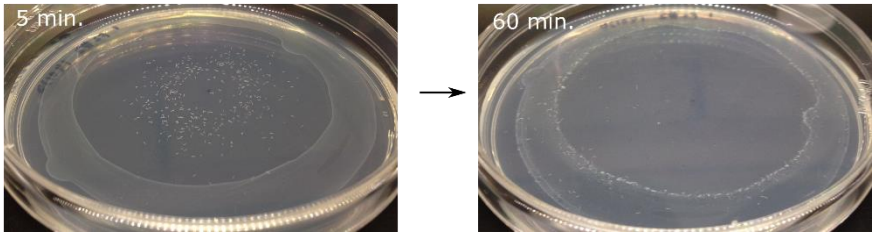


Figure S1. Photos of Edge Assay

(*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.

Table S1. Number of screened genomes and isolated mutants

	EMS-mutagenesis I			EMS-mutagenesis II			
	Day 1	**Day 3**	**Day 5**	**Day 1**	**Day 3**	**Day 5**	**Total**
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

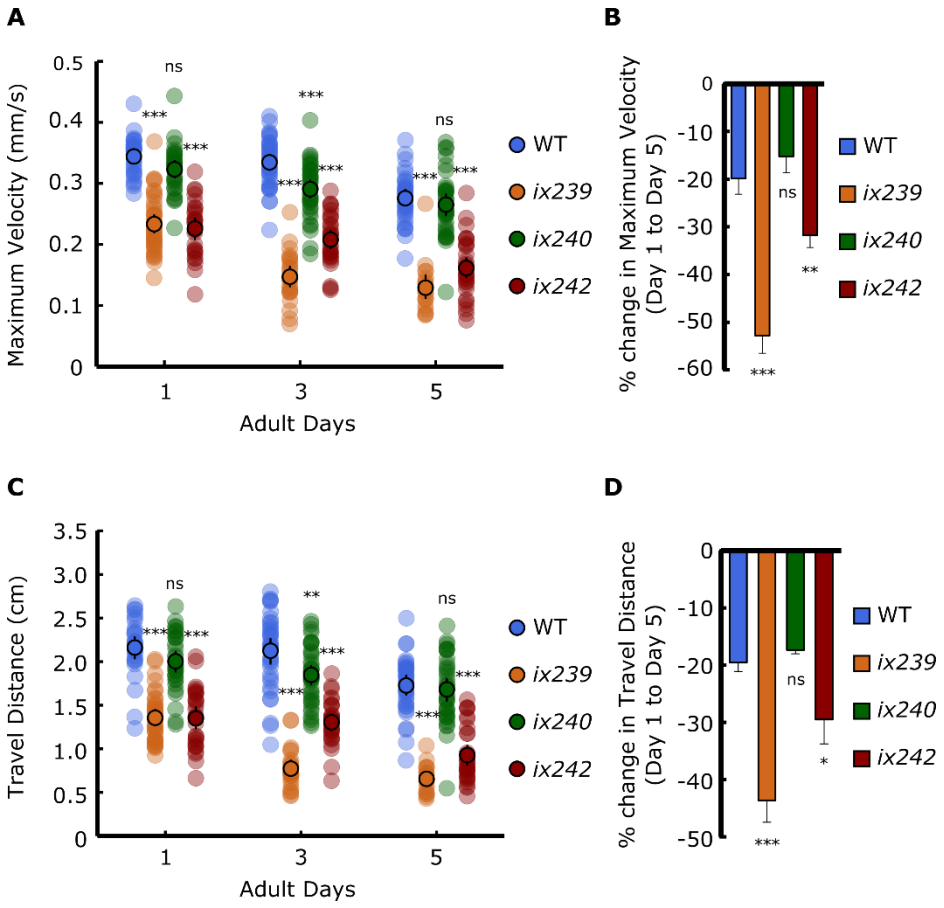


Figure S2. Maximum velocity and travel distance of isolated mutants

(A) Maximum velocities of WT, *ix239, ix240,* and *ix242* worms. (B) Percent change in maximum velocity of worms from A. (C) Travel distances of WT, *ix239, ix240,* and *ix242* worms. (D) Percent change in travel distance of worms from C**.** Error bars indicate 95% confidence intervals. For maximum velocity and travel distance experiments, n = 30–45 worms per strain for each day (10–15 worms from 3 biological replicate plates). For percent change in maximum velocity graphs, n = 3 biological replicate plates. **P* < 0.05; ***P* < 0.01; ****P* < 0.001; ns, not significant; One-way ANOVA with Dunnett's post hoc test vs. WT.

