

Figure S1. Photos of Edge Assay

(Left) Photo of Edge Assay after 5 min with worms moving away from the center. *(Right)*

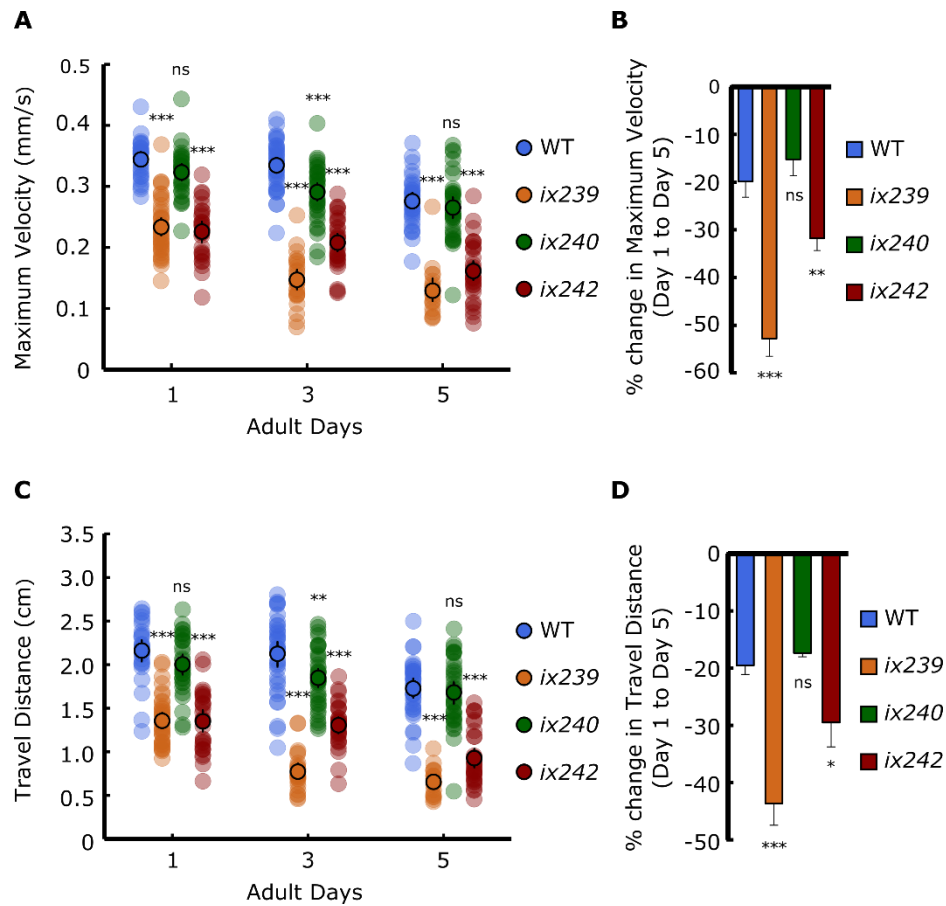
Photo of Edge Assay after 60 min with worms reaching and remaining in the edge.

6 **Table S1. Number of screened genomes and isolated mutants**

	EMS-mutagenesis I			EMS-mutagenesis II			Total
	Day 1	Day 3	Day 5	Day 1	Day 3	Day 5	
Genomes Screened	400			600			
Isolated mutants		13	23		17	17	70
Viable isolated mutants		3	8		9	2	22
Isolated mutants with reproducible deficits		0	3 (ix239, ix240, ix241)		2 (ix242, ix243)	0	5

7

8



9

10 **Figure S2. Maximum velocity and travel distance of isolated mutants**

11 (A) Maximum velocities of WT, *ix239*, *ix240*, and *ix242* worms. (B) Percent change in

12 maximum velocity of worms from A. (C) Travel distances of WT, *ix239*, *ix240*, and *ix242*

13 worms. (D) Percent change in travel distance of worms from C. Error bars indicate 95%

14 confidence intervals. For maximum velocity and travel distance experiments, $n = 30\text{--}45$

15 worms per strain for each day (10–15 worms from 3 biological replicate plates). For

16 percent change in maximum velocity graphs, $n = 3$ biological replicate plates. $*P < 0.05$;

17 $**P < 0.01$; $***P < 0.001$; ns, not significant; One-way ANOVA with Dunnett's post hoc

18 test vs. WT.

