

Fig. S1. Improved RNAi vector increases penetrance of TF depletion phenotypes.

(A) Stacked bar graph depicting the penetrance of AC invasion defects at the P6.p 4-cell stage comparing L4440-based versus T444T-based RNAi depletions in a uterine-specific RNAi-hypersensitive background. Asterisk (*) denotes a statistically significant difference between the vectors and represents a p-value < 0.03 by Fisher's exact test ($n \geq 30$ animals per treatment). (B) Stacked bar graphs depicting AC invasion defects following delayed TF-RNAi treatment at the L2 stage ($n = 30$ animals per treatment). (C) Single plane of confocal z-stack depicting early depletion of *h/h-2* at the L1 stage. The AC-specific membrane marker (magenta, *cdh-3^{1.5}*>mCherry::PLC δ^{PH}) and BM marker (green, *lam-1*>LAM-1::GFP) are overlaid in each micrograph. (D) Single plane of confocal z-stacks during the L4 stage (P6.p 8-cell stage) depicting representative phenotypes associated with TF-RNAi treatment.

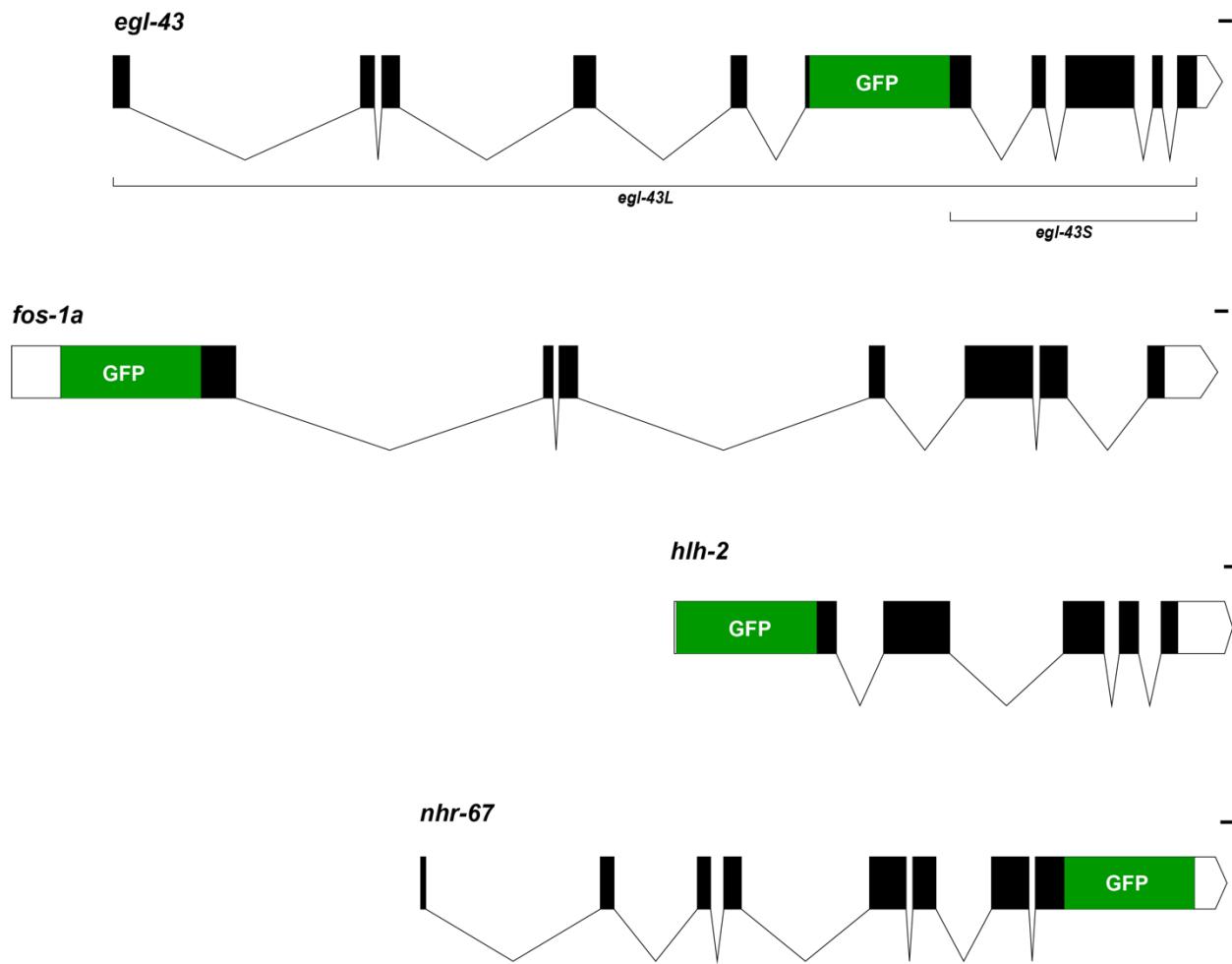


Fig. S2. Schematic of endogenous GFP-tagged loci of pro-invasive TFs. Codon-optimized GFP was integrated at the N-terminus of *fos-1A* and *hlh-2*, at the C-terminus of *nhr-67*, and internally in the *egl-43* locus (tagging both isoforms). This figure was made using <http://wormweb.org/exonintron>. Scale bar, 100 bp.

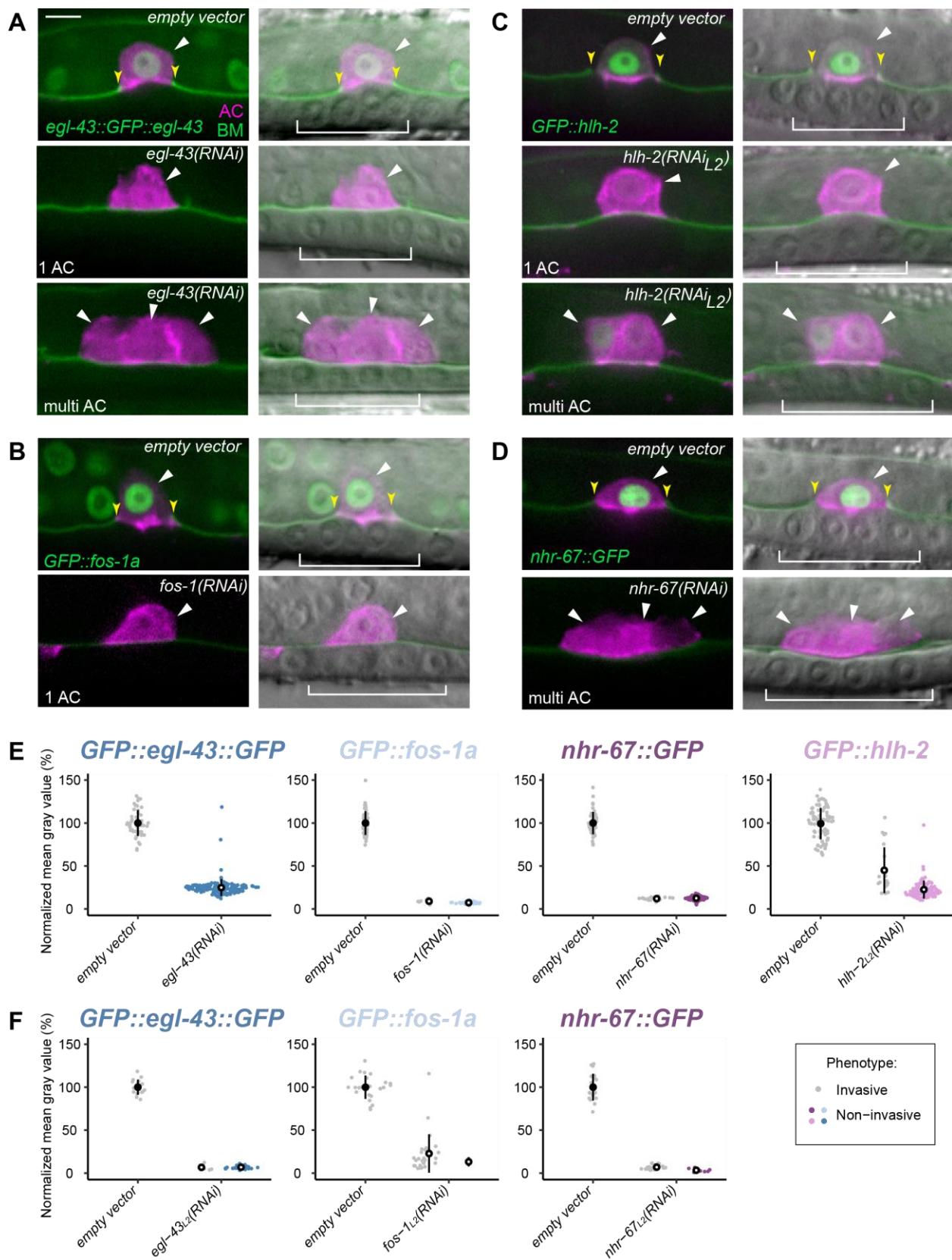


Figure S3. AC invasion phenotypes do not necessarily correlate to TF expression levels. (A-D) Single planes of confocal z-stack depicting representative phenotype (single vs. multi AC, bottom left of each image) of fluorescence alone (left; AC, magenta, expressing *cdh-3>mCherry::moeABD* and BM, green) and DIC overlay (right). (E) Sina plots of GFP-tagged TF levels, defined as the mean gray value of individual AC nuclei at the P6.p 4-cell stage following TF-RNAi knockdown. In this and all other figures, statistical significance as compared to empty vector controls is denoted as an open black circle and here represents a p-value of $< 1 \times 10^{-6}$ by Student's t test ($n \geq 50$ animals per treatment).

