Supporting Online Material for

Neuronal GPCR Controls Innate Immunity by Regulating Non-Canonical Unfolded Protein Response Genes

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Materials and Methods

Bacterial Strains

The following bacterial strains were used: *Escherichia coli* OP50 (*1*), *Pseudomonas aeruginosa* PA14 (*2*), *Salmonella enterica* serovar Typhimurium 1344 (*3*), *Salmonella enterica* SMO22 expressing GFP, *P. aeruginosa* expressing GFP. *E. coli*, *P. aeruginosa*, *S. enterica* cultures were grown in Luria-Bertani (LB) broth at 37°C.

Nematode Strains

The following *C. elegans* strains were cultured under standard conditions and fed *E. coli* OP50 (*1*). Wild-type animals were *C. elegans* Bristol N2. *octr-1(ok371)*, *pmk-1(km25)*, *daf-16(mu86)*, *ced-1(e1735),sek-1(km4)* and *pqe-1(rt13);rtIs11* strains were obtained from the *Caenorhabditis elegans* Genetics Center (University of Minnesota, Minneapolis, MN). The mutants *octr-1(ok371);sek-1(km4)*, *octr-1(ok371); ced-1(e1735)*, *octr-1(ok371);abu-1::gfp(zcEx8)*, and *octr-1(0k371);ced-1(e1735);abu-1::gfp(zcEx8)* were constructed using standard genetic techniques. FY745 *octr-1(ok371); grEx157 [Poctr-1::octr-1::gfp]* and FY746 *octr-1(ok371); grEx158[Psra-6::octr-1]* were kind gifts from Dr. Richard W. Komuniecki (University of Toledo, Toledo, OH).

C. elegans Killing Assay

C. elegans wild-type N2 animals and mutants were maintained as hermaphrodites at 20°C, grown on modified nematode growth medium (NGM) agar plates (0.35% instead of 0.25% peptone) and fed with *E. coli* OP50 as described (*1*). The bacterial lawns used for *C. elegans* killing assays were prepared by placing a 25µl drop of an overnight culture of the bacterial strains on modified NGM agar on plates 3.5cm in diameter. Full lawn plates used for *C. elegans* killing assays were prepared by spreading a 25µl drop of an overnight culture grown at 37°C of *P. aeruginosa* on the complete surface of modified NGM agar in 3.5cm diameter Petri plates. Plates were incubated at 37°C for 12~16 hours. Plates were cooled down at room temperature for at least one hour before seeding with synchronized young adult animals. The killing assays were performed at 25°C and live animals were transferred daily to fresh plates. Animals were scored at the times indicated and were considered dead when they failed to respond to touch.

C. elegans Lifespan assay on Heat-Killed Bacteria.

E. coli OP50 or *P. aeruginosa* PA14 were grown as described above. Bacteria were concentrated 1:10 and then heat-killed at 65°C for 3 hours. Bacterial death was confirmed by failure to grow on LB plates at 37°C overnight. A 25µl drop of the killed bacteria was plated on a 3.5cm plate of modified NGM agar containing 50µg/ml ampicillin. The assays were performed at 25°C.

Bacterial Lawn Avoidance Assay

The behavioral avoidance assay was performed as described (*4*). Briefly, small lawns of *P. aeruginosa* PA14 were cultured on 3.5cm NGM plates overnight at 37°C. Twenty young adult nematodes grown on *E. coli* OP50 were put in the center of each bacterial lawn. The number of nematodes was counted at 4, 6, 12, 24, 30 and 36 hours post-exposure for presence or absence on each lawn.

Profile of Bacterial Accumulation in the Nematode Intestine

To determine the profiles of bacterial accumulation in the intestine, wild-type and *octr-1(ok371)* animals were synchronized by treatment of gravid adults with sodium hydroxide and bleach. Synchronized L1 larvae were grown on *E. coli* OP50 at 20°C until they had reached young adult stage. Wild-type and *octr-1(ok371)* animals were then transferred to plates seeded with either *P. aeruginosa/*GFP or *S. enterica/*GFP (SMO22) and cultured for 48 hours at 25°C. Animals were transferred to an NGM plate seeded with *E. coli* for 15 min and transferred again to a new NGM plate seeded with *E. coli* for 30 min to eliminate *P. aeruginosa/*GFP or *S. enterica/*GFP stuck to the body of the nematodes. Animals were visualized using a Leica MZ FLIII fluorescence stereomicroscope.

Quantification of Intestinal Bacterial Loads

For the quantification of colony forming units (cfu), wild-type and *octr-1(ok371)* animals were synchronized by treatment of gravid adults with sodium hydroxide and bleach. Synchronized L1 larvae were grown on *E. coli* OP50 at 20°C until they had reached young adult stage. Wild-type and *octr-1(ok371)* animals were then transferred to plates seeded with either *P. aeruginosa/*GFP or *S. enterica/*GFP (SMO22) for 48 hours at 25°C. Animals were transferred to an NGM plate seeded with *E. coli* for 15 min to eliminate *P. aeruginosa/*GFP or *S. enterica/*GFP stuck to the body of the worms. Animals were transferred to a new NGM plate seeded with *E. coli* for 30min to further eliminate external *P. aeruginosa/*GFP or *S. enterica/*GFP. Ten nematodes per condition were transferred into 50 microliters PBS plus 0.1% Triton and ground. Serial dilutions of the lysates (10^{-1}, 10^{-2}, 10^{-3}, 10^{-4}) were plated onto LB/kanamycin to select for *P. aeruginosa/GFP* or *S. enterica/GFP* cells and grown for 24 hours at 37°C.

RNA Interference

RNA interference was used to generate loss-of-function RNAi phenotypes by feeding nematodes with *E. coli* strain HT115(DE3) expressing double-stranded RNA (dsRNA) that is homologous to a target gene (*5, 6*). Briefly, *E. coli* with the appropriate vectors were grown in LB broth containing ampicillin (100μg/ml) at 37°C overnight and plated onto NGM plates containing 100μg/ml ampicillin and 3mM isopropyl β-D-thiogalactoside (IPTG). RNAi-expressing bacteria were allowed to grow overnight at 37°C. L2 or L3 larval animals were placed on RNAi or vector control plates for 2 days at 20°C until nematodes became gravid. Gravid adults were then transferred to fresh RNAi-expressing bacterial lawns and allowed to lay eggs for 2 hours to synchronize a second generation RNAi population. The gravid adults were removed and eggs were allowed to develop at 20°C to reach L4s for subsequent assays. *unc-22* RNAi was included as a positive control in all experiments to account for RNAi efficiency.

Given the high sequence similarity among *pqn/abu* genes, the occurrence of cross-RNAi within the family is likely. In *C. elegans*, cross-RNAi is known to occur when a target mRNA shares at least 95% identity, over a span of 40 or more nucleotides, to the dsRNA encoded by the RNAi construct (*7*). To identify potential off-target cross-reactions, the BLAST algorithm was used. Our analysis revealed potential off-target cross-reactions within the *pqn/abu* family for the *abu-1, abu-7,* and *abu-8* constructs

(Table S6). No potential off-target cross-reactions for the *pqn-40/abu-12* and *pqn-46/abu-13* RNAi construct was observed (Table S6).

Tunicamycin Treatment

Tunicamycin plates were prepared by making NGM plates containing 5μg/ml of tunicamycin dissolved in DMSO or control plates containing DMSO alone. One day old plates that were seeded with *E. coli* OP50 were used. Wild-type and *xbp-1(zc12)* animals at L4 stage were transferred to tunicamycin or control plates for 5 hours at 20°C. The animals were harvested from the plates at the end of the treatment and used for RNA extraction followed by qRT-PCR analysis.

Western Blot Analysis

Whole-worm lysates were prepared in the presence of protease inhibitors. Active PMK-1 was detected using an anti-human p38 antibody from Promega, Inc. Actin was detected using a polyclonal antibody from Sigma. Blots were developed using SuperSignal chemiluminescence substrate (Pierce).

RNA Isolation

Gravid adult wild-type and *octr-1(ok371)* animals were lysed using a solution of sodium hydroxide and bleach (ratio of 5:2), washed and the eggs were synchronized for 22 hours in S basal liquid medium at room temperature. Synchronized L1 larval animals were placed onto NGM plates seeded with *E. coli* OP50 and grown at 20°C until the animals had reached the L4 larval stage. Animals were collected and washed with M9 buffer before transferring to NGM plates containing *E. coli* OP50 or *P. aeruginosa* PA14 for 4 hours at 25°C. After 4 hours, animals were collected and washed with M9 buffer, and RNA was extracted using TRIzol reagent (Invitrogen). Residual genomic DNA was removed by DNase treatment (Ambion Austin, TX).

Microarray Analysis

Total RNA was obtained as described above. cDNA was generated from 10μg of total RNA and samples were hybridized to the *C. elegans* GeneChip (Affymetrix, Santa Clara, CA) by the Duke Microarray Facility. Detailed protocols are available on the Duke Microarray Facility Web site (http://microarray.genome.duke.edu). Microarray data were subjected to the robust multichip averaging algorithm using GeneSpring GX software (Agilent Technologies, Santa Clara, CA). Analysis of variance *t* test and fold-change calculations were also performed using GeneSpring GX software. Probability calculations of enrichment were performed using the hypergeometric probability test (http://elegans.uky.edu/MA/progs/overlap_stats.html) to calculate the statistical significance of the overlap of gene groups. The GEO accession number for the microarray data is GSE27867.

Quantitative Real-Time PCR (qRT-PCR)

Total RNA was obtained as described above. qRT-PCR was conducted using the Applied Biosystems One-Step Real-time PCR protocol using SYBR Green fluorescence (Applied Biosystems) on an Applied Biosystems 7900HT real-time PCR machine in 96-well plate format. Fifty nanograms of RNA were used for real-time PCR. Twenty-five microliter reactions were set-up and performed as outlined by the manufacturer (Applied Biosystems). Relative fold-changes for transcripts were calculated using the comparative $C_T(2^{-\Delta\Delta CT})$ method (*8*) and normalized to pan-actin (*act-1, -3, -4*). Cycle thresholds of amplification were determined by StepOnePlus software (Applied Biosystems). All samples were run in triplicate. Primer sequences are available upon request.

Statistical Analysis

Animal survival was plotted as a non-linear regression curve using the PRISM (version 4.00) computer program. Survival curves were considered different than the appropriate control indicated in the main text when p-values were <0.05. Prism uses the product limit or Kaplan-Meier method to calculate survival fractions and the logrank test, which is equivalent to the Mantel-Heanszel test, to compare survival curves. A two-sample *t* test for independent samples was used to analyze the avoidance assay, cfu assay and qRT-PCR results; p-values <0.05 are considered significant. For Fig. 3B and Fig. 4C, student's exact *t*-test indicates that all differences between wild type and *octr-1(ok371)* are significantly different ($P<0.05$). All the experiments were repeated at least 3 times, unless otherwise indicated.

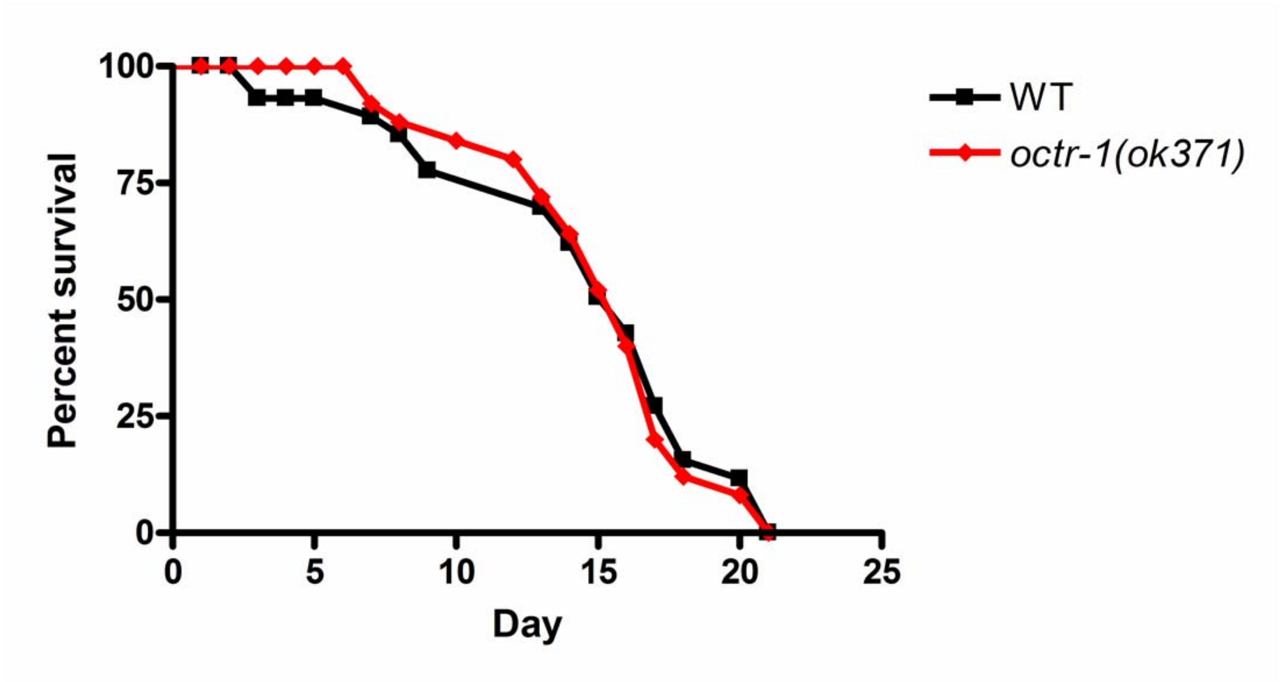

Fig. S1: *octr-1(ok371)* animals exhibit wild-type lifespan on heat-killed *E. coli* OP50. Wild-type and *octr-1(ok371)* (P=0.8297) animals were exposed to heat-killed *E. coli* OP50 and scored for survival over time. Shown is a representative assay of two independent experiments. N=45 adult animals per strain.

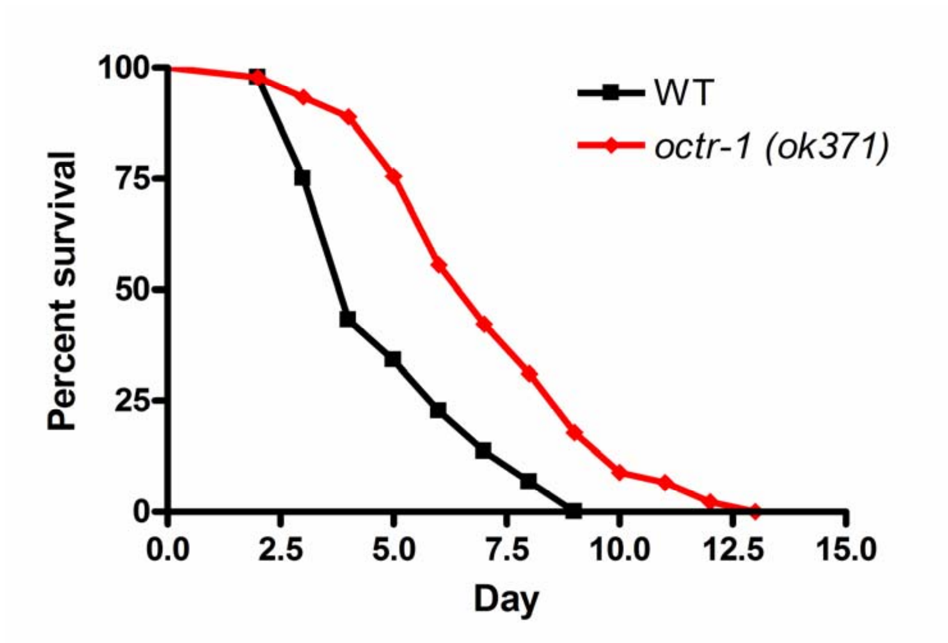

Fig. S2: *octr-1(ok371)* animals are resistant to *Salmonella enterica*. Wild-type and *octr-1(ok371)* (P<0.0001) animals were exposed to *S. enterica* strain 1344 and scored for survival over time. Shown is a representative assay of three independent experiments. N=45 adult animals per strain.