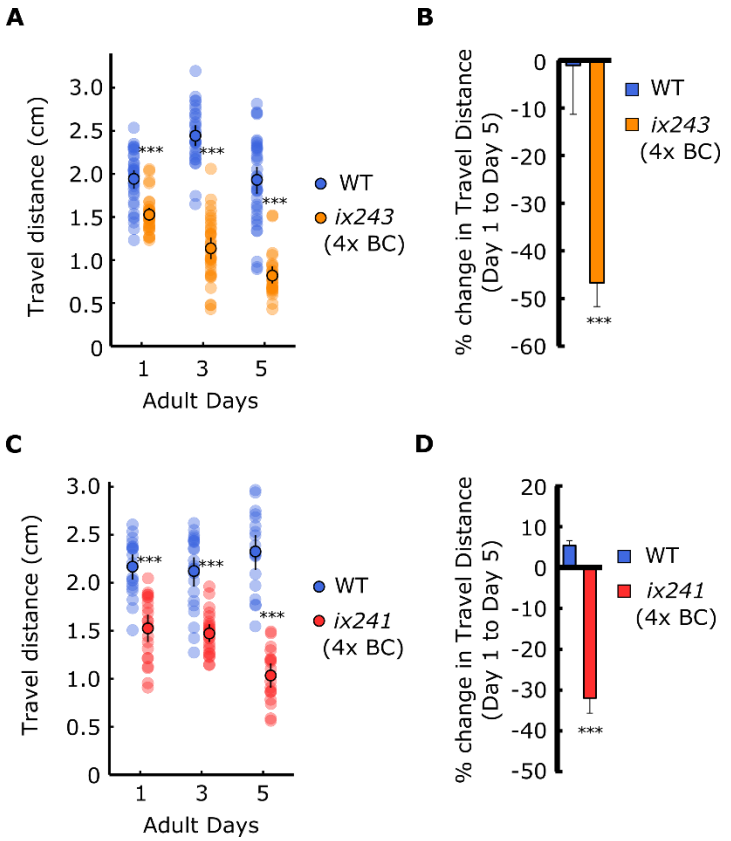


Figure S3. *ix241* and *ix243* worms show progressive locomotor decline after four backcrosses