19

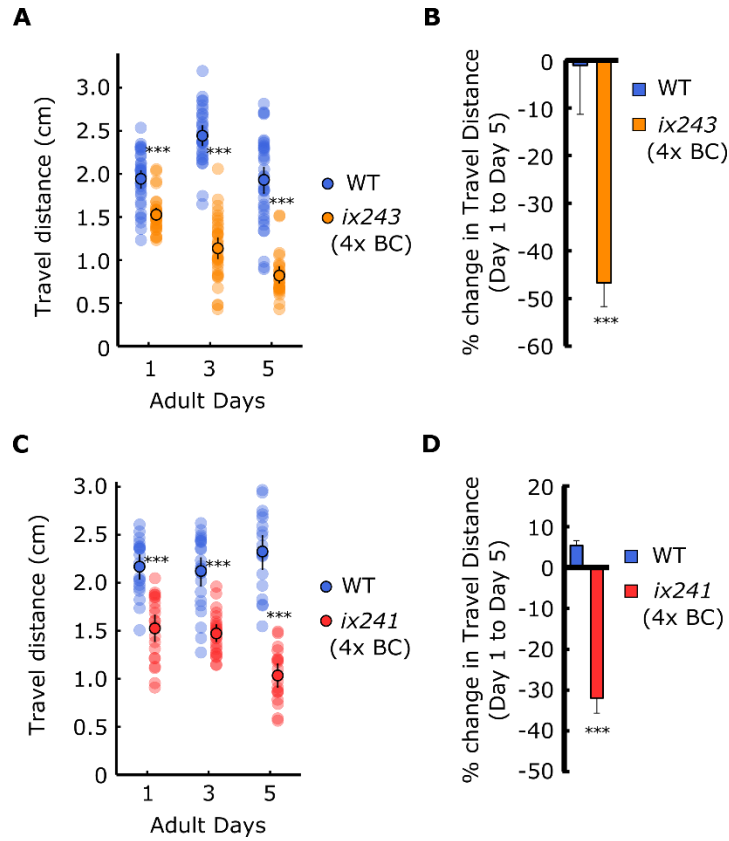


Figure S3. *ix241* and *ix243* worms show progressive locomotor decline after four backcrosses

(A) Travel distances of WT and *ix243* backcrossed four times (4x BC). (B) Percent change in travel distance of WT and *ix243*(4x BC) worms. (C) Travel distances of WT and *ix241*(4x BC) worms. (D) Percent change in travel distance of WT and *ix241*(4x BC) worms. For travel distance experiments, n = 30–45 worms per strain for each day (10–15 worms from 3 biological replicate plates). For percent change in travel distance graphs, n = 3 biological replicate plates. *** $P < 0.001$; Unpaired Student's t test vs. WT.

Table S2. Lifespan Analysis

Strain	Median Lifespan (adult days)	<i>P</i> value vs WT (Log-rank test)	Worms (Counted/Total)	FUDR
N2	18		56/90	25 µg/ml
<i>ix243</i> (4x BC)	16	<i>P</i> = 0.00078	89/90	25 µg/ml
N2	18		82/90	25 µg/ml
<i>ix243</i> (4x BC)	16	<i>P</i> < 0.0001	84/90	25 µg/ml
N2	18		87/90	25 µg/ml
<i>ix243</i> (4x BC)	16	<i>P</i> < 0.0001	87/90	25 µg/ml
N2	17		94/120	0
<i>ix241</i> (4x BC)	16	<i>P</i> = 0.095	77/120	0
N2	14		66/90	0
<i>ix241</i> (4x BC)	15	<i>P</i> = 0.12	64/90	0
N2	12		67/90	0
<i>ix241</i> (4x BC)	14	<i>P</i> = 0.024	74/90	0

