Table S1. Illumina-HiSeq 3000 sequencing run statistics. All reads 150bp, paired end. All nematodes at L1 stage. Assembled using WS242 *C. elegans* reference genome in CLC with parameters described in Materials and Methods. Overall nuclear coverage (Avg Nuc Cov) calculated for entire nuclear genome per line. Average mitochondrial coverage (Avg mtDNA Cov) calculated for whole mitochondrial genome coverage per line. Standard deviation of the mean displayed in parentheses adjacent to mean values.

Line	Total Reads	Percent Mapped	Avg Nuc Cov	Avg mtDNA Cov
N2	20,728,966	79.83%	24 (0.6)	783.3 (119.1)
gas-1 G0	18,773,512	79.95%	21.8 (0.7)	835.0 (130.0)
RC 1	19,786,862	81.69%	23.8 (0.7)	918.9 (203.9)
RC 2	19,247,616	81.07%	22.7 (0.7)	1164.8 (182.1)
RC 3	21,439,774	80.93%	25.3 (0.7)	1181.2 (184.9)
RC 4	16,474,084	79.60%	19.2 (0.7)	905.7 (141.7)
RC 5	19,538,046	82.19%	23.5 (0.5)	1093.3 (178.9)
RC 6	19,619,022	81.42%	23.3 (0.5)	1126.8 (200.9)
RC 7	21,495,750	80.90%	25.5 (0.5)	1309.4 (221.6)
RC 8	16,295,230	79.21%	18.7 (0.7)	1267.2 (196.5)
RC 9	22,938,664	82.50%	27.7 (0.7)	1418.3 (276.9)
RC 10	22,568,108	80.31%	26.5 (0.5)	1199.1 (172.4)
RC 11	20,643,212	81.39%	24.7 (0.7)	1475.5 (218.5)
RC 12	18,032,434	78.77%	20.8 (0.7)	987.9 (177.7)
RC 13	21,139,024	80.92%	25.0 (0.8)	975.3 (167.5)
RC 14	20,883,266	81.24%	24.8 (0.7)	1005.6 (167.1)
RC 15	20,963,736	80.87%	25.0 (0.8)	835.2 (140.4)
RC 16	22,865,822	80.92%	27.0 (0.8)	1200.1 (224.6)
RC 17	21,378,998	82.74%	26.0 (0.8)	1126.3 (183.5)
RC 18	21,058,244	82.17%	25.5 (1.0)	918.8 (156.3)
RC 19	20,711,046	81.42%	24.5 (0.5)	1017.7 (171.5)
RC 20	19,369,868	81.33%	23.0 (0.6)	919.8 (160.9)
RC 21	21,488,148	82.19%	26.0 (0.8)	1179.7 (189.3)
RC 22	20,626,582	82.57%	25.2 (0.7)	965.8 (163.2)
RC 23	20,960,498	82.22%	25.3 (0.7)	1046.2 (189.6)
RC 24	18,399,798	80.77%	21.8 (0.7)	697.0 (123.8)

Table S2. Two-way mixed-model ANOVA for *gas-1* G0 and *gas-1* RC life-history traits.

Fitness relative to N2

Source	SS	d.f.	MS	*F* ratio	*p* value
Strain	0.332	1	0.332	0.489	0.4919
Line(Strain)	7.896	23	0.343	20.44	<0.0001
Model	8.245	24	0.344	20.45	<0.0001
Error	1.646	98	0.017		
Total	9.892	122			

Fitness relative to *gas-1* G0

Source	SS	d.f.	MS	*F* ratio	*p* value
Strain	22.06	1	22.06	0.659	0.4257
Line(Strain)	390.8	23	16.99	16.73	<0.0001
Model	413.9	24	17.24	16.98	<0.0001
Error	99.51	98	1.015		
Total	513.4	122			

Absolute fitness

Source	SS	d.f.	MS	*F* ratio	*p* value
Strain	39790	1	39790	1.793	0.1966
Line(Strain)	279000	23	12130	5.108	<0.0001
Model	320000	24	13330	5.615	<0.0001
Error	230000	98	2375		
Total	550000	122			

Table S3: Normalization of mean mtDNA copy number. All reads 150bp, paired end. All nematodes at L1 stage. Assembled using WS242 *C. elegans* reference genome in CLC with following parameters: no masking, mismatch cost= 2, insertion cost=3, deletion cost= 3, length fraction= 0.98, read fraction= 0.98, global alignment= no, non-specific match handling= map randomly. mtDNA copy number normalized by mean coverage of corresponding single-copy nuclear genes (Norm mtDNA). mtDNA mean coverage calculated excluding AT-region (Avg Norm mtDNA Cov). Average single-copy nuclear coverage (Avg Single-Copy) calculated from average of three single copy genes: *ama-1* (Avg *ama-1 Cov*), *ego-1* (Avg *ego-1 Cov*), *efl-3* (Avg *efl-3 Cov*). Standard deviation of the mean displayed in parentheses adjacent to mean values.