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

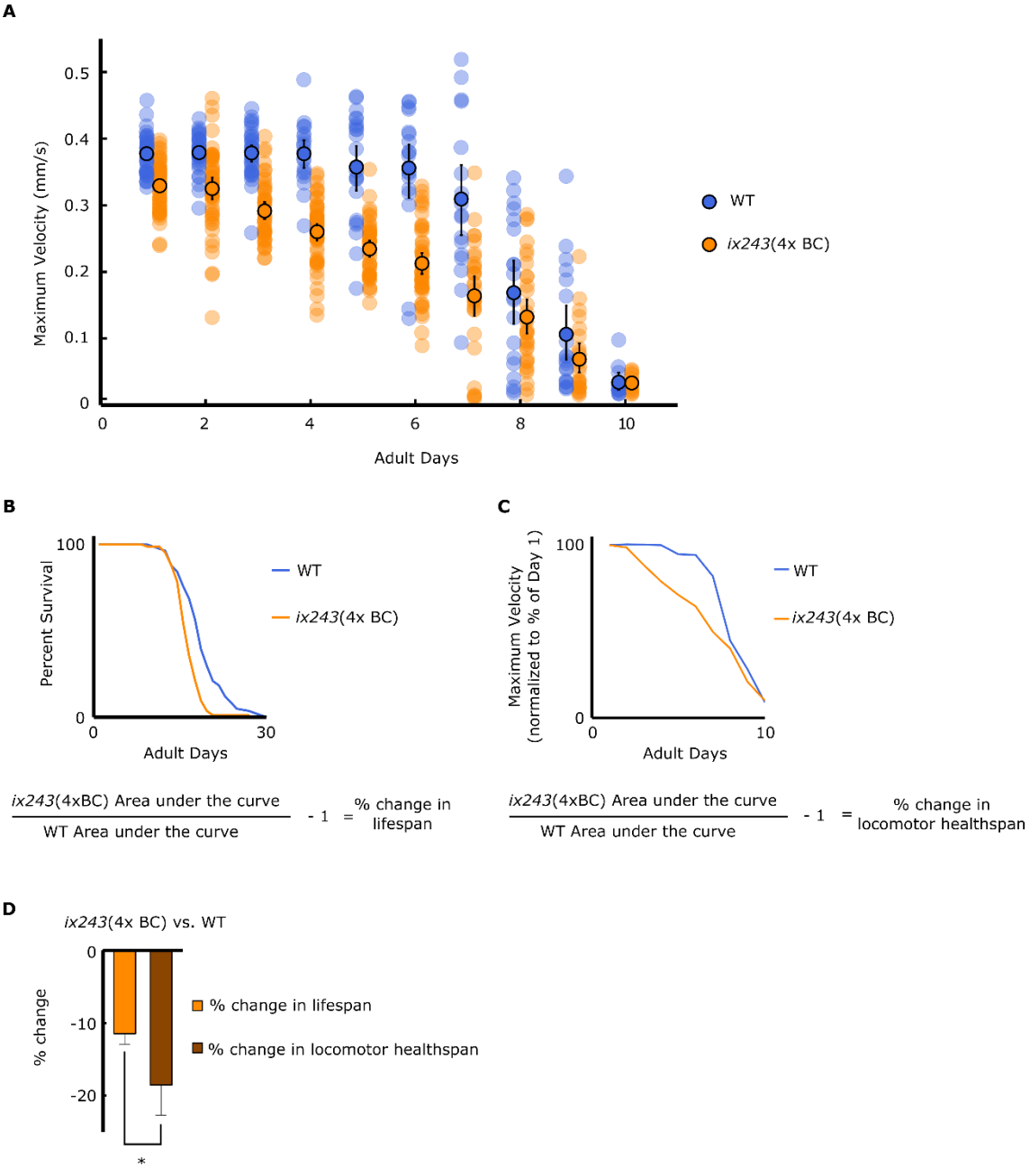


Figure S4. Greater reduction in total locomotor healthspan compared to lifespan in *ix243* worms

(A) Maximum velocities of WT and *ix243*(4x BC) worms. n = 30–45 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).