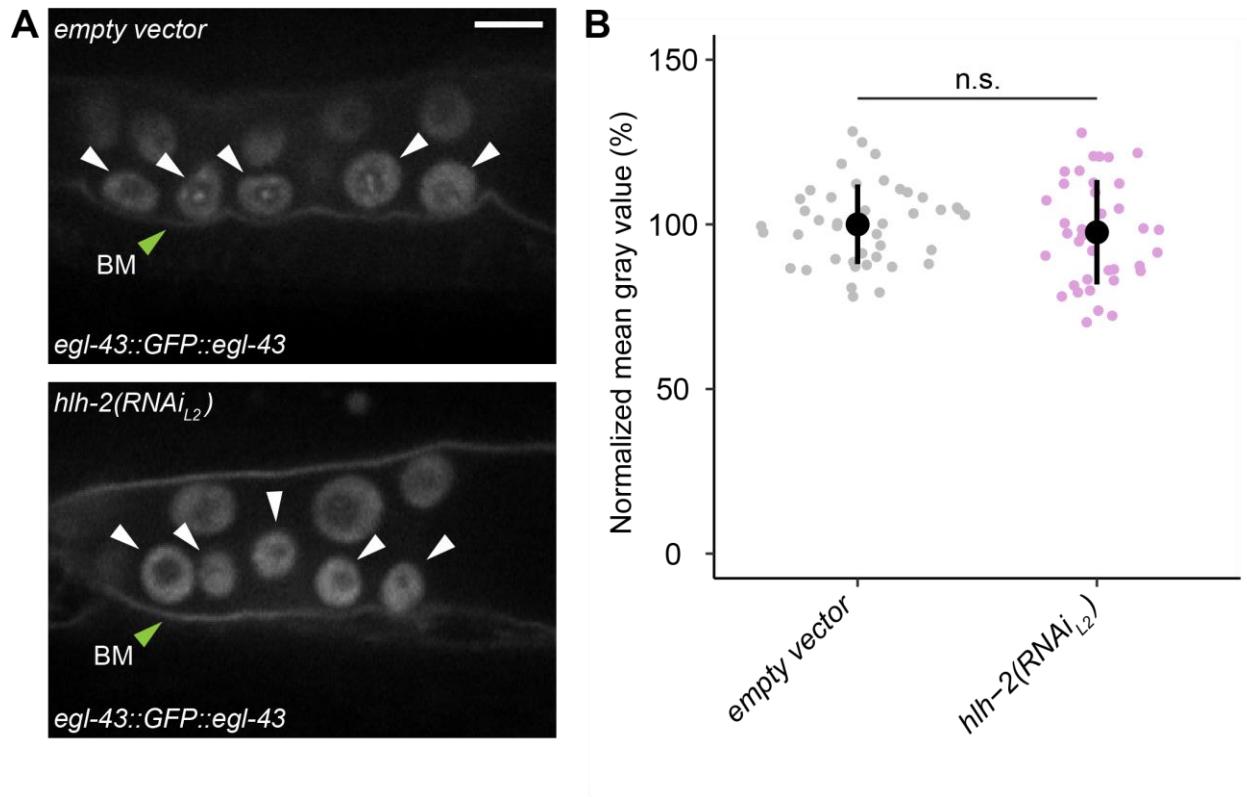


Fig S4. HLH-2 does not regulate EGL-43 expression in the ventral uterus. (A) Single plane of confocal z-stack depicting levels of *egl-43::GFP::egl-43* in the ventral uterine (VU) cells (white arrowheads) in empty vector controls (top) as compared to *hh-2(RNAi)* depletion. BM indicated by green arrowheads. (B) Sina plots of *egl-43::GFP::egl-43* levels, defined as the mean gray value of individual VU nuclei, following *hh-2* RNAi treatment ($n \geq 10$ animals, $n \geq 37$ VU cells quantified per treatment; n.s., not significant, p -value = 0.45, Student's t-test).

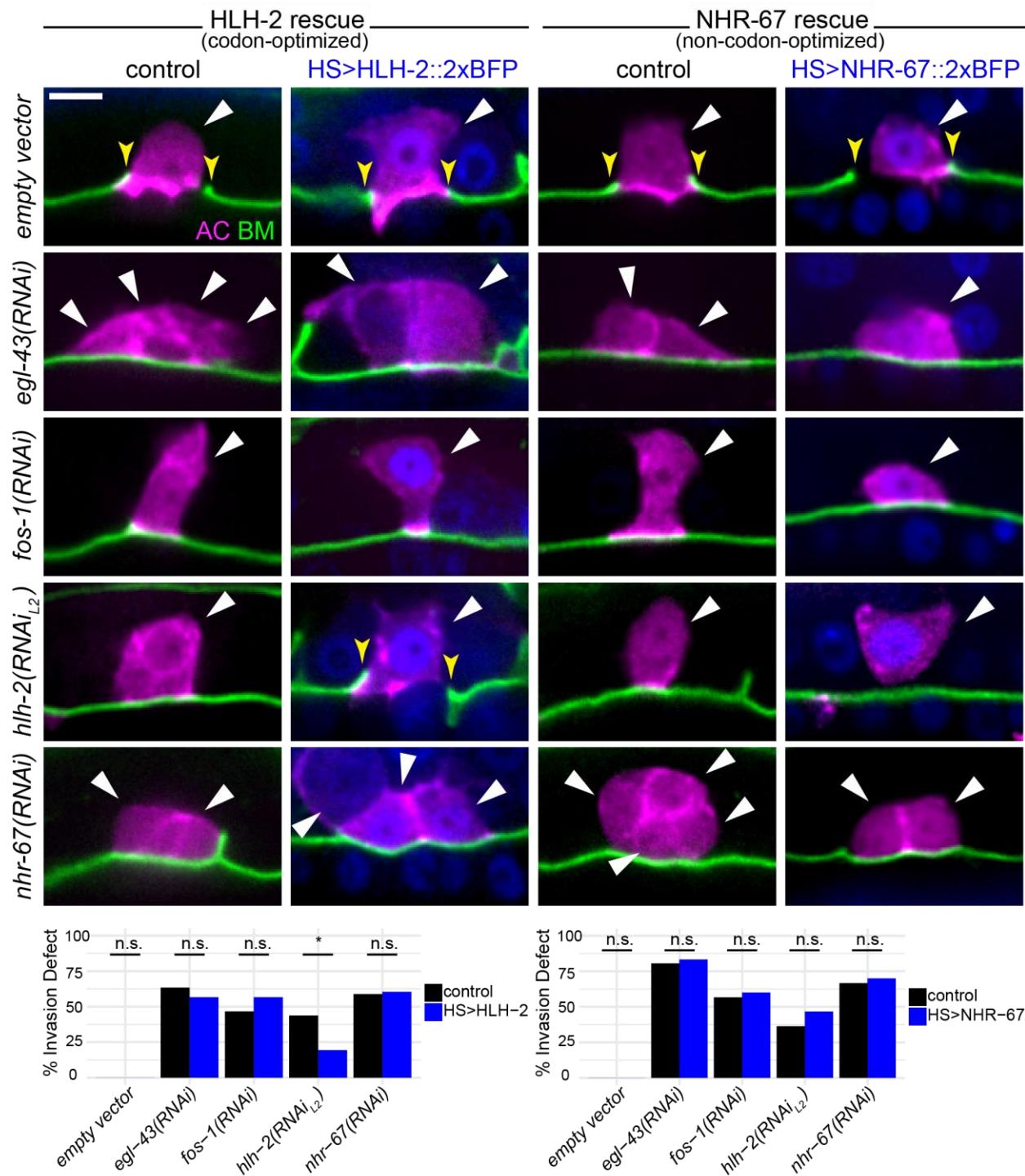


Figure S5. Induced expression of *hh-2* and *nhr-67* reveal cell cycle independent roles for *hh-2*. (A-B) Single planes of confocal z-stack depicting representative phenotype (single vs. multi AC) as fluorescence overlays (AC, magenta, expressing *cdh-3>mCherry::moeABD*, and BM, green) following no heat shock control (left) as compared

to heat shock induced expression of HLH-2::2xTagBFP (blue) (A) and NHR-67::2xTagBFP (B). (C-D) Bar graphs depict the penetrance of invasion defects in control (black) compared to heat shock induced HLH-2 (C) and NHR-67 (D) at the P6.p 4-cell stage ($n \geq 30$ animals examined for each RNAi treatment; n.s., not significant; *p-value < 1×10^{-6} ; Fisher's exact test).

