

Supplementary Tables

	HPL-2 ChIP-seq (23530)															
HPL-2 hypodermis	# Number of query intervals: 23530 # Number of db intervals: 1572 # Number of overlaps: 1226 # Number of possible intervals (estimated): 65530 # phyper(1226 - 1. 23530. 65530 - 23530. 1572. lower.tail=F) # Contingency Table Of Counts # <table><tr><td>#</td><td></td><td>in -b</td><td>not in -b</td><td></td></tr><tr><td>#</td><td>in -a</td><td>1226</td><td>22304</td><td></td></tr><tr><td>#</td><td>not in -a</td><td>346</td><td>41654</td><td></td></tr></table> # p-values for Fisher's exact test left right two-tail ratio 1 4.0067e-261 4.6837e-261 6.617	#		in -b	not in -b		#	in -a	1226	22304		#	not in -a	346	41654	
#		in -b	not in -b													
#	in -a	1226	22304													
#	not in -a	346	41654													
HPL-2 intestine	# Number of query intervals: 23530 # Number of db intervals: 1665 # Number of overlaps: 1409 # Number of possible intervals (estimated): 81142 # phyper(1409 - 1. 23530. 81142 - 23530. 1665. lower.tail=F) # Contingency Table Of Counts # <table><tr><td>#</td><td></td><td>in -b</td><td>not in -b</td><td></td></tr><tr><td>#</td><td>in -a</td><td>1409</td><td>22121</td><td></td></tr><tr><td>#</td><td>not in -a</td><td>256</td><td>57356</td><td></td></tr></table> # p-values for Fisher's exact test left right two-tail ratio 1 0 0 14.271	#		in -b	not in -b		#	in -a	1409	22121		#	not in -a	256	57356	
#		in -b	not in -b													
#	in -a	1409	22121													
#	not in -a	256	57356													
HPL-1 intestine	# Number of query intervals: 23530 # Number of db intervals: 1346 # Number of overlaps: 512 # Number of possible intervals (estimated): 88730 # phyper(512 - 1. 23530. 88730 - 23530. 1346. lower.tail=F) # Contingency Table Of Counts # <table><tr><td>#</td><td></td><td>in -b</td><td>not in -b</td><td></td></tr><tr><td>#</td><td>in -a</td><td>512</td><td>23018</td><td></td></tr><tr><td>#</td><td>not in -a</td><td>834</td><td>64366</td><td></td></tr></table> # p-values for Fisher's exact test left right two-tail ratio 1 9.3088e-21 1.4496e-20 1.717	#		in -b	not in -b		#	in -a	512	23018		#	not in -a	834	64366	
#		in -b	not in -b													
#	in -a	512	23018													
#	not in -a	834	64366													

Table S1. Number of intersections with HPL-2 ChIP-seq genomic regions and Fisher's exact test p-values.

	Hypodermal well-expressed genes (2264)	Intestinal well-expressed genes (5890)	HPL-2 hypodermis (846)	HPL-2 intestine (922)	HPL-1 intestine (739)
HPL-2 hypodermis (846)	Representation factor: 0.7 $p < 0.001$	-	-	Representation factor: 7.0 $p < 2.607\text{e-}163$	Representation factor: 6.0 $p < 4.590\text{e-}94$
HPL-2 intestine (922)	-	Representation factor: 1.0 $p < 0.383$	Representation factor: 7.0 $p < 2.607\text{e-}163$	-	Representation factor: 5.9 $p < 1.369\text{e-}100$
HPL-1 intestine (739)	-	Representation factor: 0.7 $p < 6.862\text{e-}07$	Representation factor: 6.0 $p < 4.590\text{e-}94$	Representation factor: 5.9 $p < 1.369\text{e-}100$	-

Table S2. Hypergeometric statistical test between gene sets depicted in the table.

