

Fig. S1. Establishing seam cell and hypodermis-specific promoters for RNAPol TaDa.

(A) Representative image of *srf-3* smFISH at the L2 stage, during the asymmetric seam cell division, showing high levels of transcript in seam cells. Seam cell nuclei are marked by the *SCMP::GFP* reporter and *srf-3* mRNAs appear as black spots. **(B)** Illustration of the *srf-3* locus on chromosome IV. Pink blocks signify exon sequences and grey indicate 3' UTRs. Two isoforms of *srf-3* (isoform a and b) are shown. Shaded areas near the 5' mark putative promoter or regulatory sequences tested for seam cell specific expression. With grey, the 1093 bp putative promoter sequence of isoform a (*srf-3ap*), extending from the end of the upstream gene *txt-19* 3'UTR to the *srf-3* isoform a start codon. With peach, the 2246 bp sequence starting at the same position and extending to the start codon of isoform b (*srf-3bp*) and with teal, the 1081 bp first intron of isoform a (*srf-3i1*). **(C)** Representative fluorescence images of late L4 transgenic animals carrying single-copy transgenes of transcriptional reporters driving expression of *GFP-H2B* under the *srf-3ap* promoter (grey frame), the *srf-3bp* promoter (peach frame) and the *srf-3i1::pes-10* promoter (teal frame). White arrowheads show expression in seam cell nuclei, green in intestinal and red in hypodermal. Yellow outlined areas indicate further expression in the germline. **(D-E)** Representative fluorescence images showing expression of *mCherry-H2B* under the promoter of *dpy-7* from a single-copy transgene (D) and *dpy-7syn1::mCherry-H2B* from a multi-copy transgene (E) at the L3 asymmetric cell division stage. Seam cells are marked in cyan by membrane (*arf-3::pes10::GFP-CAAX*) and nuclear (*SCMP::GFP*) reporters. Note expression of *dpy-7p::mCherry-H2B* in seam cell nuclei, indicated by white arrowheads, which is more prominent during divisions and is abolished in *dpy-7syn1::mCherry-H2B* transgenics. Scale bars are 100 µm in C and 10 µm in D and E.

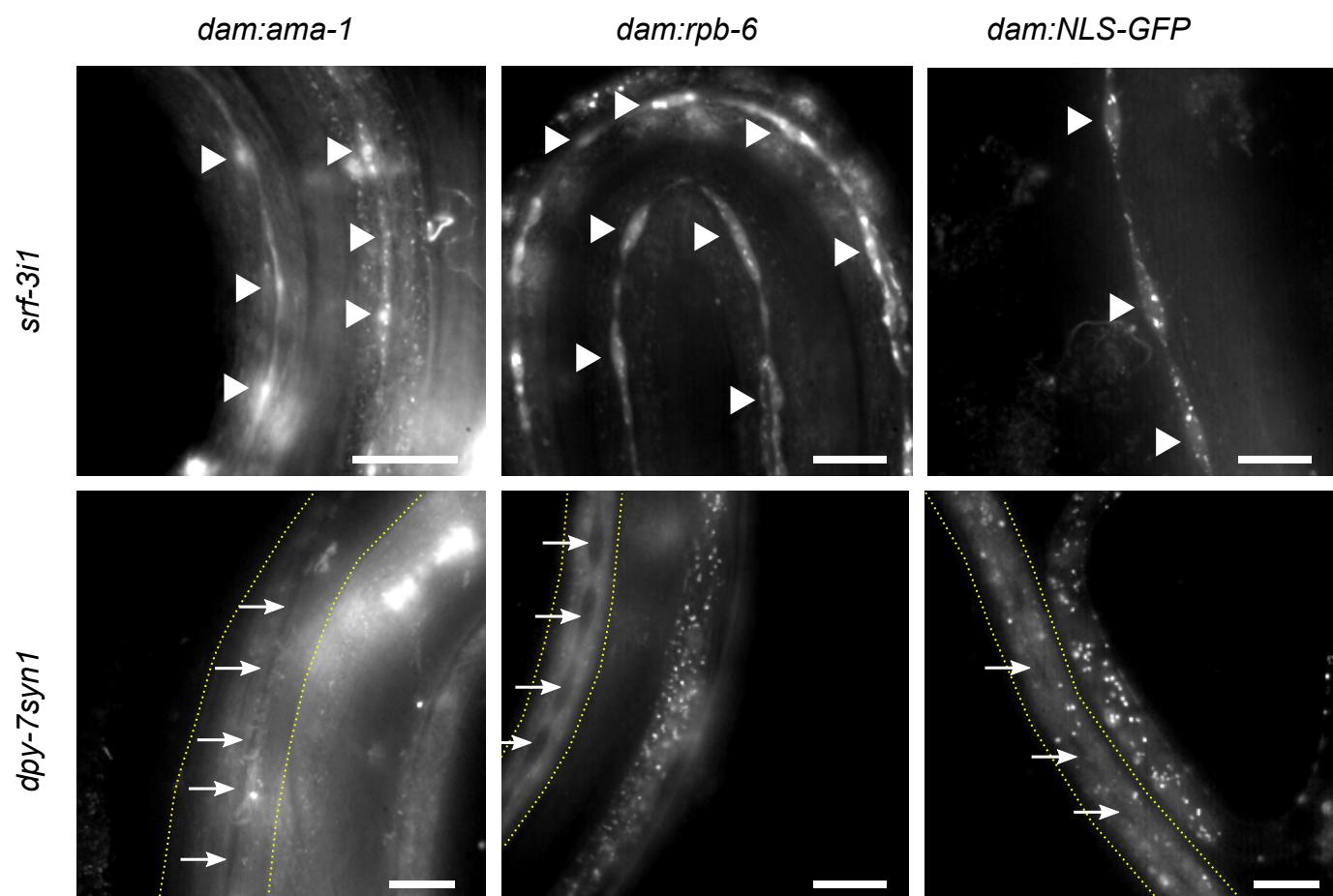


Fig. S2. Validation of expression of the RNAPol TaDa transgenes.

Confirmation of single-copy transgene expression in the expected tissue of interest, for specified transgenes, using *mCherry* expression as a proxy. Animals were imaged at the L4 stage. White arrowheads indicate expression in the seam cells, while white arrows indicate absence of expression in the seam cells in animals expressing in the hypodermis, indicated by the yellow outline. Scale bars are 20 μ m.