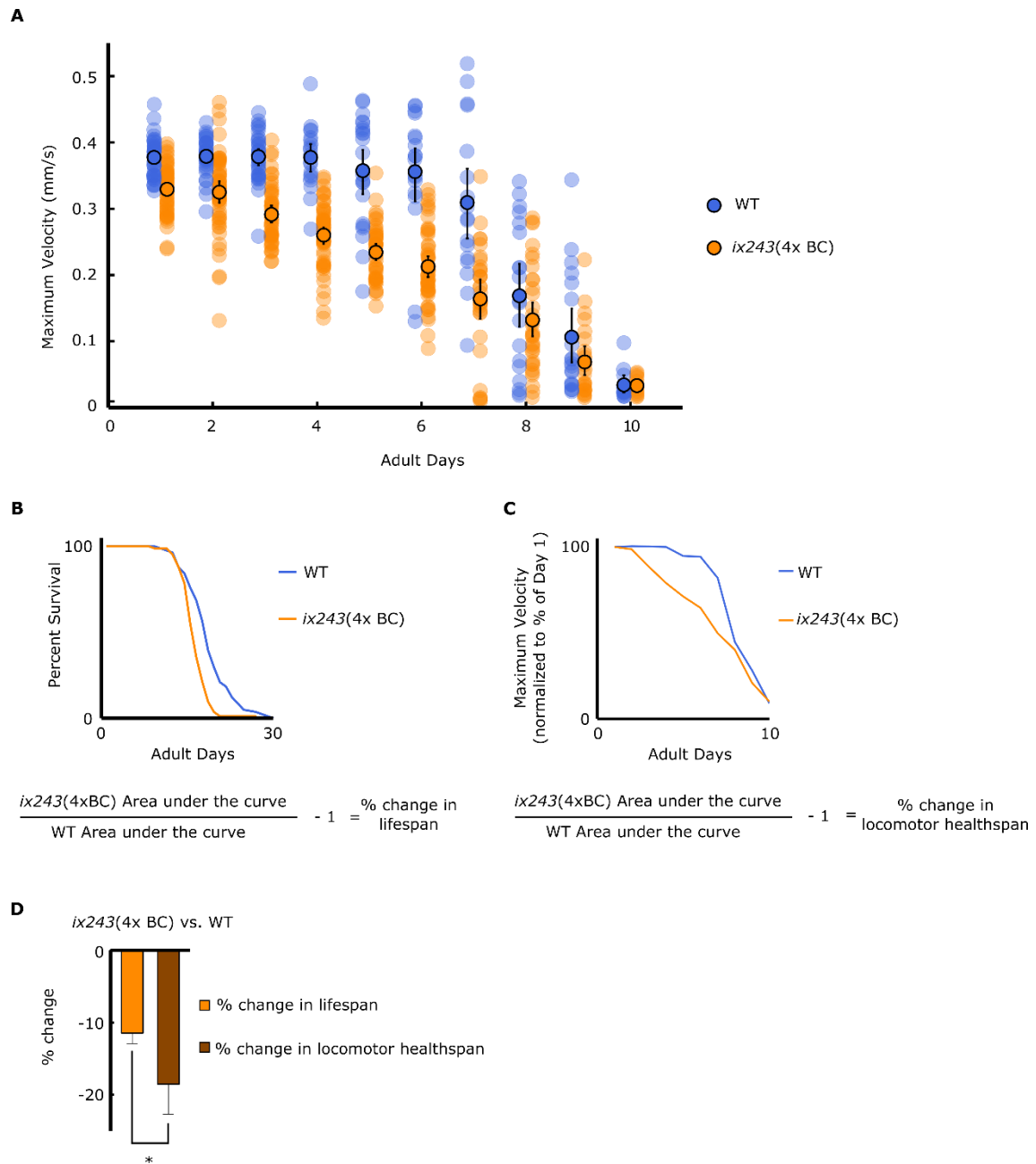


Figure S4. Greater reduction in total locomotor healthspan compared to lifespan in *ix243* worms

(A) Maximum velocities of WT and *ix243*(4x BC) worms. $n = 30\text{--}45$ worms per strain for each day (10–15 worms from 3 biological replicate plates). (B) (Top) Representative survival curve of WT ($n = 56$ worms) and *ix243*(4x BC) worms ($n = 89$ worms).

39 (Bottom) Calculation method of percent change in lifespan. (C) (Top) Representative
40 decline in maximum velocity curve of WT and *ix243*(4x BC) worms. n = 30–45 worms
41 per strain for each day (10–15 worms from 3 biological replicate plates). (Bottom)
42 Calculation method of percent change in locomotor healthspan. (D) Percent change in
43 lifespan (n = 3 biological replicate plates for WT and *ix243*(4xBC)) and locomotor
44 healthspan (n = 3 biological replicate plates for WT and *ix243*(4xBC)) of *ix243*(4xBC)
45 worms compared to WT. * $P < 0.05$; Unpaired Student's t test.

46

47 **Table S3. Development times of isolated mutant strains**

48 Development time from egg to first egg-lay (n=5 worms per strain).

Strain	Development Time (h)	% of WT
WT	70.4	100.0%
<i>ix239</i>	74.4	105.7%
<i>ix240</i>	71.2	101.1%
<i>ix241</i> (4x BC)	73.2	104.0%
<i>ix242</i>	71.8	102.0%
<i>ix243</i> (4x BC)	80.2	113.9%

