-4</i>	M4.2	PUF	Yes	Yes	
	T08B6.5	RRM	Yes	Yes	
	Y57G11C.36	KH	Yes	Yes	
<i>lsm-8</i>	Y73B6BL.32	Sm/LSm	Yes	Yes	Ste
	Y73B6BL.33	RRM	Yes	Yes	
<i>sqd-1</i>	Y73B6BL.6	RRM	Yes	Yes	Ste
	F58B3.7	RRM	No	No	
		C-X8-C-X5-C-X3-H	No	Yes	Let, Ste
	T11G6.8	X3-H			
<i>cyn-13</i>	Y116A8C.34	RRM	No	Yes	
<i>puf-3</i>	Y45F10A.2	PUF	No	Yes	
	Y57G11C.9	RRM	No	Yes	
<i>puf-11</i>	Y73B6BL.38	PUF	No	Yes	
	Y94H6A.5	DEAD/DEAH	No	Yes	
	ZK616.1	RRM	No	Yes	

Chromosome V

Gene	Sequence	Domain	<i>cog-1</i> 3'UTR	<i>lim-6::gfp; ot150</i>	Pleiotropies
<i>lsm-5</i>	F28F8.3	Sm/LSm	Yes	Yes	Ste
	F55C9.3	PAZ	Yes	Yes	
	Y38H6C.5	Zn knuckle	Yes	Yes	
		C-X8-C-X5-C-X3-H	Yes	Yes	
	Y61A9LA.8	X3-H			
<i>ergo-1</i>	R09A1.1	PAZ	Yes	Yes	
	T22H9.3	PAZ	Yes	Yes	
<i>pgl-3</i>	C18G1.4	RGG box	Yes	Yes	
	ZC317.1	DEAD/DEAH	No	No	
	Y38A10A.6	DEAD/DEAH	Yes	Yes	
<i>mut-14</i>	C14C11.6	DEAD/DEAH	Yes	Yes	
<i>sago-1</i>	K12B6.1	PAZ	Yes	Yes	
<i>spn-4</i>	ZC404.8	RRM	No	No	
		C-X8-C-X5-C-X3-H	Yes	Yes	
<i>oma-2</i>	ZC513.6	X3-H			
	C05C8.2	KH	No	No	
		C-X8-C-X5-C-X3-H	Yes	Yes	Ste, Emb
<i>pos-1</i>	F52E1.1	X3-H			

<i>rde-1</i>	K08H10.7	PAZ	Yes	Yes	
		C-X8-C-X5-C-X3-H	Yes	Yes	
	F38B7.1				
	C12D8.1	KH	Yes	Yes	
	K07C5.6	Zn knuckle	Yes	Yes	Lva
<i>snr-4</i>	C52E4.3	Sm/LSm	Yes	Yes	Lva, Let
	T07F10.3	RRM	Yes	Yes	
	W04D2.6	RRM	No	No	
<i>gut-2</i>	T10G3.6	Sm/LSm	Yes	Yes	Ste
<i>rnp-1</i>	ZK863.7	RRM	No	No	
	C50B8.1	RRM	No	No	
	F58G11.2	DEAD/DEAH	Yes	Yes	
	F58E10.3	DEAD/DEAH	Yes	Yes	Ste
	H24K24.4	RRM	No	Yes	
		C-X8-C-X5-C-X3-H	No	Yes	
	W05B10.2				
	Y59A8B.10	KH	No	Yes	
Chromosome X					
Gene	Sequence	Domain	<i>cog-1</i> 3'UTR	<i>lim-6::gfp; ot150</i>	Pleiotropies
		C-X8-C-X5-C-X3-H	Yes	Yes	
	Y60A9.3				
	F55A4.4	dsRNA-BD	Yes	Yes	
	R04A9.2	PAZ	Yes	Yes	
	F55A4.5	dsRNA-BD	Yes	Yes	
<i>fox-1</i>	T07D1.4	RRM	Yes	Yes	
	F54G2.2	Zn knuckle	Yes	Yes	
		C-X8-C-X5-C-X3-H	Yes	Yes	
	W05H7.4				
	H28G03.1	RRM	Yes	Yes	
<i>puf-9</i>	W06B11.2	PUF	Yes	Yes	
		C-X8-C-X5-C-X3-H	Yes	Yes	
	C34D10.2				
	C07A4.1	RRM	Yes	Yes	
<i>alg-1</i>	F48F7.1	PAZ	Yes	Yes	Let
<i>pab-2</i>	F18H3.3	RRM	Yes	Yes	Lva
	C36E6.1	KH	Yes	Yes	
	F19G12.3	PAZ	Yes	Yes	
		C-X8-C-X5-C-X3-H	Yes	Yes	
	K02H8.1				
<i>sup-12</i>	T22B2.4	RRM	No	Yes	Let, Ste