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## Supplementary Materials for

### **Dose-dependent functions of SWI/SNF BAF in permitting and inhibiting cell proliferation in vivo**

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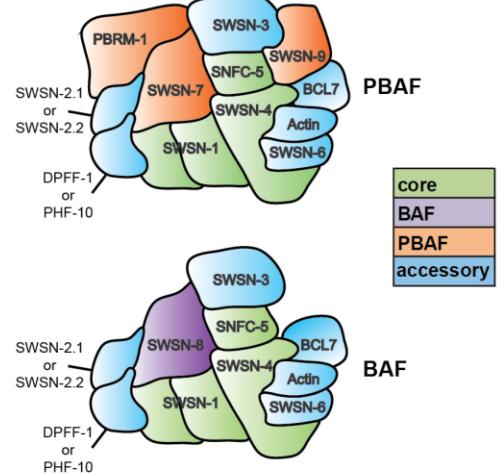
#### **This PDF file includes:**

Figs. S1 to S6  
Tables S1 and S2

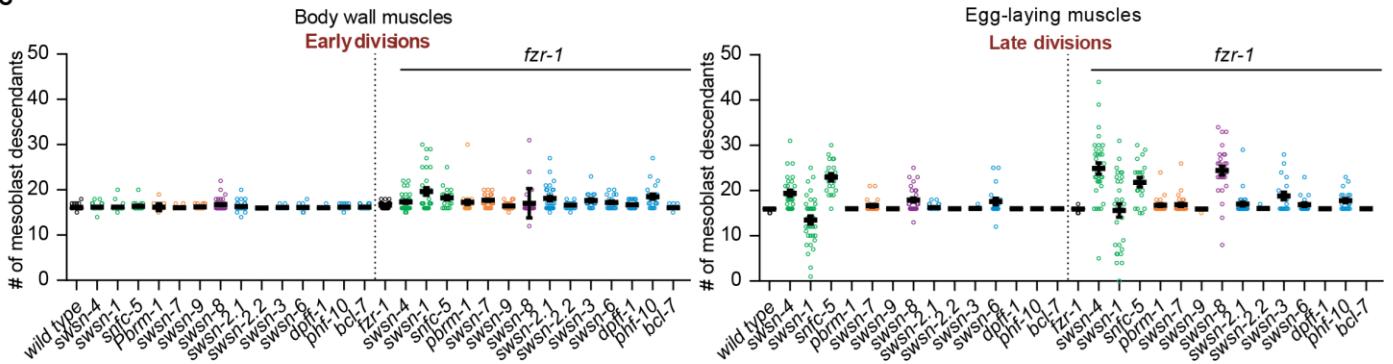
A

<i>C. elegans</i> gene	alternative <i>C. elegans</i> name	mammalian homologue(s)
<i>swn-1</i>	<i>psa-1</i>	SMARCC1/BAF155; SMARCC2/BAF170
<i>swn-4</i>	<i>psa-4</i>	SMARCA2/BRM; SMARCA4/BRG1
<i>snfc-5</i>	<i>swn-5</i>	SMARCB1/BAF47/SNF5
<i>swn-8</i>	<i>let-526, psa-10, let-104, iss-4</i>	ARID1/BAF250
<i>pbrm-1</i>	<i>tag-185</i>	PBRM1/BAF180
<i>swn-7</i>		ARID2/BAF200
<i>swn-9</i>	<i>tag-298</i>	BRD7/BRD9
<i>swn-2.1</i>	<i>ham-3</i>	SMARCD/BAF60
<i>swn-2.2</i>		SMARCD/BAF60
<i>swn-3</i>		SMARCE1/BAF57
<i>swn-6</i>	<i>psa-16</i>	ACTL6/BAF53
<i>bcl-7</i>		BCL7
<i>dpff-1</i>		DPF/BAF45
<i>phf-10</i>		PHF10/BAF45

B



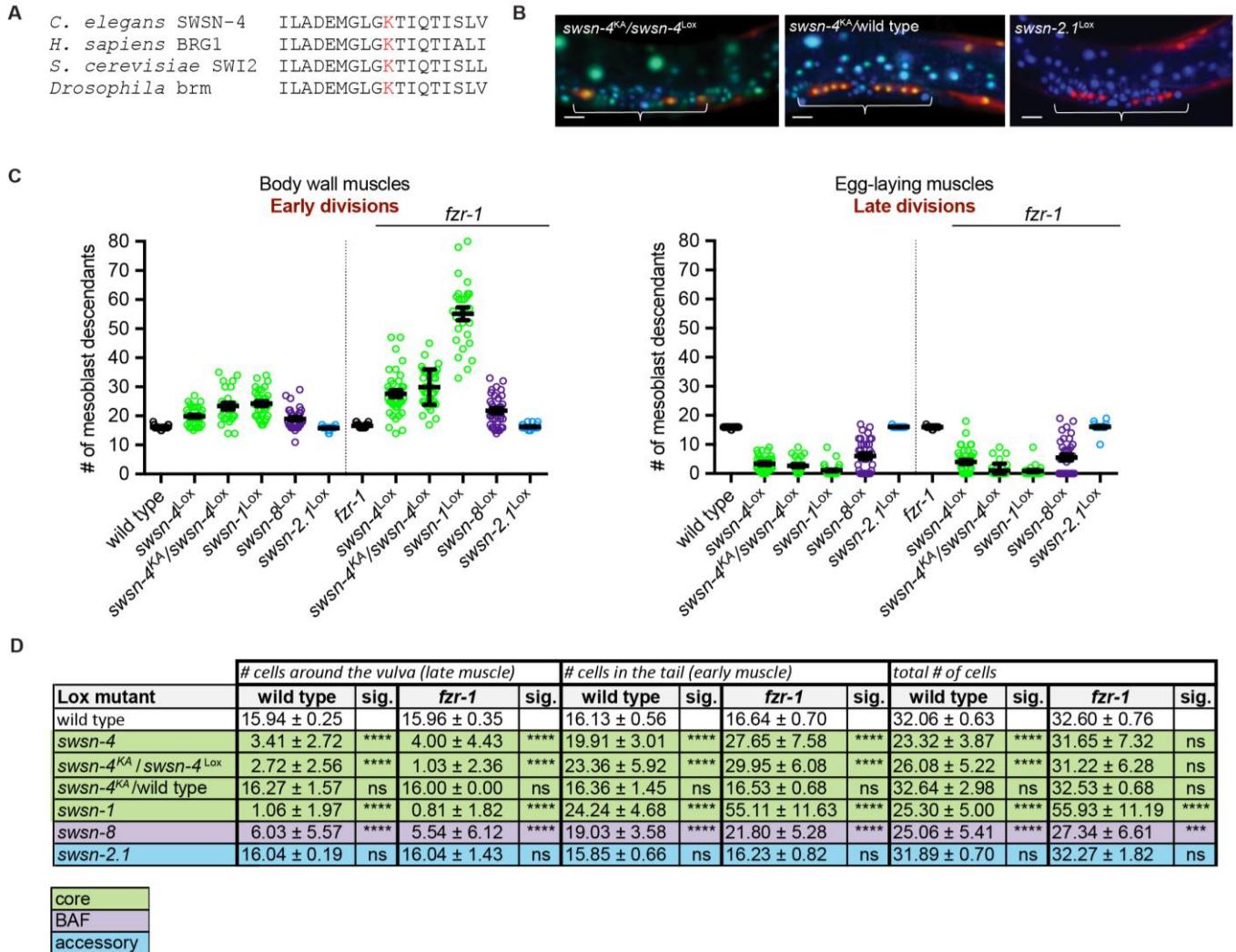
C



D

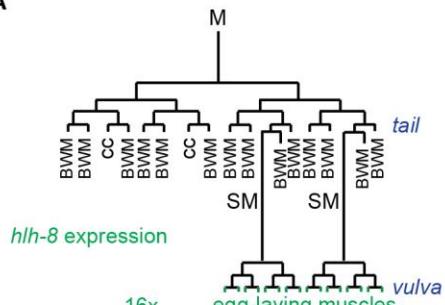
gene	# cells in the tail (Early muscle)				# cells around the vulva (Late muscle)				total # of cells			
	wild type	sig.	fzs-1	sig.	wild type	sig.	fzs-1	sig.	wild type	sig.	fzs-1	sig.
L4440	16.13 ± 0.56		16.64 ± 0.70		15.94 ± 0.25		15.96 ± 0.35		32.06 ± 0.63		32.60 ± 0.76	
<i>swn-1</i>	16.17 ± 0.79	ns	19.67 ± 4.58	**	13.49 ± 5.39	*	15.60 ± 8.15	ns	29.66 ± 5.15	*	35.27 ± 5.47	*
<i>swn-4</i>	16.20 ± 0.71	ns	17.27 ± 1.98	ns	19.40 ± 3.69	****	25.80 ± 7.09	****	35.60 ± 3.29	****	43.07 ± 6.47	****
<i>snfc-5</i>	16.40 ± 0.94	ns	18.25 ± 2.20	**	22.95 ± 3.68	****	21.85 ± 4.74	ns	39.35 ± 3.66	****	40.10 ± 5.94	****
<i>swn-8</i>	16.75 ± 1.41	*	17.03 ± 3.23	ns	17.91 ± 2.63	***	24.43 ± 5.33	****	34.66 ± 2.67	****	41.47 ± 4.31	****
<i>pbrm-1</i>	16.19 ± 0.75	ns	17.25 ± 2.58	ns	16.00 ± 0.00	ns	16.79 ± 1.62	*	32.19 ± 0.75	ns	34.04 ± 2.94	*
<i>swn-7</i>	16.08 ± 0.28	ns	17.70 ± 1.26	***	16.67 ± 1.47	**	16.87 ± 2.01	*	32.75 ± 1.60	*	34.57 ± 2.46	***
<i>swn-9</i>	16.25 ± 0.44	ns	16.46 ± 0.78	ns	16.00 ± 0.00	ns	15.96 ± 0.20	ns	32.42 ± 0.83	ns	32.25 ± 0.44	ns
<i>swn-2.1</i>	16.33 ± 1.09	ns	18.05 ± 2.56	**	16.27 ± 0.58	**	17.14 ± 2.47	*	32.60 ± 1.38	ns	35.19 ± 3.76	**
<i>swn-2.2</i>	16.00 ± 0.00	ns	16.62 ± 0.74	ns	16.00 ± 0.00	ns	16.05 ± 0.22	ns	32.00 ± 0.00	ns	32.67 ± 0.80	ns
<i>swn-3</i>	16.10 ± 0.31	ns	17.65 ± 1.63	**	16.05 ± 0.22	ns	18.80 ± 3.72	***	32.15 ± 0.49	ns	36.45 ± 4.06	****
<i>swn-6</i>	16.10 ± 0.64	ns	17.24 ± 1.41	ns	17.60 ± 3.15	**	16.90 ± 1.70	**	33.70 ± 3.16	**	34.14 ± 2.18	**
<i>bcl-7</i>	16.18 ± 0.39	ns	16.08 ± 0.40	ns	16.00 ± 0.00	ns	16.00 ± 0.00	ns	32.18 ± 0.39	ns	32.08 ± 0.40	ns
<i>dpff-1</i>	16.05 ± 0.22	ns	16.73 ± 0.88	ns	16.00 ± 0.00	ns	16.00 ± 0.00	ns	32.05 ± 0.22	ns	32.73 ± 0.88	ns
<i>phf-10</i>	16.16 ± 0.47	ns	18.52 ± 2.68	**	16.00 ± 0.00	ns	17.78 ± 2.04	****	32.16 ± 0.47	ns	36.30 ± 4.06	****

