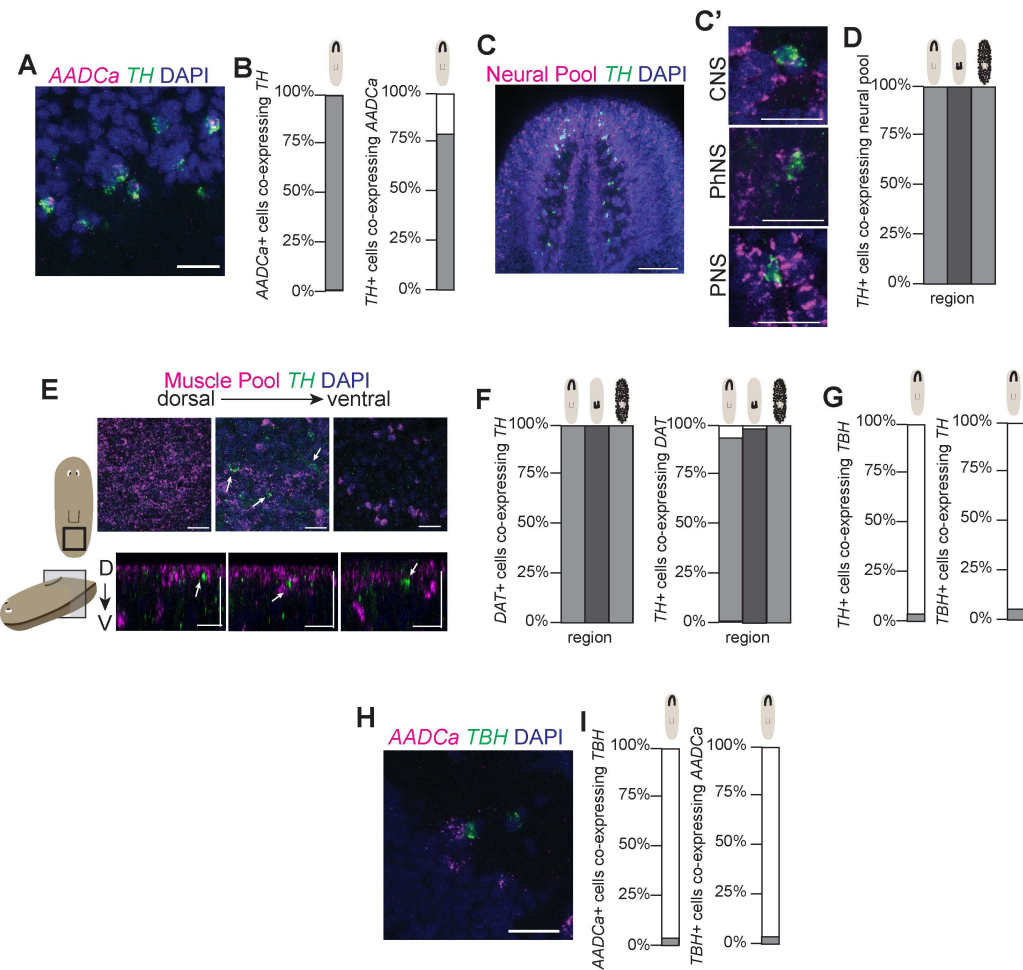