Samples (significant peaks)	Number of intersections with BLMP-1 peaks (5898)	Fisher's exact test p-values
HPL-1 intestine (1346)	169	two-tail ratio 1.8565e-09 1.701
Samples (significant peaks)	Number of intersections with L4 BLMP-1 peaks (549)	Fisher's exact test p-values
HPL-1 intestine (1346)	26	two-tail ratio 0.013515 1.701
HPL-2 intestine (1665)	34	two-tail ratio 0.0041704 1.726
HPL-2 hypodermis (1572)	14	two-tail ratio 0.097535 0.630

Table S3. Number of overlapped peaks between HP1 and BLMP-1 ChIP-seq data and Fisher's exact test p-value.

Samples (significant peaks)	Number of true intersections	p-values
HPL-2 hypodermis (1572)	1415	3.192e-26
HPL-2 intestine (1665)	945	0.002534
HPL-1 intestine (1346)	512	4.887e-06

Table S4. Number of overlapped regions and p-values from Monte Carlo Simulation between HP1 significant peaks and repetitive element coordinates annotation from UCSC based on repeat masker (cell).

Family	Type	HPL-2 hyp	HPL-2 int	HPL-1 int	Overlapping between HPL-2 hypodermis and intestine	Overlapping between HPL-1 and HPL-2 intestine	Total repetitive elements in the genome
CELE14B	DNA	282	193	94	71	94	2451

CELE42	DNA	152	112	32	83	32	963
CELE14A	DNA	92	58	26	9	26	624
PALTA5 CE	DNA	61	32	16	2	16	1434
GA-rich	Low complexity	48	28	23	9	23	1433
A-rich	Low complexity	46	26	20	-	20	4877
TIR9TA1B CE	DNA	40	48	24	11	24	585
TIR9TA1 CE	DNA	36	40	19	5	19	364
HelitronY1A CE	RC	27	17	10	-	10	1468
CELE1	DNA	75	18	-	-	7	1709
CeRep5	Unknown	44	12	-	-	3	1324
Helitron2 CE	Rolling Circle (RC)	32	14	-	-	8	624
MINISAT1 CE	Satellite	30	26	-	-	6	3455
CELE45	SINE	24	42	-	-	8	463
LR9A	Unknown	17	11	-	-	-	2150
CERP3	Unknown	17	15	-	-	-	2915
PALTTAA1 CE	DNA	17	11	-	-	4	1272
CeRep52	Satellite	15	12	-	12	-	185
HelitronY4 CE	Rolling Circle (RC)	14	21		15	-	780
CELE46B	DNA	13	13	-	-	-	1136
HelitronY1 CE	Rolling Circle (RC)	13	10	10	-	-	802
CER12-I CE	LTR	12	12	-	-	-	15
PALTTAA3 CE	DNA	10	12	-	-	-	1490
NeSL-1	LINE	10	13	-	-	-	40
CER8-I CE	LTR	-	14	13	-	13	23
CELE2	DNA	38	-	11	-	-	3158
RTE1	LINE	-	18	-	-	-	98
CER9-I CE	LTR	-	18	-	-	-	78
Vingi-2 CE	LINE	-	11	-	-	-	23
HATN1 CE	DNA	-	10	-	-	-	48
HAT1 CE	DNA	25	-	-	-	-	1659
CELE4	DNA	23	-	-	-	-	831
RC123	Satellite	21	-	-	-	-	700
PALTTAA2 CE	DNA	20	-	-	-	-	1224
CeRep3	Unknown	18	-	-	-	-	453
PAL5A CE	DNA	13	-	-	-	-	363
NPAL5A CE	DNA	13	-	-	-	-	152
NPALTA1 CE	DNA	13	-	-	-	-	258
CELE46A	DNA	10	-	-	-	-	2102

Table S5. Most frequent repetitive element families overlapped with HP1. Only repetitive elements with equal or more than 10 repetitions were considered in each individual dataset for the analysis, simple repeats were excluded.