**Fig. S1. The SWI/SNF BAF complex promotes cell cycle exit.** (A) The SWI/SNF complex consists of core, accessory, and BAF and PBAF-specific signature subunits. Table of *C. elegans* names used in this publication, alternative *C. elegans* nomenclature, and commonly used mammalian homologue names for the different subunits. (B) a schematic representation of the two conserved SWI/SNF subcomplexes (using *C. elegans* nomenclature). (C) Quantification of mesoblast lineage descendants, in the tail area (early dividing body wall muscles) and around the vulva (late dividing egg-laying muscles) at the L4 larval stage following RNAi by feeding of synchronised L1 larvae for the indicated genes, in wild type or mutant backgrounds, with (D) table of mean mesoblast cell numbers, standard deviations and tests for significance compared to wild type and *fzs-1* knockout larvae for each RNAi treatment. L4440 indicates the empty vector used in the RNAi control-treated animals.

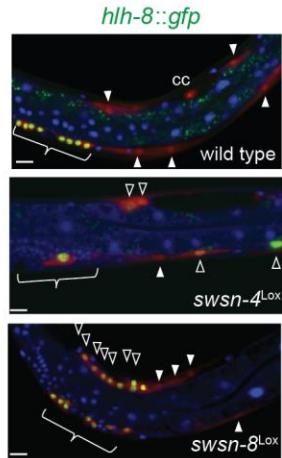
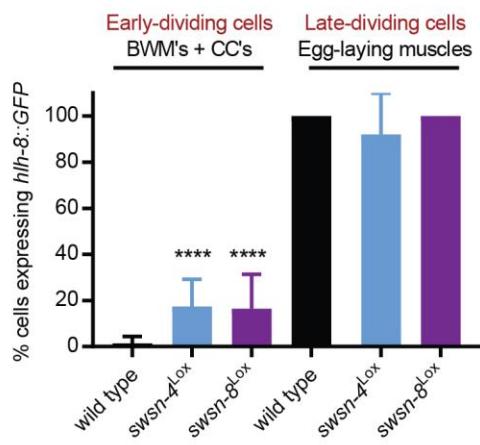


**Fig. S2. Simultaneous knockout of *fzr-1*(*Cdh-1*) increases M descendant hyperplasia early after SWI/SNF gene knockout, but does not suppress the proliferation defect of late M descendants.** (A) Illustration of the conserved lysine residue in the ATPase domain of SWSN-4, which is mutated to alanine (KA) to abolish ATPase activity. (B) Representative images of *swns-4^KA* trans-heterozygotes in the presence and absence of a wild type copy of *swns-4* (marked in cis with *Peft-3::gfp*) and of *swns-2.1^Lox* knockout larvae. Brackets indicate egg-laying muscle precursors, scale bar 10 µm. (C) Quantification of mesoblast lineage descendants in the tail area (early formed BWM) and around the vulva (late dividing egg-laying muscle precursors) at the L4 larval stage of the indicated genotypes in wild type or *fzr-1* mutant backgrounds, with (D) table of mean mesoblast cell numbers, standard deviations and tests for significance compared to wild type and *fzr-1* knockout larvae for the indicated genotypes.

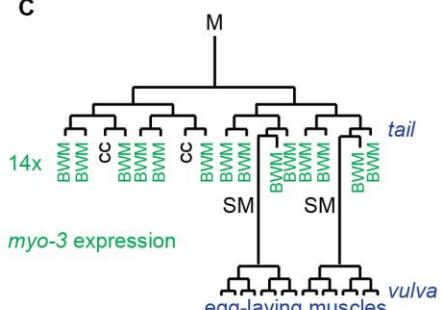
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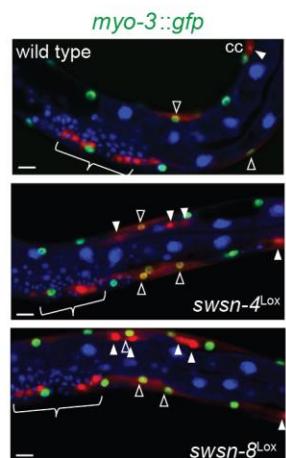
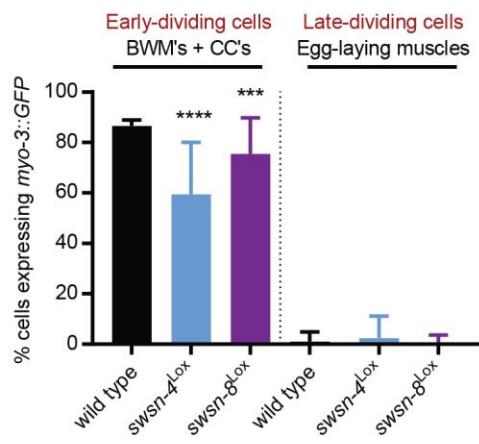
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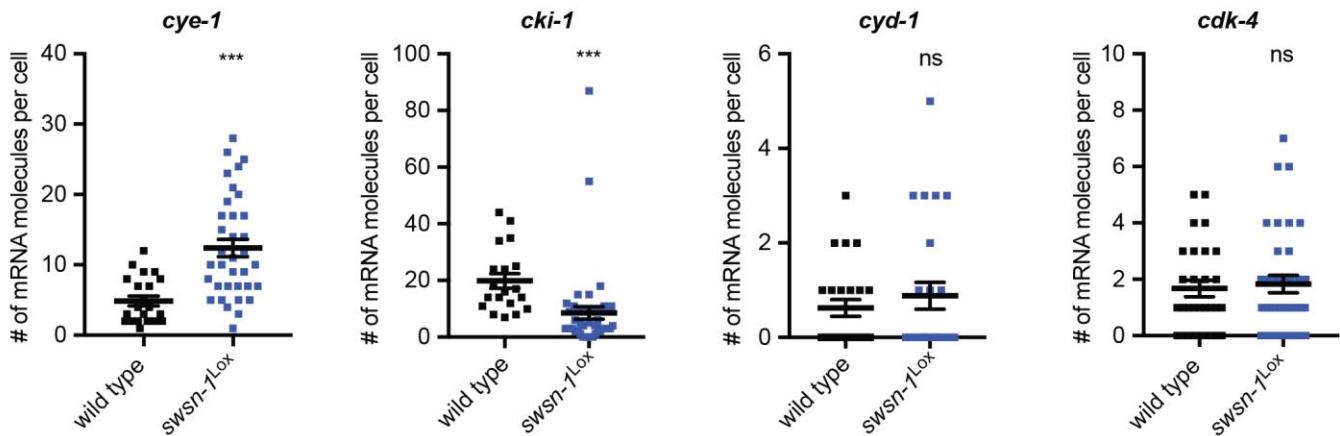
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D

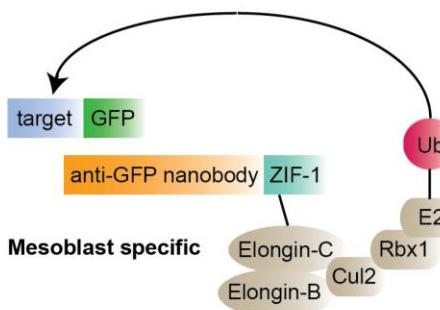


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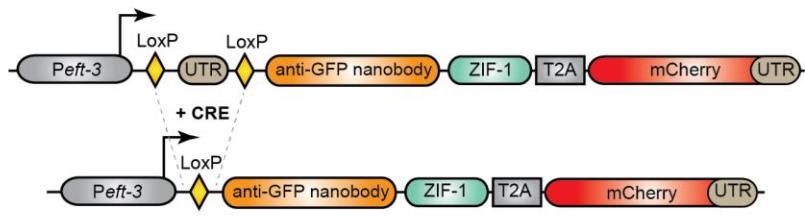


**Fig. S3. Extra M lineage descendants in the conditional SWI/SNF knockout animals correspond to a prolonged proliferative and undifferentiated state.** (A) Illustration of the wild type expression pattern of *Phlh-8::gfp*, which is restricted to the 16 egg-laying muscle precursors in early L4 larvae. (B) Percentage of mesoblast descendants expressing *Phlh-8::gfp* in early L4 larvae, for the indicated genotypes, with representative fluorescence microscopy images (right). Microscopy images: closed triangles indicate M descendants that only express the mCherry reporter. Open triangles indicate GFP expression in M descendants. Brackets indicate the vulva area. Scale bar 10  $\mu$ m. 20-30 worms were quantified for each genotype. (C) Illustration of the wild type expression pattern of *Pmyo-3::gfp* in early L4 mesoblast descendants. (D) Percentage of mesoblast descendants expressing *Pmyo-3::gfp* in early L4 larvae, for the indicated genotypes, with representative images as under B. 20-30 worms were quantified for each genotype. (E) Quantification of numbers of mRNA molecules per cell in smFISH experiments of early L4 wild-type and *swsn-1* knockout larvae for the indicated genes.