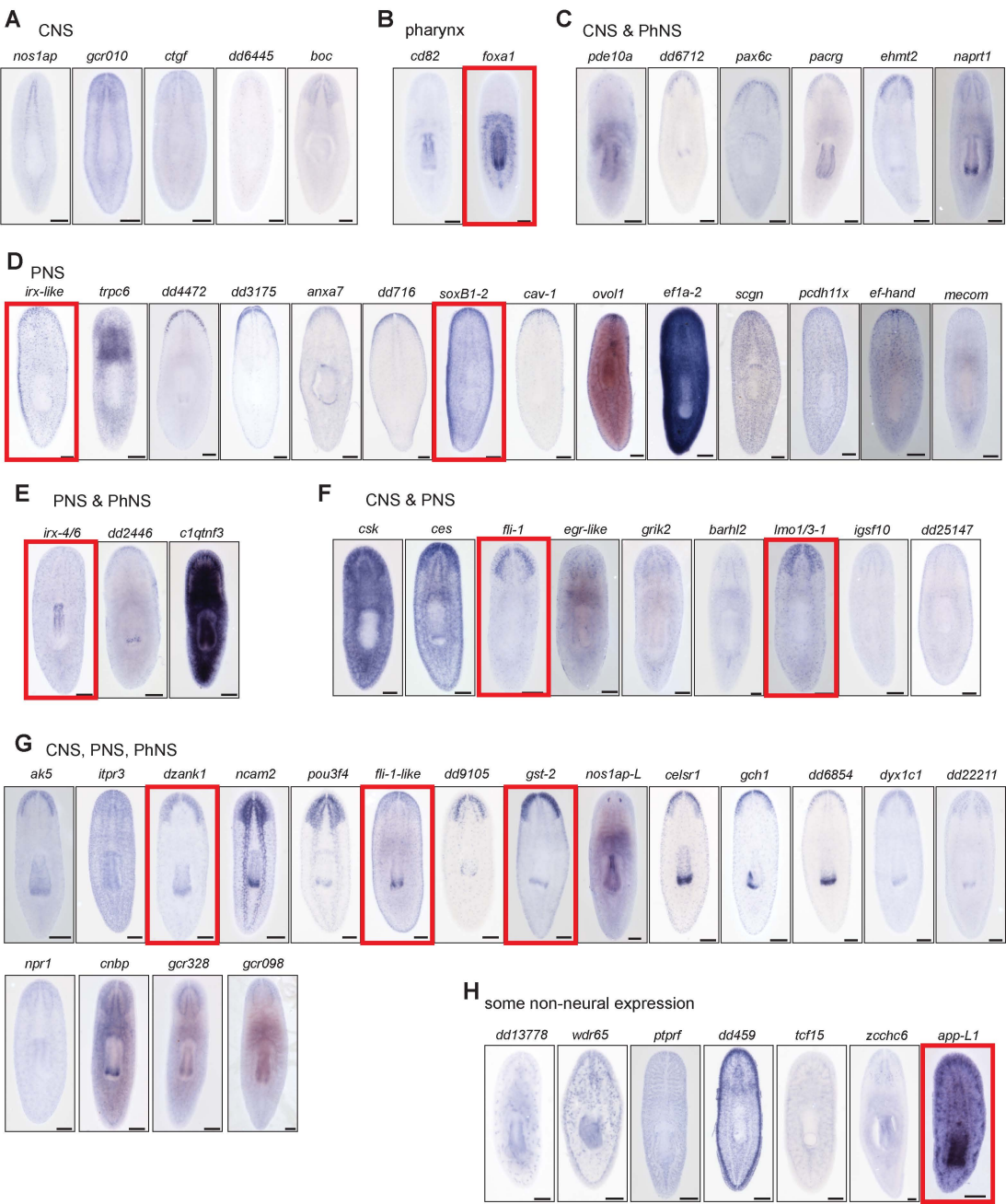