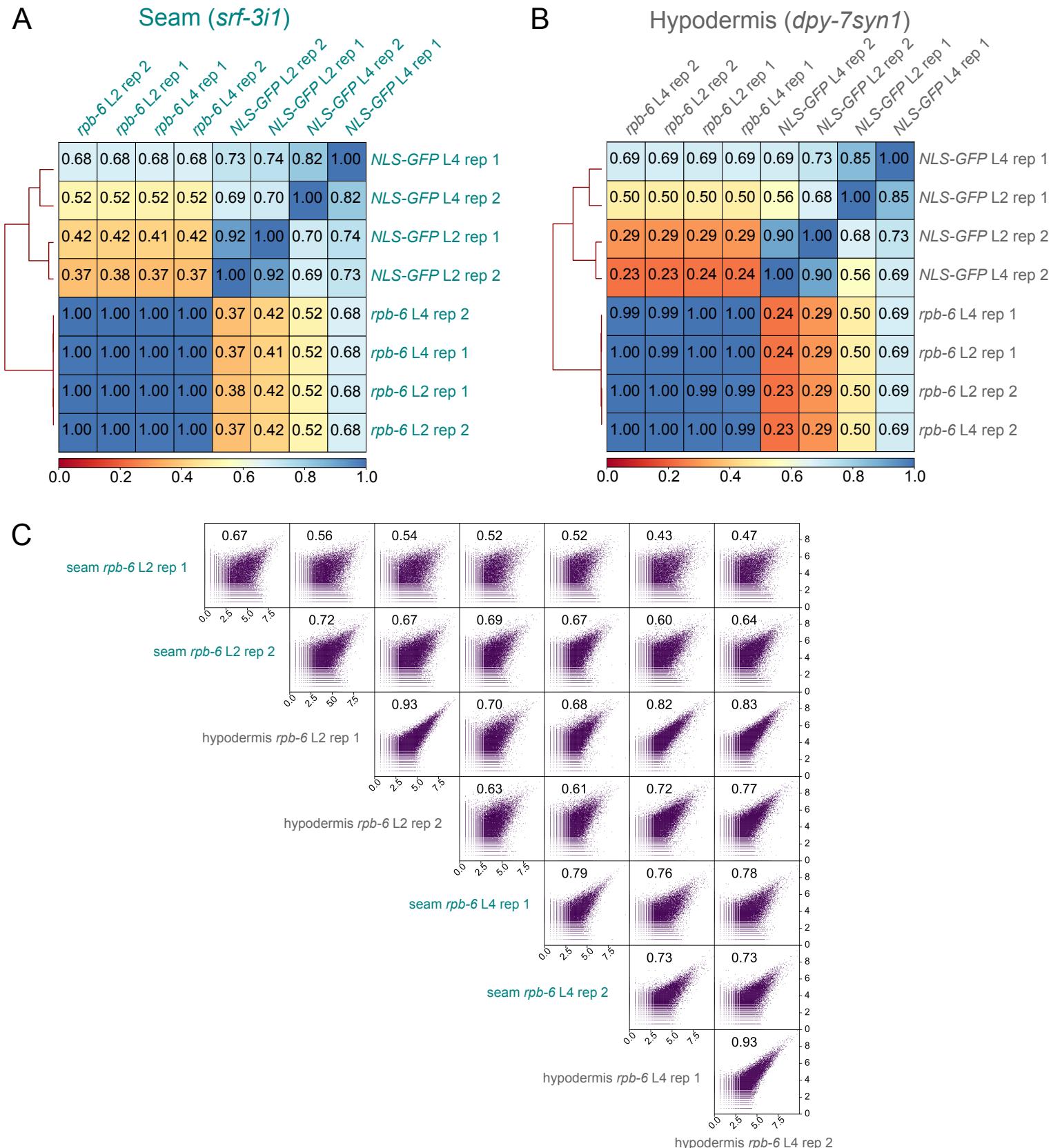


Fig. S3. RPB-6 occupancy signatures are similar across cell types and different to controls.

(A-B) Pearson correlation heatmaps based on genome-wide normalised aligned read count maps for the seam (A) and hypodermis (B). The correlation coefficient for each pairwise comparison is printed in each cell of the heatmap. For both promoters, the *dam:rpb-6* samples show higher correlation than the control samples. **(C)** Scatterplots and Pearson correlations across replicates, cell types and developmental stages based on read-count normalised scores of GATC fragments participating in protein-coding genes. The correlation coefficient r values are shown in each corresponding cell. Note that these values are not identical to those reported in Fig. 2B, likely due to differences in signal distribution across GATC fragments in protein-coding genes.

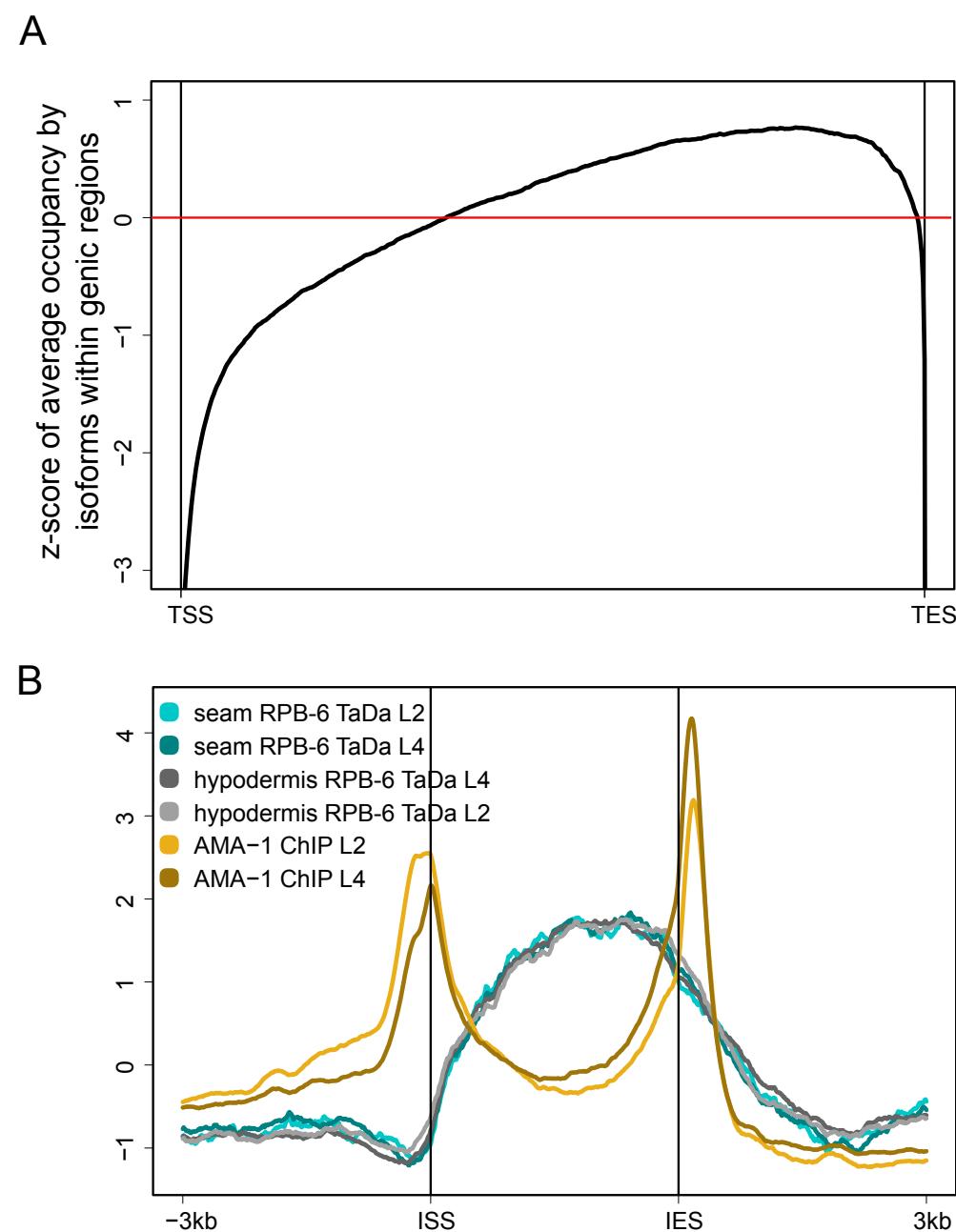


Fig. S4. Isoform positional enrichment within genes does not explain the RPB-6 occupancy signal preference for 3' regions.

(A) Deviation from the average occupancy of gene sequences by isoforms shows increased coverage of 3' regions compared to 5' regions of gene sequences annotated based on the largest transcript. Red line indicates the average isoform occupancy across the gene length. **(B)** Aggregation plot for the RPB-6 TaDa signal from the different cell types and developmental stages along with whole-animal AMA-1 ChIP-seq signal with the averaged signal anchored at the start and end sites (ISS and IES respectively) of all isoforms of *C. elegans* protein-coding genes, pushed into a pseudo-length of 3kb, along with a region 3kb upstream and 3kb downstream. In Y-axes show z-scores for the plotted sequence length in both cases.