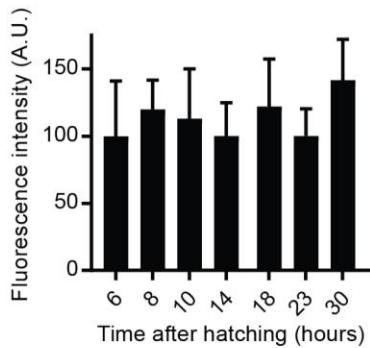
A



B



C



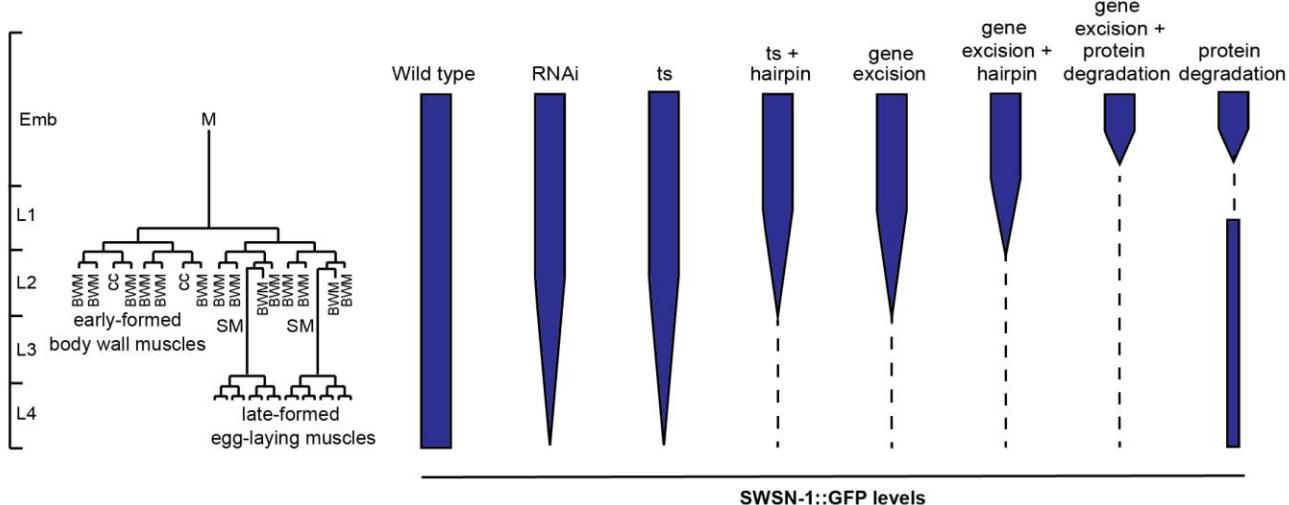
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Fig. 3	n animals scored
A	30-50
B	15-35
E	18-35
G	18-29
I	9-20

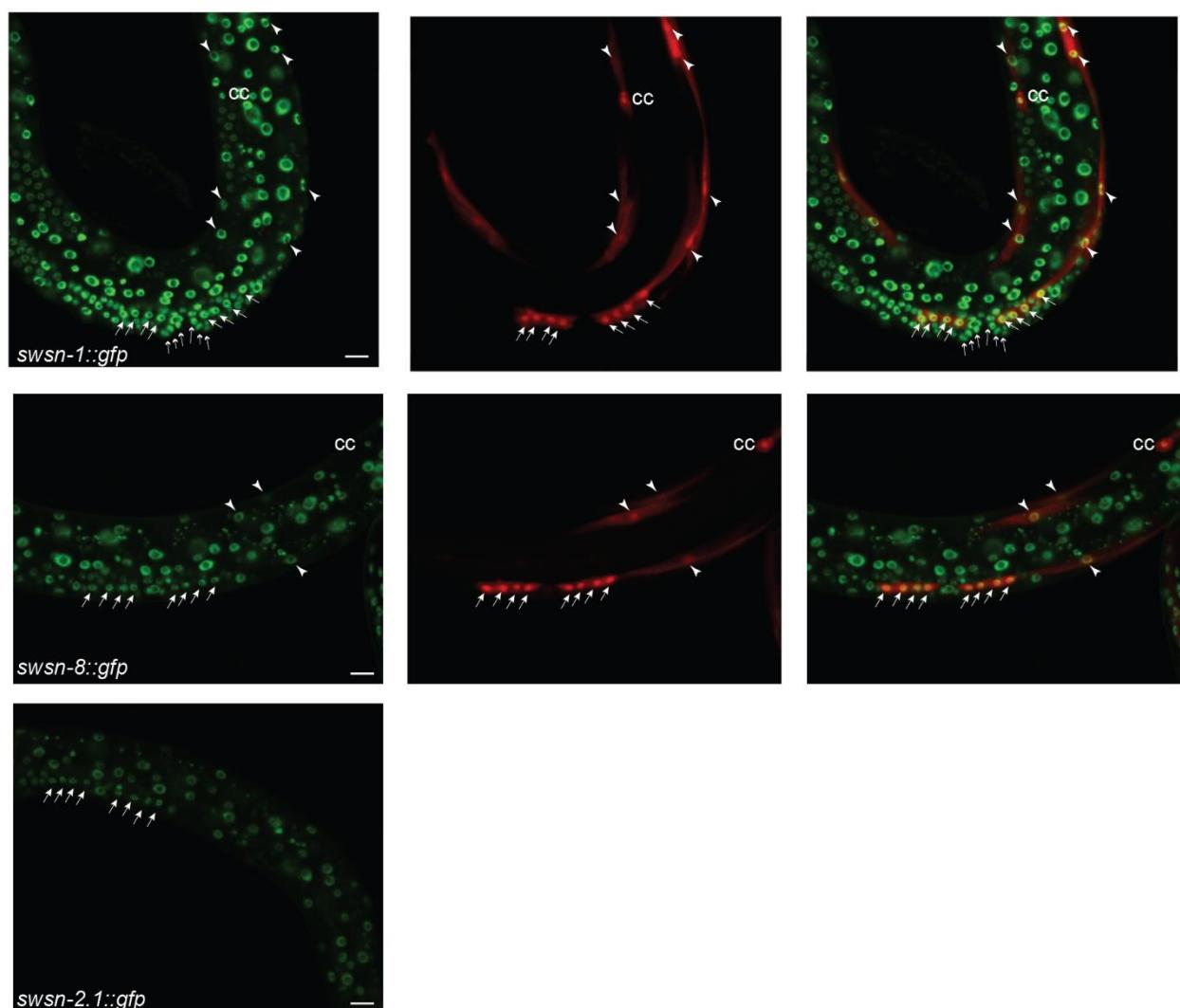
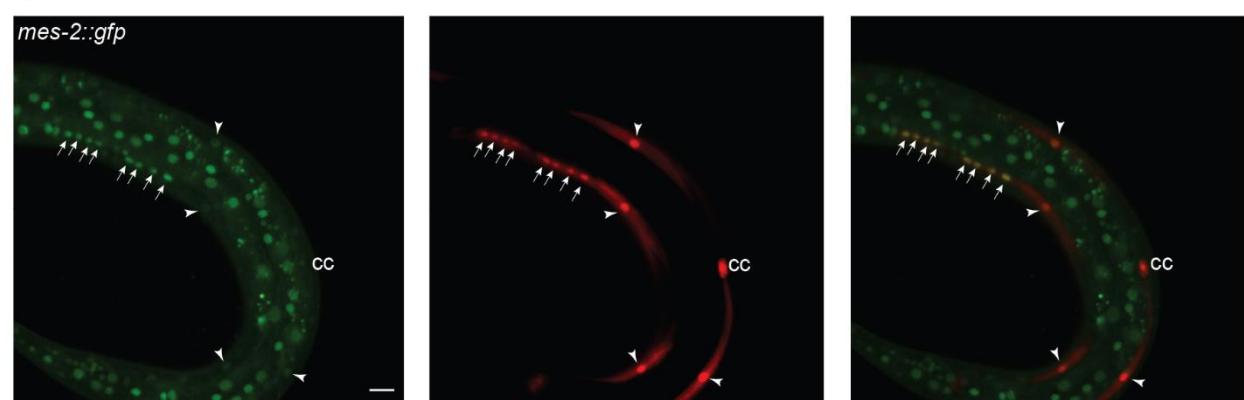
  

Fig. 3	n cells quantified
D	6-10
H	5-25

E

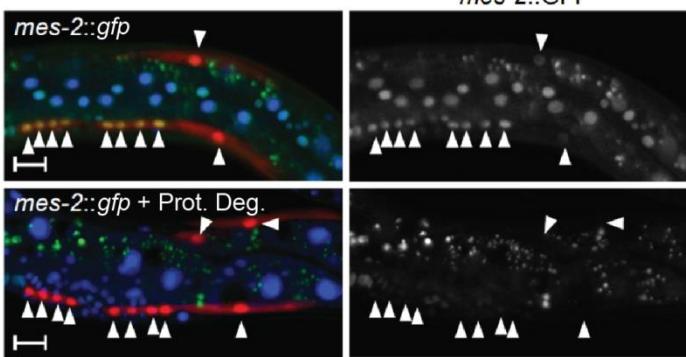


**Fig. S4. Expression of SWSN-1::GFP in M descendants over time and strategy for its inducible degradation. (A,B)** Schematic of tissue-specific protein degradation strategy (A) an anti-GFP nanobody fused to the ZIF-1 subunit of a CUL-2 E3 ubiquitin ligase leads to specific degradation of GFP-tagged proteins (Prot. Deg.). (B) Schematic of the strategy for tissue-specific expression of the anti-GFP nanobody-ZIF-1 fusion protein. A floxed STOP cassette (LoxP::let-858 UTR::LoxP) is inserted before the coding sequences of the fusion protein. Lineage-specific CRE recombinase expression leads to excision of the STOP cassette and nanobody::ZIF-1 expression from the general *eft-3* promoter. (C) Quantifications of SWSN-1::GFP levels in M lineage descendants over time, in wild type. (D) n numbers of animals/cells scored for experiments displayed in the indicated panels of Fig. 3. (E) Schematic representation of residual SWSN-1::GFP levels after depletion using the indicated methods, during the time of mesoblast lineage development.