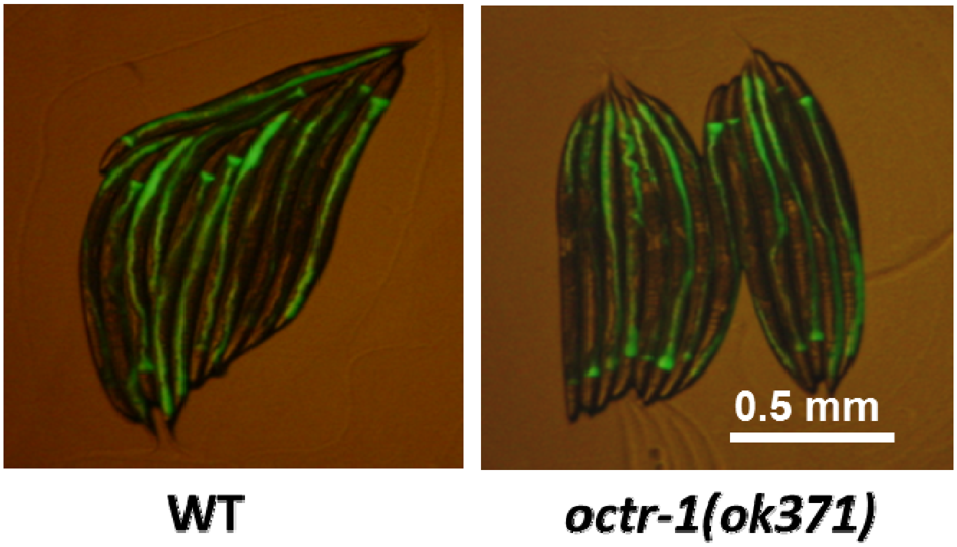

Fig. S3: *S. enterica* bacterial accumulation in the intestinal lumen is comparable in wild-type and *octr-1(ok371)* animals. Wild-type and *octr-1(ok371)* animals were fed *S. enterica* expressing GFP for 48 hours and then visualized using a MZ FLIII Leica stereomicroscope.

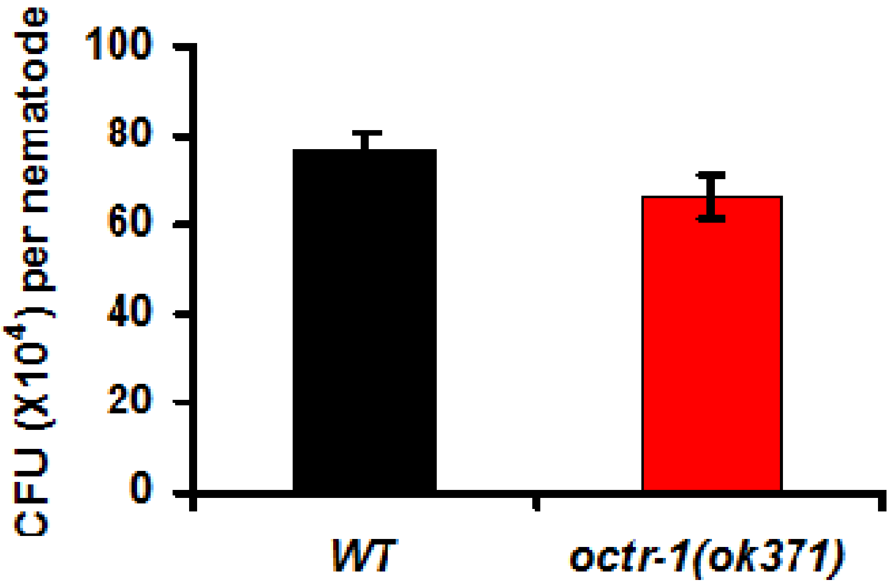

Fig. S4: *S. enterica* bacterial load is comparable in wild-type and *octr-1(ok371)* animals. Wild-type and *octr-1(ok371)* animals were fed *S. enterica* expressing GFP for 48 hours and the colony forming units were quantified. Ten animals were used for each condition. Three independent experiments were performed.

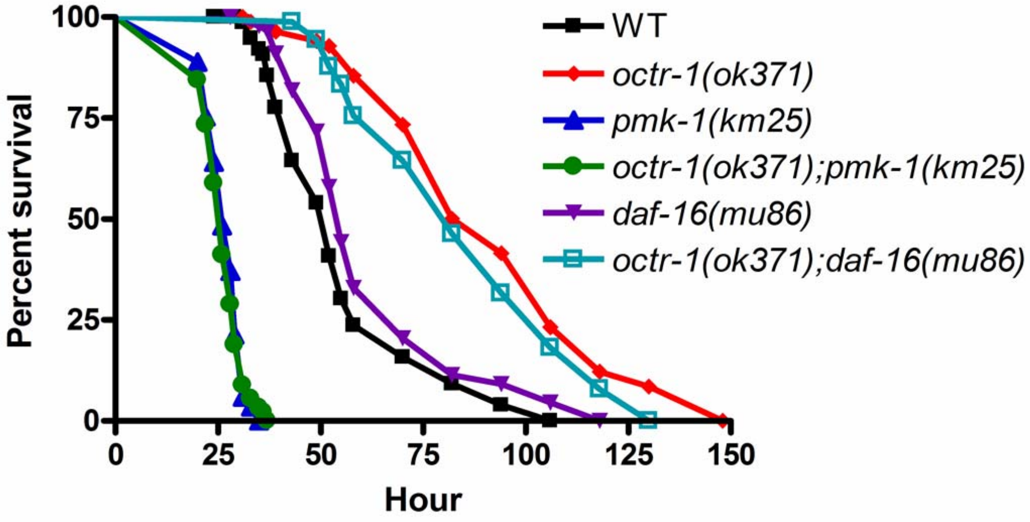

Fig. S5: Wild-type, *octr-1(ok371)*, *pmk-1(km25), octr-1(ok371);pmk-1(km25), daf-16(mu86)*, and *octr-1(ok371);daf-16(mu86)* animals were exposed to *P. aeruginosa* and scored for survival over time. Shown is a representative assay of two independent experiments. N=45 adult animals per strain. Wild-type (P<0.0001), *pmk-1(km25)* (P<0.0001), *octr-1(ok371);pmk-1(km25)* (P<0.0001), *daf-16(mu86)* (P<0.0001), *octr-1(ok371);daf-16(mu86)* (P> 0.05). P values are relative to *octr-1(ok371)* animals.

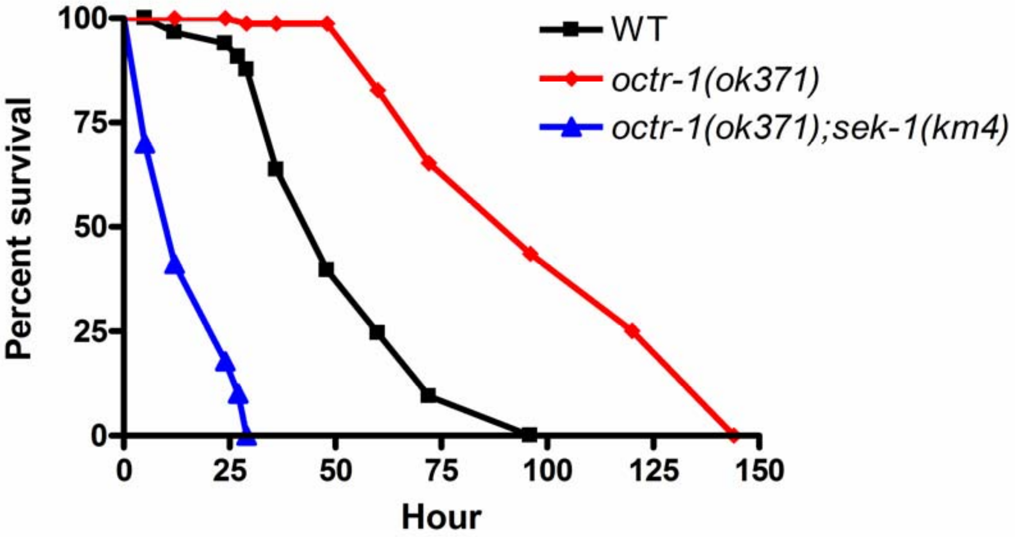

Fig. S6: Wild-type, *octr-1(ok371),* and *octr-1(ok371);sek-1(km4)* animals were exposed to *P. aeruginosa* and scored for survival over time. Shown is a representative assay of two independent experiments. N=45 adult animals per strain. *octr-1(ok371)* (P<0.0001), *octr-1(ok371);sek-1(km4)* (P<0.0001). P values are relative to wild-type animals.

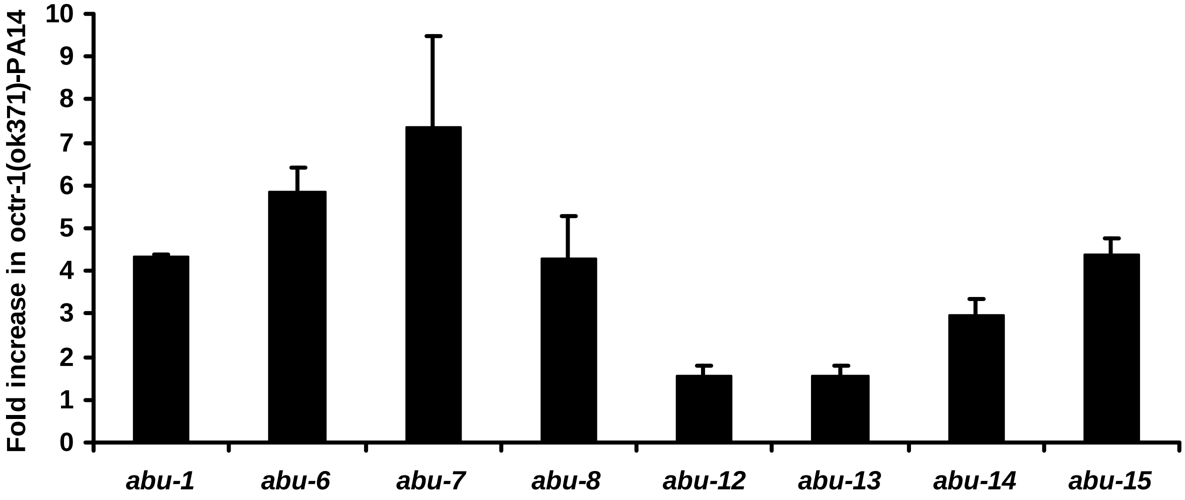

Fig. S7: Quantitative reverse transcription-PCR analysis of *abu* gene expression in *octr-1(ok371)* animals infected with *P. aeruginosa PA14* relative to *octr-1(ok371)* animals fed *E. coli* OP50. Data were analyzed by normalization to pan-actin (*act-1, -3, -4*) and relative quantification using the comparative cycle threshold method. Shown is the average of two independent experiments. Error bars are shown.

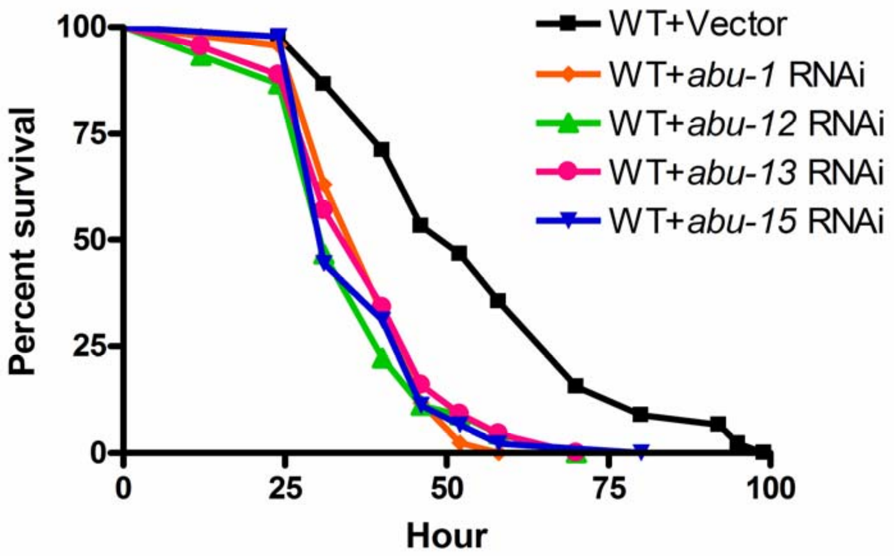

Fig. S8: *abu* genes expressed in an OCTR-1-dependent manner are required for *C. elegans* immunity against *P. aeruginosa*. Wild-type animals grown on dsRNA for vector control or dsRNA for *abu* genes were exposed to *P. aeruginosa*. *abu-1* RNAi (P<0.0001), *abu-12* RNAi (P<0.0001), *abu-13* RNAi (P<0.0001), *abu-15* RNAi (P<0.0001). P values are relative to wild-type animals. Shown is a representative assay of two independent experiments. N=45 adult animals per strain.

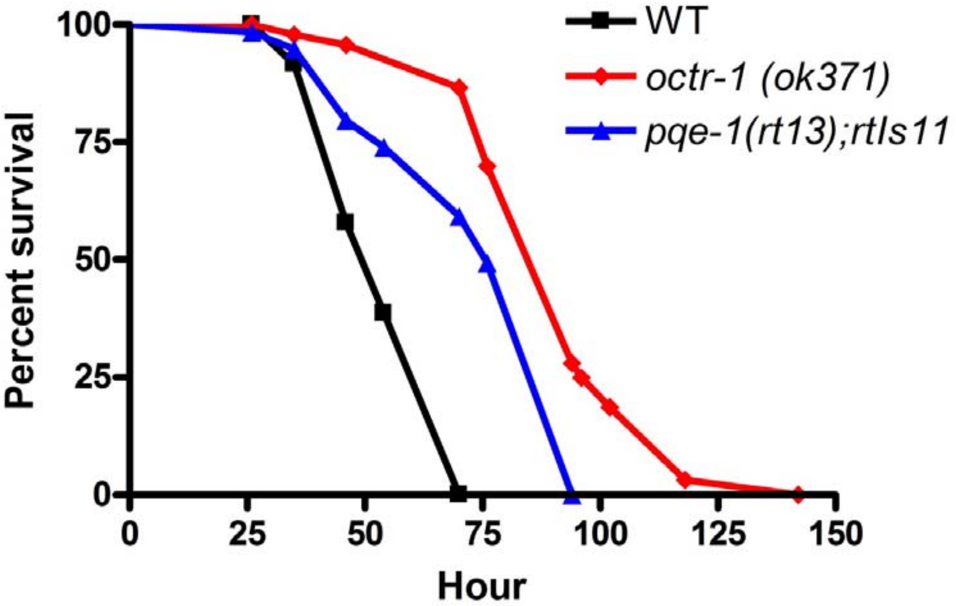

Fig. S9: Wild-type, *octr-1(ok371)*, and *pqe-1(rt13);rtIs11* animals were exposed to *P. aeruginosa* and scored for survival over time. The graph is a representative assay of three independent experiments, N=60 adult animals per strain. *octr-1(ok371)* (P<0.0001), *pqe-1(rt13);rtIs1* (P=0.003). *P* values are relative to wild-type animals.