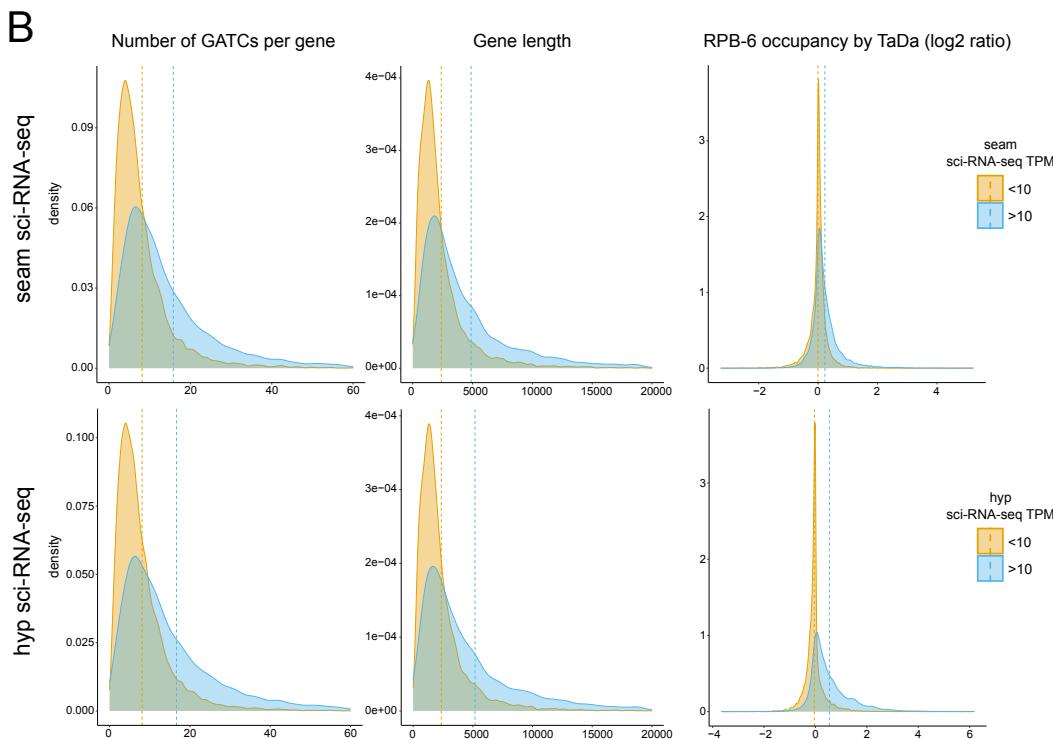
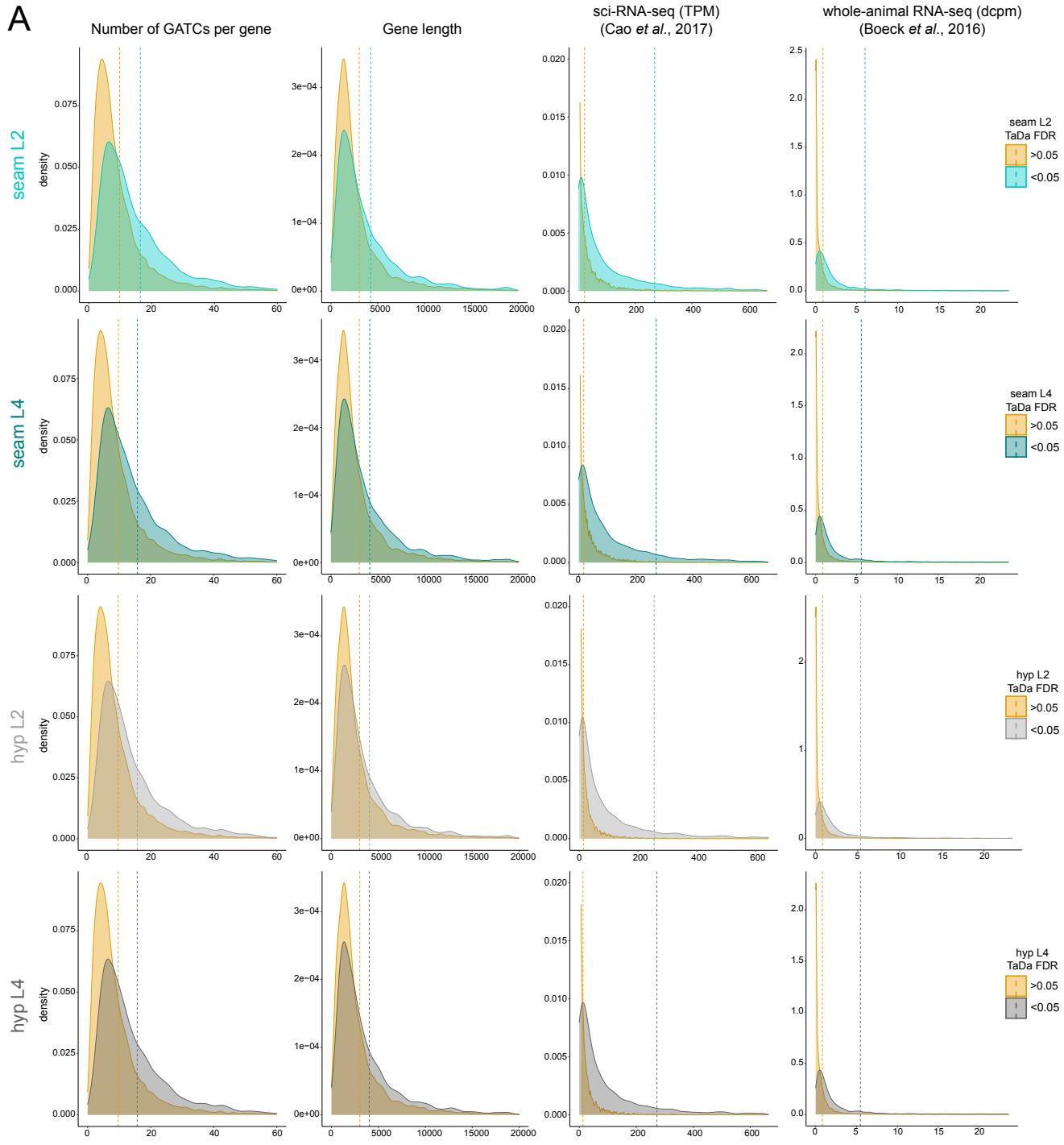


Fig. S5. TaDa-identified expressed genes show higher expression in RNA-seq experiments and are biased for GATC availability.

(A) Density plots of protein coding genes, separated in groups of expressed or non-expressed based on TaDa (FDR<0.05), per cell type and developmental stage plotted against: the number of GATCs within gene, gene length, sci-RNA-seq expression values (in TPM: transcripts per million) (Cao et al., 2017) and stage-matched whole-animal RNA-seq expression values (in dcpm: depth of coverage per base per million reads) (Boeck et al., 2016). For all cell types and stages TaDa expressed genes showed significantly increased sci-RNA-seq and whole-animal RNA-seq expression values compared to non-expressed, as well as higher numbers of GATCs and consequently longer gene lengths. **(B)** Density plots of protein coding genes, separated in groups of expressed or non-expressed based on sci-RNA-seq (TPM>10) (Cao et al., 2017), per cell type plotted against: the number of GATCs within gene, gene length and TaDa RPB-6 occupancy values ($\log_2(rpb-6:dam/NLS-GFP:dam)$). In both cell types expressed genes showed significantly longer gene length and likely consequently more GATCs than non-expressed, as well as higher RPB-6 occupancy values. In A and B dashed lines indicate the distribution mean and statistical significance of difference in the distributions was determined with a Kolmogorov-Smirnov test, $p < 2.2 \times 10^{-16}$. The X-axis is limited to the 99th percentile of values and for sci-RNA-seq the Y-axis is limited to 0.02 for visualisation.