STRAIN	DESCRIPTION	GENOTYPE	REFERENCE
BN548	FLP-Frt strain carrying <i>Pdpy-7::FLP</i> transgene on chr IV.	bqSi548[pBN266(unc-119(+) <i>Pdpy-7::FLP</i>) IV; unc-119(ed3) III	(Muñoz-Jimenez 2019)

BN577	Visual marker in pharynx - <i>Pmyo-2::GFP</i> transgene on chr IV.	bqSi577[pBN306(unc-119(+) <i>Pmyo-2::GFP</i>)] IV; may carry unc-119(ed3) III	(Muñoz-Jiménez et al. 2017)
EG4322	Strain used for MosScl into chromosome II.	ttTi5605 II; unc-119(ed9) III.	CGC
BN1010	Strain for visualization of mKate2::HPL-1	mel-28(bq17[G>F>P::mel-28]) III; hpl-1(ot841[mKate2::hpl-1]) X.	Made by crossing BN902 and OH14021
BN1011	Strain for visualization of mKate2::HPL-2	mel-28(bq17[G>F>P::mel-28]) hpl-1(ot860[mKate2::hpl-2]) III.	Made by crossing BN902 and OH14220
BN1103	Strain for tissue-specific HPL-1 DamID.	bqSi1103[pBN494(unc-119(+) <i>Phsp16.41>mCh::his-58>dam::hpl-1</i>)] II. May carry unc-119(ed9) III.	Made by injection of EG4322 and pBN494 plasmid.
BN1105	Strain for tissue-specific HPL-1 DamID co-expressing GFP in pharynx.	bqSi1103[pBN494(unc-119(+) <i>Phsp16.41>mCh::his-58>dam::hpl-1</i>)] II; bqSi577[pBN306(unc-119(+) <i>Pmyo-2::GFP</i>)] IV. May carry unc-119(ed9) III.	Made by crossing BN1103 and BN577
BN1051	Strain for control DamID in intestine.	bqSi447[pBN181(unc-119(+) <i>hsp16.41p>mCh::his-58>gfp::dam</i>)] II; bqSi997[pBN472(unc-119(+) <i>nhx-2p::FLP::SL2::mNG</i>)] IV; may carry unc-119(ed3) or unc-119(ed9) III.	Made by crossing BN448 and BN998.
BN561	Strain for control DamID in hypodermis.	bqSi447[pBN181(unc-119(+) <i>Phsp16.41::FRT::mCh::his-58::FRT::gfp::dam</i>)] II; bqSi548[pBN266(unc-119(+) <i>Pdpy-7::FLP_D5</i>)] IV. May carry unc-119(ed9) III.	Made by crossing BN550 and BN448.
BN550	Strain for control DamID in hypodermis.	FLP-Frt strain carrying <i>Phsp16.41_FRT_mCh_his-58_FRT_gfp_his-58</i> on chr II and <i>Pdpy-7::FLP-D5</i> on chr IV.	(Muñoz-Jimenez 2019)
BN448	Control strain for tissue-specific DamID	bqSi447[pBN181(unc-119(+).P <i>hsp16.41::FrT::mch::his-58::FrT::gfp::dam</i>)] II;	(Muñoz-Jimenez 2019)
BN1104	Strain for tissue-specific HPL-2 DamID.	bqSi1104[pBN495(unc-119(+) <i>hsp16.41p>mCh::his-58>dam::hpl-2</i>)] II. May carry unc-119(ed9) III.	Made by injection of EG4322 with pBN495 plasmid
BN1106	Strain for tissue-specific HPL-2 DamID co-expressing GFP in pharynx.	bqSi1104[pBN495(unc-119(+) <i>hsp16.41p>mCh::his-58>dam::hpl-2</i>)] II; bqSi577[pBN306(unc-119(+) <i>myo-2p::GFP</i>)] IV. May carry unc-119(ed9) III.	Made by crossing BN1104 and BN577.