Table S1.

Probe Set ID	**Gene Symbol**	**Gene Name**	**Description**	**Fold change**	**Corrected *P* value**
188046_s_at	F57F4.3	gfi-1	GEI-4(Four) Interacting protein	38.43	0.0014
190340_s_at	ZK678.5	wrt-4	WaRThog (hedgehog-like family)	37.41	0.0014
191688_at	F15B9.8		Thrombospondin type 1 domain	33.69	0.0014
177729_at	E01G4.6			28.59	0.0014
189762_at	K09H9.3	col-49	COLlagen	27.50	0.0015
188747_at	Y54E10BL.2	col-48	COLlagen	26.57	0.0023
177942_at	F33A8.7			26.37	0.0017
173004_s_at	T02E9.2	grl-7	GRound-Like (grd related)	25.99	0.0021
183379_at	K01D12.9			25.45	0.0030
182104_at	ZK1025.3			25.24	0.0017
173235_at	Y38C1BA.3	col-109	COLlagen	25.13	0.0023
173083_s_at	H10E21.4		calcium-binding protein	24.69	0.0042
182561_at	Y11D7A.9			23.11	0.0017

183237_s_at	ZK180.5			21.89	0.0021
185593_at	H23N18.5			20.77	0.0022
183975_s_at	F57B9.9	pqn-46	Prion-like-(Q/N-rich)-domain-bearing protein	20.49	0.0014
173611_s_at	y11d7a.11	col-120	COLlagen	20.17	0.0021
174152_s_at	C09G5.6	bli-1	BLIstered cuticle	20.05	0.0024
178715_at	C33G3.3	lgc-21	Ligand-Gated ion Channel	19.76	0.0023
183913_s_at	T10E9.3			19.67	0.0028
180505_at	F29C12.1	pqn-32	Prion-like-(Q/N-rich)-domain-bearing protein	19.62	0.0015
184102_s_at	ZK1025.2			19.40	0.0027
184102_s_at	ZK1025.8			19.40	0.0027
189482_s_at	C35B8.1	col-175	COLlagen	19.36	0.0034
174660_at	T19A5.3			19.11	0.0014
188337_at	Y57A10A.11	rol-1	ROLler: helically twisted, animals roll when moving	18.96	0.0017
177451_at	ZC373.6	dao-4	Dauer or Aging adult Overexpression	18.88	0.0021
193327_at	F53B1.4		thymidine diphosphoglucose 4,6-dehydratase	18.68	0.0015
180664_s_at	ZK180.6			18.56	0.0014

172989_s_at	R11A5.7		zinc carboxypeptidase	18.39	0.0027
190360_s_at	F27C1.8	dpy-5	DumPY : shorter than wild-type	18.23	0.0020
172497_x_at	R12E2.15			18.15	0.0032
183666_at	C52D10.13	col-138	COLlagen	18.06	0.0017
180376_s_at	M03A1.7	dao-2	Dauer or Aging adult Overexpression	17.99	0.0032
175008_at	F10D11.6			17.92	0.0014
174661_s_at	T19A5.3			17.46	0.0029
192674_s_at	B0491.2	sqt-1	SQuaT	17.40	0.0017
179686_at	C38C6.6	tag-297	Temporarily Assigned Gene name	16.95	0.0025
189968_s_at	F54C9.4	col-38	COLlagen	16.92	0.0015
176459_at	Y102A11A.5			16.88	0.0036
172346_x_at	R12E2.7			16.79	0.0039
186974_s_at	Y49F6B.10	col-71	COLlagen	16.29	0.0017
172547_x_at	R12E2.14			15.79	0.0040
188037_at	ZK377.1	wrt-6	WaRThog (hedgehog-like family)	15.52	0.0015
185764_s_at	F33D4.6			15.29	0.0023

189797_s_at	F58F6.1	col-104	COLlagen	15.00	0.0029
173576_at	ZK180.5			14.91	0.0022
194203_x_at	W04G3.8	lpr-3	LiPocalin-Related protein	14.82	0.0023
174960_at	ZK1010.7	col-97	COLlagen	14.53	0.0029
188028_at	T18H9.1	grd-6	GRounDhog (hedgehog-like family)	14.52	0.0035
186927_s_at	Y65B4BR.6	grl-16	GRound-Like (grd related)	13.99	0.0017
177696_at	C30H6.5			13.99	0.0024
185424_s_at	F33D4.6			13.88	0.0030
191001_s_at	H10E21.4		calcium-binding protein	13.87	0.0020
171795_x_at	R12E2.14			13.72	0.0041
188635_at	F58E6.13			13.06	0.0021
183724_at	Y11D7A.5			13.04	0.0046
174240_at	C34G6.6	noah-1	NOmpA Homolog (Drosophila nompA: no mechanoreceptor potential A)	12.84	0.0031
188463_at	F22D6.10	col-60	COLlagen	12.79	0.0040
175016_s_at	F44E2.4			12.74	0.0024

181956_at	C09E8.2	lips-7	LIPaSe related	12.74	0.0025
188364_s_at	F08G5.4	col-130	COLlagen	12.73	0.0021
192967_at	ZK1290.3	rol-8	ROLler: helically twisted, animals roll when moving	12.66	0.0029
191036_at	F10F2.3	lips-3	LIPaSe related	12.57	0.0029
188705_s_at	T06D8.10		peroxidase	12.47	0.0035
176471_at	Y47D7A.13			12.43	0.0033
181707_at	F10D11.6			12.41	0.0017
188853_at	R07E5.4		Glutaredoxin	12.32	0.0024
173654_at	C42D8.5	acn-1	ACE(angiotensin converting enzyme)-like Non-peptidase	12.26	0.0020
192026_at	C46A5.3	col-14	COLlagen	12.11	0.0043
183230_at	R02E4.1			12.00	0.0068
185862_at	Y59A8B.20	lon-8	LONg	11.88	0.0014
183159_at	F09F9.2			11.85	0.0035
186362_s_at	H04M03.4	glf-1	GaLactoFuranose synthesis (UGM, UDP-galactopyranose mutase)	11.56	0.0014
180375_at	M03A1.8		Dauer or Aging adult Overexpression	11.34	0.0025

192682_at	T01B7.7	rol-6	ROLler: helically twisted, animals roll when moving	11.27	0.0017
180439_at	C26B9.3			11.07	0.0014
190193_s_at	R11A5.7		zinc carboxypeptidase	10.76	0.0019
174448_s_at	F28D1.9			10.69	0.0016
187073_at	Y57A10A.23			10.69	0.0034
174628_s_at	H03E18.1			10.64	0.0032
185468_at	Y75B8A.20	grl-15	GRound-Like (grd related)	10.46	0.0048
182966_at	ZK154.1			10.37	0.0021
185646_at	T01B10.2	grd-14	GRounDhog (hedgehog-like family)	10.37	0.0034
189099_at	M195.1	col-77	COLlagen	10.23	0.0017
172353_x_at	C02E7.6			10.18	0.0047
185949_at	C42D4.13			9.75	0.0044
180614_at	T17H7.7			9.68	0.0015
190479_s_at	T05C12.10	qua-1	QUAhog (hedgehog related)	9.67	0.0030
186760_at	Y51H7C.13			9.50	0.0022
187885_at	C02D5.1	acdh-6	Acyl CoA DeHydrogenase	9.47	0.0017

183907_at	ZK1025.7			9.46	0.0027
190093_at	W05G11.3	col-88	COLlagen	9.44	0.0015
172706_x_at	F53F1.4		cuticlin	9.41	0.0017
177489_at	C05E7.2			9.41	0.0043
194238_x_at	F09B12.1	mlt-9	MoLTing defective	9.35	0.0017
194187_x_at	W01F3.3	mlt-11	MoLTing defective	9.35	0.0044
182327_at	W08F4.6	mlt-8	MoLTing defective	9.34	0.0015
172741_x_at	F41F3.3		cuticlin	9.33	0.0029
188404_at	W06B11.4	hog-1	HOG only (Hedgehog Hog domain alone)	9.33	0.0017
172799_x_at	F53F1.5		cuticlin	9.31	0.0019
187358_at	F07F6.5	dct-5	DAF-16/FOXO Controlled, germline Tumor affecting	9.18	0.0086
179510_at	F58H1.2			9.14	0.0035
184684_at	Y53F4B.27			9.13	0.0031
188391_at	F59E12.12	bli-2	BLIstered cuticle	8.99	0.0049
189221_at	F28G4.1	cyp-37B1	CYtochrome P450 family	8.95	0.0047

187278_at	C28H8.5			8.83	0.0046
173518_s_at	C34D4.15	col-113	COLlagen	8.80	0.0027
174910_at	F23H12.4	sqt-3	SQuaT	8.68	0.0030
175552_at	F49E12.6		RBB3 like protein	8.58	0.0021
184194_s_at	ZK1025.7			8.51	0.0035
183818_s_at	C05E7.1			8.46	0.0017
172325_x_at	C02E7.7			8.41	0.0037
180462_at	C07E3.10			8.39	0.0049
177032_at	F09G8.6	col-91	COLlagen	8.27	0.0068
174880_at	T23F2.1	bus-8	Bacterially Un-Swollen (M. nematophilum resistant)	8.21	0.0036
182320_at	F18G5.2	pes-8	Patterned Expression Site	8.13	0.0020
177650_at	W04G3.8	lpr-3	LiPocalin-Related protein	8.06	0.0038
177247_at	BE10.2			8.05	0.0019
192712_at	F32E10.3	clec-180	C-type LECtin	7.96	0.0034
179650_at	K08D8.4			7.94	0.0062
193712_s_at	C14F11.6		DTDP-4-dehydrorhamnose 3,5-epimerase (RFBC gene)	7.93	0.0075

173650_s_at	ZK265.2	col-63	COLlagen	7.92	0.0025
190091_at	C01B12.1	sqt-2	SQuaT	7.92	0.0017
190091_at	C01B12.8			7.92	0.0017
187162_s_at	Y38A10A.2			7.83	0.0042
181410_s_at	F26G1.5			7.82	0.0032
178517_at	C49F8.3			7.80	0.0015
177586_at	C15C6.1			7.68	0.0032
175015_at	F44E2.4			7.66	0.0018
177916_at	W04G3.3	lpr-4	LiPocalin-Related protein	7.60	0.0076
181681_at	F08F1.6	spp-13	SaPosin-like Protein family	7.60	0.0029
188276_s_at	C50B6.4	col-161	COLlagen	7.57	0.0044
188276_s_at	Y2H9A.3	col-162	COLlagen		0.0044
184220_at	C56C10.4			7.55	0.0017
189678_at	F49E12.6		RBB3 like protein	7.54	0.0020
177801_at	C29F3.5	clec-230	C-type LECtin	7.49	0.0051
185972_at	H42K12.3			7.48	0.0043

176681_at	F35B3.4			7.47	0.0097
187329_at	T19C3.2			7.47	0.0030
181055_at	T19D7.3			7.42	0.0038
180485_s_at	C45B2.7	ptr-4	PaTched Related family	7.35	0.0027
184676_s_at	ZK1290.8	wrt-10	WaRThog (hedgehog-like family)	7.26	0.0033
187901_s_at	ZK13.4	mab-7	Male ABnormal	7.21	0.0028
175115_at	Y64H9A.2			7.14	0.0035
188066_at	C24B5.3	ptr-1	PaTched Related family	7.12	0.0014
192504_at	T22H6.2			7.12	0.0033
184174_at	ZC204.12			7.11	0.0051
183941_s_at	F56D3.1			7.05	0.0034
173567_s_at	T02E9.2	grl-7	GRound-Like (grd related)	7.00	0.0025
183361_at	K01D12.8			7.00	0.0044
180616_at	T22B7.3			6.99	0.0014
184828_s_at	F09B12.1	mlt-9	MoLTing defective	6.92	0.0026
190877_at	C07D10.4	nas-7	Nematode AStacin protease	6.89	0.0019

174481_at	C45G9.6			6.85	0.0035
188311_s_at	F38A3.2	ram-2	abnormal RAy Morphology	6.79	0.0026
175393_at	Y47D7A.13		status:Partially_confirmed	6.67	0.0051
184106_at	M03F8.1			6.64	0.0063
173124_s_at	H42K12.3			6.55	0.0032
178189_at	F28C6.5			6.53	0.0029
171796_x_at	C02E7.6			6.45	0.0042
193741_at	T03G11.8	zig-6	2 (Zwei) IG-domain protein	6.43	0.0049
188461_s_at	F29B9.9	col-111	COLlagen	6.42	0.0024
178131_at	T16G1.2			6.40	0.0019
188312_at	F57B7.3	col-156	COLlagen	6.39	0.0043
181440_at	D1014.5			6.32	0.0032
181069_at	T03G6.1			6.31	0.0072
181136_s_at	F52B11.3	noah-2	NOmpA Homolog (Drosophila nompA: no mechanoreceptor potential A)	6.29	0.0029
174294_at	C25F6.7			6.26	0.0030

171807_x_at	C02E7.7			6.25	0.0041
176474_at	Y54F10AM.6			6.24	0.0037
188188_s_at	Y38F1A.3	ptr-18	PaTched Related family	6.21	0.0016
178248_at	C07E3.3			6.21	0.0032
176327_s_at	Y47D7A.5	grl-5	GRound-Like (grd related)	6.18	0.0027
188527_s_at	C42D8.5	acn-1	ACE(angiotensin converting enzyme)-like Non-peptidase	6.15	0.0020
181715_s_at	T19B10.2			6.12	0.0040
188365_at	C39E9.3	col-131	COLlagen	6.11	0.0034
182386_s_at	Y37A1B.7			6.09	0.0064
178508_at	C14A4.9			6.03	0.0027
192737_at	F49E11.10	scl-2	SCP-Like extracellular protein	5.97	0.0052
189419_at	F15B9.6		phospholipase A2	5.95	0.0033
175528_at	C35E12.5	sem-2	SEx Muscle abnormal	5.89	0.0031
185835_at	K08B12.1			5.88	0.0037
183582_at	C47E12.6			5.81	0.0045

179254_at	F25H8.6	bed-3	Zinc finger protein (BED class)	5.79	0.0020
183363_at	ZC513.1			5.79	0.0028
190570_at	F52D1.1		acid alpha-glucosidase	5.78	0.0016
178652_at	ZK84.1			5.77	0.0032
179830_at	F01D5.10			5.77	0.0036
177643_at	T26C5.2			5.76	0.0062
177870_at	C02F4.4			5.75	0.0029
183120_at	C06G1.1			5.73	0.0022
180624_s_at	F52D1.3	pqn-40	Prion-like-(Q/N-rich)-domain-bearing protein	5.69	0.0025
191612_at	F28D1.9			5.68	0.0025
176851_at	Y40B10A.6			5.68	0.0044
177505_at	T06G6.6			5.67	0.0041
190446_s_at	C31H2.2	dpy-8	DumPY : shorter than wild-type	5.64	0.0055
181714_at	T19B10.2			5.58	0.0029
172803_x_at	C34H4.4	col-107	COLlagen	5.56	0.0032
192089_s_at	F13H8.5		Phospholipase ADRAB-B (Rabbit)	5.53	0.0027