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

Table S3. Development times of isolated mutant strains

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

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

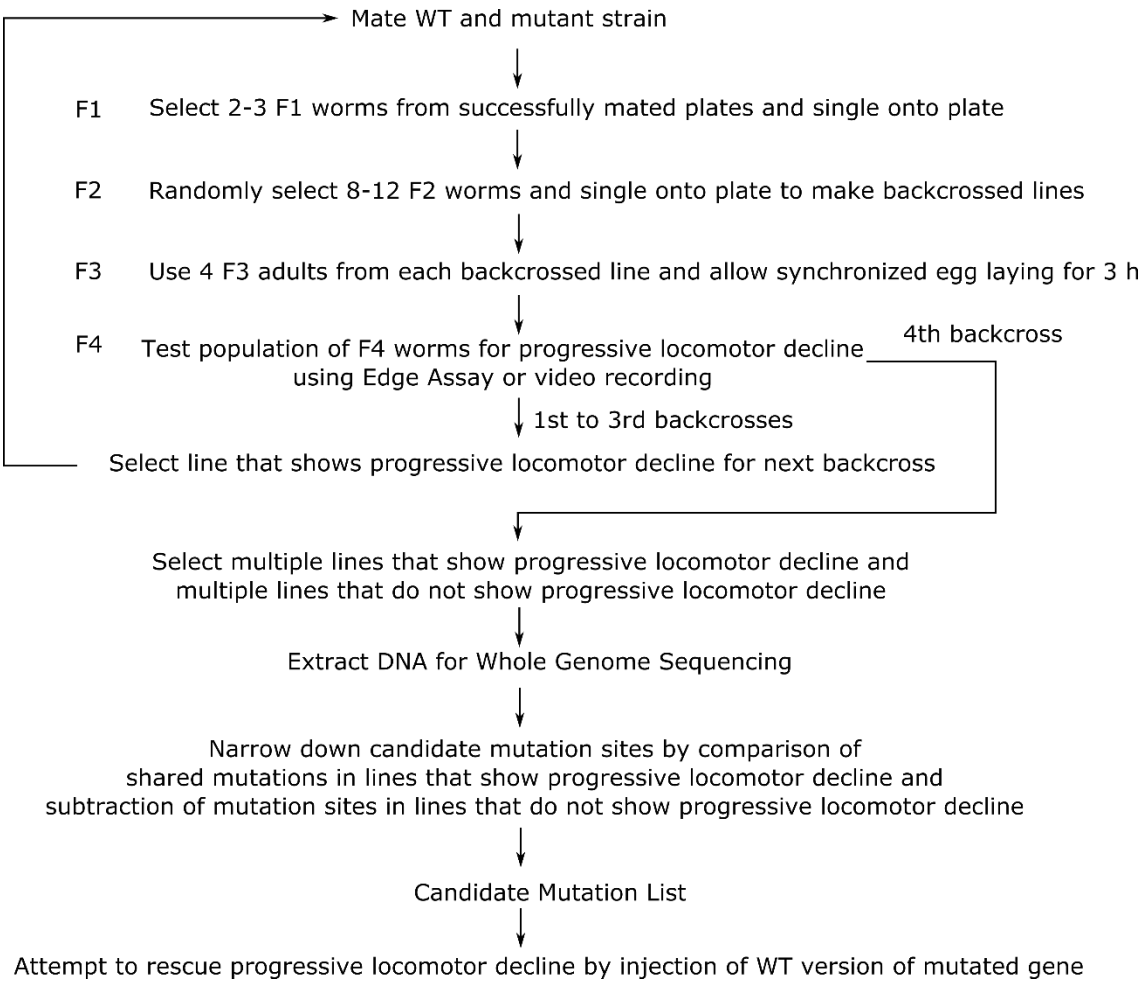


Figure S5. Strategy to identify causative mutation site

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.

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	gln-5	upstream gene variant	modifier

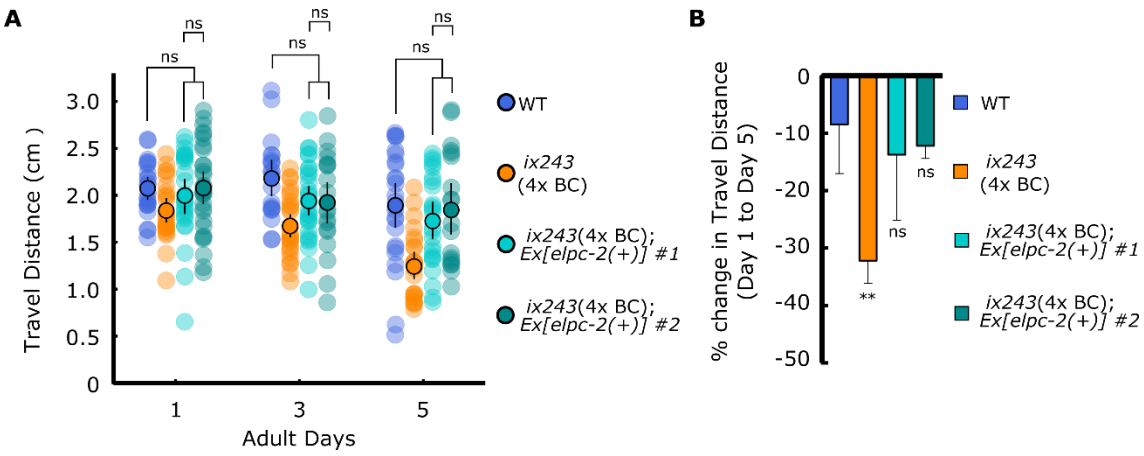


Figure S6. Wild-type *elpc-2* gene rescues progressive decline in locomotor ability of the *ix243* mutant strain

(A) Travel distance of WT, *ix243*(4x BC), *ix243*(4x BC);*Ex[elpc-2(+)] #1,* and *ix243*(4x BC);*Ex[elpc-2(+)] #2* worms. n = 30–45 worms per strain for each day (10–15 worms from 3 biological replicate plates). (B) Percent change in travel distance of worms from A. n = 3 biological replicate plates. $^{**}P < 0.01$; $^{***}P < 0.001$; ns, not significant; One-way ANOVA with Dunnett's post hoc test vs. WT.