49

50

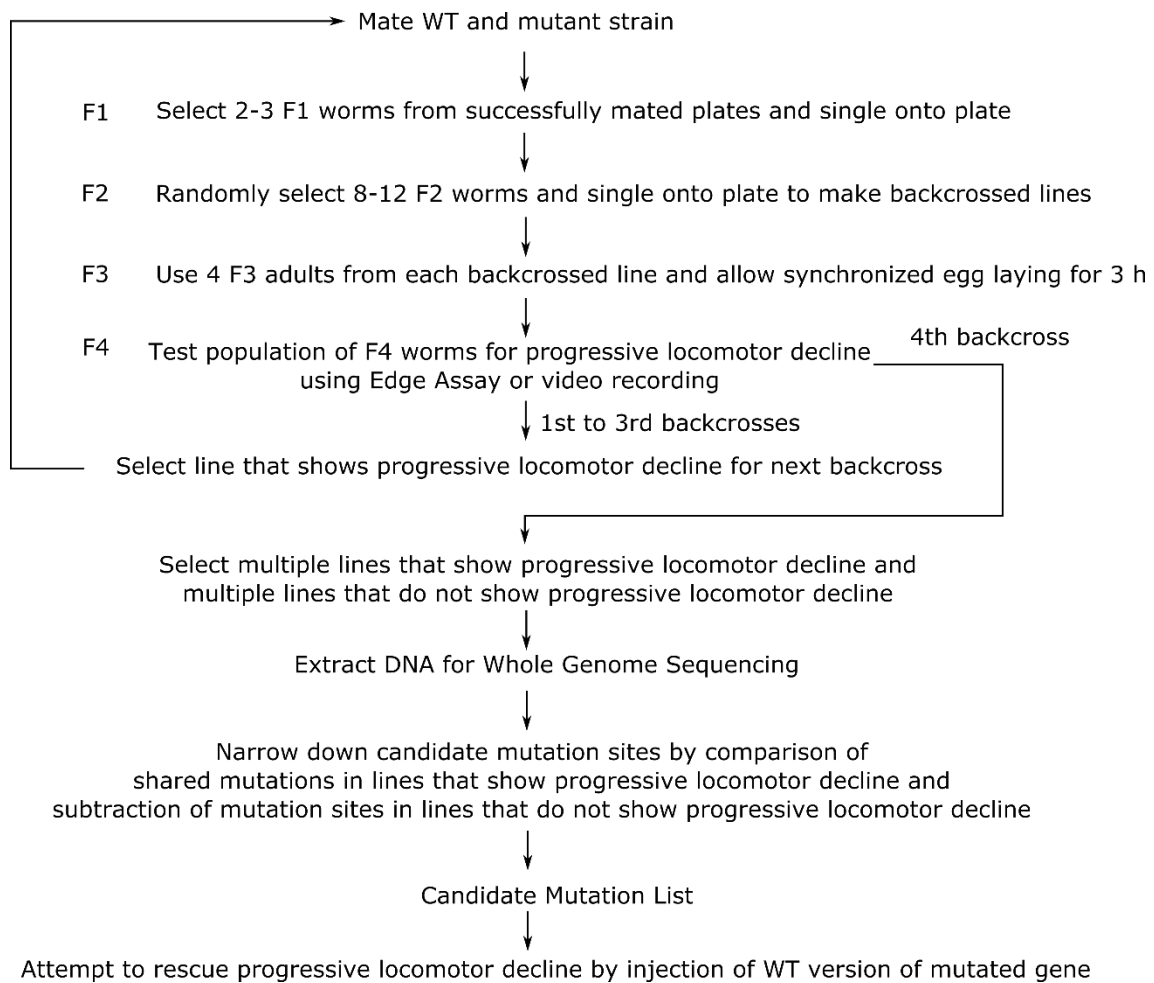


Figure S5. Strategy to identify causative mutation site

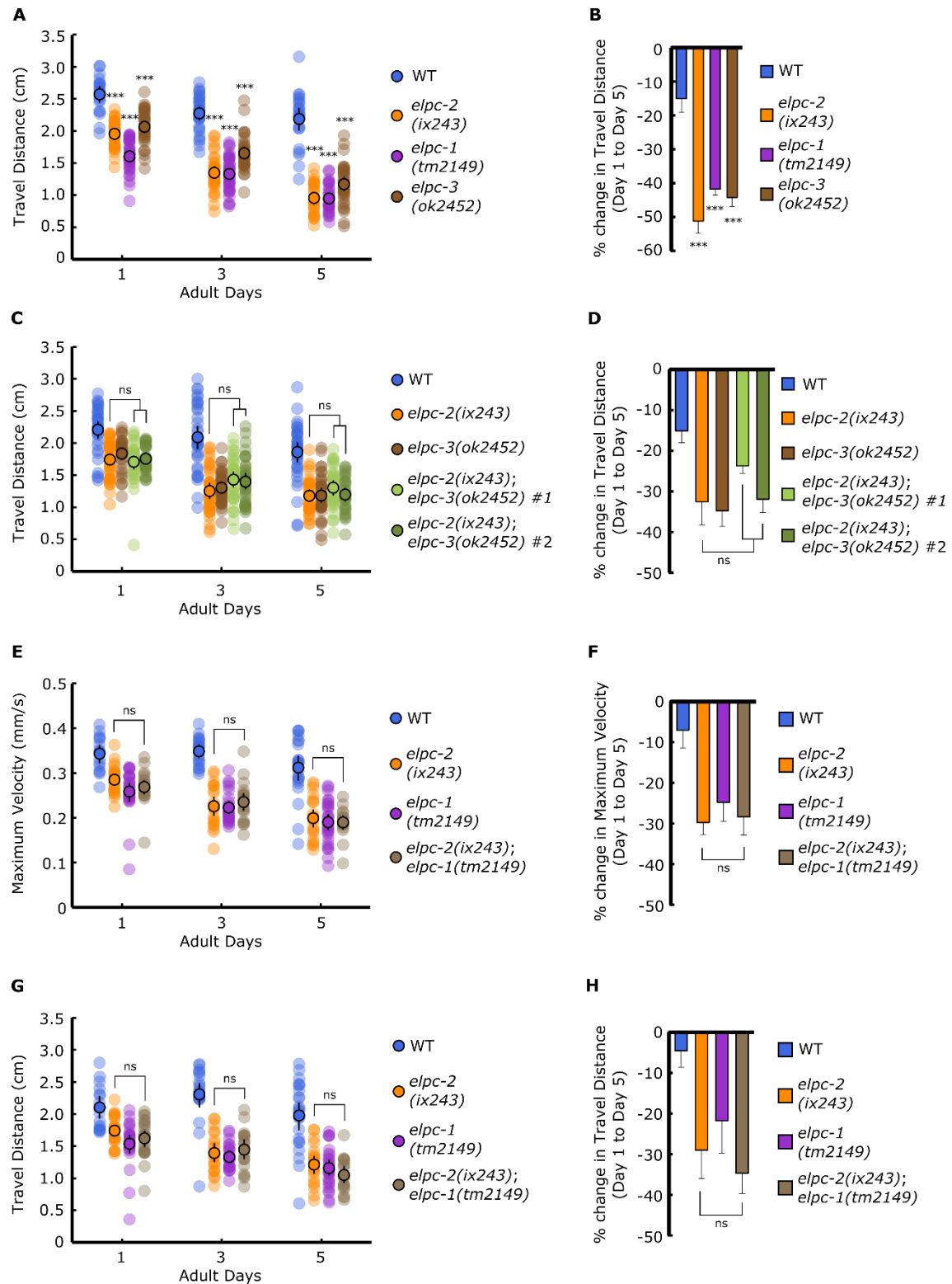
For our experiment, we pooled together the DNA of 9 mutant lines that showed a progressive locomotor decline and 9 mutant lines that did not show locomotor decline.

56 **Table S4. Remaining mutations in *ix243* mutant strains**

Chrom.	Pos.	Ref.	Alt.	Gene	Mutation Type	Effect
I	3428548	A	AGGCAGACCTAGCCCACCCTG GGCAGACCTAGCCCACCCTG	K03E5.2	downstream gene variant	modifier
I	14448378	G	GCGTCCGGTTTTGGGGTAGGTTT CCACGGCGGCCGACAATTTCCG AGTTTCGCCACTCACTATACTTA ATCAGCAATTTTATAGTGAGTTG CGAAACTCGGAAATTGTCGGCC GTCGTGGATAACTACCCCAAAA CCGGACGACCGGA	Y105E8A.27	downstream gene variant	modifier
II	1465622	C	T	Y51H7C.13	missense variant	moderate
II	1602489	C	T	bath-47	downstream gene variant	modifier
II	1717193	C	T	btb-7	downstream gene variant	modifier
II	1915528	C	T	math-31	upstream gene variant	modifier
II	2339259	G	T	F43C11.6	upstream gene variant	modifier
II	2428896	C	T	F42G2.2	downstream gene variant	modifier
II	2477652	T	A	tsr-1	upstream gene variant	modifier
II	8975684	G	T	tomm-40	upstream gene variant	modifier
III	577387	TAAAAATTT AACAAAA	T	Y55B1AL.1	downstream gene variant	modifier
III	1704981	A	T	Y22D7AR.10	upstream gene variant	modifier
III	7406703	A	T	linc-165	upstream gene variant	modifier
III	7439448	C	T	linc-165-alh-12	intergenic region	modifier
III	11024784	G	A	Y48A6B.16	upstream gene variant	modifier