191180_at	ZK1290.12	wrt-1	WaRThog (hedgehog-like family)	5.52	0.0036
177024_at	C29E4.1	col-90	COLlagen	5.47	0.0017
173639_at	C34E7.4			5.44	0.0023
172744_at	K11G9.6	mtl-1	MeTaLlothionein	5.43	0.0177
185412_at	T22B11.2			5.42	0.0029
174218_at	F11E6.8			5.41	0.0039
173664_at	ZC13.4	mab-7	Male ABnormal	5.33	0.0085
193958_at	F44C4.3	cpr-4	Cysteine PRotease related	5.32	0.0032
185608_at	H03E18.1			5.27	0.0014
184788_at	F49H12.5			5.27	0.0062
181998_at	F26B1.4	col-58	COLlagen	5.26	0.0047
190307_s_at	ZK131.8	his-14	HIStone	5.26	0.0068
190307_s_at	ZK131.1	his-26	HIStone	5.26	0.0068
190307_s_at	ZK131.4	his-10	HIStone	5.26	0.0068
172729_x_at	F11G11.12	col-73	COLlagen	5.26	0.0015
175662_at	M163.3	his-24	HIStone	5.25	0.0055

172685_x_at	K06C4.4	his-20	HIStone	5.25	0.0029
173579_s_at	W04G3.2			5.24	0.0041
183381_at	C50F7.5			5.20	0.0115
183755_s_at	F46C8.8			5.20	0.0034
188947_at	T09F5.9	clec-47	C-type LECtin	5.18	0.0113
174657_s_at	F56H1.1	che-14	abnormal CHEmotaxis	5.14	0.0043
184151_at	F26A1.9			5.13	0.0039
189278_s_at	T21D11.1		zinc protease	5.12	0.0023
193344_at	sym-1		SYnthetic lethal with Mec	5.11	0.0091
178068_s_at	C34E7.4			5.09	0.0041
184662_at	Y46G5A.29			5.09	0.0044
180055_at	ZC328.1			5.06	0.0141
177059_at	Y46C8AL.5	clec-72	C-type LECtin	5.03	0.0037
174235_at	K02C4.4	ltd-1	Lim and Transglutaminase Domain	5.02	0.0022
193091_at	T02C1.1		Zinc finger, C3HC4 type (RING finger)	5.02	0.0032
192607_at	T07F10.4	bus-19	Bacterially Un-Swollen (M. nematophilum resistant)	5.00	0.0019

174254_at	M03F4.6			5.00	0.0251
184352_at	C17H12.6			4.98	0.0117
190615_s_at	F13B12.4		cysteine synthase like	4.98	0.0030
183577_at	ZK1067.7	pqn-95	Prion-like-(Q/N-rich)-domain-bearing protein	4.91	0.0029
172824_x_at	T10C6.11	his-4	HIStone	4.89	0.0030
192786_s_at	B0286.3		saicar synthetase/air carboxlyase	4.89	0.0030
191735_at	T03D8.6			4.86	0.0023
188270_at	T21H3.2	ptr-16	PaTched Related family	4.85	0.0047
184993_at	H02F09.3			4.84	0.0041
183438_s_at	F45E4.8	nlp-20	Neuropeptide-Like Protein	4.80	0.0039
172196_x_at	K08C9.4	col-65	COLlagen	4.74	0.0033
188574_s_at	H17B01.2	col-70	COLlagen	4.73	0.0037
188574_s_at	Y51H7C.1		COLlagen	4.73	0.0091
173919_s_at	C56A3.2	ttr-44	TransThyretin-Related family domain	4.73	0.0091
184746_at	F52F10.2			4.68	0.0036
181027_at	Y42A5A.2	lact-8	beta-LACTamase domain containing	4.63	0.0036

189814_s_at	F41C6.5	col-173	COLlagen	4.63	0.0030
172825_x_at	F45F2.2	his-39	HIStone	4.62	0.0044
180122_at	C25B8.3	cpr-6	Cysteine PRotease related	4.56	0.0043
179600_at	C38C6.3			4.55	0.0025
192153_at	M153.1		pyrroline-5-carboxylate reductase	4.52	0.0024
192148_at	T07C5.1	ugt-50	UDP-GlucuronosylTransferase	4.52	0.0036
179249_at	ZK617.2	lips-6	LIPaSe related	4.52	0.0104
178343_s_at	F58G1.5	lips-9	LIPaSe related	4.50	0.0030
179786_at	C08E8.4			4.48	0.0109
189076_at	T21B10.6	cutl-15	CUTiclin-Like	4.48	0.0032
187424_s_at	C45G9.6			4.45	0.0058
192181_at	T28H10.3		vacuolar processing enzyme like	4.44	0.0170
192137_at	C05C8.3	fkb-3	FK506-Binding protein family	4.44	0.0046
175272_at	F45D3.2			4.43	0.0035
172874_x_at	F45F2.12	his-8	HIStone	4.41	0.0034
183539_s_at	C06E7.4			4.39	0.0021

180418_at	T19D7.3			4.39	0.0044
193623_at	F21F3.3		protein-S isoprenylsysteine O-methyltransferase	4.38	0.0077
181552_at	T22B7.3			4.38	0.0031
183963_at	C29F9.2			4.38	0.0131
179176_at	C52G5.2			4.36	0.0029
182683_at	ZC250.3			4.36	0.0046
184682_s_at	K09B11.10			4.34	0.0024
171956_s_at	ZK270.1	ptr-23	PaTched Related family	4.34	0.0025
175294_s_at	T17H7.7			4.34	0.0044
183103_at	F25E5.2			4.34	0.0024
189443_at	T19B10.9		max protein like	4.33	0.0022
172475_x_at	B0222.7	col-145	COLlagen	4.32	0.0068
178930_at	F19H8.2			4.31	0.0072
182733_at	C31A11.5	oac-6	O-ACyltransferase homolog	4.30	0.0035
188475_at	C44C10.1	col-180	COLlagen	4.29	0.0044
180979_at	F41E6.2	grd-5	GRounDhog (hedgehog-like family)	4.25	0.0014

193849_at	F13D11.4		dihydroflavonol-4-reductase (maize, petunia, tomato)	4.25	0.0036
172618_x_at	F07B7.9	his-50	HIStone	4.25	0.0066
184093_at	M01H9.1			4.25	0.0084
186349_at	Y51H7C.1			4.24	0.0070
193147_at	F01G10.10		lipopolysaccharide-binding protein like	4.22	0.0099
179401_at	ZK662.2			4.21	0.0026
193024_at	C15H9.1	nnt-1	Nicotinamide Nucleotide Transhydrogenase	4.20	0.0095
173928_at	F45H11.6			4.20	0.0107
185984_at	F57C12.1	nas-38	Nematode AStacin protease	4.18	0.0096
176743_s_at	F56D6.15	clec-69	C-type LECtin	4.18	0.0054
183624_at	F55G11.5	dod-22	Downstream Of DAF-16 (regulated by DAF-16)	4.17	0.0060
188368_at	ZK836.1	lon-3	LONg	4.17	0.0023
188675_at	C09G5.3	col-79	COLlagen	4.16	0.0107
180741_at	F36H9.5			4.14	0.0017
172650_x_at	K06C4.10	his-18	HIStone	4.12	0.0069
184091_at	C26F1.5	grl-10	GRound-Like (grd related)	4.12	0.0032

191038_at	C02F5.8	tsp-1	TetraSPanin family	4.11	0.0046
189952_at	R08B4.1	grd-1	GRounDhog (hedgehog-like family)	4.10	0.0083
184191_at	R09B5.9	cnc-4	CaeNaCin (Caenorhabditis bacteriocin)	4.06	0.0163
180540_at	C42D4.3			4.05	0.0104
190306_s_at	C29F3.2	wrt-8	WaRThog (hedgehog-like family)	4.04	0.0046
188116_at	F57H12.3	ora-1	Onchocerca Related Antigen family	4.04	0.0117
175229_at	C08F11.13			4.03	0.0070
182066_s_at	F59B10.1	pqn-47	Prion-like-(Q/N-rich)-domain-bearing protein	4.02	0.0041
174410_at	Y18H1A.9			4.01	0.0022
174957_s_at	F52F10.3	oac-31	O-ACyltransferase homolog	3.97	0.0038
179069_at	C08E8.4			3.97	0.0041
181713_s_at	M03F4.6			3.97	0.0041
180841_at	C32H11.5			3.95	0.0137
191057_s_at	ZC455.4	ugt-6	UDP-GlucuronosylTransferase	3.93	0.0099
172405_x_at	R09B5.8	cnc-3	CaeNaCin (Caenorhabditis bacteriocin)	3.93	0.0042
191805_s_at	F23H12.5		Thrombospondin type 1 domain	3.91	0.0121

173417_at	F35H10.10			3.90	0.0044
180192_at	C49G7.5			3.90	0.0126
182812_at	F22F4.1			3.89	0.0094
180960_at	C13C12.2			3.88	0.0058
193656_s_at	C50F2.6	fkb-5	FK506-Binding protein family	3.87	0.0059
179239_at	F53H4.3			3.86	0.0059
189600_at	F17C8.2	col-89	COLlagen	3.83	0.0057
177724_at	W04G3.1			3.82	0.0034
173335_s_at	C24B9.9	dod-3	Downstream Of DAF-16 (regulated by DAF-16)	3.81	0.0345
183601_at	C06E7.4			3.79	0.0040
194030_s_at	Y37D3B.10	dpy-18	DumPY : shorter than wild-type	3.79	0.0063
176672_at	W08G11.1			3.78	0.0106
174623_at	T27B1.2	ztf-19	Zinc finger Transcription Factor family	3.77	0.0059
178089_at	K03B8.6			3.76	0.0043
183492_at	Y39A1A.9			3.75	0.0044
181565_at	F56D6.2	clec-67	C-type LECtin	3.75	0.0038

190375_at	F46B3.5	grd-2	GRounDhog (hedgehog-like family)	3.74	0.0133
190303_s_at	Y66A7A.6	gly-8	GLYcosylation related	3.73	0.0020
185001_at	C08F11.13			3.71	0.0050
187681_at	T25D10.4			3.69	0.0062
173635_at	F16F9.2	dpy-6	DumPY : shorter than wild-type	3.68	0.0027
174044_at	K04H4.2			3.67	0.0132
179854_at	Y47D3A.2	fbxa-128	F-box A protein	3.66	0.0068
176025_at	D2007.1			3.64	0.0086
172764_x_at	F45F2.4	his-7	HIStone	3.63	0.0056
174508_s_at	K08E7.5			3.63	0.0035
191698_at	C40H1.4	elo-4	fatty acid ELOngation	3.63	0.0046
183639_at	F13A7.11			3.62	0.0047
174781_at	T27A10.6			3.62	0.0029
189723_s_at	EGAP7.1	dpy-3	DumPY : shorter than wild-type	3.61	0.0047
176330_at	Y22D7AL.14			3.61	0.0082
191887_s_at	W07B8.5	cpr-5	Cysteine PRotease related	3.60	0.0016

175803_at	Y47D3B.10	dpy-18	DumPY : shorter than wild-type	3.59	0.0056
183911_at	T19A5.3			3.59	0.0056
188441_at	F21F8.4		protease	3.59	0.0078
184629_at	Y74E4A.1	lgc-27	Ligand-Gated ion Channel	3.57	0.0052
173947_at	F13H8.5		Phospholipase ADRAB-B (Rabbit)	3.57	0.0144
182403_at	ZK418.7			3.55	0.0073
179610_s_at	T16G1.5			3.55	0.0133
185003_s_at	F52F10.3	oac-31	O-ACyltransferase homolog	3.53	0.0027
176407_at	F28A10.1		hypothetical protein	3.53	0.0114
173252_s_at	T19C4.7	nlp-33	Neuropeptide-Like Protein	3.53	0.0070
177581_at	F45G2.5	bli-5	BLIstered cuticle	3.52	0.0041
180612_s_at	F53A9.8			3.51	0.0080
172055_x_at	ZK131.6	his-12	HIStone	3.50	0.0051
172055_x_at	ZK131.10	his-16	HIStone	3.50	0.0051
172055_x_at	K06C4.11	his-19	HIStone	3.50	0.0051
172055_x_at	K06C4.3	his-21	HIStone	3.50	0.0051

172055_x_at	K06C4.12	his-22	HIStone	3.50	0.0051
172055_x_at	F35H10.11	his-29	HIStone	3.50	0.0051
172055_x_at	T10C6.12	his-3	HIStone	3.50	0.0051
172055_x_at	F35H10.1	his-30	HIStone	3.50	0.0051
172055_x_at	F17E9.13	his-33	HIStone	3.50	0.0051
172055_x_at	F17E9.9	his-34	HIStone	3.50	0.0051
172055_x_at	F08G2.2	his-43	HIStone	3.50	0.0051
172055_x_at	F07B7.10	his-51	HIStone	3.50	0.0051
172055_x_at	F07B7.4	his-52	HIStone	3.50	0.0051
172055_x_at	F07B7.3	his-53	HIStone	3.50	0.0051
172055_x_at	F07B7.11	his-54	HIStone	3.50	0.0051
172055_x_at	F54E12.5	his-57	HIStone	3.50	0.0051
172055_x_at	H02I12.7	his-65	HIStone	3.50	0.0051
172055_x_at	K06C4.2	his-28	HIStone	3.50	0.0051
172055_x_at	F45F2.3	his-5	HIStone	3.50	0.0051
172055_x_at	F45F2.4	his-7	HIStone	3.50	0.0051

191850_s_at	K08C7.2	fmo-1	Flavin-containing MonoOxygenase family	3.50	0.0129
193464_s_at	F35G2.4	phy-2	Proline HYdroxylase	3.49	0.0040
181912_at	F58H10.1			3.48	0.0028
193303_at	C06E8.5		bacterial permeability-increasing protein	3.48	0.0033
178244_at	F01D5.6			3.47	0.0106
186604_s_at	Y38C1AB.1			3.46	0.0041
186604_s_at	Y38C1AB.5			3.46	0.0041
190048_s_at	F32B5.8	cpz-1	CathePsin Z	3.45	0.0020
192146_s_at	F46BC8.6	dpy-7	DumPY : shorter than wild-type	3.44	0.0125
172363_x_at	F53A9.6			3.44	0.0132
178236_s_at	F58B3.1	lys-4	LYSozyme	3.43	0.0069
190166_at	T01B11.4	ant-1.44	Adenine Nucleotide Translocator	3.42	0.0081
192280_s_at	ZK131.5	his-11	HIStone	3.42	0.0089
192280_s_at	ZK131.9	his-15	HIStone	3.42	0.0089
192280_s_at	F08G2.1	his-44	HIStone	3.42	0.0089
193893_at	ZK909.3		guanosine-3',5'-bis(diphosphate)-pyrophosphohydrolase	3.41	0.0038

			like		
181051_at	T19D7.6		hypothetical protein	3.41	0.0104
172888_x_at	C40D2.2	math-20	MATH (meprin-associated Traf homology) domain containing	3.41	0.0074
182051_s_at	B0454.7	clec-2	C-type LECtin	3.41	0.0149
182051_s_at	C41H7.7	clec-3	C-type LECtin	3.41	0.0149
182510_at	T07G12.3			3.41	0.0036
189921_at	C05C10.4			3.40	0.0029
172991_at	C45B2.7	ptr-4	PaTched Related family	3.40	0.0047
173558_at	ZC443.3			3.36	0.0103
191527_s_at	C07A9.8		Putative membrane protein	3.36	0.0184
190551_at	W01A8.6		carboxypeptidase b like	3.36	0.0071
180840_at	C55F2.2	ilys-4	Invertebrate LYSozyme	3.35	0.0095
183689_at	C54F6.3			3.34	0.0036
178432_s_at	ZC443.3			3.34	0.0127
179896_at	F47F6.1	lin-42	abnormal cell LINeage	3.33	0.0158