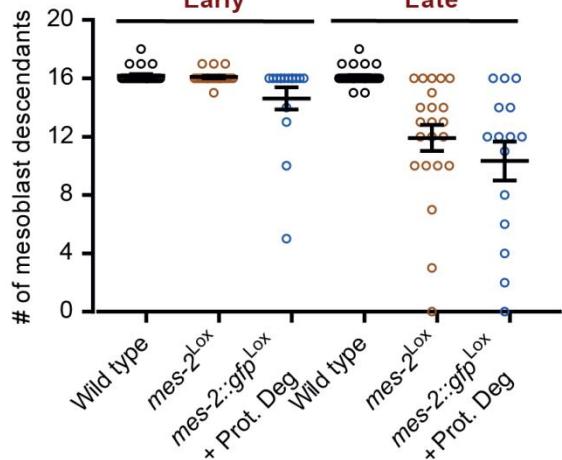
**A****B**

**Fig. S5. Expression of endogenous GFP-tagged SWI/SNF subunits *swns-1*, *swns-8* and *swns-2.1* as well as EZH2-related PcG gene *mes-2*.** (A) Representative images of L4 larvae expressing endogenous GFP-tagged SWI/SNF subunits *swns-1*, *swns-8* and *swns-2.1*. (B) Representative image of endogenous GFP-tagged EZH2-related PcG gene *mes-2*. Closed arrows indicate egg-laying muscle cells, arrowheads indicate body wall muscle cells, small open arrows indicate vulval cells (descendants of vulval precursor cells) and “cc” the coelomocytes. Scale bar 10  $\mu$ m.

A



B



**Fig. S6. Gene excision of *mes-2::gfp<sup>Lox</sup>* combined with protein degradation did not interfere with early M cell divisions. (A)** Quantifications of mesoblast descendants for the indicated genotypes, in the tail area (early) and around the vulva (late). **(B)** Expression of MES-2::GFP in L4 larvae in wild type worms (top) and after protein degradation (bottom, nanobody). Arrowheads indicate M lineage descendants.

**Table S1. Strains used in this study.** List of *C. elegans* strains used in this study, with strain names in the left-hand column and genotypes in the right-hand column.

SV1863	<i>heSi208[Peft-3::LoxP::NLS egl-13::tagBFP2::tbb-2 UTR::LoxP::NLS egl-13::mCherry:: tbb-2 UTR] V; heSi141[Phlh-8::CRE] X</i>
SV1888	<i>heSi210[Peft-3::LoxP::NLS egl-13::tagBFP2::tbb-2 UTR::LoxP::NLS egl-13::mCherry:: tbb-2 UTR] III; heSi141[Phlh-8::CRE] X</i>
SV1930	<i>swns-8(he273he287[LoxN exon 3, LoxN last intron]) I; pha-1(+) III; heSi208[Peft-3::LoxP::NLS egl-13:: tagBFP2::tbb-2 UTR::LoxP::NLS egl-13::mCherry:: tbb-2 UTR] V; heSi141[Phlh-8::CRE] X</i>
SV1871	<i>pha-1(+) III; swns-4(he268he272[LoxN start, LoxN intron 5]) IV; heSi208[Peft-3::LoxP::NLS egl-13:: tagBFP2::tbb-2 UTR::LoxP::NLS egl-13::mCherry:: tbb-2 UTR] V; heSi141[Phlh-8::CRE] X</i>
SV1897	<i>unc-119(ed3) III; pha-1(+) III; oxTi970[Peft-3::GFP::2xNLS::tbb-2 UTR + Cbr-unc-119(+)] IV; swns-4(he277[K564A]); swns-4(he268he272[LoxN start, LoxN intron 5]) IV; heSi208[Peft-3::LoxP::NLS egl-13::tagBFP2::tbb-2 UTR::LoxP::NLS egl-13:: mCherry:: tbb-2 UTR] V; heSi141[Phlh-8::CRE] X</i>
SV2044	<i>unc-119(ed3) III; oxTi970[Peft-3::GFP::2xNLS::tbb-2 UTR + Cbr-unc-119(+)] IV; swns-4(he277[K564A]); swns-4(+) IV; heSi208 [Peft-3::LoxP::NLS egl-13::tagBFP2::tbb-2 UTR::LoxP::NLS egl-13:: mCherry:: tbb-2 UTR] V; heSi141[Phlh-8::CRE] X</i>
SV2025	<i>swns-2.1(he309[LoxN first intron, LoxN last intron]) III; pha-1(+) III; heSi208[Peft-3::LoxP::NLS egl-13::tagBFP2::tbb-2 UTR::LoxP::NLS egl-13:: mCherry:: tbb-2 UTR] V; heSi141[Phlh-8::CRE] X</i>
SV1941	<i>swns-8(he273he287[LoxN exon 3, LoxN last intron]) I; fzr-1(ku298) II; unc-4(e120)II; pha-1(+)III; heSi208[Peft-3::LoxP::NLS egl-13:: tagBFP2::tbb-2 UTR::LoxP::NLS egl-13::mCherry:: tbb-2 UTR] V; heSi141[Phlh-8::CRE] X</i>
SV1894	<i>fzr-1(ku298) II; unc-4(e120) II; pha-1(+) III; swns-4(he268he272[LoxN start, LoxN intron 5]) IV; heSi208 [Peft-3::LoxP::NLS egl-13:: tagBFP2::tbb-2 UTR::LoxP::NLS egl-13::mCherry:: tbb-2 UTR] V; heSi141[Phlh-8::CRE] X</i>
SV2034	<i>fzr-1(ku298) II; unc-4(e120) II; unc-119(ed3) III; pha-1(+) III; oxTi970 [Peft-3::GFP::2xNLS::tbb-2 UTR + Cbr-unc-119(+)] IV; swns-4 (he277[K564A]); swns-4(he268he272[LoxN start, LoxN intron 5]) IV; heSi208[Peft-3::LoxP::NLS egl-13::tagBFP2::tbb-2 UTR::LoxP::NLS egl-13:: mCherry:: tbb-2 UTR] V; heSi141[Phlh-8::CRE] X</i>
SV2033	<i>fzr-1(ku298) II; unc-4(e120) II; unc-119(ed3) III; oxTi970[Peft-3::GFP::2xNLS::tbb-2 UTR + Cbr-unc-119(+)] IV; swns-4(he277[K564A]); swns-4(+) IV; heSi208 =[Peft-3::LoxP::NLS egl-13::tagBFP2::tbb-2 UTR::LoxP::NLS egl-13:: mCherry:: tbb-2 UTR] V; heSi141[Phlh-8::CRE] X</i>
SV2029	<i>fzr-1(ku298) II; unc-4(e120) II; pha-1(+) III; swns-2.1(he309[swns-2.1 LoxN first intron, LoxN last intron]) III; heSi210 [Peft-3::LoxP::NLS egl-13::tagBFP2::tbb-2 UTR::LoxP::NLS egl-13::mCherry:: tbb-2 UTR]III; heSi141[Phlh-8::CRE] X</i>
SV2027	<i>heSi219[Phlh-8::GFP::H2B::unc-54 UTR] III; heSi208 [Peft-3::LoxP::NLS egl-13::tagBFP2::tbb-2 UTR::LoxP::NLS egl-13::mCherry:: tbb-2 UTR] V; heSi141[Phlh-8::CRE] X</i>