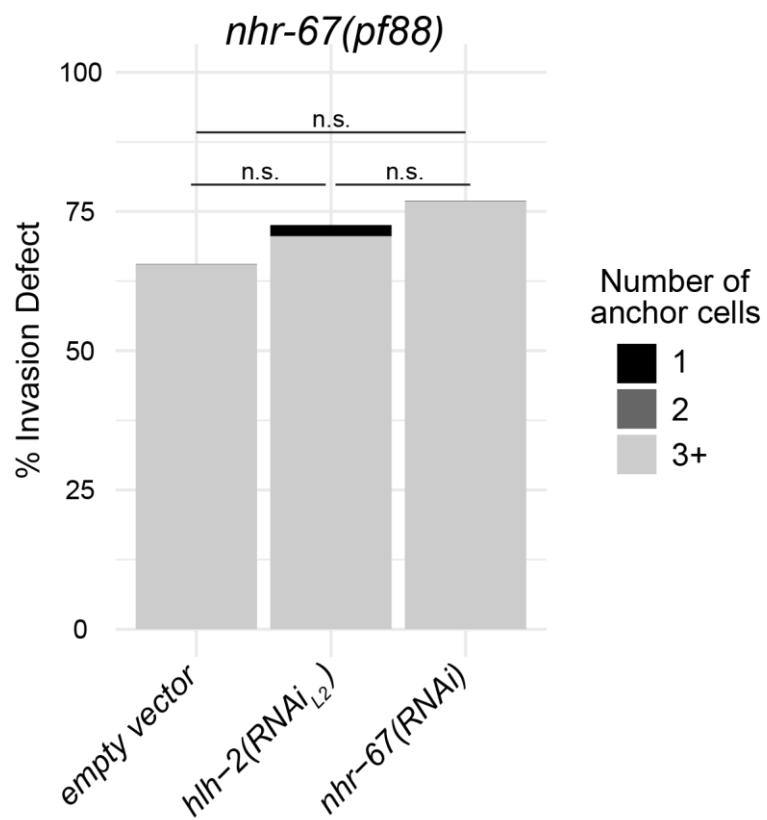


Figure S6. Depletion of *hh-2* does not significantly increase the invasion defect of an *nhr-67(pf88)* hypomorph. Bar graph depicts the penetrance of AC invasion defects at the P6.p 4-cell stage in control (empty vector) as compared to *hh-2(RNAi_{L2})* or *nhr-67(RNAi)* treatment ($n \geq 50$ animals examined for each RNAi treatment, n.s. not significant, Fisher's exact, p-value = 0.5350 (empty vector vs. *hh-2*), 0.1690 (empty vector vs. *nhr-67*) and 0.6676 (*hh-2* vs. *nhr-67*)).

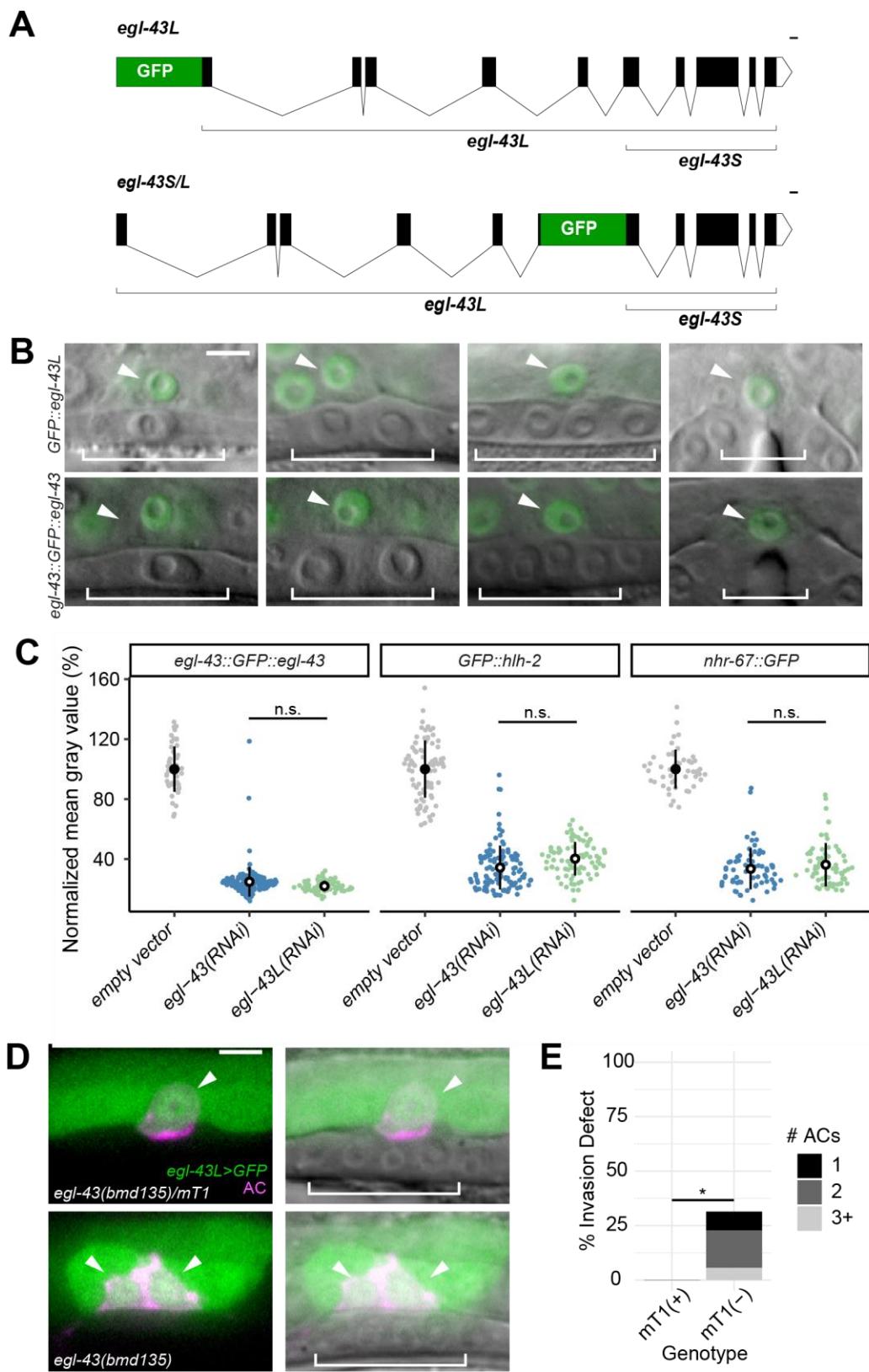


Figure S7. Both isoforms of egl-43 function redundantly to regulate AC invasion.

(A) Schematics (via <http://wormweb.org/exonintron>) of GFP insertion into the *egl-43* locus to tag the long (top) or both isoforms (bottom). Scale bar, 100 bp. (B) DIC overlaid with single confocal planes of *GFP::egl-43L* (top) and *egl-43::GFP::egl-43* (bottom). (C) Sina plots of GFP-tagged TF levels, defined as the mean gray value of individual AC nuclei, following RNAi perturbation ($n \geq 25$ animals for each treatment; n.s., not significant) between RNAi treatments targeting *egl-43L* and *egl-43*. (D) Single plane of confocal z-stacks depicting representative micrographs of control (top) versus *egl-43(bmd135)* animals expressing *egl-43L>GFP* (green) and an AC reporter (magenta). (E) Stacked bar graph depicting penetrance of AC invasion defect. Asterisk (*) denotes statistical significance between control and mT1(-) animals and represents a p-value $< 1 \times 10^{-3}$ by Fisher's exact test ($n \geq 25$ animals per treatment).