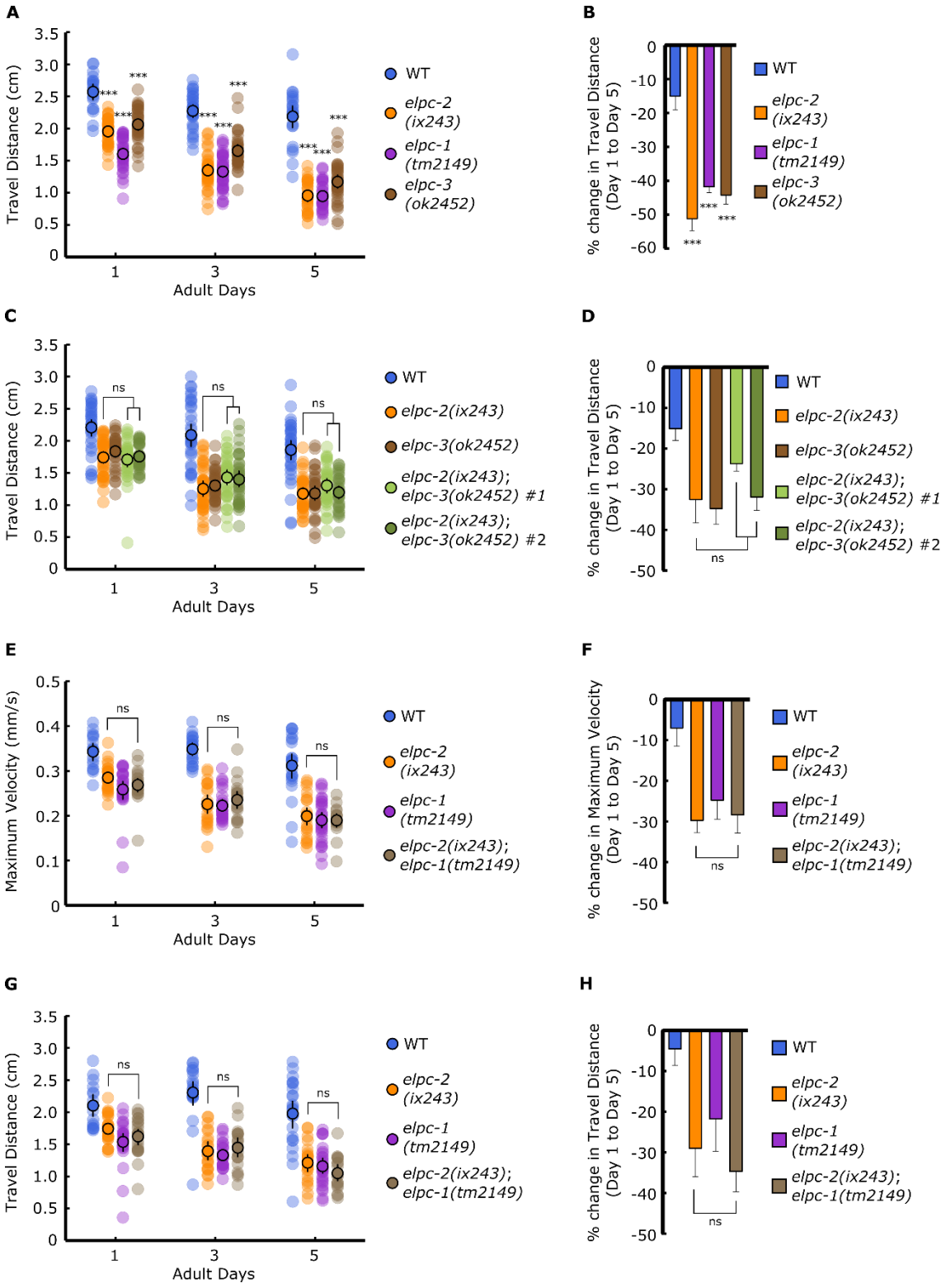


Figure S7. The Elongator complex is required to maintain adult locomotor ability

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

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

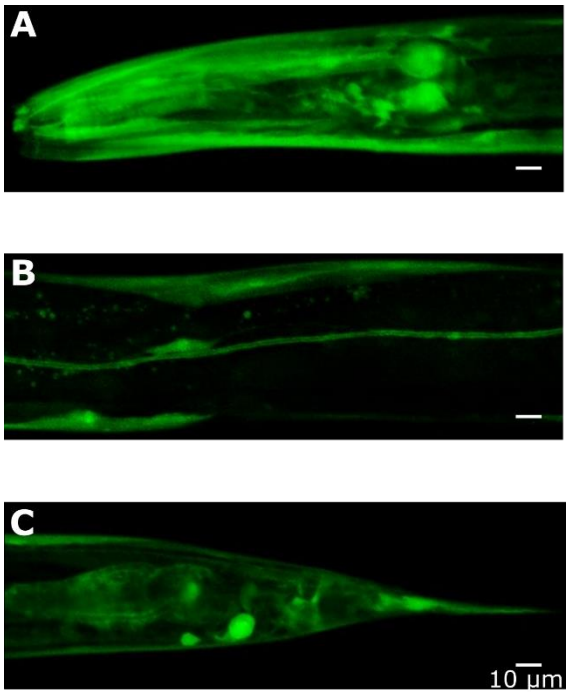
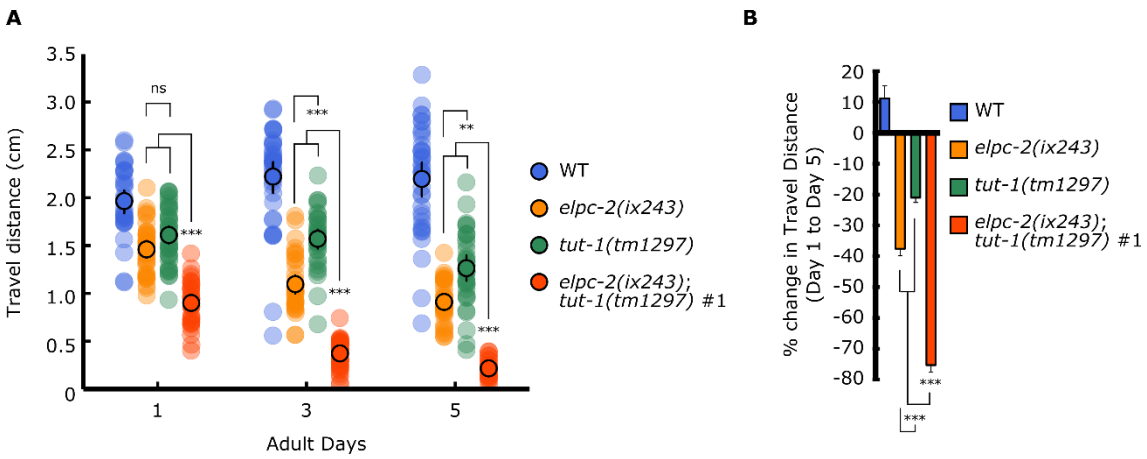


Figure S8. Expression pattern of *elpc-2* transcriptional GFP fusion

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



89

90 **Figure S9. *tut-1(tm1297)* mutant shows progressive decline in locomotor ability**

91 (A) Travel distances of WT, *elpc-2(ix243)*, *tut-1(tm1297),* and *elpc-2(ix243);tut-*

92 *1(tm1297)* worms. n = 30–45 worms per strain for each day (10–15 worms from 3

93 biological replicate plates). (B) Percent change in travel distance of worms from A. Error

94 bars indicate 95% confidence intervals. n = 3 biological replicate plates. **P* < 0.05; ***P*

95 < 0.01; ****P* < 0.001; ns, not significant; One-way ANOVA with Tukey's post hoc test.

96

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%
tut-1(tm1297)	82.0	116.5%
elpc-2(ix243);*tut-1(tm1297)*	145.4	206.5%