SV2030	<i>heSi219[Phlh-8::GFP::H2B::unc-54 UTR]III; swsn-4(he268he272[LoxN start, LoxN intron 5]) IV; heSi208[Peft-3::LoxP::NLS egl-13::tagBFP2::tbb-2 UTR::LoxP::NLS egl-13::mCherry:: tbb-2 UTR]V; heSi141 [Phlh-8::CRE] X</i>
SV2031	<i>swsn-8(he273he287[LoxN exon 3, LoxN last intron]) I; heSi219[Phlh-8::GFP::H2B::unc-54 UTR] III; heSi208[Peft-3::LoxP::NLS egl-13::tagBFP2::tbb-2 UTR::LoxP::NLS egl-13::mCherry:: tbb-2 UTR] V; heSi141[Phlh-8::CRE] X</i>
SV1578	<i>unc-119(ed3) III; hels105[Prps-27::LoxN::NLS egl-13::mCherry::let-858 UTR::LoxN::NLS:: egl-13 GFP::let-858 UTR] IV; swsn-1(os22) V; heSi164[Prps-27::LoxN::NLS egl-13::mCherry::let-858 UTR::Pswns-1::swsn-1::unc-54 UTR::LoxN::NLS egl-13::GFP ::let-858 UTR] V; heSi141[Phlh-8::CRE] X; heEx611[Phlh-8::hairpin swsn-1::unc-54]</i>
SV1818	<i>pha-1(e2123)III 7x out-crossed</i>
SV2023	<i>swsn-1(he306[swsn-1::eGFP]) V; [Peft-3::LoxP::NLS egl-13:: tagBFP2::tbb-2 UTR::LoxP::NLS egl-13::mCherry:: tbb-2 UTR] V; heSi141[Phlh-8::CRE] X</i>
SV2077	<i>swsn-1(he313he315[swsn-1::eGFP::LoxP; LoxP second intron])V; heSi208 [Peft-3::LoxP::NLS egl-13::tagBFP2::3'UTR tbb-2::LoxP::NLS egl-13::mCherry::3'UTR tbb-2] V; heSi141[Phlh-8::CRE] X</i>
SV2098	<i>fzr-1(ku298) II; unc-4(e120) II; swsn-1(he313he315[swsn-1::eGFP::LoxP; LoxP second intron]) V; heSi208[Peft-3::LoxP::NLS egl-13::tagBFP2::3'UTR tbb-2::LoxP::NLS egl-13::mCherry::3'UTR tbb-2] V; heSi141[Phlh-8::CRE] X</i>
SV2067	<i>heSi210[Peft-3::LoxP::NLS egl-13::tagBFP2::tbb-2 UTR::LoxP::NLS egl-13::mCherry:: tbb-2 UTR]III; he303[peft-3::LoxP::let-858 UTR::LoxP::vhGFP::ZIF-1::mCherry] IV ; swsn-1(he313he315[swsn-1::eGFP::LoxP; LoxP second intron]) V; heSi141[Phlh-8::CRE] X</i>
SV2161	<i>heSi210[Peft-3::LoxP::NLS egl-13::tagBFP2::tbb-2 UTR::LoxP::NLS egl-13::mCherry:: tbb-2 UTR] III; swsn-1(he313[swsn-1::eGFP::LoxP]) V; he303[peft-3::LoxP::let-858 UTR::LoxP::vhGFP::ZIF-1::mCherry] IV; heSi141[Phlh-8::CRE] X</i>
SV2155	<i>mes-2(he332he340[LoxN first intron, LoxNlast intron]) II; heSi208[Peft-3::LoxP::NLS egl-13::tagBFP2::3'UTR tbb-2::LoxP::NLS egl-13::mCherry::3'UTR tbb-2] V; heSi141[Phlh-8::CRE] X</i>
SV2185	<i>mes-2(he332he340[LoxN first intron, LoxNlast intron]) II; swsn-4(he268he272[LoxN start, LoxN intron 5]) IV; heSi208[Peft-3::LoxP::NLS egl-13::tagBFP2::3'UTR tbb-2::LoxP::NLS egl-13::mCherry::3'UTR tbb-2] V; heSi141[Phlh-8::CRE] X</i>
SV2186	<i>swsn-8(he273he287[LoxN exon 3, LoxN last intron]) I; mes-2(he332he340[LoxN first intron, LoxNlast intron]) II; heSi208[Peft-3::LoxP::NLS egl-13::tagBFP2::3'UTR tbb-2::LoxP::NLS egl-13::mCherry::3'UTR tbb-2] V; heSi141[Phlh-8::CRE] X</i>
SV2187	<i>mes-2(he332he340[LoxN first intron, LoxN last intron]) II; swsn-1(he313he315[swsn-1::eGFP::LoxP; LoxP second intron]) V; heSi208[Peft-3::LoxP::NLS egl-13::tagBFP2::3'UTR tbb-2::LoxP::NLS egl-13::mCherry::3'UTR tbb-2] V; heSi141[Phlh-8::CRE] X</i>
SV2105	<i>cki-1(he329[LoxP first intron, LoxP in UTR]) II, heSi208[Peft-3::LoxP::NLS egl-13::tagBFP2::3'UTR tbb-2::LoxP::NLS egl-13::mCherry::3'UTR tbb-2] V; heSi141[Phlh-8::CRE] X; aylS6[Phlh-8::GFP] X</i>

SV2122	<i>cki-1(he329[LoxP first intron, LoxP in UTR]) II, swsn-4 (he277[K564A]); swsn-4(+)IV; heSi208 [Peft-3::LoxP::NLS egl-13::tagBFP2::tbb-2 UTR::LoxP::NLS egl-13::mCherry::3'UTR tbb-2] V; heSi141[Phlh-8::CRE] X; aylS6[Phlh-8::GFP] X</i>
SV2295	<i>mes-2(he332he334[loxN first intron, mes-2::eGFP::LoxN]) II, heSi210 [Peft-3::LoxP::NLS egl-13::tagBFP2::tbb-2 UTR::LoxP::NLS egl-13::mCherry:: tbb-2 UTR]III; he303[Peft-3-LoxP-let-858 UTR-LoxP vhh gfp::ZIF-1mCherry] IV ; heSi141[Phlh-8::CRE] X</i>
SV2296	<i>mes-2(he332he334[loxN first intron, mes-2::eGFP::LoxN]) II, heSi210[Peft-3::LoxP::NLS egl-13::tagBFP2::tbb-2 UTR::LoxP::NLS egl-13::mCherry:: tbb-2 UTR] III; he303[Peft-3::LoxP::let-858 UTR::LoxP vhh gfp::ZIF-1::mCherry] IV ; swsn-1(he313he315[swns-1::eGFP::LoxP, LoxP second intron]) V ; heSi141[Phlh-8::CRE] X</i>
SV2081	<i>heSi210[Peft-3::LoxP::NLS egl-13::tagBFP2::tbb-2 UTR::LoxP::NLS egl-13::mCherry:: tbb-2 UTR] III ; swsn-1(he313he315[swns-1::eGFP::LoxP, LoxP second intron]) V; heSi220[Plin-31::CRE] X</i>
SV2082	<i>heSi210[Peft-3::LoxP::NLS egl-13::tagBFP2::tbb-2 UTR::LoxP::NLS egl-13::mCherry:: tbb-2 UTR] III; he303[Peft-3::LoxP::let-858 UTR::LoxP::vhhGFP::ZIF-1::mCherry] IV; swsn-1(he313he315[swns-1::eGFP::LoxP, LoxP second intron]) V; heSi220[Plin-31::CRE] X</i>
SV2117	<i>lin-35(n745) I; he317[Peft-3::Lox2772::NLS egl-13::BFP::let-858 UTR::Lox2772::NLS egl-13::mCherry] IV; heSi220[Plin-31::CRE] X</i>
SV2129	<i>he317[Peft-3::Lox2772::NLS egl-13::BFP::let-858 UTR::Lox2772::NLS egl-13::mCherry] IV; swsn-1(os22) V; heSi220[Plin-31::CRE] X</i>

**Table S2. Differentially expressed genes.** List of differentially expressed genes between control read-out strain and *swn-1::gfp<sup>Lox</sup>* + Prot. Deg. M cells at 5.5 hours of development, with a padj value <0.1. Differential expression analysis was carried out by running DESeq2 on raw transcript numbers from the replicate RNA-sequencing experiments. baseMean = normalised mean number of transcripts across all replicates and conditions. log2Fold change = log2 of the fold change difference in transcript numbers between control and *swn-1::gfp<sup>Lox</sup>* + Prot. Deg. IfcSE = standard error estimate for log2 fold change. stat= Wald statistic. pvalue = p value. padj = Benjamini-Hochberg adjusted p value (equivalent to false discovery rate).

Wormbase sequence name	baseMean	log2 FoldChange	IfcSE	stat	pvalue	padj	Gene name
F59D12.2	3.55300172	-5.1963925	1.11303548	4.66866744	3.03E-06	0.00052068	F59D12.2
R05C11.1	2.22361582	-4.5622742	1.19982322	3.80245535	0.00014327	0.0090299	arrd-26
C28F5.2	6.42940958	-4.5117297	0.91303158	4.9414826	7.75E-07	0.00015218	glb-9
F32D8.10	3.22874695	-4.4702951	1.27444141	3.50765054	0.00045208	0.02098518	F32D8.10
F43C9.2	7.43422057	-4.3882871	0.96811756	4.53280398	5.82E-06	0.00086138	F43C9.2
F10E9.12	1.93300536	-4.2995829	1.21712871	3.53256225	0.00041155	0.01991107	F10E9.12
ZK525.1	164.980828	-4.1980681	0.35919527	11.6874258	1.48E-31	9.70E-28	fip-15
F31D4.8	16.8852954	-4.1429608	0.59033242	7.01801325	2.25E-12	1.41E-09	F31D4.8
C52B9.1	6.27596045	-4.0014462	0.90009151	4.44559932	8.76E-06	0.00109479	cka-2
T25F10.3	2.40640302	-3.9657041	1.15792863	3.42482601	0.00061519	0.02658099	T25F10.3
C50D2.2	2.32471667	-3.9389373	1.11238665	3.54097859	0.00039865	0.01956213	C50D2.2
T01B10.4	2.042184	-3.8347596	1.2839331	2.986729	0.0028198	0.08043099	nhr-14
F16B4.8	17.0052536	-3.8234431	0.5927746	6.45007923	1.12E-10	4.80E-08	cdc-25.2
F35H10.10	6.8267351	-3.7446025	0.80083767	4.67585707	2.93E-06	0.00051565	F35H10.10
T28F2.3	2.91380979	-3.7231182	1.12948641	3.29629306	0.0009797	0.03752634	cah-6
T01D3.7	4.93110436	-3.7012233	1.05294867	3.51510329	0.00043958	0.02082714	T01D3.7
F55C12.4	2.50880167	-3.575991	1.06725963	3.35062896	0.00080628	0.03357067	F55C12.4
T23G11.6	2.263758	-3.4926988	1.1143712	3.134233	0.00172304	0.05679789	Iron-9
C49F8.3	1.834561	-3.4892562	1.1801507	2.956619	0.00311032	0.08651603	C49F8.3
Y73B6BL.9	117.65416	-3.4737824	0.33177041	10.4704407	1.18E-25	2.70E-22	hil-2
ZK337.2	7.51285056	-3.4037595	0.70854446	4.8038757	1.56E-06	0.00029698	klu-1
F53C3.12	2.30234	-3.342929	1.1558272	2.892239	0.00382506	0.09850844	bcmo-2
Y51A2D.15	3.71786927	-3.3219911	0.9301508	3.57145436	0.000355	0.01793294	grdn-1
C30F12.1	5.05284828	-3.2807431	0.84786963	3.86939567	0.00010911	0.00742133	rege-1
W10G6.3	2.810952	-3.251047	1.0950925	2.968742	0.00299022	0.0838481	mua-6
Y75B7AL.1	5.35856483	-3.235369	0.84643231	3.82235995	0.00013218	0.00851524	glb-33
T05A8.3	17.2049178	-3.2330046	0.87627562	3.68948369	0.00022471	0.01239775	T05A8.3
C53C11.3	3.53661071	-3.2096394	1.00188612	3.20359703	0.00135722	0.04734043	ptr-5
R05H11.2	80.3363322	-3.0819062	0.26494354	11.6323132	2.82E-31	9.70E-28	R05H11.2
C06H2.5	17.8960466	-3.0044336	0.47371263	6.3423126	2.26E-10	9.15E-08	glb-3
C18A3.4	13.3305886	-2.9701768	0.69521831	4.27229366	1.93E-05	0.00192631	osta-2
T09B4.5	38.6945977	-2.9232904	0.48964205	5.97026013	2.37E-09	7.08E-07	T09B4.5
C05G5.7	20.2421465	-2.9025752	0.49112557	5.91004707	3.42E-09	9.79E-07	C05G5.7
T06D8.1	4.79930911	-2.8861635	0.87175844	3.31073762	0.0009305	0.03632138	srap-1
T04F8.9	5.51212189	-2.8644575	0.77792652	3.68216968	0.00023126	0.01260903	T04F8.9
F15G9.5	7.27428588	-2.8467468	0.656899	4.33361414	1.47E-05	0.00162532	F15G9.5
C30G7.2	5.1870672	-2.8438054	0.84950278	3.34761163	0.00081511	0.03360502	C30G7.2