III	11416475	G	A	Y47D3B.13	upstream gene variant	modifier
III	11549303	G	A	Y66D12A.14	downstream gene variant	modifier
III	11816202	G	A	C18D11.1	upstream gene variant	modifier
III	11895783	G	A	faah-5	upstream gene variant	modifier
III	12134837	G	A	Y75B8A.6	upstream gene variant	modifier
III	12156042	G	A	linc-87	upstream gene variant	modifier
III	12190456	G	A	Y75B8A.54	upstream gene variant	modifier
III	12200963	G	A	Y75B8A.44	downstream gene variant	modifier
III	12223827	G	A	Y75B8A.16	missense variant	moderate
III	12407309	G	A	tat-1	missense variant	moderate
III	12427755	G	A	Y49E10.16	upstream gene variant	modifier
III	12476529	G	A	Y49E10.33	upstream gene variant	modifier
III	12498064	C	T	Y111B2A.3	synonymous variant	low
III	12678743	G	A	elpc-2	stop gained	high
III	12701690	G	A	spin-4	downstream gene variant	modifier
III	12750669	A	T	irld-60	missense variant	moderate
III	12810002	G	A	BE10.5	upstream gene variant	modifier
III	12838123	G	A	Y37D8A.4	synonymous variant	low
III	12892115	G	A	unc-71	upstream gene variant	modifier
III	12923518	G	A	Y37D8A.16	upstream gene variant	modifier
III	12924071	G	A	mrps-10	upstream gene variant	modifier
III	13352002	G	A	F53A2.9	downstream gene variant	modifier
III	13453318	G	A	cua-1	upstream gene variant	modifier
III	13578898	G	A	T05D4.5	upstream gene variant	modifier
IV	6722231	C	T	Y73B6A.6- Y73B6A.2	intergenic region	modifier
IV	7597770	G	A	tag-80	synonymous variant	low
IV	7597783	T	A	tag-80	missense variant	moderate
IV	17276360	A	AT	ghn-5	upstream gene variant	modifier