Table S1: Scoring table

*percentages may not necessarily sum to 100 due to rounding

Genotype	RNAi Treatment (gene, vector, L1/L2 plating)			P6.p stage	% Invaded (#ACs)				% Not invaded (#ACs)				n
					0	1	2	3+	0	1	2	3+	
<i>rrf-3(pk1426) II; unc-119(ed3) III; rde-1(ne219) V; fos-1a>RDE-1, myo-2>YFP; cdh-3>PH::mCherry; lam-1>LAM-1::GFP + unc-119(+)</i>	<i>empty vector</i>	T444T	L1	4-cell	0	100	0	0	0	0	0	0	50
	<i>egl-43(RNAi)</i>	T444T	L1	4-cell	0	12	1	0	0	27	19	41	75
	<i>egl-43(RNAi)</i>	T444T	L2	4-cell	0	63	0	0	0	37	0	0	30
	<i>egl-43L(RNAi)</i>	T444T	L1	4-cell	0	41	1	0	0	19	15	24	80
	<i>fos-1(RNAi)</i>	T444T	L1	4-cell	0	62	0	0	0	38	0	0	66
	<i>fos-1(RNAi)</i>	T444T	L2	4-cell	0	73	0	0	0	27	0	0	30
	<i>hlh-2(RNAi)</i>	T444T	L1	4-cell	0	30	0	0	21	37	6	5	115
	<i>hlh-2(RNAi)</i>	T444T	L2	4-cell	0	57	0	0	0	36	6	1	83
	<i>nhr-67(RNAi)</i>	T444T	L1	4-cell	0	7	0	0	0	13	0	81	72
	<i>nhr-67(RNAi)</i>	T444T	L2	4-cell	0	43	0	0	0	37	17	3	30
	<i>empty vector</i>	T444T	L1	8-cell	0	100	0	0	0	0	0	0	50
	<i>egl-43(RNAi)</i>	T444T	L1	8-cell	0	40	5	5	0	0	4	45	55
	<i>egl-43L(RNAi)</i>	T444T	L1	8-cell	0	78	9	5	0	7	0	2	58
	<i>fos-1(RNAi)</i>	T444T	L1	8-cell	0	90	0	0	0	10	0	0	50
	<i>hlh-2(RNAi)</i>	T444T	L1	8-cell	0	41	3	0	24	24	1	8	76
	<i>hlh-2(RNAi)</i>	T444T	L2	8-cell	0	64	1	1	0	23	1	9	81
	<i>nhr-67(RNAi)</i>	T444T	L1	8-cell	0	32	0	0	0	0	0	68	57
	<i>empty vector</i>	L4440	L1	4-cell	0	100	0	0	0	0	0	0	30
	<i>egl-43(RNAi)</i>	L4440	L1	4-cell	0	55	0	0	0	0	0	45	31
	<i>fos-1(RNAi)</i>	L4440	L1	4-cell	0	84	0	0	0	16	0	0	32
	<i>hlh-2(RNAi)</i>	L4440	L1	4-cell	0	69	0	0	9	16	0	6	32
	<i>hlh-2(RNAi)</i>	L4440	L2	4-cell	0	80	0	0	0	13	3	3	30
	<i>nhr-67(RNAi)</i>	L4440	L1	4-cell	0	40	0	0	0	7	0	53	30
<i>cdh-3(5kb)>CKI-1::GFP; zmp-1>mCherry</i>	<i>empty vector</i>	T444T	L1	4-cell	0	100	0	0	0	0	0	0	51
	<i>egl-43(RNAi)</i>	T444T	L1	4-cell	0	10	0	0	0	90	0	0	31
	<i>fos-1(RNAi)</i>	T444T	L1	4-cell	0	20	0	0	0	80	0	0	35
	<i>hlh-2(RNAi)</i>	T444T	L2	4-cell	0	92	0	0	0	8	0	0	77
	<i>nhr-67(RNAi)</i>	T444T	L1	4-cell	0	100	0	0	0	0	0	0	42
<i>laminin::GFP; zmp-1>mCherry</i>	<i>empty vector</i>	T444T	L1	4-cell	0	100	0	0	0	0	0	0	27
	<i>egl-43(RNAi)</i>	T444T	L1	4-cell	0	19	3	0	0	30	22	27	37
	<i>fos-1(RNAi)</i>	T444T	L1	4-cell	0	49	0	0	0	51	0	0	53
	<i>hlh-2(RNAi)</i>	T444T	L2	4-cell	0	56	0	0	0	31	3	10	59
	<i>nhr-67(RNAi)</i>	T444T	L1	4-cell	0	47	0	0	0	0	35	18	62
<i>egl-43>LoxP::GFP::EGL-43; cdh-3>mCherry::moeABD; laminin::GFP</i>	<i>empty vector</i>	T444T	L1	4-cell	0	100	0	0	0	0	0	0	68
	<i>egl-43(RNAi)</i>	T444T	L1	4-cell	0	0	0	0	0	8	14	78	158
	<i>egl-43(RNAi)</i>	T444T	L2	4-cell	0	16	0	0	0	78	0	6	32
<i>hlh-2>LoxP::GFP::HLH-2; cdh-3>mCherry::moeABD; laminin::GFP</i>	<i>empty vector</i>	T444T	L1	4-cell	0	100	0	0	0	0	0	0	83
	<i>hlh-2(RNAi)</i>	T444T	L2	4-cell	0	24	0	0	0	76	0	0	50
<i>fos-1>LoxP::GFP::FOS-1; cdh-3>mCherry::moeABD; laminin::GFP</i>	<i>empty vector</i>	T444T	L1	4-cell	0	100	0	0	0	0	0	0	74
	<i>fos-1(RNAi)</i>	T444T	L1	4-cell	0	18	0	0	0	9	5	68	120
	<i>fos-1(RNAi)</i>	T444T	L2	4-cell	0	93	0	0	0	7	0	0	30
<i>nhr-67>NHR-67::GFP; cdh-3>mCherry::moeABD; laminin::GFP</i>	<i>empty vector</i>	T444T	L1	4-cell	0	100	0	0	0	0	0	0	70
	<i>nhr-67(RNAi)</i>	T444T	L1	4-cell	0	15	1	0	0	0	11	73	130
	<i>nhr-67(RNAi)</i>	T444T	L2	4-cell	0	76	0	0	0	6	0	18	34
<i>egl-43L>SEC::GFP::EGL-43; laminin::GFP; cdh-3>mCherry::moeABD;</i>	N/A			4-cell	0	67	3	0	0	8	17	6	51
<i>egl-43L>SEC::GFP::EGL-43/mT1; laminin::GFP; cdh-3>mCherry::moeABD</i>	N/A			4-cell	0	100	0	0	0	0	0	0	25
<i>nhr-67(pf88); qyls227[cdh-3>mCherry::moeABD] I; qyls7[laminin::GFP] X.</i>	<i>empty vector</i>	T444T	L1	4-cell	0	34	0	0	0	0	0	66	58
	<i>hlh-2(RNAi)</i>	T444T	L1	4-cell	0	23	0	0	0	0	0	77	51
	<i>nhr-67(RNAi)</i>	T444T	L1	4-cell	0	27	0	0	0	1	0	71	65

Table S2: Rescue experiments**percentages may not necessarily sum to 100 due to rounding*

Genotype	Condition	RNAi Treatment (gene, vector, L1/L2 plating)			P6,p stage	% Invaded	% Not Invaded	n
<i>bmd142[hsp>HLH-2::2xBFP] I; qyls225[cdh-3>mCherry::moeABD] V; qyls7[laminin::GFP] X.</i>	control	<i>empty vector</i>	T444T	L1	4-cell	100	0	30
	control	<i>egl-43(RNAi)</i>	T444T	L1	4-cell	37	63	30
	control	<i>fos-1(RNAi)</i>	T444T	L1	4-cell	53	47	30
	control	<i>hlh-2(RNAi)</i>	T444T	L2	4-cell	56	44	32
	control	<i>nhr-67(RNAi)</i>	T444T	L1	4-cell	41	59	34
	heat shocked	<i>empty vector</i>	T444T	L1	4-cell	100	0	30
	heat shocked	<i>egl-43(RNAi)</i>	T444T	L1	4-cell	43	57	30
	heat shocked	<i>fos-1(RNAi)</i>	T444T	L1	4-cell	43	57	30
	heat shocked	<i>hlh-2(RNAi)</i>	T444T	L2	4-cell	81	19	31
	heat shocked	<i>nhr-67(RNAi)</i>	T444T	L1	4-cell	40	60	43
<i>bmd121[LoxP::hsp>NHR-67::2xBFP] I; qyls227[cdh-3>mCherry::moeABD] I; qyls7[laminin::GFP] X.</i>	control	<i>empty vector</i>	T444T	L1	4-cell	100	0	30
	control	<i>egl-43(RNAi)</i>	T444T	L1	4-cell	19	81	30
	control	<i>fos-1(RNAi)</i>	T444T	L1	4-cell	43	57	31
	control	<i>hlh-2(RNAi)</i>	T444T	L2	4-cell	64	36	33
	control	<i>nhr-67(RNAi)</i>	T444T	L1	4-cell	33	67	30
	heat shocked	<i>empty vector</i>	T444T	L1	4-cell	100	0	30
	heat shocked	<i>egl-43(RNAi)</i>	T444T	L1	4-cell	17	83	30
	heat shocked	<i>fos-1(RNAi)</i>	T444T	L1	4-cell	40	60	30
	heat shocked	<i>hlh-2(RNAi)</i>	T444T	L2	4-cell	53	47	30
	heat shocked	<i>nhr-67(RNAi)</i>	T444T	L1	4-cell	30	70	30