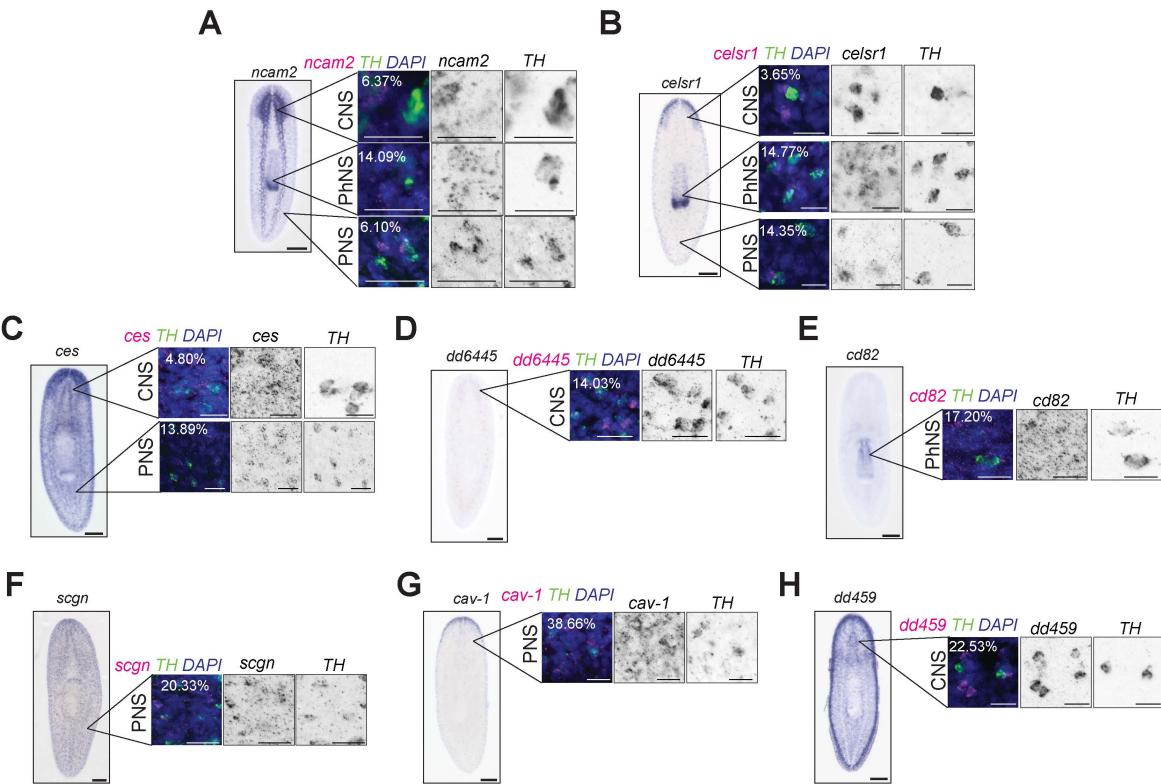
Supplementary figures



Supplementary Figure 1: Validation of markers of dopaminergic neurons. A) Co-expression of *AADCα* (magenta), *TH* (green), and DAPI (nuclei – blue) in the CNS. B) Quantification of A. N = 5 animals, 69-146 cells/region/animal. C-C') Co-expression of *TH* (green) with a pool of neural markers—*synapsin* *dd_Smed_v6_3135_0_1*, *synaptotagmin* *dd_Smed_v6_4222_0_1*, *dd_Smed_v6_6730_0_1*, and *dd_Smed_v6_6920_0_1*¹⁴⁸ (magenta)—and DAPI (nuclei – blue). Images focus on the head, while insets show the CNS, PhNS, and PNS. D) Quantification of C. Schematics above the bars indicate the region of the nervous system for quantitation. N = 8 animals, 23-142 cells/region/animal. E) Co-expression of a pool of muscle markers *myo-D* and *mhc*^{149,150} (magenta), *TH* (green), and DAPI (nuclei- blue) in the tail as well as orthogonal projections of those images. Schematic showing the location of PNS *TH*⁺ cells just ventral to the dorsal body wall muscle. F) Quantification of co-expression of *TH* and *DAT*, expanded from Fig. 1C. G) Quantification of co-expression of *TH* and *TBH*, expanded from Fig. 1D. H) Co-expression of *AADCα* (magenta), *TBH* (green), and DAPI (nuclei – blue) in the CNS. I) Quantification of H. N = 4 animals, 94-114 cells/animal. Scale bars = 50 μm (A), 20 μm (A', C, F, H). See Source Data File for more information.