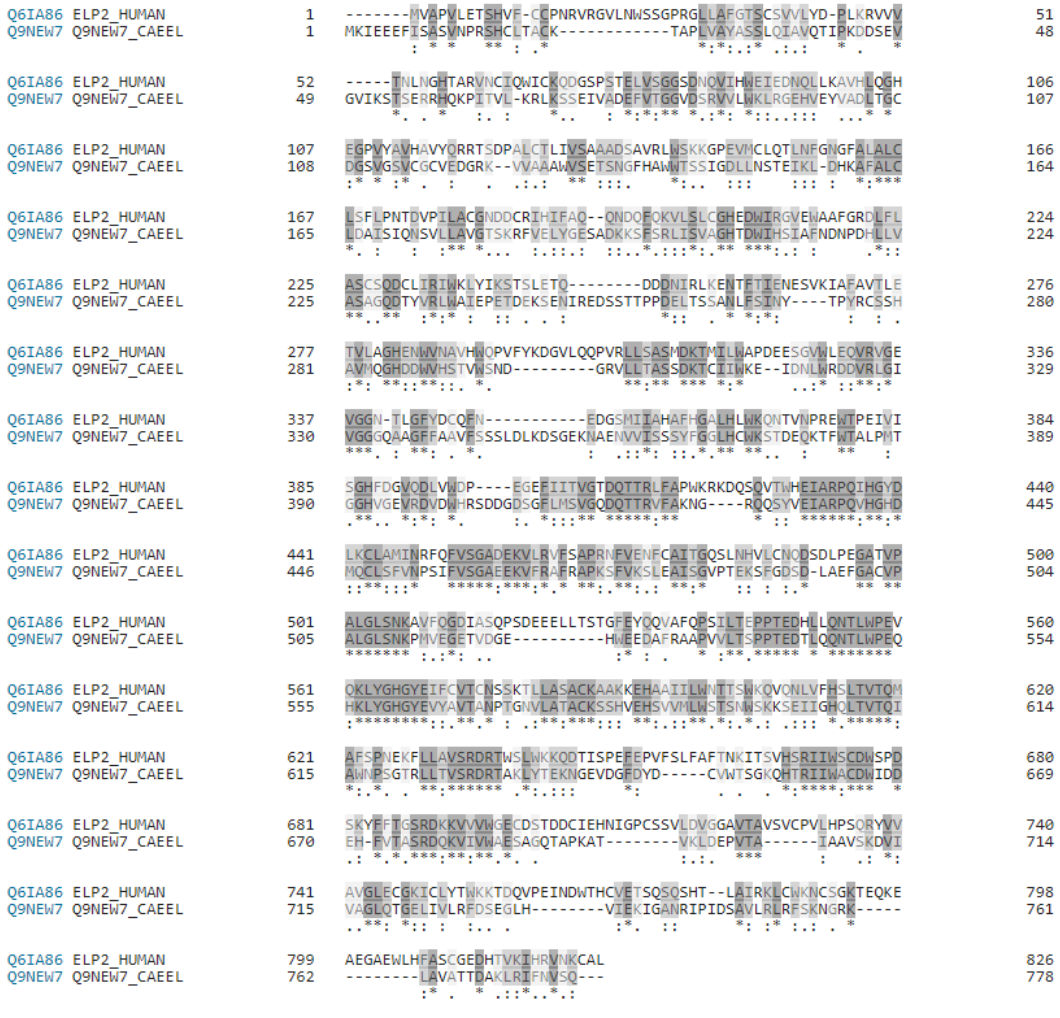


Figure S10. Amino acid alignment of *C. elegans* ELPC-2 and human ELP2

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).

Table S6. Strain list

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

Table S7. Primer list

Primer Name	**5'-3' Sequence**
5' *elpc-2*p (2090-bp upstream)	gataagtgacatgccgctgcgtccttac
3' *elpc-2UTR* (851-bp downstream)	aagagacagcgtctgattcttgaaacggta
5' *elpc-2* snp	aaatgaatttttcgccacaaaacccaaaaa
3' *elpc-2* snp	ttcgcgaaaactctcgtagtctgatcctg
5' *elpc-1* del	gaaaagcatcgagttgtccacttgaatcac
3' *elpc-1* del	cttttcagttgaattctggcatctctccaa
5' *elpc-3* del	taatagaacccagatcgagtttggcagatg
3' *elpc-3* del	aatgcatcgtatgtggttaggcggtaaaac
5' *elpc-2*p overlap ppd95.79	ctatgaccatgattacgccagataagtgacatgccgctgcgtcct
3' *elpc-2*p overlap ppd95.79	gtcctttggccaatcccgggtgattttctggaaaaaaatggtgaaaatctcg tgaaaaaac
5' ppd95.79	cccgggattggccaaaggacccaaa
3' ppd95.79	tggcgtaatcatggtcatagctgtttc