Table S3: Strains

Strain	Genotype	Description	Figure(s)	Source
NK1316	<i>rrf-3(pk1426) II; unc-119(ed3) III; rde-1(ne219) V; qyls102[fos-1a>RDE-1, myo-2>YFP]; qyls24[cdh-3>PH::mCherry]; qyls10[lam-1>LAM-1::GFP with unc-119(wt)]</i>	uterine-specific RNAi strain with AC and BM markers	1, 6, S1	Matus et al., 2015
GS9129	<i>arTi145[ckb-3>mCherry::H2B] II; lin-12(ar624[lin-12>LIN-12::GFP]) III.</i>	endogenous <i>lin-12</i> GFP reporter with somatic gonad marker	2, 7	Attner et al., 2019
DQM337	<i>egl-43(bmd88[egl-43>LoxP::GFP::EGL-43]) II; qyls225[cdh-3>mCherry::moeABD] V.</i>	endogenous <i>egl-43</i> GFP reporter with AC marker	2, S7	This study
DQM497	<i>fos-1(bmd138[fos-1>LoxP::GFP::FOS-1]) V.</i>	endogenous <i>fos-1</i> GFP reporter	2	This study
DQM352	<i>hh-2(bmd90[hh-2>LoxP::GFP::HLH-2]) I; qyls225[cdh-3>mCherry::moeABD] V.</i>	endogenous <i>hh-2</i> GFP reporter with AC marker	2	This study
DQM291	<i>nhr-67(syb509[nhr-67>NHR-67::GFP]) IV; qyls227[cdh-3>mCherry::moeABD] I.</i>	endogenous <i>nhr-67</i> GFP reporter with AC marker	2	This study
DQM335	<i>egl-43(bmd88[egl-43>LoxP::GFP::EGL-43]) II; qyls225[cdh-3>mCherry::moeABD] V; qyls7[laminin::GFP] X.</i>	endogenous <i>egl-43</i> GFP reporter with AC and BM markers	2-3, 7, S3, S4, S7	This study
DQM515	<i>fos-1(bmd138[fos-1>LoxP::GFP::FOS-1]) V; qyls227[cdh-3>mCherry::moeABD] I; qyls7[laminin::GFP] X.</i>	endogenous <i>fos-1</i> GFP reporter with AC and BM markers	2-3, 7, S3	This study
DQM350	<i>hh-2(bmd90[hh-2>LoxP::GFP::HLH-2]) I; qyls225[cdh-3>mCherry::moeABD] V; qyls7[laminin::GFP] X.</i>	endogenous <i>hh-2</i> GFP reporter with AC and BM markers	2-3, 7, S3, S7	This study
DQM368	<i>nhr-67(syb509[nhr-67>NHR-67::GFP]) IV; qyls225[cdh-3>mCherry::moeABD] V; qyls7[laminin::GFP] X.</i>	endogenous <i>nhr-67</i> GFP reporter with AC and BM markers	2-3, 7, S3, S7	This study
DQM7	<i>qyls330 [laminin::mCherry]; qyls232 [CDT-1::GFP]</i>	G1 cell cycle phase reporter with BM marker	4	Matus et al., 2015
DQM533	<i>zmp-1(qy17[zmp-1>LoxP::GFP]) III; qyls225[cdh-3>mCherry::moeABD] V</i>	endogenous <i>zmp-1</i> GFP reporter with AC marker	4	This study
DQM39	<i>qyls17 [zmp-1>mCherry] II; qyls266[cdh-3(5kb)>CKI-1::GFP] V</i>	<i>zmp-1</i> mCherry reporter with AC-specific CKI-1 over-expression	5	Matus et al., 2015
NK272	<i>qyls7[laminin::GFP]; qyls17[zmp-1>mCherry]</i>	<i>zmp-1</i> mCherry reporter with BM marker	5	Matus et al., 2015
DQM503	<i>egl-43(bmd87[egl-43>SEC::GFP::EGL-43] II/mT1; qyls227[cdh-3>mCherry::moeABD] I; qyls7[laminin::GFP] X.</i>	endogenous <i>egl-43</i> transcriptional reporter (with SEC) balanced over mT1 with AC and BM markers	6	This study
DQM444	<i>bmd121[LoxP::hsp>NHR-67::2xBFP] I; qyls227[cdh-3>mCherry::moeABD] I; qyls7[laminin::GFP] X.</i>	heat shock inducible NHR-67 with AC and BM markers	S5	This study
DQM552	<i>bmd142[hsp>HLH-2::2xBFP] I; qyls225[cdh-3>mCherry::moeABD] V; qyls7[laminin::GFP] X.</i>	heat shock inducible HLH-2 (codon-optimized) with AC and BM markers	S5	This study
DQM266	<i>nhr-67(pf88); qyls227[cdh-3>mCherry::moeABD] I; qyls7[laminin::GFP] X.</i>	nhr-67 hypomorphic mutant with AC and BM markers	S6	This study
DQM500	<i>bmd135[egl-43L>SEC::GFP::EGL-43] II/mT1; qyls227[cdh-3>mCherry::moeABD] I; qyls7[laminin::GFP] X.</i>	endogenous <i>egl-43L</i> transcriptional reporter (with SEC) balanced with mT1 balancer with AC and BM markers	S7	This study
DQM494	<i>egl-43(bmd136[egl-43L>LoxP::GFP::EGL-43]) II.</i>	endogenous <i>egl-43L</i> GFP reporter	S7	This study
DQM300	<i>egl-43(bmd88[egl-43>LoxP::GFP::EGL-43]) II.</i>	endogenous <i>egl-43</i> GFP reporter	Will be made available through the CGC (cgc.umn.edu)	
DQM497	<i>fos-1(bmd138[fos-1>LoxP::GFP::FOS-1]) V.</i>	endogenous <i>fos-1</i> GFP reporter		
DQM311	<i>hh-2(bmd90[hh-2>LoxP::GFP::HLH-2]) I.</i>	endogenous <i>hh-2</i> GFP reporter		
PHX509	<i>nhr-67(syb509[nhr-67>NHR-67::GFP]) IV.</i>	endogenous <i>nhr-67</i> GFP reporter		

Table S4: Primers

Primer	Primer sequence (5'→3')	Primer type	Amplicon	Template
DQM657	tcactatagggagacggcaATG	Forward	<i>hlh-2</i> and <i>nhr-67</i> synthesized DNAs for T444T	Twist Biosciences gene fragments for <i>hlh-2</i> , <i>nhr-67</i>
DQM658	attgggtaccggcccc	Reverse		
DQM688	gagctcAGATCTatgagcatcgacacagactc	Forward	BglII- <i>egl-43L</i> -Xhol for T444T	Twist Biosciences gene fragment for <i>egl-43L</i>
DQM689	acgtacCTCGAGctgacttgacacgtgggc	Reverse		
DQM720	TCACTATAGGGAGACCCGCAATG	Forward	BglII- <i>egl-43</i> -Sall for T444T	<i>egl-43</i> IDT gBlock
DQM722	GCCCCCCCCTCGAGGTGCGAACTTTGGCAC CGGAAC	Reverse		
DQM708	ggttgcgccacctgacttg	Forward	colony PCR screening of T444T constructs	T444T-based constructs
DM191	gttaatcgcactcaatagggcgaatgg	Reverse		
DQM433	ACGTTGTAAAACGACGCCAG	Forward	amplify left homology arm (universal)	Twist Biosciences gene fragments
DQM434	CTCCAGTGAACAATTCTCTCCTTTACTC	Reverse	amplify left homology arm (universal)	
DQM435	GCGTGATTACAAGGATGACGATGAC	Forward	amplify right homology arm (universal)	
DQM436	GAAACAGCTATGACCATGTTATCGATTCC	Reverse	amplify right homology arm (universal)	
DQM751	tcctattgcgagatgtttGgtatgtcatccgtaaaacttGTT TTAGAGCTAGAAATAGC	Forward	<i>fos-1a</i> sgRNA	pDD122
DQM747	tcctattgcgagatgtttGgtatgtcatccgtaaaacttGTT TTAGAGCTAGAAATAGC	Forward	<i>egl-43L</i> sgRNA	pDD122
DQM438	tcctattgcgagatgtttGgtatgtcatccgtaaaacttGTT TTAGAGCTAGAAATAGC	Forward	<i>egl-43</i> sgRNA	pDD122
DQM440	tcctattgcgagatgtttGAGTTTCAGAACCTCAA TGGGTTTAGAGCTAGAAATAGC	Forward	<i>hlh-2</i> sgRNA	pDD122
DQM412	AGATTGTACTGAGAGTGCACCATATGCGG TGTGAAATACCGCAC	Reverse	amplify sgRNA (universal)	pDD122

Table S5: Plasmids

Plasmid	Base vector	Description
pTNM011	pDD122	<i>egl-43</i> internal sgRNA
pTNM012	pDD282	<i>egl-43::GFP::egl-43</i> repair template
pTNM013	pDD122	<i>fos-1</i> N-terminal sgRNA
pTNM014	pDD282	<i>GFP::fos-1</i> repair template
pTNM015	pDD122	<i>hlh-2</i> N-terminal sgRNA
pTNM016	pDD282	<i>GFP::hlh-2</i> repair template
pTNM046	pDD122	<i>egl-43L</i> N-terminal sgRNA
pTNM047	pDD282	<i>GFP::egl-43L</i> repair template
pTNM051	pAP088	heat shock inducible HLH-2 (codon-optimized)
pWZ172	T444T	<i>egl-43</i> RNAi
pWZ173	T444T	<i>egl-43L</i> RNAi
pWZ174	T444T	<i>fos-1</i> RNAi
pWZ175	T444T	<i>hlh-2</i> RNAi
pWZ176	T444T	<i>nhr-67</i> RNAi
pWZ193	pAP088	heat shock inducible NHR-67