Supplementary Figure 2: Expression patterns of genes from the screen. A-G) Genes expressed in different regions of the nervous system. H) Genes with both neural and obvious non-neural expression. Red boxes denote genes for which RNAi impacted TH^+ cells (See Fig. 1L). Scale bars = 200 μm .



Supplementary Figure 3: Additional co-expression of *TH* with genes from the screen.

A-H) Representative images and quantification of co-expression with *TH* for eight genes

(*ncam2*, *celsr1*, *ces*, *dd_Smed_v6_6445_0_1*, *cd82*, *scgn*, *cav-1*, and *dd_Smed_v6_459_0_1*)

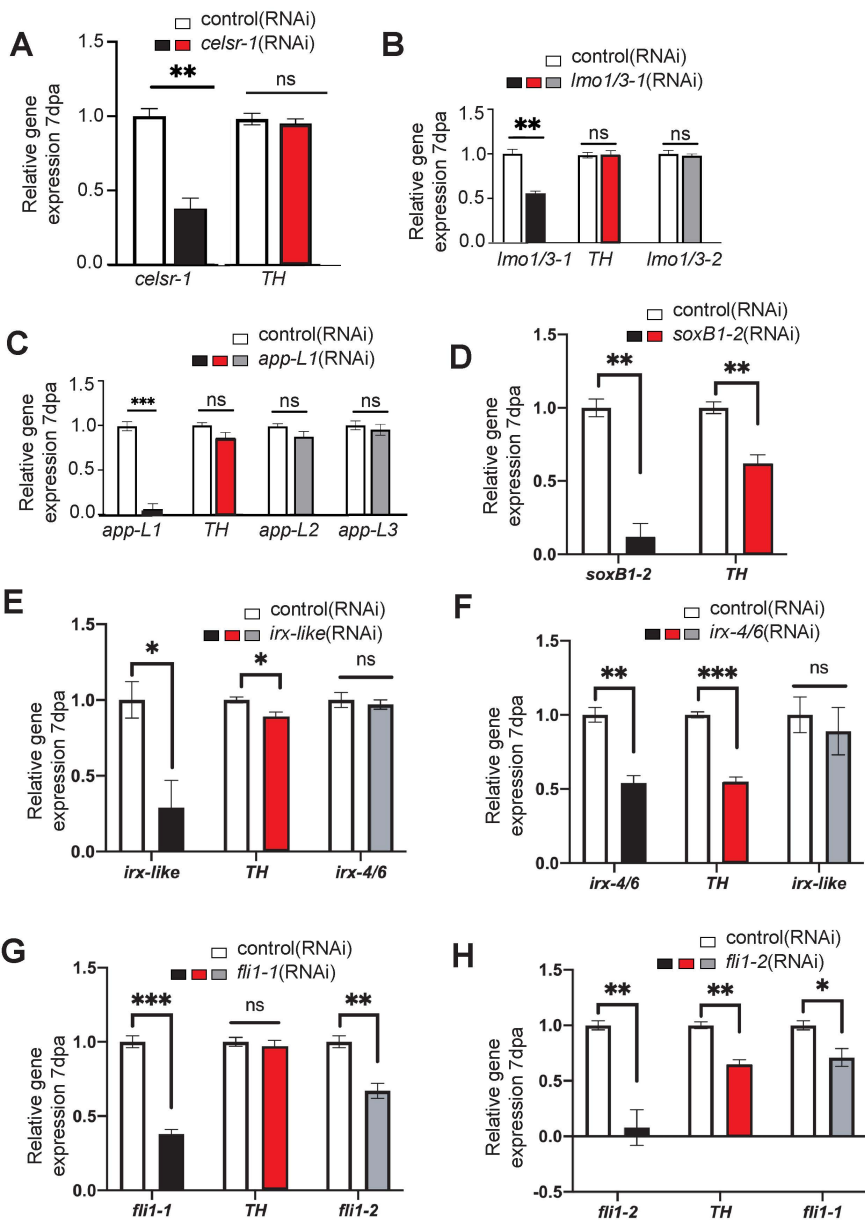
found in different regions of the nervous system. For each gene, a colorimetric ISH is shown on the left, with insets showing co-expression of the gene of interest (magenta) and *TH* (green) visualized after FISH with DAPI (blue), along with single channels shown in grayscale.