T02C12.1	8.18477688	-2.8330999	0.6620457	4.27931165	1.87E-05	0.00191987	hum-5
T21D12.9	5.53413271	-2.8011669	0.73761056	3.79762318	0.00014609	0.009124	sma-10
T05A8.8	5.12113294	-2.7894225	0.70865253	3.93623442	8.28E-05	0.00615408	T05A8.8
F32H2.5	7.452785	-2.7742985	0.66735277	4.15716935	3.22E-05	0.00291266	fasn-1
Y39A3CL.2	4.587384	-2.7483961	0.8946785	3.071937	0.00212675	0.06581414	rimb-1
K07D4.8	13.3730206	-2.7245678	0.50875507	5.35536248	8.54E-08	1.89E-05	pqn-48
T19D12.6	4.1306	-2.6874172	0.9202694	2.92025	0.0034975	0.09399201	T19D12.6
Y22D7AL.8	3.460784	-2.6471055	0.8969722	2.951157	0.00316586	0.08740584	sms-3
F19B10.10	21.3706571	-2.6428693	0.39057022	6.76669442	1.32E-11	7.33E-09	F19B10.10
ZK909.4	3.411797	-2.6322978	0.8645328	3.044763	0.00232864	0.06955533	ces-2
C54G4.5	3.21844	-2.6223438	0.8694378	3.016137	0.00256017	0.07484424	C54G4.5
F49E10.5	3.568208	-2.5731958	0.8399179	3.063628	0.00218671	0.06706558	ctbp-1
C32D5.7	4.45550972	-2.5535993	0.77568711	3.29204809	0.00099461	0.03752634	C32D5.7
C44F1.3	28.0009977	-2.5259129	0.37484168	6.73861276	1.60E-11	7.85E-09	lec-4
Y71G12B.16	15.1376572	-2.4702998	0.4310207	5.73127868	9.97E-09	2.74E-06	drag-1
C04E12.7	5.04487601	-2.3480571	0.65509138	3.58431986	0.00033796	0.0173466	scrm-3
F45E1.2	4.8447304	-2.3220069	0.70946161	3.27291415	0.00106445	0.03889765	F45E1.2
D2092.6	7.65930396	-2.305441	0.59816141	3.85421225	0.0001161	0.00781987	D2092.6
F11C1.6	6.53651	-2.30243	0.7376172	3.121443	0.00179967	0.05859595	nhr-25
F26D11.10	4.86209636	-2.2704042	0.6879095	3.30044018	0.00096533	0.03725751	che-7
W08A12.3	5.67833507	-2.2613436	0.67596583	3.34535192	0.00082178	0.03360502	W08A12.3
F25H5.1	15.1137709	-2.241816	0.63130826	3.55106396	0.00038368	0.01910045	lim-9
C39E6.4	155.991372	-2.2351062	0.23933665	9.33875434	9.75E-21	1.12E-17	mls-2
M05B5.2	9.00123501	-2.2144684	0.51320254	4.31499888	1.60E-05	0.00168689	let-522
C44C11.1	91.1495286	-2.2046676	0.25439459	8.66633043	4.46E-18	3.83E-15	ras-1
R08C7.12	11.191213	-2.1999446	0.58976361	3.73021428	0.00019132	0.01103987	R08C7.12
T01E8.3	5.83017424	-2.1953069	0.58954473	3.7237326	0.0001963	0.01106309	plc-3
F55C5.3	4.250925	-2.1756469	0.747322	2.911257	0.00359977	0.0958544	twk-24
T19E7.6	4.445232	-2.1736753	0.7269539	2.990115	0.00278873	0.08016136	T19E7.6
F08G2.7	7.01123017	-2.1661415	0.64857146	3.33986557	0.00083819	0.03397145	F08G2.7
R02E12.5	7.91289554	-2.1227029	0.59226882	3.58401936	0.00033835	0.0173466	R02E12.5
ZC132.4	20.3037772	-2.1006394	0.50494747	4.1601148	3.18E-05	0.00291266	ZC132.4
F49E12.6	35.8504122	-2.0825939	0.30810718	6.75931642	1.39E-11	7.33E-09	efl-3
H27C11.1	10.7576571	-2.0705735	0.59889043	3.45734942	0.00054552	0.02417872	nhr-97
Y65B4BL.1	9.47895146	-2.0493211	0.5005253	4.0943407	4.23E-05	0.0036357	Y65B4BL.1
F46C8.7	19.0400595	-2.0453159	0.50710685	4.03330361	5.50E-05	0.00449806	glb-16
Y38C1BA.2	4.930628	-2.0404611	0.642023	3.178174	0.00148206	0.05055851	snn-1
C50C3.9	6.33457482	-2.0280392	0.57794079	3.5090778	0.00044966	0.02098518	unc-36
C34G6.4	6.206016	-2.0231026	0.6562789	3.082687	0.00205141	0.06405978	pgp-2
F19B2.5	7.291303	-2.0210459	0.6850437	2.950244	0.00317523	0.08740584	F19B2.5
F28B4.2	10.7297493	-2.0010023	0.46792914	4.27629342	1.90E-05	0.00191987	rgl-1
C46H11.11	11.9852724	-1.9894327	0.48553403	4.09741149	4.18E-05	0.00363324	fhod-1
K12F2.2	12.4998293	-1.9860232	0.41680012	4.76492957	1.89E-06	0.00035078	vab-8
T22C8.8	7.29818737	-1.9699576	0.56617199	3.47943315	0.00050248	0.02316784	vab-9
F55A4.2	12.9881329	-1.960767	0.48435805	4.04817671	5.16E-05	0.00427249	nlf-1
T13H5.6	5.009567	-1.9595866	0.6775986	2.891958	0.00382849	0.09850844	T13H5.6
F44G4.8	8.501526	-1.9427094	0.6242212	3.112213	0.0018569	0.06017422	dep-1
F21D5.9	14.2581415	-1.9409133	0.47039129	4.12616762	3.69E-05	0.00324879	F21D5.9
F58H10.1	11.738375	-1.9400965	0.6422476	3.020792	0.00252114	0.07401821	F58H10.1
F22F1.1	277.399807	-1.9211317	0.31168151	6.16376551	7.10E-10	2.44E-07	hil-3