MRS578/B N1108	Strain for tissue-specific HPL-2 DamID in the hypodermis.	bqSi1104[hsp16.41p>mCh::his-58>dam::hpl-2] II; bqSi548[dpy-7p::FLP] IV	Made by crossing BN1104 and BN548.
BN998	FLP-Frt strain carrying <i>Pnhx-2</i> controlling expression of FLP D5::SL2::mNG transgene on chr IV and visible marker on chr II (Plmn-1::mCh::his-58).	bqSi189[pBN13(unc-119(+) lmn-1p::mCherry::his-58)] II; bqSi997[pBN472(unc-119(+) nhx-2p::FLP D5::SL2::mNG)] IV. May carry unc-119(ed3) or unc-119(ed9) III.	(Cabianca et al. 2019)
MRS579/B N1109	Strain for tissue-specific HPL-1 DamID in the intestine.	bqSi1104[pBN494(unc-119(+) <i>Phsp16.41</i> >mCh::his-58>dam::hpl-1)] II; bqSi997[pBN472(unc-119(+) <i>Pnhx-2</i> ::FLP::SL2::mNG)] IV. May carry unc-119(ed9) III.	Made by crossing BN1103 and BN998.
MRS580/B N1110	Strain for tissue-specific HPL-2 DamID in the intestine.	bqSi1103[pBN495(unc-119(+) <i>Phsp16.41</i> >mCh::his-58>dam::hpl-2)] II; bqSi997[pBN472(unc-119(+) nhx-2p::FLP::SL2::mNG)] IV. May carry <i>unc-119(ed9)</i> III.	Made by crossing BN1104 and BN998.
GM119	<i>E.coli</i> dam-3 dcm-6 knockout strain	(Arraj and Marinus 1983)	

Table S6. List of *C. elegans* and bacterial strains used.

Plasmid name	Description	Reference
pBN494	<i>Phsp-16.41</i> ::FRT::mCh::his-58::FRT::hpl-1::Dam Chr II	This publication
pBN495	<i>Phsp-16.41</i> ::FRT::mCh::his-58::FRT::hpl-2::Dam Chr II	This publication

Table S7. List of plasmids used.

Sample	Raw reads	Cut reads	Mapped reads	GATC reads (% from Raw reads)
GFP::Dam hyp (BN561) I	15,773,728	6,542,411	2,872,416	2,862,349 (18,15%)
GFP::Dam hyp (BN561) II	9,247,899	3,599,466	1,304,548	1,286,460 (13,91%)
GFP::Dam int (BN1051) I	18,066,270	7,418,519	3,660,999	3,655,161 (20,23%)
GFP::Dam int (BN1051) II	4,573,067	2,080,559	1,338,144	1,336,648 (29,23%)
Dam::hpl-2 hyp (MRS578) I	14,194,267	6,551,959	4,162,172	4,154,179 (29,27%)
Dam::hpl-2 hyp (MRS578) II	8,507,806	3,473,687	1,594,499	1,562,681 (18,37%)
Dam::hpl-1 int (MRS579) I	20,901,460	9,376,852	1,560,420	1,541,018 (39,23%)
Dam::hpl-1 int (MRS579) II	8,061,225	3,861,200	696,028	694,399 (8,61%)
Dam::hpl-2 int (MRS580) I	18,337,259	8,265,167	4,253,333	4,232,349 (23,08%)
Dam::hpl-2 int (MRS580) II	1,583,607	747,426	527,174	526,083 (33,22%)

Table S8. Quality controls metrics of sequencing libraries from DamID-seq data. Abbreviations hyp: hypodermis; int:intestine

Sample name	Dataset (GEO/ modENCODE)	Strain	Larval stage	Antibody	Temperature (°C)
ChIP dataset					
HPL-2 ChIP-seq	GSE49749/modENCODE_5976	N2	L3	HPL-2 SDQ2340	20
Histones datasets					
H3K9me1	GSE25353	N2	L3 (mixed Male and Hermaphrodite population)	AB9045	20
H3K9me2	GSE49728	N2	L3 (mixed Male and Hermaphrodite population)	HK00008	20
H3K9me3	GSE49719	N2	L3 (mixed Male and Hermaphrodite population)	AB8898	20
H3K27me3	GSE49724	N2	L3 (mixed Male and Hermaphrodite population)	UP07449	20
BLMP-1	GSE25803/modENCODE 2612	OP109	L1	GFP::3xFlag	20

Table S9. Description and references of Dataset used for comparison.