Quantification of *TH*⁺ cells expressing each gene is shown in white text in the inset. Only regions with gene expression are shown for each panel. N = 4-5 animals per gene pair, 20-295 cells/region/animal. Scale bars = 200 μm (colorimetric), 20 μm (insets). See Source Data File for more information.

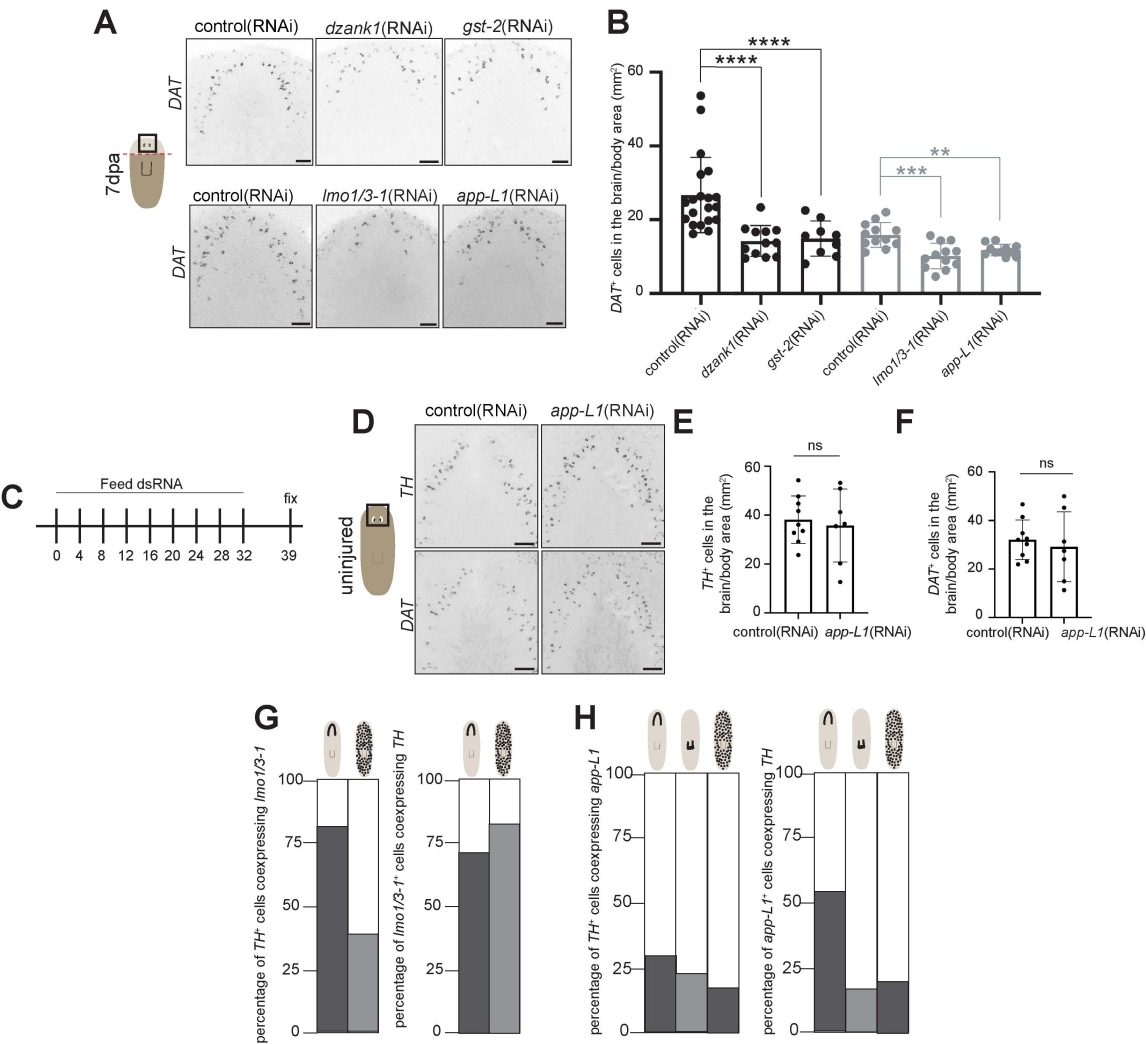
Black: Efficiency check

Red: Impact on TH

Grey: Specificity check



Supplementary Figure 4: RT-qPCR confirming knockdown efficiency, target specificity, and level of *TH* after RNAi. A-H) Relative gene expression of genes of interest 7 dpa (days post amputation) after knockdown of selected candidate genes. For each RNAi, RT-qPCR was completed using 3 biological and 3 technical triplicates. An unpaired t-test was used for all statistical analyses. Graphs show mean and standard error. Black bar graphs = knockdown checks for indicated candidate genes. Red bar graphs = evaluation of *TH* transcript. Gray bar graphs = specificity checks with paralogous genes. Level of *celsr-1* in *celsr-1*(RNAi) P = 0.0020. Level of *lmo1/3-1* in *lmo1/3-1*(RNAi) P = 0.0015. Level of *app-L1* in *app-L1*(RNAi) P = 0.0003. In *soxB1-2*(RNAi) level of *soxB1-2* P = 0.0012, level of *TH* P = 0.0062. In *irx-like*(RNAi) level of *irx-like* P = 0.0373, level of *TH* P = 0.0455. In *irx-4/6*(RNAi) level of *irx-4/6* P = 0.0029, level of *TH* P = 0.0005. In *fli1-1*(RNAi) level of *fli1-1* P = 0.0004, level of *fli1-2* P = 0.0076. In *fli1-2*(RNAi) level of *fli1-2* P = 0.0234, level of *TH* P = 0.0029, level of *fli1-2* P = 0.0491. See Source Data File for more information.