179861_at	Y47D3B.1			3.33	0.0043
184855_at	T23B12.8			3.33	0.0066
179046_at	F46A9.1			3.33	0.0114
176163_at	Y119C1B.9			3.31	0.0047
192685_at	Y45F10D.13	tag-208	Temporarily Assigned Gene name	3.31	0.0019
188294_at	F32G8.5	col-152	COLlagen	3.31	0.0117
184558_at	Y45F10A.5	nlp-17	Neuropeptide-Like Protein	3.31	0.0051
193872_s_at	F29D11.1	lrp-1	Low-density lipoprotein Receptor Related	3.30	0.0034
184400_at	F22H10.2			3.30	0.0115
186950_at	C05B5.8			3.30	0.0022
181428_at	F13B6.1			3.29	0.0075
179164_at	C06G8.1			3.29	0.0064
187228_at	R07G3.6			3.28	0.0056
174056_at	F54D1.6			3.28	0.0062
176256_s_at	Y58A7A.4			3.26	0.0062
183089_at	C15C7.5			3.26	0.0034

188104_s_at	F25H8.5	dur-1	Dauer Up-Regulated	3.26	0.0025
192924_s_at	K11C4.4	odc-1	Ornithine DeCarboxylase	3.25	0.0122
179139_at	T05D4.4	osm-7	OSMotic avoidance abnormal	3.24	0.0043
180766_at	F13B6.3			3.24	0.0141
194068_s_at	T23G11.6			3.24	0.0035
176212_at	ZC47.7	fbxa-151	F-box A protein	3.24	0.0130
176212_at	Y119D3B.19	fbxa-78	F-box A protein	3.24	0.0130
178935_at	F07D3.3			3.24	0.0059
188410_at	T23F4.4	nas-27	Nematode AStacin protease	3.24	0.0046
189705_s_at	M88.6	pan-1	P-granule Associated Novel protein	3.23	0.0054
193677_at	F32D8.7			3.22	0.0076
184711_at	C49G7.10			3.21	0.0167
189679_at	F21A3.3		EGF-domain protein	3.20	0.0030
174281_at	Y77E11A.14			3.20	0.0070
176044_at	Y41D4B.16			3.19	0.0049
185474_at	T05B11.1			3.17	0.0106

182428_s_at	Y22F5A.6	lys-3	LYSozyme	3.17	0.0107
179858_at	C49C8.5			3.17	0.0074
193127_s_at	K07E3.3	dao-3	Dauer or Aging adult Overexpression	3.17	0.0044
186676_s_at	F35H10.10			3.16	0.0014
187462_at	ZK1307.1			3.16	0.0051
179199_at	T09F5.1			3.15	0.0030
184240_at	F53F10.1			3.14	0.0048
174995_s_at	C54A12.1	ptr-6	PaTched Related family	3.14	0.0031
178449_at	C53B4.8			3.14	0.0208
177193_s_at	AC3.3	abu-1	Activated in Blocked Unfolded protein response	3.13	0.0146
177193_s_at	AC3.4	pqn-2	Prion-like-(Q/N-rich)-domain-bearing protein	3.13	0.0146
173727_s_at	F40F4.6		EGF-like repeats	3.13	0.0021
194252_x_at	F38A3.2	ram-2	abnormal RAy Morphology	3.13	0.0056
185399_at	Y75B8A.28			3.12	0.0046
187033_at	F54D1.6			3.11	0.0046
176016_at	M02H5.5	nhr-203	Nuclear Hormone Receptor family	3.11	0.0042

182019_at	W03D2.9			3.10	0.0044
185357_at	Y37D8A.16			3.09	0.0081
184205_at	Y52B11B.1			3.08	0.0037
175254_at	C05D10.3	wht-1	WHiTe (Drosophila) related ABC transporte	3.08	0.0049
174347_s_at	C49C8.5			3.08	0.0047
174252_at	ZK783.1	fbn-1	FiBrilliN homolog	3.07	0.0054
174314_at	F41C6.1	unc-6	UNCoordinated	3.07	0.0035
190937_s_at	C49A1.3		Putative membrane protein	3.06	0.0069
190688_s_at	F44E7.2		nitrophenylphosphatase	3.06	0.0459
190688_s_at	K09H11.7		nitrophenylphosphatase	3.06	0.0459
190688_s_at	C53A3.2		nitrophenylphosphatase	3.06	0.0459
177555_at	F09B9.4			3.06	0.0057
183009_at	Y38F1A.8			3.06	0.0102
178654_s_at	W04A8.4			3.06	0.0122
183630_at	C29F9.3			3.05	0.0106
188927_at	C02F5.11	tsp-2	TetraSPanin family	3.05	0.0057

175156_at	F37A8.5		Predicted Yippee-type zinc-binding protein	3.05	0.0323
190370_at	F13G3.1	ztf-2	Zinc finger Transcription Factor family	3.04	0.0054
186012_s_at	F57H12.6			3.04	0.0171
187318_at	F48E8.1	lon-1	LONg	3.04	0.0231
177378_at	R52.8	math-36	MATH (meprin-associated Traf homology) domain containing	3.03	0.0186
172360_x_at	C03A7.4	pqn-5	Prion-like-(Q/N-rich)-domain-bearing protein	3.03	0.0141
175060_at	F52F10.2			3.03	0.0022
192106_at	C34C6.3		EGF receptor/notch-like protein	3.02	0.0074
172902_x_at	F36A4.10	col-34	COLlagen	3.02	0.0067
185390_at	F49D11.6			3.02	0.0126
180978_at	M03F4.6			3.02	0.0038
182323_at	C02H6.2	fbxa-105	F-box A protein	3.02	0.0088
172627_x_at	Y105C5A.12			3.02	0.0027
172627_x_at	Y105C5A.13			3.02	0.0027
184159_at	T05E12.6			3.01	0.0148

172214_x_at	ZK525.1	flp-15	FMRF-Like Peptide	3.00	0.0035
183802_at	T05E7.4			3.00	0.0035
185238_at	Y67A10A.8			2.99	0.0078
174388_at	F47B7.2			2.99	0.0043
181121_at	C46F2.1			2.99	0.0043
181793_at	C09E8.3	mlt-10	MoLTing defective	2.99	0.0030
184295_at	Y37H2A.14			2.98	0.0126
191984_at	R06B10.1		protein-tyrosine phosphatase	2.98	0.0059
193268_at	Y1A5A.1		LIM domain containing proteins (2 domains)	2.98	0.0133
190139_s_at	E03H4.10	clec-17	C-type LECtin	2.97	0.0468
174132_at	C38H2.2			2.97	0.0046
178723_at	F54D5.3			2.97	0.0032
187503_at	C14B9.3			2.97	0.0100
184116_s_at	T05E12.6			2.96	0.0085
182346_at	ZC123.1			2.96	0.0040
184853_at	C18A11.1			2.96	0.0343

191502_at	ZC443.5	ugt-18	UDP-GlucuronosylTransferase	2.96	0.0119
184912_s_at	W04H10.4	clec-118	C-type LECtin	2.96	0.0057
184912_s_at	T27D12.3	clec-144	C-type LECtin	2.96	0.0057
193761_at	F44C4.5	ppt-1	Palmitoyl Protein Thioesterase	2.96	0.0164
176818_s_at	C02F12.7	tag-278	Temporarily Assigned Gene name	2.95	0.0034
184811_at	T27A10.6			2.95	0.0074
188632_at	K08E3.1	tyr-2	TYRosinase	2.95	0.0115
175382_at	Y39A1A.9			2.94	0.0087
173839_at	K02G10.5		zinc-finger DNA-binding protein	2.93	0.0056
171945_x_at	C09E8.3	mlt-10	MoLTing defective	2.93	0.0042
189452_at	F46C8.2	col-174	COLlagen	2.93	0.0072
187509_at	B0280.7			2.93	0.0062
183555_at	C34H4.3	tag-244	Temporarily Assigned Gene name	2.93	0.0041
187920_at	F46G10.7	sir-2.2	yeast SIR related	2.93	0.0045
175193_at	T25F10.3			2.93	0.0034
174404_s_at	F14E5.5	lips-10	LIPaSe related	2.92	0.0147

187972_at	C03C11.2	fog-3	Feminization Of Germline	2.92	0.0071
189261_at	F21A3.2			2.92	0.0211
189346_at	F48F7.2	syn-2	SYNtaxin	2.92	0.0121
189344_s_at	F08F3.7	cyp-14A5	CYtochrome P450 family	2.91	0.0054
185780_at	Y50E8A.16	haf-7	HAlF transporter (PGP related)	2.90	0.0050
191020_at	T18D3.3		cobalt uptake like protein	2.90	0.0168
188525_at	F42G9.2	cyn-6	CYclophyliN	2.89	0.0043
177917_at	C02D4.1	jud-4	JUDang (Korean for resistant to alcohol)	2.89	0.0056
181441_s_at	T01D1.3			2.89	0.0033
193885_at	B0393.5		EGF-like aspartic acid and asparagine hydroxylation sites	2.89	0.0039
177997_at	F11F1.6			2.89	0.0084
175576_s_at	Y75B7AR.1			2.88	0.0077
178038_at	T23F6.1			2.88	0.0065
176141_s_at	Y58A7A.3			2.88	0.0107
188085_s_at	R09H10.4	ptr-14	PaTched Related family	2.87	0.0038

189864_s_at	F19C7.7	col-110	COLlagen	2.87	0.0113
189259_s_at	T02D1.5	pmp-4	Peroxisomal Membrane Protein related	2.87	0.0061
188390_at	F56C11.2	ptr-11	PaTched Related family	2.86	0.0025
184534_s_at	C17H12.8			2.86	0.0082
183876_at	C07G3.2			2.86	0.0352
179537_at	C50B8.4			2.86	0.0181
190184_at	ZK822.3	nhx-9	Na/H eXchanger	2.85	0.0056
176188_at	Y71D11A.1	cdh-12	CaDHerin family	2.85	0.0099
187353_s_at	Y110A2AL.8	ptc-3	PaTChed family	2.85	0.0025
177317_at	VC5.3	npa-1	Nematode Polyprotein Allergen related	2.84	0.0034
178149_s_at	T07C4.4	spp-1	SaPosin-like Protein family	2.83	0.0068
177519_at	F35E2.9			2.83	0.0165
185492_at	K02E10.4			2.83	0.0117
181310_at	Y38H6C.9			2.83	0.0080
176209_at	Y58A7A.5			2.82	0.0125
174283_s_at	F38B6.4		GARS/AIRS/GART	2.82	0.0024

179373_at	C50F4.9			2.82	0.0143
178194_at	R07E3.6			2.82	0.0157
178409_s_at	F58B3.3	lys-6	LYSozyme	2.81	0.0187
181888_at	T05C1.3			2.81	0.0048
175025_at	T14B4.7	dpy-10	DumPY : shorter than wild-type	2.80	0.0165
192930_s_at	ZC455.10	fkb-4	FK506-Binding protein family	2.79	0.0110
176686_at	D1014.7			2.78	0.0057
179226_at	C06B3.7			2.77	0.0256
181933_at	T27A3.5			2.77	0.0117
181835_at	F55G11.7			2.77	0.0271
178767_at	C10C5.2			2.77	0.0142
178724_s_at	F54D5.3			2.77	0.0067
193545_s_at	F57B7.4	mig-17	abnormal cell MIGration	2.77	0.0068
193293_at	C52E4.1	cpr-1	Cysteine PRotease related	2.77	0.0029
191066_s_at	ZC455.6	ugt-5	UDP-GlucuronosylTransferase	2.76	0.0069
190830_at	T21C9.8	ttr-23	TransThyretin-Related family domain	2.76	0.0122

189736_s_at	K11D12.4	cpt-4	Carnitine Palmitoyl Transferase	2.76	0.0023
177255_at	M195.2			2.76	0.0089
173210_s_at	F14B8.5			2.75	0.0017
186061_at	R107.1	nac-2	NADC (Na+-coupled dicarboxylate transporter) family	2.75	0.0038
181014_at	C39H7.4			2.75	0.0063
184451_at	Y57G7A.1			2.75	0.0216
185406_at	Y95B8A.2			2.75	0.0184
175707_s_at	F15C11.1	sem-4	SEx Muscle abnormal	2.75	0.0044
178087_s_at	F58B3.2	lys-5	LYSozyme /// LYSozyme	2.74	0.0024
194056_s_at	F35C11.1	clec-62	C-type LECtin	2.74	0.0051
179947_at	T02C5.1			2.73	0.0061
190075_at	K09C8.1	pbo-4	PBOc defective (defecation)	2.72	0.0021
182755_at	F47F6.3	oac-30	O-ACyltransferase homolog	2.72	0.0031
178853_at	F30F8.5			2.72	0.0078
180846_at	C27D9.2			2.72	0.0071
190585_at	ZK970.7		OV-17 antigen precursor	2.72	0.0047

173778_s_at	C01B10.10			2.71	0.0160
180315_at	F44G3.10			2.71	0.0478
180453_at	F53A9.1			2.71	0.0096
193133_s_at	ZK337.1			2.71	0.0048
189455_at	C27A2.4			2.70	0.0066
173583_s_at	C14H10.2			2.70	0.0035
174952_s_at	ZK337.1			2.70	0.0058
193263_at	ZC410.4	twk-8	TWiK family of potassium channels	2.70	0.0014
172386_x_at	B0213.5	nlp-30	Neuropeptide-Like Protein	2.70	0.0065
184787_at	F46G11.2			2.70	0.0147
173238_s_at	K11D12.4	cpt-4	Carnitine Palmitoyl Transferase	2.69	0.0042
175797_at	R31.1	sma-1	SMAll	2.69	0.0074
173388_s_at	F09B12.3			2.69	0.0051
180611_at	Y38H8A.1			2.69	0.0087
185334_s_at	R02F11.1			2.69	0.0051
176271_at	C52D10.1			2.69	0.0034

178412_at	R02D5.3			2.68	0.0097
184533_at	C17H12.8			2.68	0.0026
180814_s_at	F09B12.3			2.67	0.0032
183735_at	K03H9.3			2.67	0.0063
176227_s_at	Y71H2AM.15			2.67	0.0041
182253_at	Y80D3A.5	cyp-42A1	CYtochrome P450 family	2.67	0.0132
173395_s_at	Y47D3B.10	dpy-18	DumPY : shorter than wild-type	2.67	0.0051
187377_at	F37A4.5			2.66	0.0064
177298_at	M163.1			2.66	0.0259
176819_s_at	Y49C4A.8	ugt-29	UDP-GlucuronosylTransferase	2.66	0.0098
182143_s_at	F42C5.7	grl-4	GRound-Like (grd related)	2.65	0.0075
190013_at	T21D12.2	dpy-9	DumPY : shorter than wild-type	2.65	0.0079
179860_at	K04C2.5			2.65	0.0058
190541_at	C30G12.2		Alcohol dehydrogenase	2.65	0.0101
194211_x_at	C03A7.14	abu-8	Activated in Blocked Unfolded protein response	2.65	0.0178