57

58



68

69 **Figure S7. The Elongator complex is required to maintain adult locomotor ability**

70 (A) Travel distances of WT, *elpc-1(tm2149)* and *elpc-3(ok2452)* worms. (B) Percent
 71 change in travel distance of worms from A. (C) Travel distances of WT, *elpc-2(ix243)*,

72 *elpc-3(ok2452)*, and *elpc-2(ix243);elpc-3(ok2452)* worms. (D) Percent change in travel
73 distance of worms from C. (E) Maximum velocities of WT, *elpc-2(ix243)*, *elpc-1(tm2149)*,
74 and *elpc-1(tm2149);elpc-2(ix243)* worms. (F) Percent change in maximum velocity of
75 worms from E. (G) Travel distances of WT, *elpc-2(ix243)*, *elpc-1(tm2149)*, and *elpc-*
76 *1(tm2149);elpc-2(ix243)* worms. (H) Percent change in travel distance of strains from G.
77 For maximum velocity and travel distance experiments, n = 30–45 worms per strain for
78 each day (10–15 worms from 3 biological replicate plates). For percent change in
79 maximum velocity graphs, n = 3 biological replicate plates. *** $P < 0.001$; ns, not
80 significant; One-way ANOVA with Dunnett's post hoc test vs. WT for A, B; One-way
81 ANOVA with Tukey's post hoc test for C–H.

82

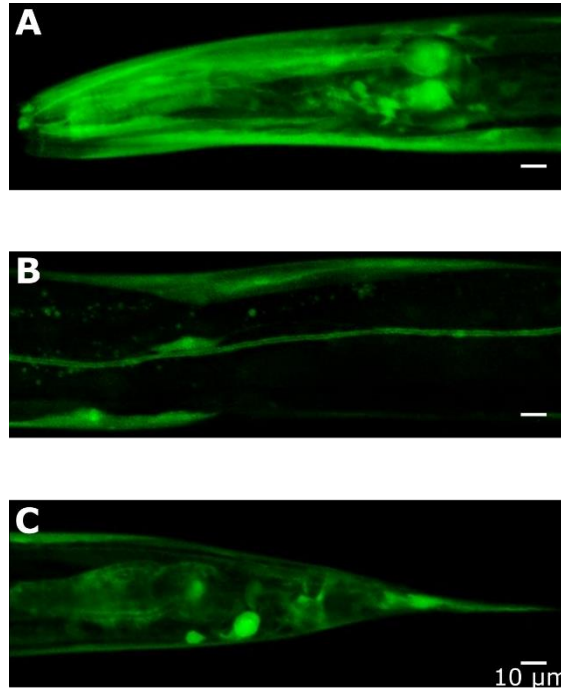


Figure S8. Expression pattern of *elpc-2* transcriptional GFP fusion

(A) *elpc-2p::GFP* expression in pharynx, neurons, and head muscles. (B) *elpc-2p::GFP* expression in body wall muscles and canal cell. (C) *elpc-2p::GFP* expression in coelomocytes, intestine, and tail. Scale bars: 10 μ m.

Table S5. Development times of *tut-1(tm1297)* and *elpc-2(ix243);tut-1(tm1297)*

mutants

Development time from egg to first egg-lay (n = 5 worms per strain).