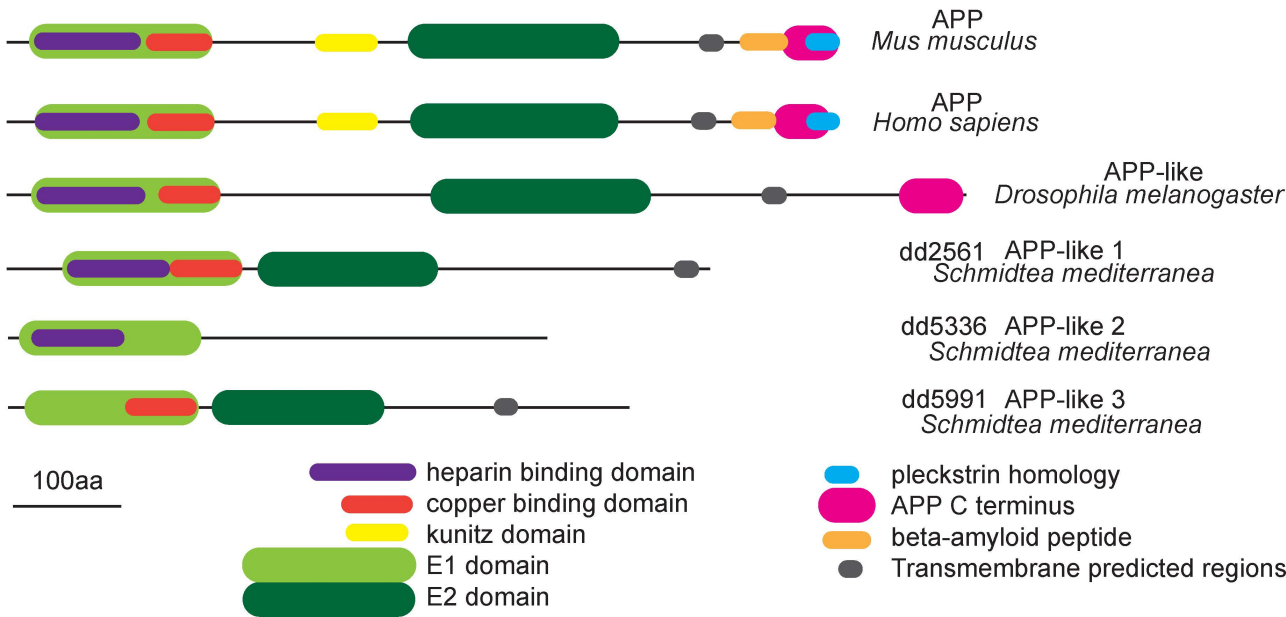


Supplementary Figure 5: *lmo1/3-1* and *app-L1* are required for proper expression of *DAT*.

A) Inverted grayscale FISH images showing *DAT*⁺ cells in the regenerated tiara 7 dpa (days post amputation) after knockdown of *dzank1*, *gst-2*, *lmo1/3-1* or *app-L1*. B) Quantification of animals from A. Left - One-way ANOVA with Dunnett's multiple comparisons test. Right – Brown-Forsyth and Welch ANOVA with Dunnett's T3 multiple comparisons test. **** P < 0.0001, control vs *lmo1/3-1*(RNAi) P = 0.0009; control vs *app-L1*(RNAi) P = 0.0028. N = 9 animals (*gst-2*), N = 11 (*app-L1*), N = 12 (*dzank1*, control 2, *lmo1/3-1*), N = 20 (control 1). C) Long-term RNAi maintenance paradigm. D) Inverted grayscale FISH images showing either *TH*⁺ (top) or *DAT*⁺ cells (bottom) in the maintained tiara after knockdown of *app-L1*. E-F) Quantification of D. Unpaired t-test. G) Expanded quantification of co-expression of *TH* and *lmo1/3-1* from Fig. 2E. H) Expanded quantification of co-expression of *TH* and *app-L1* from Fig. 2F. Schematics above the bars indicate the region of the nervous system analyzed. Scale bars = 50 μm. Bars depict mean and standard deviation. See Source Data File for more information.