Line	Avg Norm mtDNA Cov	Avg Single Nuc Cov	Avg *ama-1* Cov	Avg *ego-1* Cov	Avg *efl-1* Cov
N2	120.6 (16.1)	20.5 (6.5)	23.2 (7.0)	26.4 (7.3)	11.8 (7.2)
gas-1 G0	128.2 (16.8)	19.4 (6.5)	19.8 (6.1)	27.0 (8.7)	11.2 (7.3)
RC 1	116.5 (22.9)	20.5 (7.9)	24.4 (8.0)	27.1 (6.8)	9.9 (7.3)
RC 2	157.8 (20.1)	19.3 (7.4)	20.9 (6.4)	27.2 (7.5)	9.8 (5.8)
RC 3	164.2 (20.2)	21.3 (7.3)	24.5 (7.6)	28.1 (7.6)	11.2 (7.7)
RC 4	133.2 (17.6)	18.0 (6.8)	20.3 (6.9)	24.8 (6.8)	8.8 (5.6)
RC 5	153.5 (20.1)	20.5 (7.2)	22.7 (6.7)	28.0 (6.7)	10.9 (7.1)
RC 6	165.7 (23.8)	20.0 (6.9)	24.6 (8.9)	25.1 (7.1)	10.3 (6.1)
RC 7	207.0 (28.8)	22.4 (6.4)	24.4 (6.5)	28.8 (7.3)	13.9 (9.1)
RC 8	223.0 (27.6)	15.3 (5.7)	18.0 (4.9)	20.2 (5.3)	7.8 (5.2)
RC 9	192.1 (33.1)	22.1 (7.4)	23.2 (7.0)	30.1 (8.3)	12.9 (6.5)
RC 10	186.7 (20.1)	22.4 (6.5)	25.9 (7.9)	28.4 (7.8)	13.1 (6.9)
RC 11	230.1 (24.9)	20.3 (6.5)	23.4 (6.8)	26.4 (9.5)	11.2 (6.5)
RC 12	133.7 (20.5)	19.3 (7.4)	20.5 (6.5)	27.6 (7.5)	9.7 (6.0)
RC 13	164.6 (25.3)	20.8 (5.9)	24.6 (6.5)	25.6 (9.5)	12.3 (6.0)
RC 14	123.3 (17.8)	21.5 (8.2)	21.8 (6.6)	31.2 (7.9)	11.5 (6.5)
RC 15	117.2 (17.3)	20.5 (7.1)	24.6 (7.0)	26.6 (6.3)	10.4 (6.5)
RC 16	172.3 (27.7)	23.6 (7.0)	24.7 (6.8)	31.9 (8.2)	14.2 (8.1)
RC 17	161.1 (20.5)	21.9 (7.1)	23.3 (7.1)	29.9 (9.7)	12.6 (6.8)
RC 18	110.8 (17.0)	21.3 (8.3)	23.5 (7.1)	30.0 (8.5)	10.3 (6.0)
RC 19	165.9 (24.6)	20.2 (6.2)	20.2 (6.2)	27.9 (8.1)	12.5 (7.5)
RC 20	157.7 (25.0)	19.4 (5.8)	20.7 (6.6)	25.5 (6.8)	11.8 (6.3)
RC 21	170.5 (22.1)	22.3 (7.0)	25.8 (9.6)	28.5 (8.2)	12.5 (7.3)
RC 22	156.6 (22.4)	21.1 (6.2)	24.4 (7.1)	26.7 (6.3)	12.1 (7.3)

RC 23	121.9 (19.3)	22.4 (8.6)	23.4 (6.6)	32.3 (9.3)	11.3 (5.9)
RC 24	98.2 (14.7)	19.3 (7.1)	25.0 (7.8)	23.4 (6.3)	9.4 (6.2)