Table S6: CRISPR reagents

Gene	Guide	Left homology arm sequence	Right homology arm sequence
egl-43 (internal)	aagtcagatgccatcacaag	CTAAGATGAGAACCGTTACAGAGTCCTTTA TAGAATTGGTTTATAATAGAGATGTATGGAA ACCGGGCAAAGTTAATTAGGATCTTACGCCAA CAAGAAAATTTAAGATAAGTAACGCCAAACTT GAGCAGGAGTTGAAAGTTCAGTGATTACAATTGA AGTTTTATTATTATTATCTTGGCTAGAA TAGATGGAGCATCTCACAGGACTGGACTTATAT AATGGCTATCTGCCTGCCTACCTGCCTTC GTTTATTACTGTATTGCGCAATAAACTCA TGCATTCTATTGTTAGAAGTTAAAAAAACAAAT ATTTAGAAAACGTTACATGACTTGTAGTTGG CTCGCATGTTGGCAGAAGGCAGGCACAGGGAAAC CCTGAAGGCACTTAGGCAGGTTGCTGGACAAA ATACCTGCTGATTGCTGATTATTCTACTAAT ATAATCAGATGAAACATGGACAATTGGTACAA ATACTAATAGGGTGTACTGCTATAACTCTC CGAACAAACCTAACAGTCATTACATTCACTAT CACGTGTTATCAATCAATTTCAGCGGCTCTCA AACAAACACTCTCATATTCAATTGCTCCTAAAGCCG TTTCGGTGCATTGTCAGGACCCGGAGAGTTCAT TCAGTGAGTTATTAGAGTTCTAAGAATAAA ACTGAGCACTGTAATAATCTATCGCAATGCTC CTGGGCTAAAGCTCTTAAAGAGGAGGATAAAA CTGAATAAACCCCATAATCTCACAAACAGGGGGAA AAACTCGAGGCGTGGTCAGAAGGTTATTGCTCT CTGTACTAATAAAACGGAACGATTCAATGATG TGCCCCCACCTGAGGTGGTCCCTCCTTAATTGT TTACCCCGTGAGAAAAGTGCAGGAGGCCATGATG CTCCGCCCTTCTCTCAACCAAATAAGCACAG CGCGCCGCCATCCCTCGCATCTTCTTGG GGTGTGTCACAGGGCTATTCTTGACGTGCG CTTCCCACCTTACCTAGTGTATTCAATCCGT CTTATTCAATTAGTGAATAAAATTCCAGGAGGGT GGACGTGCCAACGTGTCAGTCAG 	ATGCCATCACAAAGCGGCACTAACGAGCATGAC CAGTTTGCAGATGACTGCACTCTACAAACCATTG ATGGCGCAACTTGCCTGGATTGAGCGGAGCAGGTG GATTAGGTTCCGTGCCATATTGGCCACATATACTT CAAATGGCAACACAGGTTAGTTATTATTGAAA TCAACTATAGATACCGTCTCCCCTATTACTATTGCA TCCCATATTCAACTTGCACGCTTATATTGAGTT TCCGTTGTCACATGAAATGATCAATTGGCCA ATTTTTATTATTCTCTCTATAGTTGTAGTTG ATAAAAATATCAAATCGTCATAATGAACCGAGATA AGCATTCAAAAGTGAATAGTGGGCTGCAATAGAG GAAATAAGGTAATTTCCTCACCCCCCTGACTATA CAACACTCTTGAGAGTATCCATGGACAACAATCAT CGTACCTTAATTAAACCTACCTTAAGCCTCC ACCTCTCATCTCCGCTTAATGATACCTTCA TTCCCGCATCTGGGGCTTAATCCTCTTCT CTCTCCTCAAGCGGCTAATGAACATGCACTCATT TTCAGGCACACATTCCGCTGCTTCTGCC GCCAATCCAGAAGCGTACAAACTGATGCA CGACGTGTCATCTCCAGATGCCAGTGTCCAG GTTTGTGAATGTTATATGGTAATCAAAAAAAA GTGGAGTAGTCTCTTACTCTTATCAATAATTGATT TATTCTATTCACTTCTAGACTGAGAAGCTAA TATATTGATAGAAAACACAAAAAAATCAATT TTCCAGTGGACATGCCAGTGAATCTCACC CAACTGAACCAAGTCGACCTAACAGCTACAC CCTCCTCGACGCTGAAATGAAACTACATCAA GTCGACGATGGAGAGGATCGTACAGCATCGGA GACTCTGGGAATGATGATGATGACTCAGAAC TGAGGTTAGATGAGTCGTCACACAAACGTC CGAAAAAGCGCCGACATCTCACACAATTCCGAC ATACTCGCTGTCACAACTCGGTGCTCAGGCTT GAATTGACGTTCTGGCATGCTCAGCGCTCG TTAATTATAATCCAGCAGTCCATGCCACTCAT TTC
egl-43L (N-terminus)	gatgctcatcctaaaaactt	TATTTCCGTCAGCAATTACTTCCAAAATTCA AACTAAGTCATAGTTGTTAGTTAAGTTGG TCTTGATTAGGAGCAGTCGTTAAACTCGCAG CCGACCTCGATGGAGTCGCGATAGCCTACTC CTGGAAAAAACGTTGCTCTGCTTCACCTCAT GATATCAGGAAACTTATTACAGACATTAGCCGA CAAATAACCGCTTGGCTTACTAGAAATGCTC AATAGATTCAATTAGTAGGTGTAGATATTCA CTTTGTTATTCTAAGTATCGAAGTACATATG TTAGAAAGTAAATAAAATTGCTATTCTACTTAA GAATTTCATTTAAAGTCTTAGTAAGCTG GGGTTTCAAGCTGCAACTTCAAGTGAAGAT GCTCTCCTCGTCAAGCATCTGTCACTCTACGA TTGGCTGATGGCGTGTCTCCATCTTCC ACCGCCCACTTTGAGACAGGAGAGGCTCTC GCTCCTCTCGCATCCACAAATGGAAGGCCCT TTCCATCTCTTCTTCTGGTTAGTTGAA GTATCCTAAAGTATCTTGACGTTTACTATAT GACTCTGGAGAGACATTGAGTTTGGTCAA ATATAGAATGTCAAATTGAGAGCAATCTC ATATGTCATTTCATCAAAATTGTTATCTC GTGGTGTGAGAACCTCAAAAATACTCTA AATTAAGAATTCTGATTAAAAGTACTAGCA AATTGTCATGAAAATCTCAACGAATTCTC AGTCATCTACCAATGAAATTGGCTTGAAC TTTCACCATCTACTAAAATTCAATAAAATA TCTCTCCCAAACCTACACCTCCCTCAATCT CAGCTTACTCTAACCTCTATCCAAATTGTC TCTACCGTACCATCTCCCTGTTGCTCTCA ATGACAAAGCCAGCCTGAACAGCCATATCCA TTTCGTTGATTGTTCTCGTTACAAGATGTAT TACTCATCTTCGCCCCAAAAGTGTCTGAA TGTACAGTTCTGTTCTCCACGTACAGTT TAAGTTTCAGG	ATGAGCATCGACACAGACTTCTCACGAGTGTGA GGTAAAGGAGGATGAGCTACATGAAATGTGCTC ATTCAGTAACTCAAATTGCACTCGGAAGGACCAT CGGTGTGATTGATAAGGTGAGCTTGGTGTCAA TTTTACGCCCTAGACATTGCTTAGAGGTGTC CTAGAAAAAGAGTAAAGCTTATTCCGGGCTC TAAAAAAACTCCACCGGAAAAAAACAGGTC GCTTGAACGAAATCTTATAGCTGAGTAACCTAT TAAGCTTCACTGATGTTACACTCATATTGTTAG AGTATGTTATGATAACAGTAATTAGTTGTTAAT TGATAAAATAATGACTTTAAATTACAAA TTTTAAATATTCTACAGCTTAAATTGATACC TTGGTGCCTAATCTACCTAATCTACAGTAC CCAAACATTCTCAATCTCTCTAATGATT TCGAATTACAATTCTCCAGAACCCAAA AATTATCGGGACCCGAAATGTTGGGCCATGTG TTCCCTCCCTGCTTCTCTCTCAAAATT CCTGCTTCCACCTTCCGCTCCCCCGTCC TACCACTTTGTTAACCTGGGGCACACTGTAAC CATTACATTAGGATT