188061_s_at	F52E4.6	wrt-2	WaRThog (hedgehog-like family)	2.64	0.0067
189803_at	F38B6.5	col-172	COLlagen	2.63	0.0040
187829_s_at	F55C12.7	tag-234	Temporarily Assigned Gene name	2.63	0.0230
177832_at	K02E2.8			2.63	0.0259
180607_at	C10G6.1			2.63	0.0029
174610_at	F39C12.3	tsp-14	TetraSPanin family	2.63	0.0041
175256_at	C05E11.3			2.63	0.0067
173974_s_at	Y73B6BR.1	pqn-89	Prion-like-(Q/N-rich)-domain-bearing protein	2.63	0.0082
184283_at	Y51H4A.25			2.62	0.0135
174547_at	F19H8.4			2.62	0.0071
190702_at	K01H12.2	ant-1.3	Adenine Nucleotide Translocator	2.62	0.0085
190009_at	F49E12.10		ERG-3 like protein	2.62	0.0080
172809_x_at	Y41E3.2	dpy-4	DumPY : shorter than wild-type	2.62	0.0041
172343_x_at	B0213.6	nlp-31	Neuropeptide-Like Protein	2.61	0.0128
176002_at	M02H5.8			2.60	0.0106
187775_at	F40B5.3			2.60	0.0082

174273_at	F01G10.9			2.60	0.0071
192458_at	F27C8.1	aat-1	Amino Acid Transporter	2.60	0.0044
183631_at	C08F11.5	fbxa-98	F-box A protein	2.60	0.0081
190366_at	F44F4.11	tba-4	TuBulin, Alpha	2.60	0.0039
189983_at	B0365.5	clec-225	C-type LECtin	2.59	0.0260
178077_at	F57F5.3			2.59	0.0086
177877_at	F35E2.5			2.58	0.0050
188132_at	M110.1	col-76	COLlagen	2.58	0.0038
186715_at	F46C5.2			2.58	0.0025
188653_at	C44F1.2	attf-1	AT hook Transcription Factor family	2.58	0.0228
186995_at	Y65B4BR.2	lpr-1	LiPocalin-Related protein	2.58	0.0076
175546_at	R06C1.6			2.58	0.0061
180204_at	F35E12.9			2.58	0.0132
185640_s_at	F43B10.2	tag-343	Temporarily Assigned Gene name	2.58	0.0109
183859_at	F13H10.1			2.58	0.0099
191861_at	Y32F6B.3	crp-1	Cdc-42 Related Protein	2.57	0.0104

185158_s_at	C33C12.4			2.57	0.0238
175438_at	C36E8.2	glb-11	GLoBin	2.57	0.0082
194109_s_at	Y75B12B.6	plc-2	PhosphoLipase C	2.57	0.0171
193318_at	C29F3.6	srx-58	Serpentine Receptor, class X	2.57	0.0074
184002_at	C09F12.1	clc-1	CLaudin-like in Caenorhabditis	2.57	0.0102
178465_at	C08B6.11			2.57	0.0055
183449_s_at	F45H10.4	drr-1	Dietary Restriction Response (WT but not eat-2 lifespan increased)	2.56	0.0113
175462_s_at	T12A7.1	gem-4	Gon-2 Extragenic Modifier	2.56	0.0117
191899_at	M04G7.2		protein-tyrosine phosphatase	2.56	0.0209
181791_at	T06A1.5			2.56	0.0037
188661_s_at	F42E11.4	tni-1	TropoNin I	2.56	0.0068
187219_at	C34C12.6			2.55	0.0070
185243_at	B0336.11			2.55	0.0091
183440_s_at	R09A1.3			2.54	0.0148
181555_at	B0496.7	valv-1	VALVe cells defective	2.54	0.0277

189987_s_at	C26C6.3	nas-36	Nematode AStacin protease	2.54	0.0032
182169_at	F47G6.2			2.54	0.0043
187962_at	K02E2.4	ins-35	INSulin related	2.54	0.0073
181137_at	F46G10.1			2.54	0.0071
178929_at	F47G9.3	cutl-18	CUTiclin-Like	2.53	0.0069
177920_at	D1086.3			2.53	0.0447
183702_at	K05B2.4			2.53	0.0076
190134_s_at	T10B10.1	col-41	COLlagen	2.52	0.0024
186070_at	Y71H2B.7	gpa-17	G Protein, Alpha subunit	2.52	0.0167
180193_at	F14F9.4			2.52	0.0118
182629_at	C50D2.1			2.52	0.0044
179131_at	T08G5.3			2.52	0.0073
184771_at	H02F09.2			2.51	0.0048
192474_s_at	C31C9.2		D-3-Phosphoglycerate dehydrogenase	2.50	0.0114
176677_at	D1014.6			2.50	0.0014
189362_at	F56H11.3	elo-7	fatty acid ELOngation	2.50	0.0155

189558_at	C14H10.3			2.50	0.0045
173668_s_at	F52G2.3			2.50	0.0062
185287_at	Y53F4B.25			2.50	0.0082
182502_at	F18E9.4			2.50	0.0165
183378_at	F55G11.8			2.49	0.0072
189150_at	ZC416.4	kgb-2	Kinase, GLH-Binding	2.49	0.0116
183148_at	F20D6.1			2.49	0.0122
192012_s_at	T19D12.2			2.49	0.0122
177276_at	ZK6.8			2.49	0.0145
188448_at	D1069.2	cpn-2	CalPoNin	2.49	0.0027
185554_s_at	Y39B6A.1			2.49	0.0188
177369_at	R52.3	math-35	MATH (meprin-associated Traf homology) domain containing	2.49	0.0212
179076_at	K10G4.3			2.49	0.0209
184948_at	Y57G11B.2			2.48	0.0042
184596_s_at	F57H12.7	mec-17	MEChanosensory abnormality	2.48	0.0049

189194_at	F27E5.3		homeobox domain	2.48	0.0119
185193_at	Y50E8A.12			2.48	0.0255
189100_at	ZK896.6	clec-187	C-type LECtin	2.48	0.0102
187906_at	F31F6.5	daf-6	abnormal DAuer Formation	2.48	0.0045
185970_at	ZK1055.4			2.48	0.0103
175163_at	F45H7.4	prk-2	Pim (mammalian oncogene) Related Kinase	2.47	0.0058
177670_at	ZC64.2	ttr-48	TransThyretin-Related family domain	2.47	0.0058
174579_s_at	H24G06.1			2.47	0.0042
177410_at	C01A2.2			2.47	0.0061
183222_at	ZC449.1			2.47	0.0163
185758_at	C14C11.3	hex-2	HEXosaminidase	2.46	0.0052
180332_at	Y51H4A.9	col-137	COLlagen	2.46	0.0095
177325_at	R57.2			2.46	0.0088
176222_at	Y82E9BL.10	fbxa-14	F-box A protein	2.46	0.0029
176395_at	Y71G12B.18			2.46	0.0453
177868_s_at	T28F3.8			2.46	0.0078

181536_at	F52B11.5			2.46	0.0041
193469_at	T05A7.5	fut-6	FUcosyl Transferase	2.45	0.0078
175126_s_at	K08D8.5			2.45	0.0056
192138_at	B0207.7		serine/threonine-protein kinase	2.45	0.0078
176217_at	Y54E5A.1			2.45	0.0047
187668_at	F47D12.6			2.45	0.0041
178710_at	F59C6.2			2.45	0.0362
180523_at	F47B10.5			2.44	0.0360
175870_s_at	Y34F4.4			2.44	0.0062
181653_at	T22H9.3			2.44	0.0132
182106_at	C34H4.1			2.44	0.0417
183713_at	C24G7.2			2.44	0.0055
174896_at	C14H10.3			2.44	0.0051
178927_at	K08D8.5			2.44	0.0051
179316_at	F58H1.6			2.44	0.0094
181618_at	ZK418.2		hypothetical protein	2.43	0.0125

191666_s_at	R12A1.4	ges-1	abnormal Gut Esterase	2.43	0.0061
175405_s_at	C15C7.7			2.43	0.0051
182667_at	C13D9.1	srr-6	Serpentine Receptor, class R	2.43	0.0261
188964_at	D1081.5		ankyrin motif	2.43	0.0058
181216_s_at	Y53H1B.2			2.43	0.0042
181111_at	C24G6.7	grl-1	GRound-Like (grd related)	2.43	0.0216
177631_at	ZK596.3			2.43	0.0078
174407_at	F08F1.8	tth-1	Tetra THymosin (four thymosin repeat protein)	2.43	0.0055
193439_at	Y70D2A.1		7 transmembrane receptor (rhodopsin family)	2.43	0.0094
171752_x_at	C18C4.5			2.42	0.0061
180514_at	K10H10.4			2.42	0.0064
172761_x_at	T10C6.14	his-1	HIStone	2.42	0.0027
180072_s_at	F13D12.9			2.42	0.0139
180759_at	F36H9.2			2.42	0.0081
183895_at	Y43F8C.1	nlp-25	Neuropeptide-Like Protein	2.42	0.0372
192613_at	Y70C5C.6	nhr-112	Nuclear Hormone Receptor family	2.41	0.0097

173242_s_at	M01D7.5	nlp-12	Neuropeptide-Like Protein	2.41	0.0051
193329_at	F41E6.6	tag-196	Temporarily Assigned Gene name	2.41	0.0035
187176_s_at	D2096.6			2.41	0.0058
186597_at	F19C6.5			2.41	0.0099
194180_x_at	B0273.4	unc-5	UNCoordinated	2.40	0.0046
177267_at	ZC8.3	set-30	SET (trithorax/polycomb) domain containing	2.40	0.0087
180911_at	F52E1.9			2.40	0.0033
176260_at	Y58A7A.1			2.40	0.0170
188965_at	F55H12.3		LDL receptor	2.40	0.0080
193529_at	F55C5.2		glycerophosphoryldiester phophodiesterase like	2.40	0.0142
176064_s_at	R05G9R.1			2.40	0.0041
191718_s_at	C43C3.1	ifp-1	Intermediate Filament Protein, class E	2.40	0.0029
174461_at	F58A4.11	gei-13	GEX Interacting protein	2.39	0.0040
179620_s_at	T10G3.3			2.39	0.0112
178656_at	F36D1.6			2.39	0.0163
174906_s_at	C25F6.2	dlg-1	Drosophila Discs Large homolog	2.39	0.0080

190104_at	E04D5.3	cut-4	CUTiclin	2.39	0.0062
182439_at	Y17D7B.4			2.39	0.0062
191638_s_at	C55B7.3		protein-tyrosine phosphatase	2.39	0.0166
192126_s_at	T24A11.3	toh-1	TOllisH (Tolloid and BMP-1 family)	2.39	0.0132
176748_s_at	C18C4.5			2.39	0.0078
188716_s_at	ZK430.8	mlt-7	MoLTing defective	2.38	0.0184
193013_at	T02E1.7		Yeast hypothetical protein YG5Y like	2.38	0.0200
187522_at	F25B5.1	dct-6	DAF-16/FOXO Controlled, germline Tumor affecting	2.38	0.0065
193419_at	F35B12.9			2.37	0.0068
183663_s_at	Y41C4A.8			2.37	0.0132
172635_x_at	Y38E10A.15			2.37	0.0058
184823_at	C01B10.4			2.37	0.0165
189519_at	R08F11.3	cyp-33C8	CYtochrome P450 family	2.36	0.0068
193520_at	W06B3.2	sma-5	SMAll	2.36	0.0068
172871_x_at	ZK131.7	his-13	HIStone	2.36	0.0113

172871_x_at	ZK131.2	his-25	HIStone	2.36	0.0113
172871_x_at	ZK131.3	his-9	HIStone	2.36	0.0113
178071_at	F56D5.2			2.36	0.0095
190628_at	F32A5.4			2.36	0.0051
193579_at	Y43C5B.2		Src homology domain 2, tyrosine-protein kinase	2.35	0.0376
188486_s_at	K10B4.6	cwn-1	WNT family	2.35	0.0040
181326_at	F15E6.2	lgc-22	Ligand-Gated ion Channel	2.35	0.0068
172292_x_at	D2092.8			2.35	0.0097
172184_x_at	Y46C8AL.2	clec-174	C-type LECtin	2.34	0.0207
181939_at	F35C11.4			2.34	0.0029
188734_at	ZK945.1	lact-2	beta-LACTamase domain containing	2.34	0.0196
174286_at	F48F7.1	alg-1	Argonaute (plant)-Like Gene	2.34	0.0318
177951_s_at	PDB1.1			2.34	0.0043
180471_at	Y17G7B.8			2.33	0.0022
178834_at	F47B8.2			2.33	0.0110
188168_at	R07G3.2	lips-17	LIPaSe related	2.33	0.0016

188998_s_at	C05A9.1	pgp-5	P-GlycoProtein related	2.33	0.0161
171745_x_at	F56C11.2	ptr-11	PaTched Related family	2.33	0.0300
191856_s_at	K12F2.1	myo-3	MYOsin heavy chain structural genes	2.33	0.0043
186843_at	Y65B4BL.6			2.33	0.0123
178872_at	C25F9.12			2.33	0.0452
178872_at	C25F9.6			2.33	0.0452
179914_at	F35E12.8			2.32	0.0127
176383_at	C52D10.1			2.32	0.0037
179012_at	K08E4.7			2.32	0.0382
189538_s_at	C01B7.4	tag-117	Temporarily Assigned Gene name	2.32	0.0147
172564_x_at	F26A10.1			2.32	0.0099
174629_at	W01A11.3	unc-83	UNCoordinated	2.32	0.0077
182039_at	F37C4.3	oac-23	O-ACyltransferase homolog	2.31	0.0233
179402_at	F52H3.5			2.31	0.0399
189580_at	M04G12.2	cpz-2	CathePsin Z	2.31	0.0072
184051_at	C26F1.1			2.31	0.0062

186748_at	ZK512.1			2.31	0.0035
192277_at	R07B7.11	gana-1	GAlactosidase/N-Acetylgalactosaminidase	2.31	0.0085
178938_at	C50B6.9			2.31	0.0040
172191_x_at	ZK1025.4			2.31	0.0066
172191_x_at	C27C7.2			2.31	0.0066
189629_at	ZC373.7	col-176	COLlagen	2.30	0.0144
187705_at	T25D10.1			2.30	0.0369
193301_at	T05A7.4	hmg-11	HMG	2.30	0.0065
173117_at	H10E21.4		Hypothetical protein (H10E21.4)	2.30	0.0107
190566_at	T12G3.1		Drosphila REF (2)P like	2.30	0.0106
193986_s_at	F08C6.4	sto-1	STOmatin	2.29	0.0091
184208_at	Y17G7B.14			2.29	0.0148
175391_at	ZK678.8	bus-17	Bacterially Un-Swollen (M. nematophilum resistant)	2.29	0.0088
192213_s_at	Y57G11A.1	tag-273	Temporarily Assigned Gene name	2.29	0.0050
190899_at	F21H7.1	gst-22	Glutathione S-Transferase	2.29	0.0121
180562_at	B0218.8	clec-52	C-type LECtin	2.29	0.0083

179730_at	F19C7.1			2.29	0.0033
191134_at	F17A9.3		BZIP transcription factor	2.29	0.0279
190234_at	R10H1.4	isl-1	Inhibitor of Serine protease Like protein	2.29	0.0279
190234_at	R10H1.1		trypsin inhibitor	2.29	0.0279
188240_at	C54H12.1	ptr-6	PaTched Related family	2.29	0.0035
173090_s_at	F35C5.8	clec-65	C-type LECtin	2.28	0.0067
174389_s_at	K02E10.4			2.28	0.0131
179704_at	C16D9.4			2.28	0.0062
190177_at	R05H10.6	cdh-7	CaDHerin family	2.28	0.0062
179563_at	C25D7.16			2.28	0.0068
179563_at	C25D7.5			2.28	0.0068
184284_s_at	T28F3.9			2.28	0.0349
184284_s_at	Y51H4A.25			2.28	0.0349
193258_at	F27E5.4	phg-1	PHarynx-associated GAS (growth arrest protein) related	2.28	0.0134
191624_at	F47B10.7	acbp-3	Acyl-Coenzyme A Binding Protein	2.28	0.0065
176071_at	B0403.3			2.27	0.0078