Strain	Development Time (h)	% of WT
WT	70.4	100.0%
<i>tut-1(tm1297)</i>	82.0	116.5%
<i>elpc-2(ix243);tut-1(tm1297)</i>	145.4	206.5%

Q6IA86	ELP2_HUMAN	1	-----HIVAPVLETSSVVF-CEPNRVRGVLNWSGPRGLAFGTSCSVVLYD-PLKRVVV	51
Q9NEW7	Q9NEW7_CAEEEL	1	MKIEEEFTSSASVNPESHCLTAEEK-----TAPLVAYASSLQIAVQTIRKDSSEV	48
			: * * * * *	
Q6IA86	ELP2_HUMAN	52	-----TNLNGHTARVNCITQWICKODGSPSTELVSGGSDNOVTHNEIEDNOLLKAVH-LQSH	106
Q9NEW7	Q9NEW7_CAEEEL	49	GVIKSTISERRHOKPIITVL-KRLKSSSEIVADEFTGGVDSRVVLLKRLRGEHVEYVADLTGC	107
			: : : * * * * *	
Q6IA86	ELP2_HUMAN	107	EGPVYAVHVVYQRTSDPALCTLIISAAADSAVRLNSKKGPEVMCLQTLNFGNGFALALC	166
Q9NEW7	Q9NEW7_CAEEEL	108	DGSMGSGCGVEDGRK--VVAAMVSETSNGFHAMTSSIGDLLNSTEIKL-DHKAFALC	164
			: * * * * *	
Q6IA86	ELP2_HUMAN	167	LSFLPNTDVPILACGNDDCRIHIFAQ--QNDQFQKVLSCGHEDWIRGVLEIAAFGRDLFL	224
Q9NEW7	Q9NEW7_CAEEEL	165	LDATSIQSVLLAVGTSKRFVELYGESADKKSFSRLTSVAGHTDWIHSIAFNDNPDLILV	224
			: : * * * * *	
Q6IA86	ELP2_HUMAN	225	ASCSDCLIRINKLYIKSTSLETO-----DDNIRLKENITETIENESVKIAFAVITL	276
Q9NEW7	Q9NEW7_CAEEEL	225	ASAGQDTYVRLWATEPETDEKSENIREDSSTTPPELTSANLESINY----TPYRCSSH	280
			: * * * * *	
Q6IA86	ELP2_HUMAN	277	TVLAGHENNVNAVHNPVFYKDGVLQPPVRLLSASMDKTMILNAPDEESGVHLEQVRVE	336
Q9NEW7	Q9NEW7_CAEEEL	281	AVMQGHDDNVHSTVNSND-----GRVLLTASSDKTCTINKE--IDNLRRDDVRLGI	329
			: * * * * *	
Q6IA86	ELP2_HUMAN	337	VGGN-TLGFYDCQFN-----EDGSHITAHAFHGAHLNKNONTVPRENTPELVI	384
Q9NEW7	Q9NEW7_CAEEEL	330	VGGGQAAGFFAAVFSSSLDKDSGEKIAENVVSISSYFGGLHCKNSTDEQKTFMTALPHT	389
			: * * * * *	
Q6IA86	ELP2_HUMAN	385	SGHFDGVODLVNDP---EGEFTITVGTDDTTRLFAPWKRKQDSQVTHHEIARPOIHGYD	440
Q9NEW7	Q9NEW7_CAEEEL	390	GGHVGEVRDWDHRSDDGDSGLHMSVGDDOTTRVFAKNG---RQSYVEIARPOVHGHD	445
			: * * * * *	
Q6IA86	ELP2_HUMAN	441	LKCLAMINRFQFVSGADEKVLRFVSAPRNFVENFCATTGQSLNHVLCNODSDLPEGATVP	500
Q9NEW7	Q9NEW7_CAEEEL	446	MQCLSFVNPISIFVSGAEKVFRAFRAPKSEFKLEAISGVPTKSEFGDSD-LAEFGACVP	504
			: * * * * *	
Q6IA86	ELP2_HUMAN	501	ALGLSNKAVFOGDIASQPSDEEELLTSTGFEYQVAFQPSILTTEPPTEDHLLONTLWPEV	560
Q9NEW7	Q9NEW7_CAEEEL	505	ALGLSNKPMVEGETVDGE-----HNEEDAFRAAPVVLTSPTEDTLQONTLWPEQ	554
			: * * * * *	
Q6IA86	ELP2_HUMAN	561	OKLYGHGYEIFCYTICNSKTLASACKAAKKEHAATILNNTTSNKQVONLVFHS-LTVQM	620
Q9NEW7	Q9NEW7_CAEEEL	555	HKLYGHGYEYVAVTANPTIGNVLATAACKSSHVEHVSVMILNSTSNKSKSEIGHCLTYTQI	614
			: * * * * *	
Q6IA86	ELP2_HUMAN	621	AFSPNEKFLLAISRDRTWSLNKKODTISPEFEPVFSLFAFTNKITSVHSRIIWSCDWSPD	680
Q9NEW7	Q9NEW7_CAEEEL	615	AMNPSGTRLLTVSRDRTALEYTEKNGEVDGFOYD-----CVMTSGKHTRIIWACDWIDD	669
			: * * * * *	
Q6IA86	ELP2_HUMAN	681	SKYFFTGSRDKKVVWNGECSDTDDCIEHNIGPCSSVLGVGAVTAVSVCPVLHPSORYVV	740
Q9NEW7	Q9NEW7_CAEEEL	670	EH-FVITASRDQKVIIVWAEASAGQTAPKAT-----VKLDEPVTA-----IAAVSKDVI	714
			: : * * * * *	
Q6IA86	ELP2_HUMAN	741	AVGLECGKICLYTNKKTDQVPEINDWTHCVETSSQSOSHT--LAIRKLCHKIKCSGKTEQKE	798
Q9NEW7	Q9NEW7_CAEEEL	715	VAGLQTGELLIVLRFDSGLH-----VIEKIGANRIPIDSAVLRIRFSKNGRK-----	761
			: * * * * *	
Q6IA86	ELP2_HUMAN	799	AEGAELHFAISCGEDHTVKIHRVKNKCAL	826
Q9NEW7	Q9NEW7_CAEEEL	762	-----LAVATTDAKLRIFNVSQ---	778
			: * * * * *	