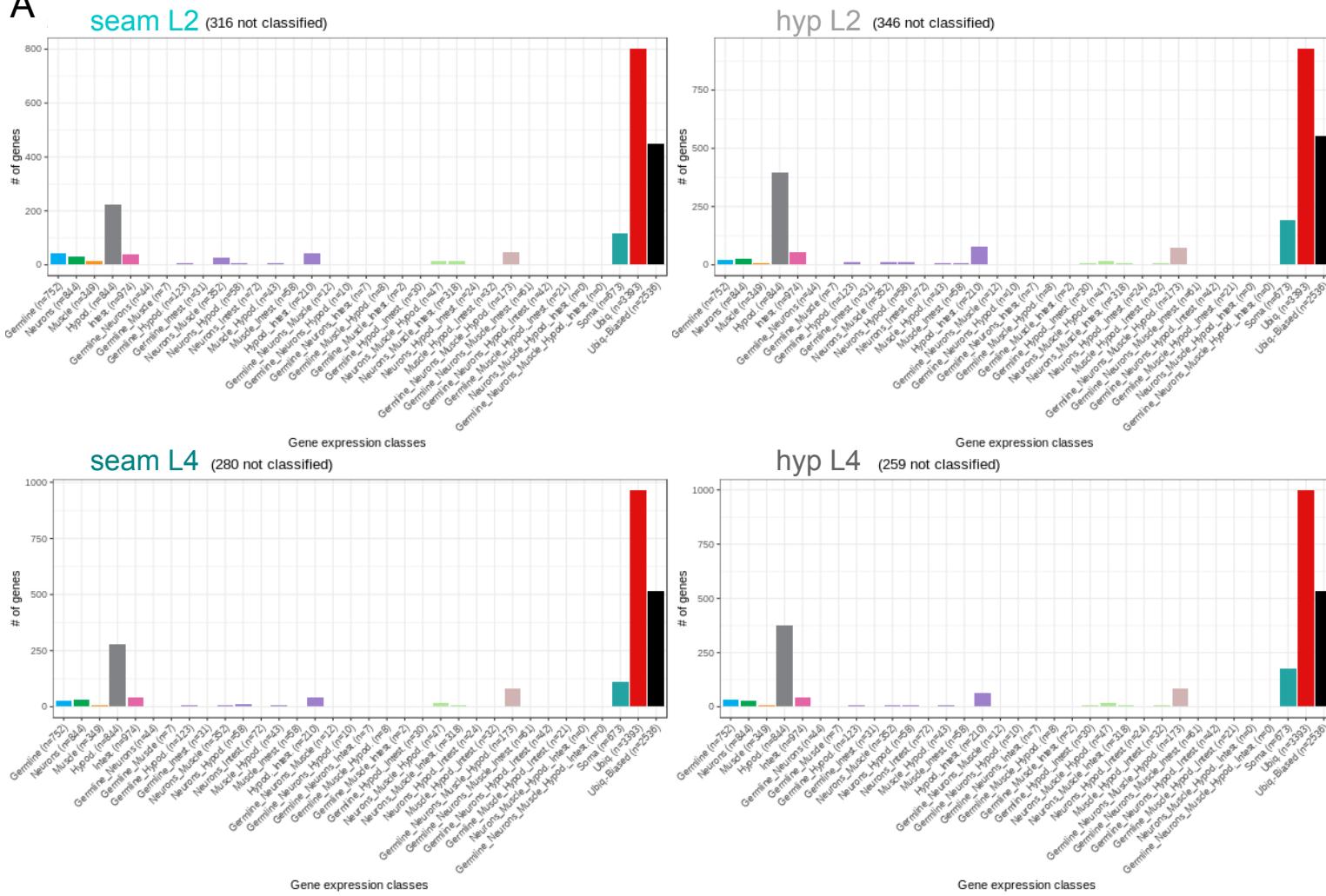
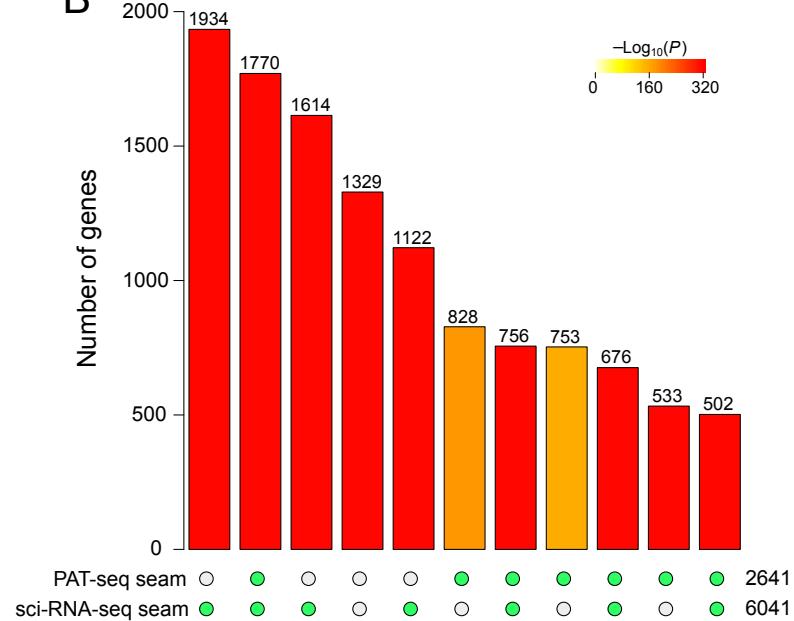
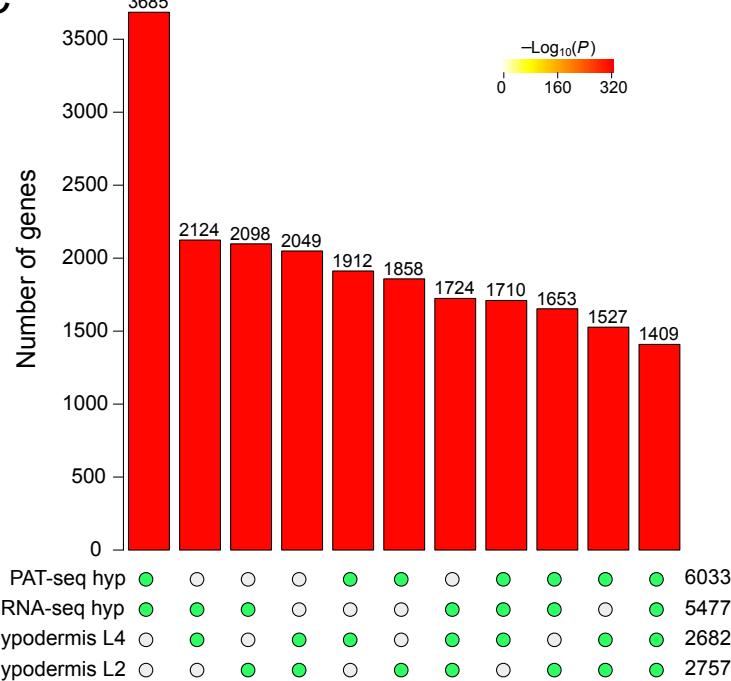
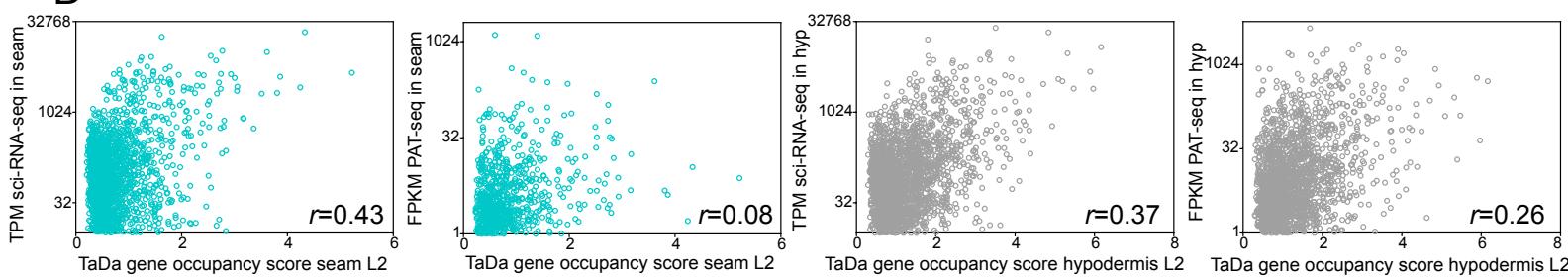
A**B****C****D**

Fig. S6. TaDa-identified expressed genes overlap significantly with other published transcriptomes.

(A) Barplots of numbers of TaDa-identified expressed genes for each cell type and developmental stage that are in common with gene-sets classified based on their tissue specificity (Serizay et al., 2020). **(B-C)** Barplots of the sizes and statistical significance, assessed by a Fisher's exact test, of all possible intersections between TaDa, sci-RNA-seq genes over a 10 TPM threshold (Cao et al., 2017) and PAT-seq-identified sets of expressed genes (Blazie et al., 2017) in the seam cells (B) and the hypodermis (C). All overlaps are highly significant. **(D)** Correlation scatterplots of expression levels for L2 genes common between seam (left) or hypodermis (right) TaDa sets and the sci-RNA-seq or the PAT-seq datasets for seam cells and hypodermis. For TaDa the $\log_2(dam:rpb-6/dam:NLS-GFP)$ scores are used as a measure of expression levels, for sci-RNA-seq the values are transcripts per million reads (TPM) and for PAT-seq fragments per kilobase of transcript per million reads (FPKM). All correlation analyses showed significant although weak correlation (indicated by the r values) across methods with $p < 0.0001$ for all.