Table S4. *gas-1* G0 mutations lost within RC lines. List of four mutations present in the backcrossed *gas-1* G0 ancestor compared to the wildtype (N2) reference strain sequence that were subsequently lost within individual RC lines during laboratory evolution. Ch = chromosome, Mut Type = mutation type, Ref Codon = reference codon in N2 sequence, Ref AA = reference amino acid in N2 sequence, Mut Codon = mutation codon in *gas-1* G0, Mut AA = mutation amino acid in *gas-1* G0, Line(s) = RC lines numbers in which each mutation was lost. The chromosome X SNP residing within an intron of *fox-1* was lost by three RC lines each belonging to the higher-fitness class (Figure 1) and noted as having high male frequency; the other three SNPs (on chromosomes II, V and X) were lost by different RC lines each belonging to the lower-fitness class and not noted to have evolved high male frequency.

Ch	Position	Mut Type	Gene	Type	Ref Codon	Ref AA	Mut Codon	Mut AA	Line(s)
II	1302680	G:C → C:G	emc-2	Exon	GTC	Val	GTG	Val	RC6
V	18718740	A:T → T:A	Y17D7C.2	Intron					RC1
X	2445717	A:T → T:A	fox-1	Intron					RC3, RC12, RC24
X	14203413	G:C → A:T	ceh-37	Intron					RC14

Table S5. mtDNA single-nucleotide polymorphisms. Variant refers to alleles differing from the WS242 reference genome and wildtype N2 control. Ref Nuc = reference nucleotide, Ref Cov = coverage of reference allele, Var Nuc = variant nucleotide, Ref Codon = reference codon, Ref AA = reference amino acid, var codon = variant codon, Var AA = variant amino acid, site specific variant frequency (Var Freq) was calculated by dividing number of variant calls (Var Cov) by the total coverage at the position (Ref Cov + Var Cov).

Line	Pos	Gene	Ref Nuc	Ref Cov	Var Nuc	Var Cov	Total Cov	Var Freq	Ref Codon	Ref AA	Var Codon	Var AA
N2	5079	cytb	G	6	A	640	646	0.9907	GGG	Gly	GGA	Gly
N2	4391	tRNA-Gln	C	3	T	740	743	0.9960				
N2	8429	cox-1	A	5	G	870	875	0.9943	GTA	Val	GTA	Val
RC 3	2154	nduo-1	T	7	C	1095	1102	0.9936	ATA	Met	ACA	Thr
RC 3	9145	cox-1	C	1246	T	33	1279	0.0258	CCG	Pro	CTG	Leu
RC 4	219	nduo-6	G	772	T	30	802	0.0374	AGT	Ser	ATT	Met
RC 5	1977	nduo-1	C	683	T	403	1086	0.3711	TCA	Ser	TTA	Leu
RC 13	227	nduo-6	G	40	T	721	761	0.9474	GTT	Val	TTT	Phe
RC 13	5079	cytb	G	919	A	66	985	0.0670	GGG	Gly	GGA	Gly
RC 14	8057	cox-1	T	1073	A	45	1118	0.0403	ATT	Met	ATA	Met
RC 17	851	tRNA-Glu	G	1052	T	39	1091	0.0357				
RC 18	227	nduo-6	G	5	T	662	667	0.9925	GTT	Val	TTT	Phe
RC 19	10846	16S-rRNA	G	939	T	30	969	0.0310				
RC 19	11734	nduo-5	G	881	T	23	904	0.0254	GGT	Gly	GTT	Val
RC 22	1977	nduo-1	C	1	T	907	908	0.9989	TCA	Ser	TTA	Leu
RC 24	227	nduo-6	G	1	T	542	543	0.9982	GTT	Val	TTT	Phe

Table S6. RC line nuclear mutations. RC line mutations were identified by mapping to WS424 N2 reference sequence. All mutations in *gas-1* RC lines compared to *gas-1* G0 progenitor and wildtype (N2) Denver lab reference strain sequence to eliminate Denver-lab N2 variants. Ch = chromosome, Ref Nuc = reference nucleotide, Mut Nuc= mutation nucleotide, Cov = coverage at position. Mutation type was categorized as either intergenic (IG), intronic (IN), exonic (EX), or pseudogene (PS). Ref codon = reference codon in WS424 genome, Ref AA = reference amino acid in WS424 genome, Mut codon= mutation codon, Mut AA = mutation amino acid, Syn/Non indicates if mutation was synonymous or non-synonymous.