<i>fos-1A</i> (N-terminus)	ccactctttatatacgaga	<p>CTTAGACATCCCATCCAAATTTAACATGTTGCGTGTGCTTGGGTCAACAAACGACACATACCTGTTA GTGTCATCCTCGTCCCGCGTGCACGCATCGCAC TGAATCATCGGTATTCATCACCTCTCTGCAAT CAACGAGCCAATGCCAATTGGGTTATTGAGTT AGAAACTCGGGAAAGCTTCACAGAAGAAATAATTAA GCTGAATTGGCAAAAGAGAGCACCTGCTCCCCGG AATGTCATACTTTGAGATAAAAAGAAGGGAGA CGACGACGTCTCGGTTCTCTATCCCAAACAAAT ACCATTTGTTCCCATCTCGTCTCGATGTTG CTGACTCACCATCAATATCTAAACAGAAAGCACC CAATGGTTGCCTTTTGCTCTTCTGACAG TTTCTGTTTTTGATGTTACATAAATACCGTA CACCCACCATCTAGTCATTGTCACATATTGAA TCAAAAGTTCAAAAACCTCGTCACCTTAA CACAGTCCGTCGGCCACCCCGTACCGAGCCGG CGTTTCTGGTGTATCATTGGGGTGGCTCTT TGAAAATTCAAATTGGTGTGTCCTCCCGAAGG TGTGGGCGGAGCTGCGCACCGTCCGGTGGC CGTTGCTCGACAGTTCTTCCCTCGCTC CTTCTCTCTCAACCAAAACCTGCCCCACAC GCAACTTCTTGTATCGCTGTCCTGTC AAAGATAACAATCACCCGTGTTGCTAATCTCA CCTAGAAGAGTCATCTCGTGAATCAGAATCCCT TTTCTCCCTACTTTCACTTCTATTCCGG TTACTCACCTCTGTGTTGGCCCCGATCGTGTG TCAGCACGTCTGCTATATAAGAGAGTGCA</p>	<p>ATGTTCGAACACCATCGTCGACGACTAACAC CACGAGCTCTGGTTCTGGCTCCGATTCCAATCACT ACTTCGAATTGGTCCAGGAACCGATCAACCAA GCGCACCCGACATCAGTCATTGTTCACCGCGAC AACATCACCATCAGATCCACCAACAAACCGAC AACTCACCTCAACTCCGTCACCCATATTATCCA TCAAATGTCATATGGACTCCCTTATTCTTGGAACT GATTTCCTGCAGGTATGATACATCACAAATATCTTC CTTAATTCACTGTTACTCAAAGTCACACTATTCCC TTGCTAATAATCACGAGTTGATAGAGCTTTAAA TCATTACTTCACTCATTTCACTCAACCTCGAGC CTTACATTGTCAGTTGATCTCTTCTTCCCATATA AAAATGAGGATATAGTAGCTTACTTCATTTAGTT AATATTAATTGCAAAAGTCAACACAAAAAGTAAA GCGTCACTAATTCTTGTGCAAAAGTCAG AAAAAGTTACCTAGCTCTGAATCTTCCCTCAA AAATGTTCTTACAGCCATCTCCCCGGATTAG TTCGGAAAAATAAAACTATTGGTTATGGATTAAA TGATATGGTAGGTGGTCACGAGGAATCTAAA AGAAGATGCCGACGTGTTACACACTTACAGTA ATCTATCTATCTTACCTTCTCATGCACCTGCTAAT TTGTCATCTTACCTCTCATGCACCTGCTAAT CCCTTGGATTGTTCTGTTGCACCTGTTGAAA AAAGATAAGTAATACTTATATGTTAACCTTCCGG TGCCAGTGAATAATTACAGGCACGCAAATTNTTA AATATTCAAAAAATCTGTCACCTCTGTTGAGC TTG</p>
<i>hfh-2</i> (N-terminus)	agttttcagaacccatcaatgg	<p>GACTGGTGAATGAATGGTGGGAGAAGAGAGATGGA GGACCCCGGGATAATAGAGGAGATGGTGTGTCGA GGAGGTAGAGAGAGATGGTGTGGGCGTGCACCT CTCCCGATCATCGTCTCTCGCTCTGGATGTA GACGGTCCCCGGAGAAAGAATGTCTGCGTCTA TGTACACCAATATACTGTTATGTCCTGGAATGG GCTTTATACCGTCCCTCCACTACCACCC CGAAGAACATTCCCTAGCCACCCGATAGCCGCT AAAGAGGGGGAGTCACCTCTGTT TGTCATAATCTGTCGTTACTAGCTTCAA GTTCATGATCTACTGTAATAACATAGCACATA TTTGAATGAAATACATAATGTCATCCATCTG ATTTGAAATTAAAATTCTCTCCCTCCAAATTTC AATTGGATCTTACCAAATAATTGATCTGCA TTACTTTCTCACTCTACAAATGTTACGAATCC TTACCAATTGAAATTAAACAAGAACGCAAATGT ATTGTAGGGCAGTTTTTCAATTATTGAGGTTA TCAAAAAATGTATATTGTCATCCGAAATGTTACTA GCTCACGTTAAAGCTTCATATATCTTACCT ACGTCTGAAATTAAACTAATTATTGATGGGCT GAAACCCCTTGTATCCATACCCCTTACTGTTATT TTATGCTTTGGATGTCATCCATCGATAAT CATCTACAATGACATCTACATTACAACATTCTT GATACCCTCAACATCATTACCTCCCTACAAATT GTTCTCTTCAAGTAATTGCTCTAATAATT ACCGGAACCTAGTAGATCTATTGTCACGTCACAA TTATTATTCTTATTGATCTACCTTCCCTTTGA TCTCGTTGCCATTAAACAAACGAGGAGAATC GATTATTCTCTTCTTCTATTCTCAATT CAAATGGGGTGTCTGACGAAATCTAATCAGA ATATATTACTAACCTAATTCTCACCTGCTGCTC CAGCCCAATTCCCTACTTATCCCTCCCTCTCCC CGCTTCTCCGCTGACTTTATTCTTGACATTACT ACTATAATCGTCTTCATATCATTGCGAGAAATA AGATTTCAAGAACCTCA</p>	<p>ATGGCGGATCCAAATAGCCAACCTACGTCAGCCAC AACTGTTGCAACTGCCGCCATTGCTCAACCACAGG TTATGCTTCAAATGTCATATGATTATCCTTATAATA TTGATCCGACACGATTAGTCAGATGCCTGATTATTGG AGTGGTTAGTCCTTTTCTTGAATCTTAA TTCAATTATATCATTGTTAAACCAACAAACAT GTTTCGTAATTGTTAAAGTCGCTGTTAATCAG TTGAAATATTGGATAATTGCAAGAAAAGGATATA AGTTGGTATTACTTATCTGAAATTGTTGAATTGTT GATTATAAGCTCGCAAATTAAAATTACTTTA AGTGAACAAAATGTATAACTCTTTAATGTTCTA AAATTGGTAAAATCTGTTGCTCTAGTAAGTAG TTATTAAACCAAAATGTTATATCTCATCTCAAGT GCAAGTCATCAAATAACATTTCAGGATACCATC TCAACCCGATCTCTCCGATGCAAACACGGATATT GATTATTCTCATGCCCTCTCCACACATCCAC AACTGAAACCCCTGCTCCGTAAGTCGCTCAA CTGCAACATCTGATATTAGCAAATTCTGCAACAT CATCCACTCAACGACGGCTCCATCTACTGCTCCA GCTCCAACCTCAACTACTGATGTCGTTGAGTTAAA GCAAACACAGCTCCAGCCACGAAATTCTGCGAGAA ACATCAGCGATTGTTGCTCCACAGCCTCTACTAA TCTTACCGCACAATTGACGCAAATGTCATCAATGT ATACATGGCCACAAACATATCCAGGTTACCTTCCA CCTTCAGAAGATAACAAAGCAAGTGAAGCTGTTAA TCCATACATCTCAATCCCTCCAAACATATACATTG TGCTGATCCATCAGTTGCCGACTTCTCATGTCATC AGCAGCAACTGCTGGACAGCCGGTACGTTCTAT TCTCTGGTTTACTGCTGTTACTGTTTACCA CAAGTTAATCTCGACGAATGATTGCTGGCCCTCC TCAGCCGCAAGCATTACGTATGCAATACTCGCT TCTTGTGATGTGAGGCCGCCCTCTGAAGATTG AGATGTCATGCAAAGGGGGCATCTTCTGAGAAGA ACACCCCTGTGCGCACTAACGACCTCC</p>
<i>nhr-67</i> (C-terminus)	ccacgtcattcgattcgatcatat agagagttaatgttgaagagg	N/A (made by SunyBiotech)	N/A (made by SunyBiotech)