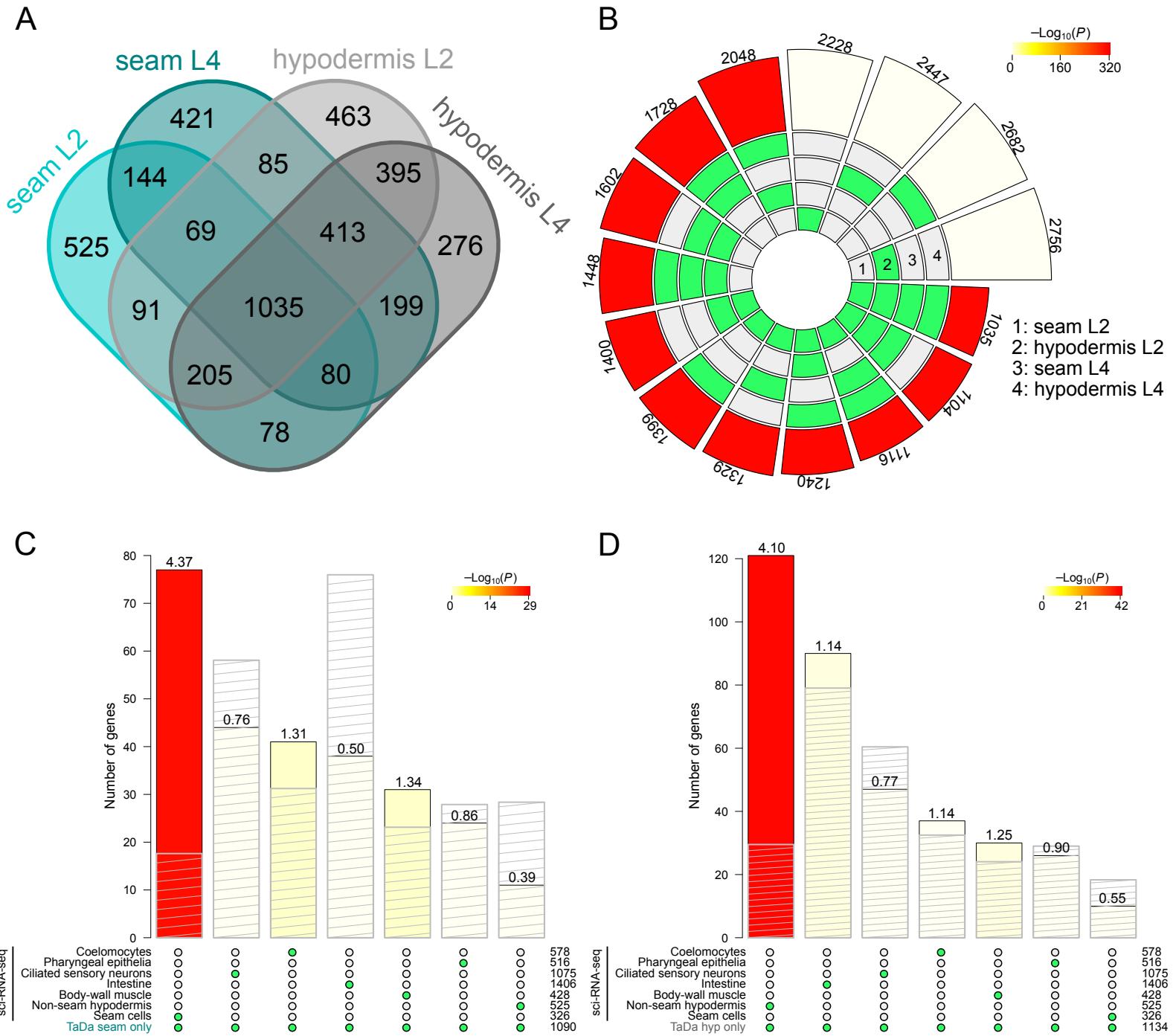


Fig. S7. Intersections of TaDa-identified expressed gene sets show significant overlap across cell types and reveal seam cell and hypodermal-specific genes.

(A-B) Multiple intersections of all the acquired gene-sets expressed in the seam and hypodermis in both stages. The Venn diagram (A) presents the number of genes that are shared across datasets or are unique to the cell type and/or developmental stage. The circular plot (B) reports the sizes of all pairwise and higher-order intersections between the sets (indicated in green whether they are included in each comparison) and indicates that they are highly significant (in red) with a Fisher's exact test. **(C-D)** Barplots representing intersections between TaDa seam-only (C) or TaDa hypodermis-only (D) gene sets and cell-type-specific genes from 7 non-related cell types from sci-RNA-seq (genes with a TPM>10 and 5-fold higher than the 2nd most expressing cell type) (Cao et al., 2017). The colour of the bar signifies statistical significance assessed by a Fisher's exact test, gridded bars indicate expected overlap based on gene set and genome size and the enrichment fold between observed and expected overlaps is printed on top of bars. The most significant intersections are those between gene sets specific for the same-cell type ($p\leq 7.06\times 10^{-29}$).

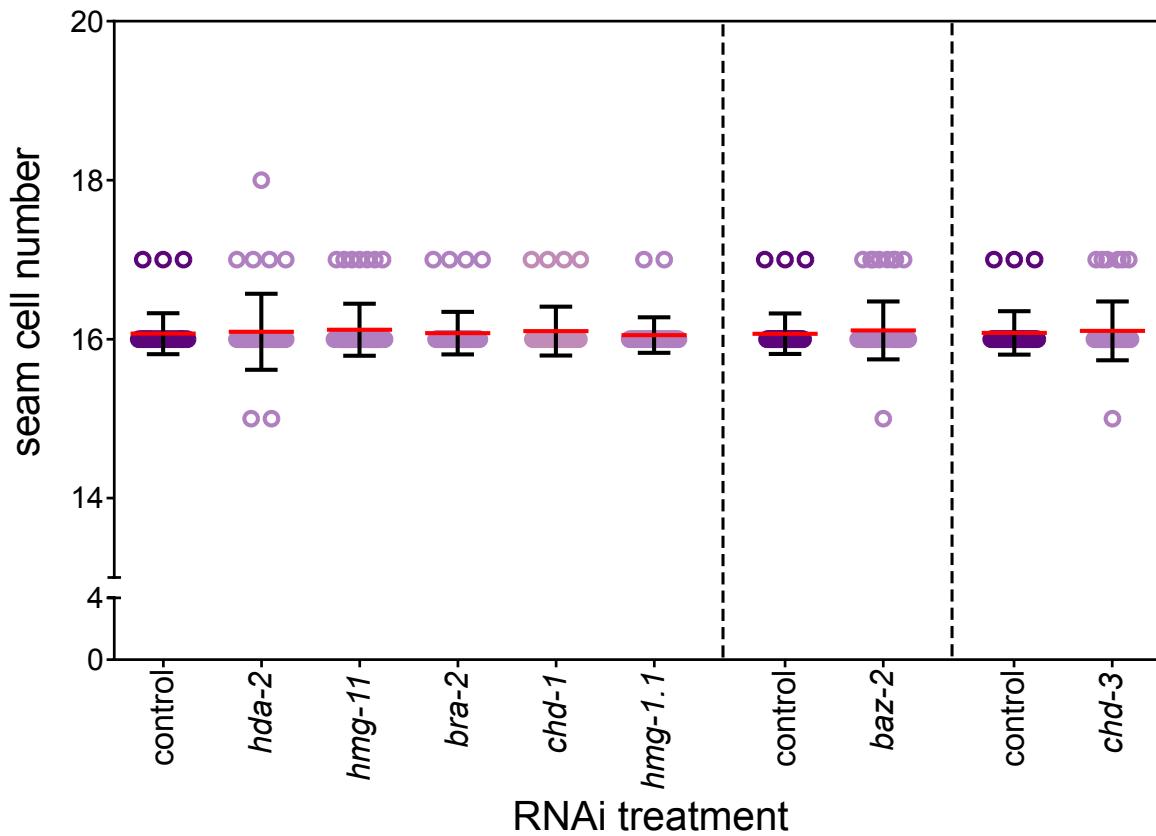


Fig. S8. RNAi-screen for putative chromatin factors regulating seam cell patterning.