F44E2.10	6.21366462	-1.8427425	0.560391	3.28831557	0.00100789	0.03752634	F44E2.10
K08E5.2	10.0644874	-1.8359864	0.50786962	3.61507429	0.00030026	0.01574654	nac-3
F08C6.7	19.2132654	-1.8302918	0.33971451	5.38773523	7.14E-08	1.69E-05	unc-98
T10B10.4	78.8627584	-1.8061174	0.22284895	8.10467085	5.29E-16	4.04E-13	T10B10.4
C13C4.4	6.77314	-1.7916252	0.5638847	3.17729	0.00148658	0.05055851	C13C4.4
F07C6.4	75.8379683	-1.7900074	0.28719129	6.23280547	4.58E-10	1.66E-07	F07C6.4
F42G4.3	27.3709441	-1.7898437	0.45143419	3.96479438	7.35E-05	0.00567039	zyx-1
F37A8.5	76.2385642	-1.7883321	0.42707635	4.18738266	2.82E-05	0.00261979	F37A8.5
W02D9.10	231.826969	-1.7807756	0.17414601	10.2257617	1.52E-24	2.61E-21	W02D9.10
W02B8.1	11.1459889	-1.7393745	0.45727691	3.8037663	0.00014251	0.0090299	W02B8.1
F33C8.3	13.392557	-1.7311253	0.44211294	3.91557249	9.02E-05	0.00638768	tsp-8
R12H7.1	11.3029177	-1.7286201	0.4599535	3.75824979	0.00017111	0.01022173	unc-9
F46H6.1	12.1698361	-1.7256188	0.40488584	4.26198844	2.03E-05	0.00196052	rhi-1
F01G12.5	21.3031616	-1.7233596	0.50033445	3.44441525	0.0005723	0.02520304	let-2
K05G3.3	8.77310247	-1.7034448	0.51339676	3.31798908	0.00090668	0.03579824	cah-3
F45E1.7	12.5462391	-1.7012888	0.45570649	3.73329956	0.00018899	0.01100292	sdpn-1
Y54E5B.1	22.918993	-1.7000122	0.37867361	4.48938655	7.14E-06	0.00096218	smp-1
C48A7.1	20.4225952	-1.6974015	0.4800832	3.53564022	0.00040679	0.01982011	egl-19
F26F4.5	69.362556	-1.6942338	0.5324367	3.182038	0.00146243	0.05023438	F26F4.5
C33B4.3	20.1540679	-1.6777202	0.44775727	3.74694131	0.000179	0.01060135	shn-1
T12A7.2	14.9463862	-1.6744993	0.4188446	3.99790112	6.39E-05	0.00504642	T12A7.2
T22C1.7	16.0317699	-1.6701133	0.51854941	3.22074088	0.0012786	0.04527815	jph-1
Y43F8B.2	131.674773	-1.6661172	0.29707585	5.60838977	2.04E-08	5.40E-06	Y43F8B.2
T06C10.4	14.9329536	-1.6581618	0.39525078	4.19521434	2.73E-05	0.00256556	fip-10
F25H8.3	68.0917646	-1.6452291	0.36980542	4.44890461	8.63E-06	0.00109479	gon-1
F42G8.11	7.494057	-1.570831	0.5154163	3.047694	0.00230605	0.06950667	sph-1
Y15E3A.5	34.3150071	-1.5555013	0.34113445	4.55978952	5.12E-06	0.00078173	Y15E3A.5
T11F9.11	14.0183837	-1.5408766	0.4653	3.31157652	0.00092772	0.03632138	dhs-19
F53G12.5	64.3063346	-1.5375681	0.35278471	4.35837509	1.31E-05	0.00155205	mex-3
C26E6.2	32.989894	-1.5174407	0.32067506	4.73201965	2.22E-06	0.00040189	flh-2
C01F6.6	14.903184	-1.5082342	0.39397825	3.82821694	0.00012907	0.00844519	nrf1-1
C18H9.7	28.8862293	-1.5069442	0.26982069	5.58498414	2.34E-08	5.95E-06	rpy-1
Y71H10B.1	82.2056788	-1.493053	0.33418276	4.46777383	7.90E-06	0.00104421	Y71H10B.1
T23G4.1	29.8797578	-1.4787024	0.36961652	4.00063937	6.32E-05	0.00504638	tlp-1
C01C10.3	40.80348	-1.4708649	0.33590336	4.37883361	1.19E-05	0.00143807	acl-12
B0034.3	22.668541	-1.4276013	0.4612311	3.095198	0.00196682	0.06253367	casy-1
F54G8.3	21.5379352	-1.4261671	0.36790784	3.87642493	0.000106	0.00735593	ina-1
F14B4.2	47.1906766	-1.4198141	0.30492629	4.65625356	3.22E-06	0.00053957	hxk-1
B0464.4	22.3489578	-1.4176703	0.31762951	4.46328285	8.07E-06	0.00104623	bre-3
C02B10.5	76.6244438	-1.4051987	0.28046548	5.0102375	5.44E-07	0.00010985	C02B10.5
F52D2.6	51.6522398	-1.4013905	0.27038398	5.18296421	2.18E-07	4.55E-05	F52D2.6
Y22F5A.3	29.0937367	-1.3968047	0.30195512	4.62586854	3.73E-06	0.00059598	ric-4
T19H5.4	24.186515	-1.3666714	0.4702452	2.906296	0.00365736	0.09663866	T19H5.4
T07A9.7	69.768756	-1.3417783	0.19979611	6.71573806	1.87E-11	8.57E-09	gpa-4
ZK617.1	11.843322	-1.3393497	0.4396667	3.046284	0.00231689	0.06950667	unc-22
C12C8.1	21.208646	-1.3382157	0.4553537	2.938849	0.00329434	0.09016769	hsp-70
T13B5.1	173.407423	-1.3133264	0.20830019	6.30496985	2.88E-10	1.10E-07	snf-3
Y47D3A.17	19.7880015	-1.3096509	0.37304252	3.51072823	0.00044688	0.02098518	obr-1
W03G9.1	36.648037	-1.2985345	0.34454586	3.76882919	0.00016402	0.01004749	snf-1
R02E12.2	51.607165	-1.2969935	0.4192553	3.093565	0.00197767	0.06253367	mop-25.1

H24G06.1	55.8792185	-1.2849119	0.37585582	3.4186299	0.00062937	0.02702369	H24G06.1
C33A11.1	57.3803494	-1.2795917	0.29830158	4.28959085	1.79E-05	0.00186325	nfki-1
T05H10.4	26.231066	-1.2763515	0.32124182	3.97317983	7.09E-05	0.00553655	T05H10.4
Y41C4A.13	57.5326835	-1.2749685	0.21247159	6.00065415	1.97E-09	6.14E-07	sup-1
C17C3.1	23.7159656	-1.2745038	0.3490298	3.6515615	0.00026065	0.01409976	C17C3.1
T06E6.2	289.64723	-1.2610586	0.4138514	3.047129	0.00231038	0.06950667	cyb-3
ZK637.1	42.2349534	-1.2308499	0.35530066	3.46424897	0.00053171	0.02371997	svop-1
R03E9.3	38.925582	-1.2307769	0.27917095	4.40868529	1.04E-05	0.00127586	abts-4
C45G3.1	25.8782562	-1.2208324	0.28278052	4.31724349	1.58E-05	0.00168689	aspm-1
ZK524.2	50.937348	-1.204126	0.36210148	3.32538269	0.00088297	0.03520891	unc-13
W09D6.5	86.3311025	-1.1838784	0.19695918	6.01078054	1.85E-09	6.04E-07	W09D6.5
F57F5.5	56.7328472	-1.181782	0.30123409	3.92313493	8.74E-05	0.00637325	pkc-1
B0365.3	121.591287	-1.1720173	0.35497551	3.30168489	0.00096106	0.03725751	eat-6
T14F9.4	49.0579525	-1.1714267	0.2999811	3.90500178	9.42E-05	0.00660534	peb-1
K08H10.2	289.368135	-1.1708231	0.26950927	4.34427785	1.40E-05	0.00157373	K08H10.2
C06G3.2	30.9144771	-1.1642116	0.3072336	3.78933664	0.00015105	0.00934878	klp-18
Y47D3A.6	19.1540876	-1.155003	0.34523977	3.34550953	0.00082132	0.03360502	tra-1
C53C11.5	14.167833	-1.1482234	0.395382	2.904086	0.00368327	0.0969397	C53C11.5
Y56A3A.29	38.7753507	-1.1387706	0.3287043	3.46442265	0.00053137	0.02371997	ung-1
F47F6.1	234.291006	-1.1276089	0.35214588	3.20210747	0.00136426	0.04734043	lin-42
Y47D9A.2	34.982855	-1.09523	0.3743581	2.925621	0.00343769	0.09334756	scpl-3
T27F2.2	21.502562	-1.0913504	0.3736086	2.921106	0.00348791	0.09399201	sipa-1
C07A9.12	13.112497	-1.0893231	0.3592731	3.03202	0.00242923	0.07224606	C07A9.12
T20D4.6	36.1342034	-1.0745024	0.25581677	4.20028136	2.67E-05	0.00254365	arrd-22
W06F12.1	101.632259	-1.0576398	0.23369696	4.52568926	6.02E-06	0.0008616	lit-1
AC7.2	25.5425187	-1.0370702	0.2924635	3.5459818	0.00039115	0.01933254	soc-2
F55F1.1	76.5125781	-1.0370287	0.19733068	5.25528356	1.48E-07	3.17E-05	F55F1.1
Y105C5B.21	36.63704	-1.0324217	0.3565687	2.895435	0.00378633	0.09815882	jac-1
Y53G8AM.8	22.655643	-1.0292847	0.3288706	3.129756	0.00174951	0.05723411	Y53G8AM.8
F08B6.4	32.644672	-1.0254591	0.30736653	3.33627433	0.00084909	0.0341127	unc-87
C14B4.2	122.379923	-1.0214436	0.25068799	4.07456136	4.61E-05	0.00391006	C14B4.2
F42G9.9	19.352785	-1.019695	0.3294334	3.0953	0.00196614	0.06253367	ptl-1
F08F1.8	22.177381	-1.0171508	0.3298314	3.083851	0.0020434	0.06405978	tth-1
ZK381.5	54.3891759	-1.0079839	0.21728418	4.63901181	3.50E-06	0.00057263	prkl-1
B0336.1	45.914659	-0.9816407	0.3362004	2.919808	0.00350247	0.09399201	wrm-1
C43E11.6	45.4056406	-0.9423236	0.28600161	3.29481911	0.00098485	0.03752634	nab-1
W04D2.1	56.4428428	-0.9397792	0.21608755	4.34906696	1.37E-05	0.00156542	atn-1
C10E2.6	78.0954021	-0.93889	0.26687946	3.51803017	0.00043476	0.02074182	mct-6
C35D10.13	223.161433	-0.9193072	0.26484215	3.47115147	0.00051823	0.02357782	C35D10.13
K04H4.1	172.087543	-0.914601	0.25215287	3.62716873	0.00028655	0.01514286	emb-9
F52G3.1	79.9325294	-0.9035247	0.26561538	3.40162795	0.00066986	0.02840693	F52G3.1
ZK177.6	97.5760965	-0.9023406	0.20013999	4.50854716	6.53E-06	0.00089685	fzy-1
Y49E10.6	879.392385	-0.9012024	0.24202955	3.72352235	0.00019646	0.01106309	his-72
ZK1151.1	213.511523	-0.8990057	0.3101886	2.898256	0.00375245	0.09764889	vab-10
Y113G7B.23	422.381722	-0.8882372	0.2805206	3.166389	0.00154344	0.05197767	swns-1
F43G9.9	21.338275	-0.883303	0.2957611	2.986542	0.00282152	0.08043099	cpn-1
F54B11.3	72.3270871	-0.8675679	0.22002523	3.94303817	8.05E-05	0.00614146	unc-84
Y59H11AR.2	104.367155	-0.8546834	0.24826824	3.44258036	0.00057619	0.02521302	catp-7
Y69A2AR.7	39.515101	-0.849774	0.25884596	3.2829332	0.00102733	0.03774202	epg-9
F26B1.3	328.541295	-0.8389909	0.2449029	3.42581052	0.00061297	0.02658099	ima-2