Line	Ch	Position	Ref Nuc	Mut Nuc	Cov	Type	Gene	Ref Codon	Ref AA	Mut Codon	Mut AA	Syn/Non
RC 1	I	12,782,722	A	G	6	IG						
RC 1	II	4,642,450	A	T	7	IG						
RC 1	II	14,338,105	G	A	9	IG						
RC 1	V	9,603,829	T	C	7	IG						
RC 1	X	8,651,733	A	T	5	IG						
RC 2	III	7,425,423	C	A	8	IG						
RC 2	IV	7,591,706	A	G	5	EX	tag-80	AAG	Lys	AGG	Arg	Non
RC 2	V	5,084,795	A	G	6	EX	Y58A7A.4	GAT	Asp	GAC	Asp	Syn
RC 2	V	5,084,806	C	A	6	EX	Y58A7A.4	GCA	Ala	TCA	Ser	Non
RC 2	V	17,412,257	C	A	6	IG						
RC 2	X	5,283,318	G	A	5	IN	Y34B4A.2					
RC 3	I	1,413,024	T	C	7	EX	set-29	AAT	Asn	AAC	Asn	Syn
RC 3	I	15,01,842	C	T	11	IN	Y92H12A.5					
RC 3	I	13,203,218	T	G	23	IG						
RC 3	III	7,415,219	A	C	21	IG						
RC 3	V	1,164,088	C	T	24	IN	T21H3.5					
RC 3	V	13,645,972	T	C	8	IG						
RC 3	X	7,607,385	C	T	30	IN	twk-17					
RC 4	I	10,137,355	C	T	5	IG						
RC 4	X	4,028,900	A	T	7	IG						
RC 5	III	3,386,567	T	A	5	IG						
RC 5	III	3,897,472	A	G	10	IN	tir-1					
RC 5	X	4,037,336	G	A	6	IG						
RC 5	X	14,679,813	T	A	36	IN	slt-1					
RC 5	X	17,447,220	G	A	11	IG						
RC 6	I	8,623,736	A	G	28	EX	fer-1	AGA	Arg	GGA	Gly	Non
RC 6	II	6,669,203	C	T	6	EX	T19D12.1	AAC	Asn	AAT	Asn	Syn
RC 6	III	12,004,543	A	T	6	IG						
RC 6	III	12,004,552	G	A	6	IG						
RC 6	IV	6,794,092	C	T	32	EX	C17H12.3	CTC	Leu	CTT	Leu	Syn

RC 6	IV	8,580,642	T	C	5	IG						
RC 6	X	6,687,376	A	T	21	IG						
RC 6	X	7,206,440	C	T	28	IG						
RC 6	X	13,634,317	A	T	31	IG						
RC 7	III	2,500,192	T	G	6	IG						
RC 7	III	4,947,709	A	G	32	IG						
RC 7	V	19,683,735	G	T	5	IN	mrp-7					
RC 7	X	14,763,281	G	T	31	EX	Y16B4A.2	GGG	Gly	GGT	Gly	Syn
RC 8	III	2,282,489	G	T	6	IN	Y54F10BM.3					
RC 8	X	17,441,843	G	A	5	IG						
RC 9	II	4,308,972	A	T	10	IG						
RC 9	V	6,086,004	C	A	5	IG						
RC 10	IV	12,731,956	G	A	5	IG						
RC 10	V	10,340,073	C	T	28	IN	K07C5.2					
RC 10	X	4,425,834	G	A	22	IG						
RC 11	IV	7,642,263	T	C	22	IN	nlp-20					
RC 11	V	5,358,409	T	G	22	IG						
RC 11	X	2,347,297	C	A	17	IN	T01B6.1					
RC 11	X	2,884,067	C	T	16	IG						
RC 12	X	11,976,631	C	G	6	IG						
RC 12	X	14,908,742	G	C	5	IG						
RC 13	I	34,362	C	G	22	IG						
RC 13	I	9,403,794	C	G	24	IN	F16A11.1					
RC 13	I	12,181,325	C	A	23	EX	abdh-11.2	TTC	Phe	TTA	Phe	Syn
RC 13	III	1,849,254	A	T	5	IN	pqn-82					
RC 13	III	4,634,881	C	T	24	IN	F10F2.2					
RC 13	IV	5,871,330	C	T	25	PS	srv-18					
RC 13	IV	7,899,075	G	A	13	IN	atic-1					
RC 13	IV	11,272,487	C	T	22	IG						
RC 13	V	11,114,001	G	A	22	IN	math-33					
RC 13	V	14,297,743	G	A	20	PS	F14D7.4					
RC 13	X	3,821,608	G	T	17	IN	fkh-9					
RC 14	IV	8,574,587	A	T	6	IG						
RC 15	V	9,981,010	G	A	6	IG						
RC 16	II	694,578	T	G	6	IG						
RC 16	II	3,797,273	T	A	13	EX	Y8A9A.2	CTG	Leu	CAG	Gln	Non
RC 16	II	4,260,898	T	C	5	IG						
RC 16	III	12,347,900	T	C	5	IN	pph-4.1					
RC 16	V	4,140,793	G	A	24	EX	lgc-29	ACG	Thr	ACA	Thr	Syn
RC 17	III	5,357,452	C	T	5	IG						