174396_at	B0496.3	unc-82	UNCoordinated	2.27	0.0030
190608_s_at	C09D4.3		SER/THR protein kinase	2.27	0.0063
175450_at	F56D5.6			2.27	0.0086
172997_s_at	F56C9.7			2.27	0.0072
172321_x_at	C03A7.3	abu-7	Activated in Blocked Unfolded protein response	2.27	0.0286
179118_at	C25D7.4	fbxa-82	F-box A protein	2.27	0.0113
182465_at	Y17D7B.3			2.27	0.0454
189079_s_at	C25A11.4	ajm-1	Apical Junction Molecule	2.26	0.0046
177956_at	F13G3.2	srd-53	Serpentine Receptor, class D (delta)	2.26	0.0128
184547_at	K12C11.6			2.26	0.0084
184547_at	K12C11.7			2.26	0.0084
184733_at	T06C12.10	cgt-1	Ceramide Glucosyl Transferase	2.26	0.0051
192278_s_at	T16A9.4		endothelin converting enzyme 1	2.26	0.0140
173480_s_at	Y5H2B.5	cyp-32B1	CYtochrome P450 family	2.26	0.0240
192917_s_at	F07A11.4		ubiquitin carboxyl-terminal hydrolase	2.26	0.0061

192943_at	ZK1251.3		3-oxo-5-alpha-steroid 4-dehydrogenase	2.26	0.0225
188084_s_at	K04B12.1	plx-2	PLeXin	2.26	0.0073
188090_at	F56H1.1	che-14	abnormal CHEmotaxis	2.26	0.0067
183083_at	C15C7.7			2.26	0.0050
179913_at	E04F6.9			2.25	0.0058
188307_at	Y53F4B.28	ptr-20	PaTched Related family	2.25	0.0070
180039_at	Y54E5A.1			2.25	0.0096
192216_at	F58H1.7			2.25	0.0068
177270_at	JC8.12			2.25	0.0071
172371_x_at	F44E7.3			2.25	0.0330
171862_s_at	R08E3.1			2.24	0.0036
179417_at	F56D5.6			2.24	0.0065
175833_s_at	C48D5.1	nhr-6	Nuclear Hormone Receptor family	2.24	0.0151
175786_at	T05A6.1	cki-1	CKI family (Cyclin-dependent Kinase Inhibitor)	2.24	0.0264
183691_at	F35C8.2			2.24	0.0283
171805_x_at	F22F1.1	hil-3	Histone H1.3	2.24	0.0049

172472_x_at	B0222.8	col-10	COLlagen	2.23	0.0073
172472_x_at	B0222.6	col-144	COLlagen	2.23	0.0073
176616_s_at	F10E9.6	mig-10	abnormal cell MIGration	2.23	0.0046
180618_at	F14D2.7			2.23	0.0233
182935_at	F36A4.3			2.23	0.0266
193393_at	C53D6.2	unc-129	UNCoordinated	2.23	0.0123
178138_at	F38B7.2			2.23	0.0219
186179_at	K05F1.10			2.23	0.0144
194078_s_at	D2085.1	pyr-1	PYRimidine biosynthesis	2.22	0.0070
192344_at	C28G1.5			2.22	0.0103
188299_at	Y71F9B.5	lin-17	abnormal cell LINeage	2.22	0.0045
178165_at	F46F3.3			2.22	0.0255
176619_s_at	E01A2.3	lin-44	abnormal cell LINeage	2.22	0.0027
190822_s_at	R07B1.3		membrane glycoprotein	2.22	0.0021
174029_at	T14F9.4	peb-1	Pharyngeal Enhancer Binding	2.22	0.0138
177374_at	LLC1.2			2.22	0.0051

172511_x_at	T28F3.8			2.21	0.0117
186477_at	F36H12.14			2.21	0.0214
173561_s_at	R12C12.9			2.21	0.0154
188068_at	F37A8.4	nlp-10	Neuropeptide-Like Protein	2.21	0.0040
172899_x_at	F08G2.3	his-42	HIStone	2.21	0.0157
173620_s_at	C03A7.11	ugt-51	UDP-GlucuronosylTransferase	2.21	0.0252
193472_at	ZK524.1	spe-4	defective SPErmatogenesis	2.20	0.0099
178687_at	F15H9.1			2.20	0.0254
171737_x_at	T12G3.1		Drosphila REF (2)P like	2.20	0.0307
184813_at	C35A11.2		hypothetical protein	2.20	0.0327
191646_at	F53F4.5	fmo-4	Flavin-containing MonoOxygenase family	2.20	0.0073
192520_s_at	F36H2.5			2.20	0.0160
178944_at	F45D3.2			2.20	0.0082
175504_at	F17C11.11			2.20	0.0232
180642_at	F53A9.2			2.20	0.0163
175264_at	C05D10.4			2.20	0.0023

190213_s_at	C16C8.2		peroxidase precursor	2.20	0.0079
172356_at	K02E11.7			2.20	0.0098
193686_at	F32A11.6	moe-3	See oma	2.20	0.0068
184258_at	Y62E10A.3			2.20	0.0365
178042_at	W01B6.4			2.19	0.0125
175817_at	F48E3.1	gly-12	GLYcosylation related	2.19	0.0123
189512_at	C03G6.15	cyp-35A2	CYtochrome P450 family	2.19	0.0253
171905_x_at	K10D6.2			2.19	0.0051
184953_at	Y113G7B.3	fbxa-115	F-box A protein	2.19	0.0205
180447_at	F54C9.11			2.19	0.0057
191301_s_at	F47B10.2		histidine ammonia-lyase	2.18	0.0067
184183_s_at	R04B3.3			2.18	0.0023
185055_at	C10H11.6	ugt-26	UDP-GlucuronosylTransferase	2.18	0.0148
173015_s_at	Y54G2A.9	clec-81	C-type LECtin	2.18	0.0031
172323_x_at	C03A7.7	abu-6	Activated in Blocked Unfolded protein response	2.18	0.0103

191621_s_at	R31.1	sma-1	SMAll	2.18	0.0058
176169_at	Y82E9BL.14	fbxa-80	F-box A protein	2.18	0.0095
193265_at	K10C3.3	zig-1	2 (Zwei) IG-domain protein	2.18	0.0036
188182_at	F54C1.9	sst-20	Sperm Specific Transcript	2.18	0.0132
174426_at	F13H6.1			2.18	0.0025
183736_at	B0511.3	fbxa-125	F-box A protein	2.17	0.0303
187985_at	F44G3.6	skr-3	SKp1 Related (ubiquitin ligase complex component)	2.17	0.0058
184125_at	C05D12.1		hypothetical protein	2.17	0.0023
180698_s_at	R12E2.9	inx-15	INneXin	2.17	0.0120
183575_at	T14A8.2			2.17	0.0107
183964_at	T24A6.7			2.17	0.0344
173148_s_at	R12H7.2	asp-4	ASpartyl Protease	2.17	0.0062
172309_x_at	C08E3.13			2.17	0.0113
172309_x_at	C08E3.1			2.17	0.0113
189882_at	ZK484.2	haf-9	HAlF transporter (PGP related)	2.16	0.0042
192403_s_at	F42G8.11	sph-1	SyaptoPHysin	2.16	0.0126

180882_s_at	F18C5.5			2.16	0.0275
185439_at	H20J04.1			2.16	0.0401
192034_s_at	D1009.1			2.16	0.0058
193321_at	R04E5.10	ifd-1	Intermediate Filament, D	2.16	0.0190
173609_at	Y39B6A.1			2.16	0.0038
183874_s_at	Y56A3A.7			2.16	0.0062
178900_s_at	F45D3.4			2.16	0.0254
177219_at	M28.8			2.16	0.0302
188592_at	E03A3.4	his-70	HIStone	2.16	0.0173
177492_at	F41E7.8	cnc-8	CaeNaCin (Caenorhabditis bacteriocin)	2.16	0.0122
180391_s_at	F54A5.2	cutl-20	CUTiclin-Like	2.15	0.0036
190607_at	C09D4.3		SER/THR protein kinase	2.15	0.0400
181113_at	F40E10.5			2.15	0.0360
175726_s_at	H01A20.1	nhr-3	Nuclear Hormone Receptor family	2.15	0.0203
172671_x_at	K03A1.6	his-38	HIStone	2.15	0.0024
189790_s_at	T10H10.1	hum-6	Heavy chain, Unconventional Myosin	2.15	0.0156

186846_s_at	F36G3.1			2.15	0.0116
171801_s_at	W03G11.4			2.15	0.0046
181683_at	M03E7.2			2.14	0.0114
185566_at	C05E11.3			2.14	0.0102
175453_at	F48F7.2	syn-2	SYNtaxin	2.14	0.0377
178054_at	C06G8.3			2.14	0.0153
175390_at	F15D4.8	flp-16	FMRF-Like Peptide	2.14	0.0098
189026_s_at	F32A7.5			2.14	0.0025
174641_at	F08B12.1			2.14	0.0056
182552_at	F22A3.2	ttr-35	TransThyretin-Related family domain	2.14	0.0062
193811_at	F22D6.12		beta-1,6-N-acetylglucosaminyltransferase	2.14	0.0048
179038_at	F26A3.5			2.14	0.0035
177516_at	T21C9.9			2.14	0.0186
181659_at	F35D2.2			2.13	0.0051
178718_at	T22A3.4	set-18	SET (trithorax/polycomb) domain containing	2.13	0.0041
177487_at	C29F3.7			2.13	0.0030

187413_at	C04F6.2			2.13	0.0046
180934_at	K10B3.1			2.13	0.0059
191679_s_at	F56F4.5	opt-3	OligoPeptide Transporter	2.13	0.0049
172974_s_at	F19C7.1			2.13	0.0029
187260_s_at	ZK1320.2			2.12	0.0081
192199_at	F11E6.8			2.12	0.0066
185519_at	C25E10.9	swm-1	Sperm activation Without Mating	2.12	0.0054
179607_at	C18E9.9			2.12	0.0127
185711_at	T15B7.14			2.12	0.0271
179161_at	C44F1.5	acy-3	Adenylyl Cyclase	2.12	0.0096
174902_at	K10D6.4			2.12	0.0061
183989_at	F07G6.7	fbxa-53	F-box A protein	2.12	0.0111
175519_at	F59C6.11			2.11	0.0338
189671_at	C50H11.15	cyp-33C9	CYtochrome P450 family	2.11	0.0058
188754_at	T27B1.2	ztf-19	Zinc finger Transcription Factor family	2.11	0.0089

174012_s_at	F53B2.8			2.11	0.0277
185685_at	ZC513.10	fbxa-223	F-box A protein	2.11	0.0407
192037_at	F26D10.9	atgp-1	Amino acid Transporter GlycoProtein subunit	2.11	0.0069
178854_at	M05B5.2			2.11	0.0039
188523_at	R13F6.9	sma-3	SMAll	2.11	0.0148
182513_at	F08F1.8	tth-1	Tetra THymosin (four thymosin repeat protein)	2.11	0.0027
191801_s_at	F33C8.1	tag-53	Temporarily Assigned Gene name	2.11	0.0042
187919_s_at	T09B4.7			2.11	0.0391
180214_at	T13C2.3			2.11	0.0098
174122_s_at	T11B7.4	alp-1	ALP/Enigma encoding	2.11	0.0057
189597_s_at	F59F4.1		acyl-CoA oxidase I	2.11	0.0058
174578_at	H24G06.1			2.11	0.0047
182301_at	H12D21.9			2.11	0.0137
181532_at	F13H8.4	nmgp-1	Neuronal Membrane GlycoProtein	2.10	0.0050
188229_s_at	Y60A3A.18	skr-4	SKp1 Related (ubiquitin ligase complex component) /// SKp1 Related (ubiquitin ligase complex component)	2.10	0.0135

186153_s_at	T27A10.7	cgr-1	CRAL/TRIO and GOLD domain suppressor of activated Ras	2.10	0.0068
174147_at	T21H8.1			2.10	0.0066
185227_at	F19F10.4	ttr-10	TransThyretin-Related family domain	2.10	0.0112
172516_x_at	Y39G8B.1			2.10	0.0045
180378_at	C17F4.5	fbxc-50	F-box C protein	2.10	0.0041
189973_at	T23H4.3	nas-5	Nematode AStacin protease	2.10	0.0374
182172_at	B0344.2	wrt-9	WaRThog (hedgehog-like family)	2.10	0.0038
189457_at	B0213.15	cyp-34A9	CYtochrome P450 family	2.10	0.0209
179413_at	K06A4.4			2.10	0.0064
193037_s_at	T22B7.1	egl-13	EGg Laying defective	2.10	0.0049
174178_at	C14C11.8	pqn-13	Prion-like-(Q/N-rich)-domain-bearing protein	2.10	0.0159
172735_x_at	T10E10.2	col-167	COLlagen	2.10	0.0145
172735_x_at	T10E10.1	col-168	COLlagen	2.10	0.0145
172735_x_at	T10E10.6	col-170	COLlagen	2.10	0.0145
180690_at	F35E12.4			2.10	0.0165

180658_at	T01B6.1			2.10	0.0047
179806_at	W05H9.1			2.09	0.0473
188756_s_at	Y116F11B.3	pcp-4	Prolyl Carboxy Peptidase like	2.09	0.0056
178229_at	F01D5.7			2.09	0.0041
177629_at	ZK593.3			2.09	0.0262
178065_at	T21H8.1			2.09	0.0091
190357_at	T28D6.4		Ank repeat (8 domains)	2.09	0.0219
176453_at	Y39G10AR.6	ugt-31	UDP-GlucuronosylTransferase	2.09	0.0180
179078_s_at	F54C9.3			2.08	0.0203
172859_x_at	C07E3.4		Protein-tyrosine phosphatase	2.08	0.0303
174251_s_at	Y54G2A.4			2.08	0.0036
180008_at	K06A1.2			2.08	0.0229
193844_at	C34D1.5	zip-5	bZIP transcription factor family	2.08	0.0403
175227_s_at	Y116A8C.38			2.08	0.0102
175227_s_at	Y116A8C.24			2.08	0.0102
181671_s_at	F56C9.7			2.08	0.0043

180799_at	C55C3.1			2.08	0.0051
181585_at	C29F5.3			2.08	0.0275
184254_at	C46H11.7			2.08	0.0205
179117_at	F32B4.2			2.08	0.0169
173680_at	T02C5.3	igcm-3	ImmunoGlobulin-like Cell adhesion Molecule family	2.08	0.0034
172746_x_at	T07H6.3	col-166	COLlagen	2.08	0.0106
172746_x_at	T10E10.5	col-169	COLlagen	2.08	0.0106
190301_s_at	C05E11.5	amt-4	AMmonium Transporter homolog	2.07	0.0165
182227_s_at	K12F2.2	vab-8	Variable ABnormal morphology	2.07	0.0097
185201_s_at	Y116A8C.4			2.07	0.0098
185280_at	H43E16.1			2.07	0.0047
193566_at	C06C6.4	nhr-63	Nuclear Hormone Receptor family	2.07	0.0279
190228_s_at	T04C9.6	frm-2	FERM domain (protein4.1-ezrin-radixin-moesin) family	2.07	0.0092
186270_s_at	F53C3.12	bcmo-2	Beta-Carotene 15,15'-MonoOxygenase	2.07	0.0187
174021_at	F16H11.5	nhr-45	Nuclear Hormone Receptor family	2.07	0.0120
193319_at	C44H4.2	sym-5	SYnthetic lethal with Mec	2.07	0.0205