F36D4.3	121.253849	-0.8377846	0.23025789	3.63846226	0.00027427	0.01472063	hum-2
F55G1.4	44.1313926	-0.8357662	0.24486556	3.41316344	0.00064213	0.02740038	rod-1
F23B12.8	27.600287	-0.8280302	0.2677484	3.092568	0.00198433	0.06253367	bmk-1
T05G5.3	276.949613	-0.8123365	0.18823952	4.31544096	1.59E-05	0.00168689	cdk-1
ZK484.4	56.7676944	-0.8005727	0.24351448	3.28757724	0.00101053	0.03752634	ZK484.4
C04C11.2	55.1867623	-0.7839628	0.20514353	3.82153317	0.00013262	0.00851524	arrd-25
F32A7.5	104.836748	-0.7447384	0.20094506	3.70617935	0.00021041	0.01175213	maph-1.1
Y69A2AR.30	328.04706	-0.742828	0.19888859	3.73489477	0.00018779	0.01100292	mdf-2
C26C6.5	79.8945488	-0.7325429	0.20456325	3.58100904	0.00034227	0.01741773	dcp-66
F28C1.3	45.2670596	-0.7281156	0.22618113	3.21917032	0.00128562	0.04529342	F28C1.3
T09B9.4	50.8616853	-0.7170812	0.22199847	3.23011756	0.00123739	0.04427548	T09B9.4
ZC168.4	67.219783	-0.7161476	0.2427856	2.949712	0.00318071	0.08740584	cyb-1
R04A9.2	49.5885729	-0.7154935	0.20641934	3.4662134	0.00052784	0.02371997	nrde-3
C34F11.3	51.6688035	-0.7136762	0.21156448	3.373327	0.00074266	0.03129116	ampd-1
D2023.2	110.557242	-0.7043079	0.16978086	4.1483352	3.35E-05	0.00298802	pyc-1
F20D12.5	147.844297	-0.6614121	0.208454	3.172941	0.00150903	0.05106922	exc-9
C27C12.2	53.358324	-0.6432961	0.2050648	3.137039	0.00170663	0.05664048	egrh-1
B0379.4	113.443821	-0.6412742	0.19499571	3.28865768	0.00100666	0.03752634	scpl-1
T22F3.3	95.1072598	-0.6361966	0.17064347	3.72822116	0.00019284	0.01103987	pygl-1
F33G12.6	49.705523	-0.6355775	0.2051498	3.098114	0.00194757	0.06252238	F33G12.6
Y67D8C.10	133.64517	-0.5802355	0.16460114	3.52509984	0.00042332	0.02033728	mca-3
Y104H12BR.1	118.31027	-0.5789008	0.1741458	3.32423046	0.00088663	0.03520891	plst-1
F32D1.10	567.140468	-0.5477174	0.16680072	3.28366336	0.00102467	0.03774202	mcm-7
C09B8.6	111.136355	-0.539317	0.15010844	3.59284941	0.00032708	0.01702311	hsp-25
F09C8.2	128.706889	-0.5064155	0.15854173	3.19420918	0.00140214	0.0484057	F09C8.2
H06O01.1	353.54509	0.3345586	0.1152489	-2.902923	0.00369697	0.0969397	pdi-3
E04A4.5	332.97673	0.3721427	0.1283115	-2.900306	0.00372798	0.09738108	timm-17B.1
Y54E2A.11	261.127657	0.40159095	0.10672878	-3.7627241	0.00016807	0.01012859	eif-3.B
C30C11.4	612.850295	0.4374191	0.1410602	-3.100938	0.00192908	0.06221977	hsp-110
C15H9.6	522.148047	0.4648205	0.1520833	-3.056354	0.00224047	0.06840894	hsp-3
F15C11.2	123.306095	0.52678942	0.16289909	-3.233839	0.00122138	0.04397991	ubql-1
F53E10.6	64.851635	0.5352744	0.1784134	-3.000193	0.00269809	0.07803344	F53E10.6
C08F8.1	57.347649	0.5571294	0.1915618	-2.908354	0.00363337	0.09637554	pfd-1
Y57G11C.15	615.380944	0.55748832	0.174102	-3.2020788	0.0013644	0.04734043	sec-61
F32D8.6	155.961671	0.59641036	0.17688563	-3.3717288	0.00074698	0.03129116	emo-1
F22B5.10	45.47339	0.6026689	0.200371	-3.007766	0.00263176	0.07661097	F22B5.10
F15D4.3	138.472852	0.6049805	0.1974035	-3.06469	0.00217896	0.06706558	romo-1
Y82E9BR.3	1184.61847	0.6206881	0.16477274	-3.7669343	0.00016526	0.01004749	Y82E9BR.3
T05E11.5	137.615195	0.62932279	0.13729553	-4.5837093	4.57E-06	0.00071323	imp-2
F46H5.2	92.783169	0.6294835	0.2114079	-2.977578	0.00290535	0.08180238	F46H5.2
M117.2	1072.4932	0.64478735	0.16833944	-3.8302809	0.000128	0.00844519	par-5
Y38C1AA.4	86.1533312	0.66617637	0.18060889	-3.6885026	0.00022558	0.01239775	tcl-2
F25H2.10	787.551724	0.6854658	0.2339459	-2.930019	0.00338941	0.09240184	rla-0
F01F1.8	1122.23847	0.6880134	0.2236028	-3.076945	0.00209134	0.06501137	cct-6
Y22D7AL.5	1003.66427	0.7059176	0.2368409	-2.980556	0.00287726	0.08134467	hsp-60
T18H9.7	35.14044	0.7167174	0.2280709	-3.14252	0.001675	0.05586057	tag-232
Y48B6A.14	891.905536	0.7178651	0.2291007	-3.133404	0.00172791	0.05679789	hmg-1.1
T04G9.5	214.171898	0.72336038	0.13470518	-5.3699522	7.88E-08	1.80E-05	trap-2
C36E8.3	40.9462701	0.72422026	0.22443818	-3.226814	0.00125177	0.04455775	pxd-1
Y54E10A.16	107.088777	0.73173143	0.18997868	-3.8516503	0.00011732	0.00782543	mab-31

F37C12.13	72.1164343	0.73275845	0.21945071	-3.3390571	0.00084063	0.03397145	exos-9
C29F9.7	75.0175792	0.75354503	0.19143894	-3.9362161	8.28E-05	0.00615408	pat-4
ZC190.4	216.929465	0.78472061	0.18396304	-4.2656429	1.99E-05	0.00195626	ZC190.4
F29C12.3	30.3107875	0.80194063	0.24644915	-3.2539801	0.001138	0.04136548	rict-1
F47B7.1	1051.28895	0.80564111	0.1778382	-4.5301916	5.89E-06	0.00086138	F47B7.1
R53.7	39.8465429	0.80979406	0.24612746	-3.2901411	0.00100137	0.03752634	aakg-5
C01G6.1	1019.26807	0.81166624	0.2004927	-4.048358	5.16E-05	0.00427249	aqp-2
T24H7.1	891.665078	0.8121701	0.2660965	-3.052164	0.00227198	0.0690641	phb-2
T08B2.10	885.248143	0.8195439	0.2710568	-3.023513	0.00249858	0.0739882	rps-17
F31E3.2	157.13697	0.83650502	0.23508971	-3.5582375	0.00037335	0.01872208	F31E3.2
K08C7.3	213.035409	0.84964394	0.21593739	-3.9346773	8.33E-05	0.00615408	epi-1
B0035.4	32.116959	0.8677055	0.2750063	-3.155221	0.00160377	0.05374569	pfd-4
T03F7.1	48.2000073	0.87290811	0.22264291	-3.9206642	8.83E-05	0.00637325	snf-11
C54E4.2	66.3144792	0.89144973	0.2454862	-3.6313639	0.00028193	0.01501427	test-1
C50F4.13	345.092877	0.9065933	0.3066341	-2.956597	0.00311055	0.08651603	his-35
T07H6.2	22.2073095	0.95987477	0.29685099	-3.2335239	0.00122273	0.04397991	mom-1
T01C3.6	1621.34819	1.0369024	0.3554531	-2.917129	0.0035327	0.09443442	rps-16
Y38A10A.5	339.158508	1.04043675	0.26551121	-3.918617	8.91E-05	0.00637325	crt-1
R13F6.4	127.442829	1.06426169	0.23595708	-4.5104038	6.47E-06	0.00089685	ten-1
D1054.8	32.4693758	1.14113837	0.26214888	-4.3530164	1.34E-05	0.00156353	D1054.8
T01A4.3	27.505256	1.1620759	0.3874103	-2.9996	0.00270334	0.07803344	T01A4.3
F22F4.2	52.1975498	1.16637195	0.21603663	-5.3989546	6.70E-08	1.64E-05	inx-3
T01G9.3	22.6406325	1.18953561	0.34231777	-3.4749456	0.00051096	0.02340183	dma-1
T28F4.1	144.292672	1.3032711	0.16678337	-7.8141548	5.53E-15	3.80E-12	T28F4.1
C09D8.1	153.020119	1.66427405	0.1827058	-9.1090378	8.31E-20	8.16E-17	ptp-3
F38B6.6	2.789607	2.8937525	0.9578417	-3.021118	0.00251844	0.07401821	F38B6.6
F59B2.6	67.0238931	3.86820996	0.40968808	-9.4418416	3.66E-21	5.03E-18	zif-1