Table S7: RNAi vectors

RNA Target	Synthetic gene block
<i>egl-43L(RNAi)</i>	TCACTATAGGGAGACCGGCAATGAGCAGTCAGACAGACTTCTCACGAGTGTGAGGTAAGGAGGATGAGCTACATGGAA ATGTGCTCATTCAGTAACTCAAATTGCACTCGAAGGACCATCGGTGATTGATAAGGCTACACCGAATGATTGAATGC TCTCTCATCTAACCTGATTAAGGAAGCTGATGACGGAGAAGATGCCAATATTGTATGAGGCAGGAGGATAGAAAGACT TTTCTACAAACCAGTAAGATTCAATATTGGAGAGCGTCTTCTACAAAGACTGTCGAAGGAGGTGTGATGAGGAGG ATCAGGATGATCTGAGAATTAAATTGTAAAAGATGAAGATCGGCCGAGACTACTCAAAGCTGCACAAAGAGCAGCAG TGAAGACAGCAATCTAACCGGTTTGAGGAGTATTCGAGAACACGGCAACTGTACCTGGTCAAACGCCCTCCGACGG ATCACACAAGTGTGGAGTTGTCCAAGAGTTTCAAGTCAAGCGGTCAAACAAACACTCTCATATTCTATTGCTCCTAA AGCCGTTCCGGTGTCAATTGTGTCACACACAATTCTCAAATCTGTGCAAGGACCGGAGAGTTCATTGACAGCG TTGGACGTGCCAACGTTGCAAAGTCAGGGGGGGGCCGGTACCAAT
<i>egl-43(RNAi)</i>	TCACTATAGGGAGACCGGCAATGCCATCACAGGGCACTAACAGGAGCATCGGACAGCTTGGAGATGACTGCACTCTACA AACATTGATGGCGCAACTTGGCGATTGAGCGGAGCAGGTGGATTAGTGTCCGATATTGGCCACATATACTCAAAT GGCAACACAGGCACCACATTCCCGCTTGTCTTCTGCGGCCATCCAGAAGCTACAAACTGATGCAAGCAGCAGCTG TGCATCTCCAGATGCCAGTGTCCAGTGGACATGCCAGTGAATCTCACCAACTACAACACTGAACCAAGCTGACCTAACAGCT ACACAAAACCTCTCGACGCTGAAATGAAACTACATCAAAGTCCGACGATGGAGAGGATGTCAGCAGCATGGAGAC TCTGGGAATGATGATGATGACTCAGAAGCTGGAGTTCTAGATGAGTCGTCCACAACAGTCAACGAAAAGCGTCCG ACATCTCACACAATTCCGACATACTCGCTGCTCCACAACGCTGTCAGGCTTGAATTGACGCTTCCATTGGCATGCTTC AGCGCTCGCTTAATTATAATTCAGCAGTGTCCATGCCCTACTCATTTCTAAGGACATGCGAGGAGGAAAGCATCATC ACCAAGCTGAGCAGTGGAAAGGATAGGTACAGCTGCAAGTCTGTCAGAAAGTGTCCCAGAGTCAACGAGCATT GACAAGACATTAAGGACACATACAGGAGAGCAGCTTATAAGTCAATTGCAAGGAGGAAAGTCTCAATCTCTCAAAT TTGCAACGCCACGTTAGAAACATTCTAAATAAGCGAACACCTCGCTGACACCCCCACAATCATCATGTCACAGTCTGC ACAATTCAACCTCAACCTCCACTACTACTACCTACCGTCCATCATCTCTTCATCTTCAGGAACGTCCGGTGC AAAGTTACCGGGCCCCCTCGAGG
<i>fos-1(RNAi)</i>	CTCACTATAGGGAGACCGGCAAGTATGGTACAGTATAGCACGGTAAGAAATCGTCGGTGGAGAAAACCTAAAGAAG AGGATAATATGGAGGATGACGATGATAAGAGGCTGAAACGTCGCAAGGAATAAGAAGCTGCTGCAAGATGTCGGC AAAGGAGAATTGATTGATGAGGAAATTGCAAGATCAAGTAATGACTCTAAAAATAGCAACGACAAAAAAATGGCGGAATG CAACACATCCGAAATAAGCTCAACAGTCTCAAAACTATTGGAACAGCATGATTGAAACTGAGTCGCGAAGAACAGAAC CATGAGATAATCGATTGATAATCCACCATCACAGTCCACCATCACACCATATCTTCACACATTGAGGAGTTCATCC ACACAGTGTGACTCTGTACCATATTCTATTGATCAGGACATTCTCATCGTCTGAACAACACTCACCAAGTTGAGGACT ATAAGCCTCAATTGATCAATTACTCTCTCCAACTCTCATGTTAACATGAAATATCAATTCTATGCCACC ACCAGCTTACCGGCAAGCACGAGTGTCTGTTGAATTCTATCCCTATCCGGTTTGCATGCCACTCATTAC GGTCGTTGAAACGTTTCGAGAACCGGAACGCAAATTCACCGGAGTCAAGTGTGGACAAACACTGACATCATTGACCA TGCCAGACGACGTTGAACGTCGTCAGCTCTCGACGCTTCCAGAATCGTGAAGGAAATCAGCCGATCACTACTCCAGCA GGCCTTCCGTCGGGGGGAAATCAAAACACCGCAGAGTACAGGAATGGACTATTGGAGGCCACCCAGGC CCATTGACTGCTTCTCCAACACTGGTCTGACACCTTCTGGTCAAGGAAACATGAACACTGCTTCAACTCCAAACCCGAT TCAACCACATCCGGATGTCATCTCGGACACTCTAGGTGCACTCGAGGGGGGGCCG
<i>hlh-2(RNAi)</i>	TCACTATAGGGAGACCGGCAATGGGGATCCAATAGCCAACCTACGTCAAGGCCACAACGTTGCAACTGCGGCCATTGCTC AACACAGGTTATGCTTCAAATGCAATGATTATCTTATAATTGATCCGACAACGATTGAGTCCTGATTATTGGAGT GGATACCATCTCAACCGTATCTCGATGCAAACACGGATATTGATTATTGATCAGCCTCTTCAAACACATCCACCAAC TGAACACCCCTGCTTCCGTAGCTGCTCCAACTCTGCAACATCTGATATTAGCAATTGCAACATCATCCACTTCAACGA CGGCTCATCTACTGCTCCAGCTCAACTACTGATGTGCTTGAAGGCAACACAGCTCCAGGCCAGAATT TGCAGAAACATCGCATTGTTGCTCCACAGCCTCTACTAATCTACCGCACCAATTGAGCAGTCAATGTCATCAATGTC GGCCACAAACATATCCAGGTTACCTCCACCTCAGAAGATAACAAAGCAAGTGAAGCTGTTAACATCCACATCTCAATCC CCAACATATACATTGGTCTGATCCTCATGTTGCGACTTCTCATCGTATCGAGCAGCAACTGCTGGACAGCGGAATGTC TTGGTGGAGATAACCAACTTGGTACTACAATCATCAATTCCACCGAGCGTATGAGCCCACACTTGTACCAAATGGATA TCCAGGAATGCCAACAGGATCAAGTGCATCATGTTGCAAGTCAAGGCTTCAACTCGCATTCTCATCGTCTCAAGGCTTCT TCGTCGGGTACAAGGCCCTCCATCTGAAATTCAACTCGCATTCTCATCGTCTCAAGGCTTCTGATAATGAATCAATGA GTGATGACAAAGATA CGGATAGGAGATCACAGAATAATGTCGAGAAAGAGTACGAGTGTGACATCAGGGGGGGCCG GTACCAAT
<i>nhr-67(RNAi)</i>	TCACTATAGGGAGACCGGCAATGAGTACTGCGGTTTACAGATGTCGTTCAAGCAGTCGAATTCTATTGGATGTTGATTG TAGAGTCTGTGAAGATCATTGTCGGGGAAAGCATTACAGTATTCTCTGCGACGGGTGCTGGATTCTTAAACGTC TCCGTCGTATCGTAACAGTGTGCAAAACAAAGGAGCTCCATCGGAGAACATGCAAAAGTGGACAAACACACCGC ACCAAGTGCAGAGCTGCCACTAAGAAAGTGTCTGGAATTGGGATGAAACAGATGCTGCAACATGAGAGAGGGC GTAACACTCAAGTTAACAGCACAACAGATGATGTTGATCATGGATCCTCTCTAATTGCGGAAATGGGATCAGAAAGTGA TGCACAAATTCTCCGACATCATCAATGAAATGTCGACACAGTGGCGGACTGCTGCTGCAATTCTGACTTGTGGAT TTTGTCAAGAACCTTGTGAAATGGAGTACCTAACAGAACGGCAATGACAATGTTCAACAAATTGGGAGCAGCACTTCT CATGCAACTGAAACACGTGCCATAACTCTAAGCAAATAAGGACTGAGACGATATCCGGTAGCTCAGAGCAAAGAAATGCG GTTGCTAACCGCTTGAATAATTGAAACGTTACAATTGGATAATAGAGAATACATGATGTTGAAACATTTCACAATGTGGAG AGATAACACCAAGTGCACATTCAAAATTGCTTCTGAGTACATGTTGAAACATTTCACAATAGAACCGAACCGACGAGATA TCCAATGATAATGCAATTGCCGATTCCAACACTCTCAATAATTGATGTTCTATTCCGCCCTCAATTGGATCAGCTCAA TGCAGACTTATTCAAGACATGTCAGGCCACCAACAACCCACTCTACGTCACTGTTCCAATGGGGGGGGCCG TACCAAT