Quantification of seam cell number at the late L4 stage of RNAi treated animals carrying the *SCMp::GFP* reporter in a WT background ($39 \leq n \leq 63$ animals per treatment). Targeted chromatin factors are indicated on the X-axis and sets of treatments performed on the same day are separated from others by dashed lines, having their respective control. No significant changes to the mean or variance were observed in both backgrounds for the presented treatments.

Table S1. List of genes expressed in seam cells and hypodermis at L2 and L4 by TaDa and their overlap with sci-RNAseq and PAT-seq.

[Click here to download Table S1](#)

Table S2. List of genes (including transcription and chromatin factors) expressed in seam cells at L2 and L4 by TaDa.

[Click here to download Table S2](#)

Table S3. List of strains used in this study.

Strain	Background	Genotype
N2	N2	wild isolate <i>C. elegans</i> from Bristol, UK
JR667	N2	<i>unc-119(e2498::Tc1)</i> III; <i>wls51[SCMp::GFP + unc-119(+)]</i> V
EG6699	N2	<i>ttTi5605</i> II; <i>unc-119(ed3)</i> III; <i>oxEx1578</i> .
MBA250	N2	<i>icbls2[arf-3::pes-10::GFP:CAAX::unc-54]</i> I; <i>icbSi2[dp-7p::mCherry:H2B::unc-54 3'UTR+cb-unc-119]</i> IV; <i>wls51[SCMp::GFP+unc-119(+)]</i> V
MBA467	N2	<i>icbSi25[pDK16(srf-3ap::GFPo-H2B::unc-54 3'UTR + cb-unc-119)]</i> II; <i>unc-119(ed3)</i> III
MBA468	N2	<i>icbSi26[pDK1(psr-3ap::GFPo-H2B::unc-54 3'UTR + cb-unc-119)]</i> II; <i>unc-119(ed3)</i> III
MBA488	N2	<i>icbEx121[pDK18(dpy-7syn1::mCherry-H2B::unc-54 3'UTR) pBJ36, pRF4]; icbls2[arf-3::GFP:CAAX::unc-54 3'UTR]</i> I; <i>wls51[SCMp::GFP + unc-119(+)]</i> V
MBA489	N2	<i>icbEx122[pDK18(dpy-7syn1::mCherry-H2B::unc-54 3'UTR) pBJ36, pRF4]; icbls2[arf-3::GFP:CAAX::unc-54 3'UTR]</i> I; <i>wls51[SCMp::GFP + unc-119(+)]</i> V
MBA490	N2	<i>icbEx123[pDK18(dpy-7syn1::mCherry-H2B::unc-54 3'UTR) pBJ36, pRF4]; icbls2[arf-3::GFP:CAAX::unc-54 3'UTR]</i> I; <i>wls51[SCMp::GFP + unc-119(+)]</i> V
MBA496	N2	<i>icbSi32[pDK26(srf-3bp::GFPo-H2B::unc-54 3'UTR + cb-unc-119)]</i> II; <i>unc-119(ed3)</i> III
MBA497	N2	<i>icbSi33[pDK26(srf-3bp::GFPo-H2B::unc-54 3'UTR + cb-unc-119)]</i> II; <i>unc-119(ed3)</i> III
MBA540	N2	<i>icbSi42[pDK32(srf-3i1::pes-10::GFPo-H2B::unc-54 3'UTR + cb-unc-119)]</i> II; <i>unc-119(ed3)</i> III
MBA541	N2	<i>icbSi43[pDK32(srf-3i1::pes-10::GFPo-H2B::unc-54 3'UTR + cb-unc-119)]</i> II; <i>unc-119(ed3)</i> III
MBA542	N2	<i>icbSi44[pDK32(srf-3i1::pes-10::GFPo-H2B::unc-54 3'UTR + cb-unc-119)]</i> II; <i>unc-119(ed3)</i> III
MBA687	N2	<i>icbSi71[pDK62(cb-unc-119 + dpy-7syn1::wormCherry::Dam-myc:ama-1::unc-54 3'UTR)]</i> II; <i>unc-119(ed3)</i> III
MBA688	N2	<i>icbSi72[pDK65(dpy-7syn1::wormCherry::Dam-myc:rpb-6::unc-54 3'UTR + cb-unc-119)]</i> II; <i>unc-119(ed3)</i> III
MBA692	N2	<i>icbSi76[pDK54(srf-3i1::pes-10::wormCherry::Dam-myc:NLS-GFP::unc-54 3'UTR + cb-unc-119)]</i> II; <i>unc-119(ed3)</i> III
MBA693	N2	<i>icbSi77[pDK64(dpy-7syn1::wormCherry::Dam-myc:NLS-GFP::unc-54 3'UTR + cb-unc-119)]</i> II; <i>unc-119(ed3)</i> III
MBA694	N2	<i>icbSi78[pDK46(cb-unc-119 + srf-3i1::pes-10::wormCherry::Dam-myc:ama-1::unc-54 3'UTR)]</i> II; <i>unc-119(ed3)</i> III
MBA698	N2	<i>icbSi82[pDK55(srf-3i1::pes-10::wormCherry::Dam-myc:rpb-6::unc-54 3'UTR + cb-unc-119)]</i> ; <i>unc-119(ed3)</i> III
MBA1138	N2	<i>icbEx261[pDK133(srf-3i1::Δpes-10::mir-42-44::p10 3'UTR), myo-2::dsRed, pBJ36]; unc-119(e2498::Tc1)</i> III; <i>wls51[SCMp::GFP + unc-119(+)]</i> V
MBA1139	N2	<i>icbEx262[pDK133(srf-3i1::Δpes-10::mir-42-44::p10 3'UTR), myo-2::dsRed, pBJ36]; unc-119(e2498::Tc1)</i> III; <i>wls51[SCMp::GFP + unc-119(+)]</i> V
MBA1140	N2	<i>icbEx263[pDK133(srf-3i1::Δpes-10::mir-42-44::p10 3'UTR), myo-2::dsRed, pBJ36]; unc-119(e2498::Tc1)</i> III; <i>wls51[SCMp::GFP + unc-119(+)]</i> V
MBA1141	N2	<i>icbEx267[pDK147(dpy-7syn1::mir-42-44::p10 3'UTR), myo-2::dsRed, pBJ36]; unc-119(e2498::Tc1)</i> III; <i>wls51[SCMp::GFP + unc-119(+)]</i> V
MBA1142	N2	<i>icbEx265[pDK139(srf-3i1::Δpes-10::mir-47::p10 3'UTR), myo-2::dsRed, pBJ36]; unc-119(e2498::Tc1)</i> III; <i>wls51[SCMp::GFP + unc-119(+)]</i> V
MBA1143	N2	<i>icbEx266[pDK139(srf-3i1::Δpes-10::mir-47::p10 3'UTR), myo-2::dsRed, pBJ36]; unc-119(e2498::Tc1)</i> III; <i>wls51[SCMp::GFP + unc-119(+)]</i> V
MBA1144	N2	<i>icbEx264[pDK139(srf-3i1::Δpes-10::mir-47::p10 3'UTR), myo-2::dsRed, pBJ36]; unc-119(e2498::Tc1)</i> III; <i>wls51[SCMp::GFP + unc-119(+)]</i> V
MBA1145	N2	<i>icbEx268[pDK148(dpy-7syn1::mir-47::p10 3'UTR), myo-2::dsRed, pBJ36]; unc-119(e2498::Tc1)</i> III; <i>wls51[SCMp::GFP + unc-119(+)]</i> V
MBA1146	N2	<i>icbEx269[pDK148(dpy-7syn1::mir-47::p10 3'UTR), myo-2::dsRed, pBJ36]; unc-119(e2498::Tc1)</i> III; <i>wls51[SCMp::GFP + unc-119(+)]</i> V
MBA1192	N2	<i>icbEx292[pDK158(srf-3i1-mut::Δpes-10::outtron::>hda-1 fragment>::srf-3a intron5::<hda-1 fragment<::p10 3'UTR), myo-2::dsRed, pBJ36]</i> ; <i>wls51[SCMp::GFP + unc-119(+)]</i> V

Table S4. Primers used in this study (general oligos and smFISH probes).