RC 17	V	12,864,657	A	G	11	IN	T07F10.6						
RC 17	V	12,864,661	C	G	11	IN	T07F10.6						
RC 18	I	6,644,090	C	A	18	IG							
RC 18	III	7,415,236	G	A	25	IG							
RC 18	IV	3,208,939	G	C	25	PS	puf-4						
RC 18	IV	17,063,015	A	C	8	IN	Y116A8C.467						
RC 18	V	6,087,148	A	T	6	IG							
RC 18	V	9,603,864	C	T	6	IG							
RC 18	X	17,445,113	G	A	8	IG							
RC 19	I	8,008,052	C	G	27	EX	C54G4.2	CCA	Pro	CGA	Arg	Non	
RC 19	III	1,441,904	C	T	21	EX	Y82E9BR.2	CGT	Arg	TGT	Cys	Non	
RC 19	IV	7,128,174	A	G	6	IN	str-50						
RC 19	V	2,763,471	A	G	20	IG							
RC 19	X	14,908,867	G	C	9	IG							
RC 20	I	12,360,758	A	T	21	IN	oac-43						
RC 20	II	1,422,675	T	C	14	IN	Y51H7C.10						
RC 20	II	13,505,040	C	T	18	EX	F54F11.1	CAA	Gln	TAA	Stop	Non	
RC 20	III	958,048	T	A	35	IG							
RC 20	IV	9,047,795	C	G	5	IG							
RC 20	IV	15,020,193	G	A	23	IN	Y41E3.7						
RC 20	V	14,756,564	C	T	24	IG							
RC 20	X	10,549,806	C	T	21	IN	syd-2						
RC 20	X	12,276,980	G	T	7	IG							
RC 21	II	696,862	T	C	5	IG							
RC 22	I	10,116,399	C	A	23	EX	Y106G6D.4	GCC	Ala	GAC	Asp	Non	
RC 22	I	10,948,653	T	G	8	IG							
RC 22	III	490,793	C	T	27	IG							
RC 22	IV	16,615,359	T	G	17	IG							
RC 22	V	10,379,220	G	C	29	EX	AC3.12	GTA	Val	CTA	Leu	Non	
RC 22	X	11,787,528	T	A	9	IG							
RC 23	IV	8,573,847	G	A	9	IG							
RC 23	V	6,173,736	G	T	14	EX	ttn-1	GAA	Glu	TAA	Stp	Non	
RC 23	V	17,173,442	C	A	27	IG							
RC 23	X	13,697,074	A	T	27	IG							
RC 24	I	10,225,483	T	C	9	EX	ced-12	TTA	Phe	TCA	Ser	Non	
RC 24	II	7,026,963	C	A	18	IN	C52E12.1						
RC 24	II	7,188,583	T	G	9	IG							
RC 24	II	7,188,585	G	T	9	IG							
RC 24	IV	11,614,944	C	G	10	IG							
RC 24	V	12,312,064	A	G	14	IG							

| RC 24 | V | 20,588,961 | A | G | 19 | IN | F26F2.7 | | | | | |

Table S7: Summary of *gas-1* RC line SNP-containing genes predicted to interact within two degrees of *gas-1*. Table is organized by "RC line SNP" = RC line genes containing SNPs predicted to interact with genes in *gas-1* network; i.e., "*gas-1* Interaction". Interaction values were obtained from Gene Orienteer. Asterisks denote interactions below the threshold minimum of 4.6. Note that two different mutation sites where observed within mitochondrial gene, *nduo-1*: 1977 bp and 2154 bp and are counted as two distinct mutations for a total of 13 mutations in 12 genes. Also note that each SNP-containing gene can interact with multiple genes within the *gas-1* network.