175142_at	F17C11.12			2.07	0.0092
190223_at	K11E4.2		Src homology domain 2	2.07	0.0162
173944_at	K10D3.4		serine proteinase inhibitor (kunitz type)	2.07	0.0127
184693_s_at	C32H11.11			2.07	0.0475
184693_s_at	C32H11.8			2.07	0.0475
181688_at	W06D11.4			2.06	0.0038
190007_at	R186.6		Rhodanese-like domain	2.06	0.0162
186385_at	T25F10.3			2.06	0.0156
188332_at	K06A4.3	gsnl-1	GelSoliN-Like	2.06	0.0272
183590_at	C50E3.6			2.06	0.0044
172422_x_at	K10D6.2			2.06	0.0051
177152_at	Y45G5AM.3			2.06	0.0249
173224_s_at	C17C3.4	ins-11	INSulin related	2.06	0.0113
178031_at	C27H2.2			2.06	0.0062
189061_at	F26A1.4		Casein kinase	2.06	0.0180
176925_at	Y42H9B.1	col-115	COLlagen	2.06	0.0196

184065_at	Y38F1A.7			2.06	0.0067
186941_at	F54H5.4	mua-1	MUscle Attachment abnormal	2.06	0.0492
177499_at	C38H2.2			2.06	0.0076
190579_at	C17G1.3	ugt-23	UDP-GlucuronosylTransferase	2.06	0.0032
174406_at	F13B10.1	tir-1	TIR (Toll and Interleukin 1 Receptor) domain protein	2.06	0.0108
175943_at	C02D5.2			2.05	0.0161
173782_at	M60.5	kqt-2	potassium channel, KvQLT family	2.05	0.0111
181149_at	F40A3.1			2.05	0.0162
192140_at	C06B8.7		Human M130 antigen like protein	2.05	0.0140
186214_at	Y41G9A.5			2.05	0.0079
184708_s_at	C43E11.5			2.05	0.0238
184708_s_at	C50F2.5			2.05	0.0238
186029_at	T28C12.3	fbxa-202	F-box A protein	2.05	0.0344
186628_at	Y38E10A.18	nhr-234	Nuclear Hormone Receptor family	2.05	0.0057
173614_at	C46H11.11	fhod-1	Formin HOmology Domain	2.05	0.0283
185754_at	C14F11.2			2.04	0.0050

193825_at	C01C4.1	nlp-1	Neuropeptide-Like Protein	2.04	0.0029
172679_x_at	B0035.9	his-46	HIStone	2.04	0.0239
172679_x_at	F54E12.3	his-56	HIStone	2.04	0.0239
172679_x_at	F22B3.1	his-64	HIStone	2.04	0.0239
189825_at	C08F8.7	rap-3	RAP homolog (vertebrate Rap GTPase family)	2.04	0.0499
178996_at	C43F9.8	efn-2	Eph(F)riN	2.04	0.0052
178067_at	F48F7.7			2.04	0.0144
184716_at	Y46G5A.10			2.04	0.0150
178771_at	F59C6.14			2.04	0.0112
178771_at	F59C6.3			2.04	0.0112
175603_at	R12H7.1	unc-9	UNCoordinated	2.04	0.0041
174912_at	T04F8.6			2.03	0.0162
183641_at	F08B12.4			2.03	0.0089
186488_at	T15H9.4			2.03	0.0249
175732_at	F39C12.2	add-1	ADDucin	2.03	0.0058
184655_at	T21E12.5			2.03	0.0128

172951_s_at	C39F7.2			2.03	0.0047
172823_x_at	B0035.7	his-47	HIStone	2.03	0.0067
180954_at	C45G7.5	cdh-10	CaDHerin family	2.03	0.0085
173164_s_at	C18D11.1			2.03	0.0066
178886_at	F32D8.3			2.03	0.0041
185356_at	F35D11.2	pqn-35	Prion-like-(Q/N-rich)-domain-bearing protein	2.03	0.0243
178403_at	F10A3.2	fbxa-88	F-box A protein	2.02	0.0101
179499_s_at	C06H5.1	fbxa-156	F-box A protein	2.02	0.0322
179499_s_at	C06H5.2	fbxa-157	F-box A protein	2.02	0.0322
182330_s_at	Y37A1A.2			2.02	0.0166
177161_at	R11.2			2.02	0.0113
190135_at	F07C3.10	nhr-36	Nuclear Hormone Receptor family	2.02	0.0126
173571_s_at	T27E4.6	oac-50	O-ACyltransferase homolog	2.02	0.0100
185693_at	W02F12.2			2.02	0.0085
182615_at	C54D10.9			2.02	0.0074
190144_at	F22E10.1	pgp-12	P-GlycoProtein related	2.02	0.0062

187944_at	C18D1.3	flp-4	FMRF-Like Peptide	2.02	0.0179
178355_at	C29F7.1			2.02	0.0162
172198_x_at	F15D3.3	col-66	COLlagen	2.02	0.0133
178264_at	F01D5.8			2.02	0.0063
177569_s_at	F35E2.6	oac-19	O-ACyltransferase homolog	2.02	0.0160
187654_s_at	F11G11.9			2.02	0.0430
193749_at	F33D4.1	nhr-8	Nuclear Hormone Receptor family	2.02	0.0090
172061_x_at	T21C12.1	unc-49	UNCoordinated	2.02	0.0041
189584_s_at	F41E6.5			2.02	0.0099
187036_at	F13E9.13			2.02	0.0140
185717_s_at	F21C10.7			2.01	0.0071
182433_s_at	C25D7.12			2.01	0.0226
191828_at	R08E3.1			2.01	0.0042
179646_at	C18E9.8			2.01	0.0070
189660_at	F59D6.3		aspartyl protease	2.01	0.0326
193267_at	F13D11.1			2.01	0.0362

181257_at	F17C11.2			2.01	0.0070
172545_x_at	W08E12.4			2.01	0.0302
172545_x_at	W08E12.5			2.01	0.0302
180524_at	T22B2.6			2.01	0.0100
173737_at	C01C10.3	acl-12	ACyLtransferase-like	2.01	0.0127
184698_at	Y49E10.16			2.01	0.0070
193164_at	C37E2.2			2.01	0.0075
173777_s_at	F14H8.6	cng-1	Cyclic Nucleotide Gated channel	2.00	0.0081
171910_x_at	C01G6.1	aqp-2	AQuaPorin or aquaglyceroporin related	2.00	0.0042

Table S2. Representation factors for gene sets among OCTR-1-regulated genes.

Gene set	Genes in Set	Genes in Common	Representation Factor	*p*-value
PMK-1-induced genes	144	21	2.9	<1.001e-05
DAF-16-induced genes	263	44	3.3	<1.612e-12
CED-1-induced genes	218	43	3.9	<7.827e-15

The representation factor is the number of overlapping genes divided by the expected number of overlapping genes drawn from the group of OCTR-1-regulated genes and the group corresponding to a give gene set.
For details, see http://elegans.uky.edu/MA/progs/overlap_stats.html

PMK-1-induced genes from Troemel *et al*., 2006. PloS Genet 2, e183.
DAF-16-induced genes from Murphy *et al*., 2003. Nature 424, 277-283.
CED-1-induced genes from Haskins *et al*., 2008. Dev Cell 15, 87-97.

Table S3. *pqn/abu* genes are up-regulated by ER stress in *xbp-1(zc12) III* mutant animals.

Genes	Induction in *xbp-1**	
abu-1	1.42±0.16	1.45±0.29[§]
abu-6	2.12±0.17	1.75±0.28[§]
abu-7	1.60±0.22	1.22±0.49[§]
abu-8	1.97±0.24	1.77±0.29[§]
abu-12/pqn-40	1.41±0.07	
abu-13/pqn-46	1.68±0.11	
abu-14/pqn-95	1.15±0.03	
abu-15/pqn-5	1.60±0.07	

*Shown is the mean±SD of fold increase in tunicamycin-treated versus untreated *xbp-1* mutant animals. Student's exact *t*-test indicates that all differences between tunicamycin-treated animals and untreated animals are significantly different (P<0.05); N=3.

[§] Induction by tunicamycin in *xbp-1* observed by Urano et al. J Cell Biol. 2002 Aug 19;158(4):639-46.

Table S4. Prediction of signal peptide and transmembrane domains in PQN/ABU protein sequences

	Signal peptide	**TM region**
ABU-1/PQN-2	Y	1
ABU-6	Y	1
ABU-7	Y	1
ABU-8	Y	1
PQN-5/ABU-15	Y	1
PQN-13	Y	1
PQN-32	Y	1
PQN-35	none	1
PQN-40/ABU-12	Y	1
PQN-46/ABU-13	none	none
PQN-47	none	1
PQN-89	Y	4
PQN-95/ABU-14	Y	2

Signal peptide in PQN/ABU proteins

	Signal peptide probability	**Probable cleavage site**
ABU-1/PQN-2	1	aa 19-20
ABU-6	0.999	aa 21-22
ABU-7	0.997	aa 19-20
ABU-8	0.996	aa 19-20
PQN-5/ABU-15	0.997	aa 21-22
PQN-13	0.999	aa 18-19
PQN-32	0.999	aa 31-32
PQN-35	0.006	
PQN-40/ABU-12	0.999	aa 19-20
PQN-46/ABU-13	0	

PQN-47	0	
PQN-89	0.993	aa 22-23
PQN-95/ABU-14	0.999	aa 24-25

The amino acid sequences were predicted with the use of SIGNALP tool
http://www.cbs.dtu.dk/services/SignalP/

Transmembrane domains in PQN/ABU proteins

	TM domains (aa residues)	**TMPRED score**	**Orientation**
ABU-1/PQN-2	1 to 22	1695	o-i
ABU-6	3 to 22	2063	o-i
ABU-7	3 to 22	2267	o-i
ABU-8	3 to 22	2277	o-i
PQN-5/ABU-15	3 to 22	2073	o-i
PQN-13	1 to 19	1397	i-o
PQN-32	1 to 23	1501	o-i
PQN-35	56 to 79	2661	i-o
PQN-40/ABU-12	35 to 57	1521	i-o
PQN-46/ABU-13	none		
PQN-47	657-659	2318	o-i
PQN-89	6 to 24	1437	i-o
	271 to 293	1088	o-i
	306 to 323	772	i-o
	366-388	3266	o-i
PQN-95/ABU-14	6 to 24	1960	i-o
	345 to 369	531	o-i

Transmembrane (TM) domains were predicted using TMPRED program available at http://www.ch.embnet.org/software/TMPRED_form.html
The algorithm is based on the statistical analysis of TMbase,

a database of naturally occurring transmembrane proteins.
The prediction is made using a combination of several weight-matrices for scoring.
Scores above 500 are considered significant.
o-i N terminus out

Table S5: *abu* genes are up-regulated in wild-type animals following *P. aeruginosa* infection for 4 hours at 25°C.

Gene name	Induction in PA14-infected WT animals*
abu-1	2.00±0.25
abu-6	1.91±0.12
abu-7	2.03±0.06
abu-8	1.84±0.16
abu-12	1.46±0.03
abu-13	1.54±0.08
abu-14	1.21±0.02
abu-15	2.07±0.11

* Shown is the mean±SD of fold increase in *P. aeruginosa* PA14-infected wild-type animals versus *E. coli* OP50-exposed wild-type animals. Student's exact *t*-test indicates that all differences between *P. aeruginosa* PA-14-exposed animals and *E. coli* OP50-exposed animals are significantly different ($P<0.05$); N=3.

Table S6

RNAi construct	**Cross-reacting *pqn/abu* genes**
abu-1	*abu-2*, *abu-4*, *abu-5*, *pqn-76*, *pqn-78*, *pqn-79*, *pqn-91*
abu-7	*abu-6*, *abu-8*, *abu-9*, *abu-10*, *pqn-5*, *pqn-54*, *pqn-57*
abu-8	*abu-6*, *abu-7 abu-9*, *abu-10*, *pqn-5*, *pqn-54*, *pqn-57*
pqn-40/abu-12	NONE per this analysis
pqn-46/abu-13	NONE per this analysis

To identify potential off-target cross-reactions, the BLAST algorithm was used.
In *C. elegans*, cross-RNAi is known to occur when a target mRNA shares at least 95% identity, over a span of 40 or more nucleotides, to the dsRNA encoded by the RNAi construct.

abu-1

IDENTITY	**CHRO**	**STRAND**	**START**	**END**	**SPAN**	**GENE**
100	V	minus	10381800	10380316	1278	*abu-1*
87	IV	plus	15291875	15293411	1260	*pqn-91*
87	IV	plus	15291875	15293411	1265	*pqn-91*
89	IV	plus	15590665	15591740	544	*pqn-5/abu-15*
90	IV	plus	15590665	15591740	438	*pqn-5/abu-15*
89	IV	plus	15595003	15593928	544	*pqn-78*
90	IV	plus	15595003	15593928	438	*pqn-78*
89	IV	plus	15595538	15596613	544	*pqn-79*
90	IV	plus	15595538	15596613	438	*pqn-79*
89	IV	plus	15579054	15580129	544	*pqn-76*

90	IV	plus	15579054	15580129	438	*pqn-76*
87	V	plus	2274522	2272440	541	*Y5H2A.4*
89	V	plus	2274522	2272440	335	*Y5H2A.4*
87	V	plus	2274522	2272440	358	*Y5H2A.4*
88	V	plus	2274881	2275976	435	*abu-4*
84	V	plus	2274881	2275976	555	*abu-4*
83	X	plus	1410647	1408831	568	*abu-2*
78	X	plus	1410647	1408831	189	*abu-2*

abu-7

IDENTITY	**CHRO**	**STRAND**	**START**	**END**	**SPAN**	**GENE**
100	V	plus	5164743	5163380	1317	*abu-7*
96	V	plus	5194592	5192977	1338	*abu-8*
98	V	plus	5158608	5159882	871	*pqn-5/abu-15*
95	V	plus	5158608	5159882	396	*pqn-5/abu-15*
97	V	plus	5161877	5160587	873	*abu-6*
99	V	plus	5161877	5160587	369	*abu-6*
83	V	plus	1464990	1466350	827	*pqn-54*
80	V	plus	1464990	1466350	391	*pqn-54*
82	X	plus	8322059	8323291	794	*abu-9*
82	X	plus	8320934	8319616	794	*pqn-57*

abu-8

IDENTITY	CHRO	STRAND	START	END	SPAN	GENE
100	V	plus	5194592	5192977	1338	*abu-8*
96	V	plus	5164743	5163380	1337	*abu-7*
93	V	plus	5158608	5159882	871	*pqn-5/abu-15*
95	V	plus	5158608	5159882	396	*pqn-5/abu-15*
93	V	plus	5161877	5160587	873	*abu-6*
98	V	plus	5161877	5160587	368	*abu-6*
83	V	plus	1464990	1466350	827	*pqn-54*
80	V	plus	1464990	1466350	391	*pqn-54*
82	X	plus	8322059	8323291	723	*abu-9*
82	X	plus	8320934	8319616	723	*pqn-57*

pqn-40/abu-12

IDENTITY	CHRO	STRAND	START	END	SPAN	GENE
100	X	plus	457649	450446	2325	*pqn-40*

pqn-46/abu-13

IDENTITY	CHRO	STRAND	START	END	SPAN	GENE
100	III	plus	6944683	6941833	1113	*pqn-46*

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