Oligo name	Sequence 5' -> 3'
DK27	CTCATCTGAAAGAGGATCTGGCATGGAATGGCCGATGAGGACGATTATC
DK28	CGAGATGGCTAGCACTTAATAACTGCATGCTACCAATCAGCAGTTGAA
DK33	CTTACTTGCACTTATAATCAGACTCACTAGGCTAGCTTCACTTGGTTTCAG
DK34	TTCTCCTTACTCATCCTAGGATTCAGATGGTACCTGAA
DK35	GGTACCATCTGAATCCTAGGTAGAGTAAAGGAGAAATT
DK36	CCGATCCCCCGGGCACTTAAGCTTGTAGAGCTCGTCATT
DK37	GACGAGCTCTACAAGCTTAAGCTGGGGATCGGTGGAG
DK38	CACGGGCGCAGATGTTAATTAAATTACTTGTGGAAGTGTACT
DK39	ACTTCCAGCAAGTAATTAAACATCTCGCGCCCGTGCCT
DK40	GGCCCCGGGCTACGTTAACGACTCACTTAAAAAACAGTTATGTTGGTATA
DK41	AGGCCCTTGAAGTAGAGGGTACCCAGACTCACCAACTTTGTATAGAAAAGTT
DK42	CCACTTCAAAAAGCGCGATTTTCTCATCCTAGGGTTACTACTTATAC
DK43	CTCATCTGAAAGAGGATCTGGCATGCTATGACTGCTCAAAGGAA
DK44	GCGAGATGGCTAGCACTTAAATTACATGCTGTTAGTTCATCCA
DK46	ACATTTCGTTCTGATAAGTTAACATTATGGTCTAAAGGGTGAAGA
DK47	GTAATGGGACTTAGAAGTCAGAGGCAATTACTGCTGGAAGTGTACT
DK48	GGGGACAAAGTTGTACAAAAAAGCAGGCTATGGTCAGCAAGGGAGAGGCA
DK49	CTTGTAGAGCTCGTCATT
DK50	AGGAATGGACGAGCTCACAAAGTGCCTGGGGGATCGGGAGC
DK59	AATTCTCTCTTAACTCATCCTAGGATTTCTTTGATTGTGAAGATT
DK64	TTGCACTTAAATCAGACTCACTAGGCTAGGTGAGTTCTAACCT
DK65	CGGGGATCCCTCTAGACTGACCAAGGGCTGATTTCTTTGATTGTGAAG
DK66	GGCCGTGAATTCTCACAACTCAAAAGGAATCAGGCCCTGGTCGACT
DK67	TGAAACATTCTCTCTTAACTCATCCTAGCTCAAGCAAGGGTCCTCCT
DK89	GGGGACAACTTGTATAGAAAAGTTGGTAGTTAACCTAACCT
DK90	GGGGACTGCTTTTGACAAACTGCTCAGCTCCAAGCAAGGGTCTCCT
DK102	CTCATGACAACTAACCTGCCAATTGTTCTCGGATGACCTAGGATGACGTATTCCCTGTGCTC
DK103	GTAAGCTTAAACAAAGTTCATTGGCTCGATCAAGTAAATT
DK107	GAACAACTTCTCTTAACTCATCCTAGGCTGAAAGTTAAAATTACAG
DK113	GGGGACAACTTGTATAGAAAAGTTGCGGAATTCTTGTATAACG
DK114	GGGGACTGCTTTTGACAAACTTGTATCAAGAACAAATGAA
DK217	TTAATCTGTAATTAACTTCAGGCTAGTTGCGGACCTTGTTGGGTG
DK218	ATTTGTTATTAAACAGATTCTTAATAAACCTTACAGGAACGAAATAC
DK219	TATTCTTACATTGTTCTGATAACCTAGTTGCGGACCTTGTTGGGTG
DK220	TTAATCTGTAATTAACTTCAGGCTAGGAGAGCCGACTGAAACTGAA
DK221	ATTTGTTATTAAAACGATTCTTAAATGATTACCGCACACCTTGCC
DK222	TATTCTTACATTGTTCTGATAACCTAGGAGAGCCGACTGAAACTGAA
DK247	TGCAAGACTAAGGTATGACTCTGTTTACAGCGAC
DK248	TCGAAGACTAAAGCTCGGTATTCCATCGCGAAGT
MB100	ATCGGGAGGCGAACCTAAGT
MB106	AGGCAGAAATGTAACAAAGACTCG
MB270	CGGGAAATTCTCTGATAACGATAATTGGTTATTGTGTC
MB271	CGGGAAATTCTCATTTATCACACCCCTGTTCTT

efl-3 probe (1:50)		srf-3 probe (1:50)	
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aactgtgtatgtatcatgt	aatgtttttgttgcgttgcgt		
aaaacccctgtttccggat	cttcgtatgttgcggat		
tataagcgctgtatcgact	tgtgcgtatgttgcgtatgt		
aaccaggacatgttgcgtatgt	cacccgttgcgtatgttgcgt		
acccttttaatgtggccaaq	ctccgttgcgtatgttgcgt		

Table S5. List of transgenes and injection mixes used in this study.