RC Line SNP	*gas-1* Interaction	Interaction Value	RC Line
C55F2.1	T22D1.3	9.2	RC 13
C55F2.1	Y57G11C.3	13.91	RC 13
C55F2.1	R04B5.6	14.72	RC 13
ced-12	hda-1	5.52	RC 24
F10F2.2	C31C9.2	5.68	RC 13
F10F2.2	T22D1.3	21.36	RC 13
F26F2.7	sod-3	4.76	RC 24
F26F2.7	sod-2	4.76	RC 24
F26F2.7	ero-1	14.41	RC 24
math-33	hda-1	6.33	RC 13
math-33	prdx-2	6.75	RC13
math-33	idh-1	13.18	RC 13
math-33	T22D1.3	15.55	RC 13
nduo-1	gas-1	7.58	RC 22
nduo-1	gas-1	7.58	RC 3
nduo-1	gas-1	7.58	RC 5
pph-4.1	hda-1	15.44	RC 16
slt-1	sod-3	5.32	RC 5
slt-1	unc-9	5.34	RC 5
slt-1	sdha-2	5.53	RC 5
slt-1	sdha-1	5.69	RC 5
slt-1	sod-1	6.04	RC 5
slt-1	sod-5	6.04	RC 5
slt-1	hda-1	10.97	RC 5
syd-2	unc-9	5.02	RC 20
tir-1	emb-8	5.29	RC 5
tir-1	duox-2	5.39	RC 5
tir-1	vps-34	6.01	RC 5
tir-1	sod-1	6.47	RC 5
tir-1	sod-5	6.47	RC 5
tir-1	lpd-5	7.76	RC 5
tir-1	hda-1	8.89	RC 5
tir-1	bli-3	21.92	RC 5

Y41E3.7	T05H4.4	5.35	RC 20
Y41E3.7	T05H4.5	5.35	RC 20
Y41E3.7	F08F8.2	5.35	RC 20
Y92H12A.5	gpd-2	12.12	RC3
*F16A11.1	cts-1	*0.79	RC 13
*F16A11.1	rnr-1	*0.79	RC 13
*F54F11.1	F08F8.2	*1.02	RC 20
*F54F11.1	Y56A3A.19	*1.02	RC 20
*fer-1	sod-2	*4.28	RC 6
*fer-1	sod-3	*4.17	RC 6
*fkh-9	unc-1	*1.61	RC 13
*K07C5.2	acdh-12	*0.86	RC 10
*K07C5.2	cts-1	*0.86	RC 10
*K07C5.2	DC2.5	*0.86	RC 10
*K07C5.2	ivd-1	*0.86	RC 10
*K07C5.2	let-721	*0.86	RC 10
*K07C5.2	sdha-1	*0.86	RC 10
*K07C5.2	shda-2	*0.86	RC 10
*K07C5.2	T27E9.2	*0.86	RC 10
*K07C5.2	trxr-1	*0.86	RC 10
*K07C5.2	Y57G11C.3	*0.86	RC 10
*nduo-6	gas-1	*2.05	RC 13
*nduo-6	gas-1	*2.05	RC 18
*nduo-6	gas-1	*2.05	RC 24
*ppfr-1	hda-1	*2.05	RC 6
*puf-4	hda-1	*2.04	RC 18
*puf-4	sod-1	*2.04	RC 18
*puf-4	sod-2	*2.04	RC 18
*puf-4	sod-3	*2.04	RC 18
*R05D7.4	fat-5	*4.37	RC 13
*R05D7.4	fat-6	*4.37	RC 13
*R05D7.4	fat-7	*4.37	RC 13
*R05D7.4	Y56A3A.19	*3.35	RC 13
*set-29	alh-1	*3.13	RC 3
*set-29	alh-2	*3.13	RC 3
*set-29	C31C9.2	*3.13	RC 3
*set-29	emb-8	*3.47	RC 3
*set-29	gspd-1	*3.86	RC 3
*T01B6.1	fat-6	*1.32	RC 11
*T01B6.1	fat-7	*1.32	RC 11
*T01B6.1	sod-1	*0.97	RC 11