Figure S10. Amino acid alignment of *C. elegans* ELPC-2 and human ELP2

C. elegans ELPC-2 and human ELP2 were aligned using Clustal Omega (Sievers *et al.* 2011). An asterisk (*) indicates positions that are conserved; colon (:) indicates positions that are strongly similar (> 0.5 in the Gonnet PAM 250 matrix); period (.) indicates positions that are weakly similar (< 0.5 in the Gonnet PAM 250 matrix).

109 **Table S6. Strain list**

Strain	Genotype	Obtained From
CB408	<i>unc-43(e408) IV</i>	CGC
CB190	<i>unc-54(e190) I</i>	CGC
MT7929	<i>unc-13(e51)</i>	CGC
AM725	<i>rmIs290 [unc-54p ::Hsa-sod-1 (127X)::YFP]</i>	CGC
VC1937	<i>elpc-3(ok2452) V</i>	CGC
CF1038	<i>daf-16(mu86) I</i>	CGC
n/a	<i>elpc-1(tm2149) I</i>	National BioResource Project (Japan)
n/a	<i>tut-1(tm1297) IV</i>	National BioResource Project (Japan)
OF1260	<i>ix239</i>	This study
OF1261	<i>ix240</i>	This study
OF1262	<i>ix241</i>	This study
OF1263	<i>ix241</i> (4x backcrossed)	This study
OF1264	<i>ix242</i>	This study
OF1265	<i>elpc-2(ix243) III</i>	This study
OF1266	<i>elpc-2(ix243) III</i> (4x backcrossed)	This study
OF1267	<i>elpc-2(ix243) III ; ixEx244[elpc-2(+); lin-44p ::RFP]</i>	This study
OF1268	<i>elpc-2(ix243) III ; ixEx245[elpc-2(+); lin-44p ::RFP]</i>	This study
OF1269	<i>elpc-2(ix243) III ; ixEx246[lin-44p ::RFP]</i>	This study
OF1270	<i>ixEx247[lin-44p ::RFP]</i>	This study
OF1271	<i>elpc-1(tm2149) I ; elpc-2(ix243) III</i>	This study
OF1272	<i>elpc-2(ix243) III ; elpc-3(ok2454) V (#1)</i>	This study
OF1273	<i>elpc-2(ix243) III ; elpc-3(ok2454) V (#2)</i>	This study
OF1289	<i>elpc-2(ix243) III ; tut-1(tm1297) IV</i>	This study

110

111

112 **Table S7. Primer list**

Primer Name	5'-3' Sequence
5' <i>elpc</i> -2p (2090-bp upstream)	gataagtgacatgccgctgcgtccttac
3' <i>elpc</i> -2UTR (851-bp downstream)	aagagacagcgtctgattcttgaaacggta
5' <i>elpc</i> -2 snp	aaatgaatttttcgccacaaaacccaaaaa
3' <i>elpc</i> -2 snp	ttcgcgaaaactctcgtagtctgatcctg
5' <i>elpc</i> -1 del	gaaaagcatcgcgagttgtccacttgaatcac
3' <i>elpc</i> -1 del	cttttcagttgaattctggcatctctcaa
5' <i>elpc</i> -3 del	taatagaaccagatcgagtttggcagatg
3' <i>elpc</i> -3 del	aatgcatcgtatgtggtaggcggtaaaac
5' <i>elpc</i> -2p overlap ppd95.79	ctatgaccatgattacgccagataagtgacatgccgctgcgtcct
3' <i>elpc</i> -2p overlap ppd95.79	gtcctttggccaatcccgggtgattttctggaaaaaatgggaaaaatctcg tgaaaaaac
5' ppd95.79	cccgggattggccaaaggacccaaa
3' ppd95.79	tggcgtaatcatgggtcatagctgttc

113

114

115

116

117