Extrachromosomal array number		Genetic contents	Composition of injection mix
<i>icbEx121</i>		[<i>pDK18(dpy-7syn1::mCherry-H2B::unc-54 3'UTR)</i> <i>pBJ36, pRF4]</i>	pDK18 10 ng/μl, pRF4 35 ng/μl, pBJ36 80 ng/μl
<i>icbEx122</i>		[<i>pDK18(dpy-7syn1::mCherry-H2B::unc-54 3'UTR)</i> <i>pBJ36, pRF4]</i>	pDK18 10 ng/μl, pRF4 35 ng/μl, pBJ36 80 ng/μl
<i>icbEx123</i>		[<i>pDK18(dpy-7syn1::mCherry-H2B::unc-54 3'UTR)</i> <i>pBJ36, pRF4]</i>	pDK18 10 ng/μl, pRF4 35 ng/μl, pBJ36 80 ng/μl
<i>icbEx261</i>		[<i>pDK13(srf-3'1::Apes-10::mir-42-44::p10 3'UTR), myo-2::dsRed, pBJ36]</i>	pDK133 50 ng/μl, myo-2::dsRed 5 ng/μl, pBJ36 70 ng/μl
<i>icbEx262</i>		[<i>pDK133(srf-3'1::Apes-10::mir-42-44::p10 3'UTR), myo-2::dsRed, pBJ36]</i>	pDK133 50 ng/μl, myo-2::dsRed 5 ng/μl, pBJ36 70 ng/μl
<i>icbEx263</i>		[<i>pDK133(srf-3'1::Apes-10::mir-42-44::p10 3'UTR), myo-2::dsRed, pBJ36]</i>	pDK133 50 ng/μl, myo-2::dsRed 5 ng/μl, pBJ36 70 ng/μl
<i>icbEx264</i>		[<i>pDK139(srf-3'1::Apes-10::mir-47::p10 3'UTR), myo-2::dsRed, pBJ36]</i>	pDK139 50 ng/μl, myo-2::dsRed 5 ng/μl, pBJ36 70 ng/μl
<i>icbEx265</i>		[<i>pDK139(srf-3'1::Apes-10::mir-47::p10 3'UTR), myo-2::dsRed, pBJ36]</i>	pDK139 50 ng/μl, myo-2::dsRed 5 ng/μl, pBJ36 70 ng/μl
<i>icbEx266</i>		[<i>pDK139(srf-3'1::Apes-10::mir-47::p10 3'UTR), myo-2::dsRed, pBJ36]</i>	pDK139 50 ng/μl, myo-2::dsRed 5 ng/μl, pBJ36 70 ng/μl
<i>icbEx267</i>		[<i>pDK147(dov-7syn1::mir-42-44::p10 3'UTR), myo-2::dsRed, pBJ36]</i>	pDK147 50 ng/μl, myo-2::dsRed 5 ng/μl, pBJ36 70 ng/μl
<i>icbEx268</i>		[<i>pDK148(dpy-7syn1::mir-47::p10 3'UTR), myo-2::dsRed, pBJ36]</i>	pDK148 50 ng/μl, myo-2::dsRed 5 ng/μl, pBJ36 70 ng/μl
<i>icbEx269</i>		[<i>pDK148(dpy-7syn1::mir-47::p10 3'UTR), myo-2::dsRed, pBJ36]</i>	pDK148 50 ng/μl, myo-2::dsRed 5 ng/μl, pBJ36 70 ng/μl
<i>icbEx292</i>		[<i>pDK158(srf-3'1-mut::delta-pes-10::outron::hda-1 fragment>::srf-3a intron5::<hda-1 fragment<::p10 3'UTR), myo-2::dsRed, pBJ36]</i>	pDK158 50 ng/μl, myo-2::dsRed 5 ng/μl, pBJ36 70 ng/μl
Single-copy insertion number		Genetic contents	Composition of injection mix
<i>icbS125</i>		[<i>pDK16(srf-3'ap::GFPo-H2B::unc-54 3'UTR + cb-unc-119)</i>]	pDK16 50 ng/μl, pCFJ601 50 ng/μl, pMA122 10 ng/μl, pGH8 10 ng/μl, myo-2::dsRed 2.5 ng/μl, pCFJ104 5 ng/μl
<i>icbS126</i>		[<i>pDK16(srf-3'ap::GFPo-H2B::unc-54 3'UTR + cb-unc-119)</i>]	pDK16 50 ng/μl, pCFJ601 50 ng/μl, pMA122 10 ng/μl, pGH8 10 ng/μl, myo-2::dsRed 2.5 ng/μl, pCFJ104 5 ng/μl
<i>icbS132</i>		[<i>pDK26(srf-3'bp::GFPo-H2B::unc-54 3'UTR + cb-unc-119)</i>]	pDK26 50 ng/μl, pCFJ601 50 ng/μl, pMA122 10 ng/μl, pGH8 10 ng/μl, myo-2::dsRed 2.5 ng/μl, pCFJ104 5 ng/μl
<i>icbS133</i>		[<i>pDK26(srf-3'bp::GFPo-H2B::unc-54 3'UTR + cb-unc-119)</i>]	pDK26 50 ng/μl, pCFJ601 50 ng/μl, pMA122 10 ng/μl, pGH8 10 ng/μl, myo-2::dsRed 2.5 ng/μl, pCFJ104 5 ng/μl
<i>icbS142</i>		[<i>pDK32(srf-3'1::pes-10::GFPo-H2B::unc-54 3'UTR + cb-unc-119)</i>]	pDK32 50 ng/μl, pCFJ601 50 ng/μl, pMA122 10 ng/μl, pGH8 10 ng/μl, myo-2::dsRed 2.5 ng/μl, pCFJ104 5 ng/μl
<i>icbS143</i>		[<i>pDK32(srf-3'1::pes-10::GFPo-H2B::unc-54 3'UTR + cb-unc-119)</i>]	pDK32 50 ng/μl, pCFJ601 50 ng/μl, pMA122 10 ng/μl, pGH8 10 ng/μl, myo-2::dsRed 2.5 ng/μl, pCFJ104 5 ng/μl
<i>icbS144</i>		[<i>pDK32(srf-3'1::pes-10::GFPo-H2B::unc-54 3'UTR + cb-unc-119)</i>]	pDK32 50 ng/μl, pCFJ601 50 ng/μl, pMA122 10 ng/μl, pGH8 10 ng/μl, myo-2::dsRed 2.5 ng/μl, pCFJ104 5 ng/μl
<i>icbS171</i>		[<i>pDK62(cb-unc-119 + dpy-7syn1::wormCherry::Dam-myc::ama-1::unc-54 3'UTR)</i>]	pDK62 50 ng/μl, pCFJ601 50 ng/μl, pMA122 10 ng/μl, pGH8 10 ng/μl, myo-2::dsRed 2.5 ng/μl, pCFJ104 5 ng/μl
<i>icbS172</i>		[<i>pDK65(dpy-7syn1::wormCherry::Dam-myc::pb-6::unc-54 3'UTR + cb-unc-119)</i>]	pDK65 50 ng/μl, pCFJ601 50 ng/μl, pMA122 10 ng/μl, pGH8 10 ng/μl, myo-2::dsRed 2.5 ng/μl, pCFJ104 5 ng/μl
<i>icbS176</i>		[<i>pDK54(srf-3'1::pes-10::wormCherry::Dam-myc::NLS-GFP::unc-54 3'UTR + cb-unc-119)</i>]	pDK54 50 ng/μl, pCFJ601 50 ng/μl, pMA122 10 ng/μl, pGH8 10 ng/μl, myo-2::dsRed 2.5 ng/μl, pCFJ104 5 ng/μl
<i>icbS177</i>		[<i>pDK64(dpy-7syn1::wormCherry::Dam-myc::NLS-GFP::unc-54 3'UTR + cb-unc-119)</i>]	pDK64 50 ng/μl, pCFJ601 50 ng/μl, pMA122 10 ng/μl, pGH8 10 ng/μl, myo-2::dsRed 2.5 ng/μl, pCFJ104 5 ng/μl
<i>icbS178</i>		[<i>pDK46(cb-unc-119 + srf-3'1::pes-10::wormCherry::Dam-myc::ama-1::unc-54 3'UTR)</i>]	pDK46 50 ng/μl, pCFJ601 50 ng/μl, pMA122 10 ng/μl, pGH8 10 ng/μl, myo-2::dsRed 2.5 ng/μl, pCFJ104 5 ng/μl
<i>icbS182</i>		[<i>pDK55(srf-3'1::pes-10::wormCherry::Dam-myc::pb-6::unc-54 3'UTR + cb-unc-119)</i>]	pDK55 50 ng/μl, pCFJ601 50 ng/μl, pMA122 10 ng/μl, pGH8 10 ng/μl, myo-2::dsRed 2.5 ng/μl, pCFJ104 5 ng/μl

Table S6. List of RNAi clones used in this study.

WormBase Gene ID	Public Name	Sequence Name	Ahringer RNAi library Geneservice_location
WBGene00009899	<i>efl-3</i>	<i>F49E12.6</i>	II-6K03
WBGene00000275	<i>bub-1</i>	<i>R06C7.8</i>	I-3H11
WBGene00001834	<i>hda-1</i>	<i>C53A5.3</i>	V-9F11
WBGene00009672	<i>F43G9.12</i>	<i>F43G9.12</i>	I-4C12
WBGene00001974	<i>hmg-4</i>	<i>T20B12.8</i>	III-3P10
WBGene00010369	<i>chd-1</i>	<i>H06O01.2</i>	I-3M20
WBGene00003664	<i>nhr-74</i>	<i>C27C7.3</i>	I-5P17
WBGene00001976	<i>hmg-11</i>	<i>T05A7.4</i>	II-3N12
WBGene00006554	<i>tbx-35</i>	<i>ZK177.10</i>	II-4O24
WBGene00001835	<i>hda-2</i>	<i>C08B11.2</i>	II-5N08
WBGene00001971	<i>hmg-1.1</i>	<i>Y48B6A.14</i>	II-9G13
WBGene00017757	<i>bra-2</i>	<i>F23H11.1</i>	III-1E22
WBGene00001470	<i>baz-2</i>	<i>ZK783.4</i>	III-4E11
WBGene00006970	<i>zag-1</i>	<i>F28F9.1</i>	IV-1P04
WBGene00003606	<i>nhr-7</i>	<i>F54D1.4</i>	IV-6C03
WBGene00020062	<i>nhr-270</i>	<i>R13D11.8</i>	V-1B09
WBGene00003649	<i>nhr-59</i>	<i>T27B7.1</i>	V-2M07
WBGene00001210	<i>egl-46</i>	<i>K11G9.4</i>	V-4L02
WBGene00003717	<i>nhr-127</i>	<i>T13F3.3</i>	V-10J08
WBGene00000482	<i>chd-3</i>	<i>T14G8.1</i>	X-6G01
WBGene00007433	<i>swn-7</i>	<i>C08B11.3</i>	II-5N10