extracellular N-terminus

intracellular C-terminus

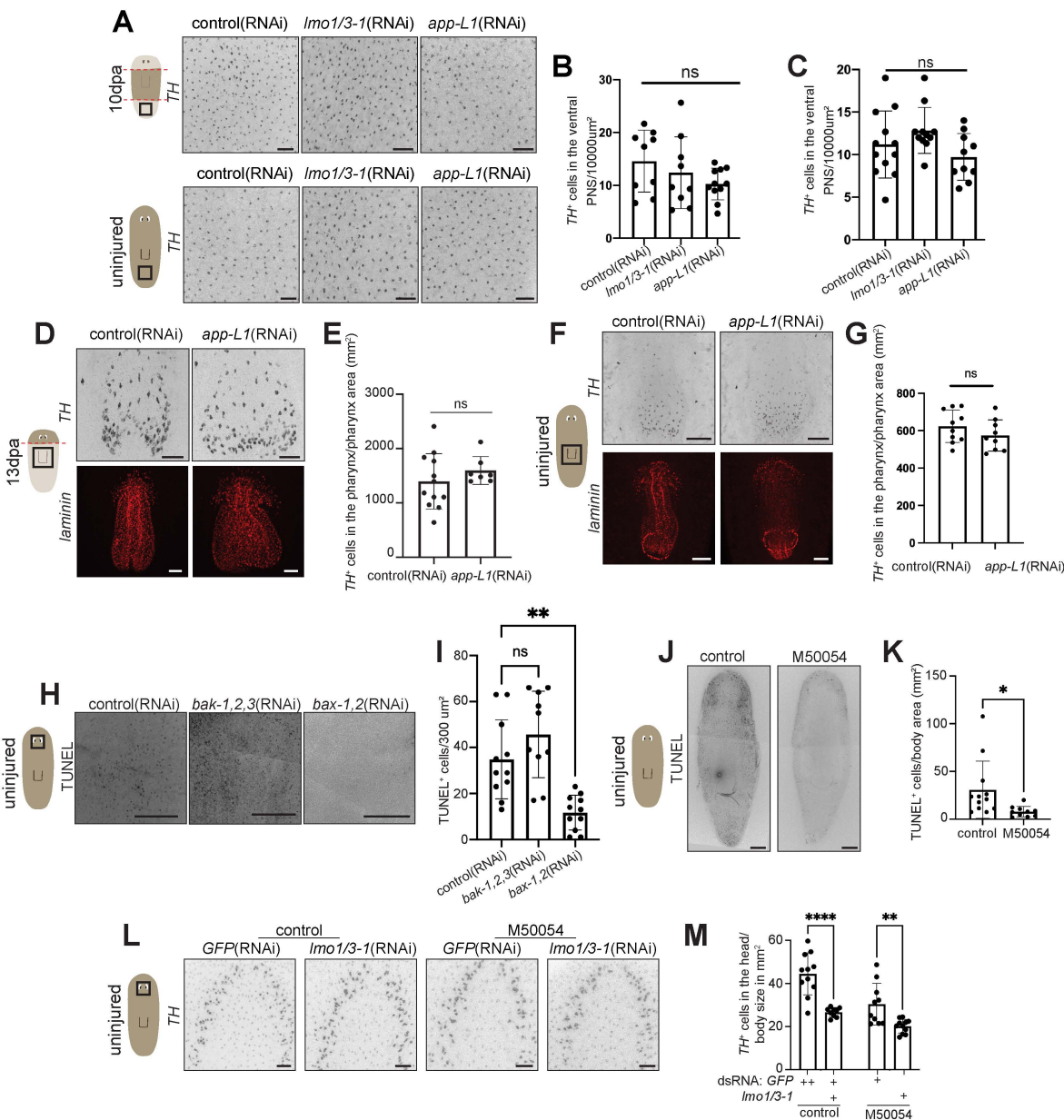


Supplementary Figure 6: APP domain analysis Ovals denote protein domains and regions.

Purple = heparin binding domain, dark orange = copper binding domain, yellow = kunitz

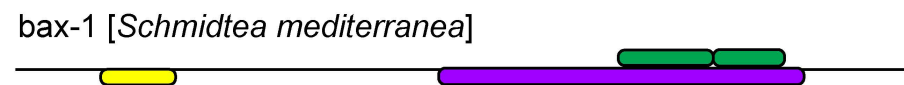
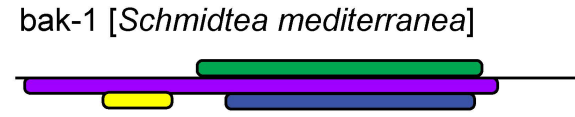
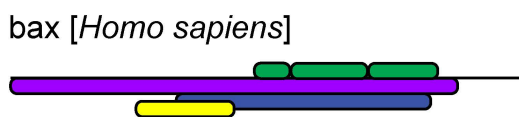
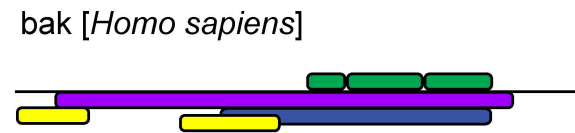
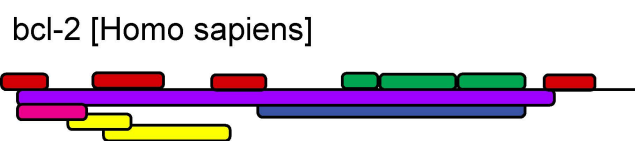
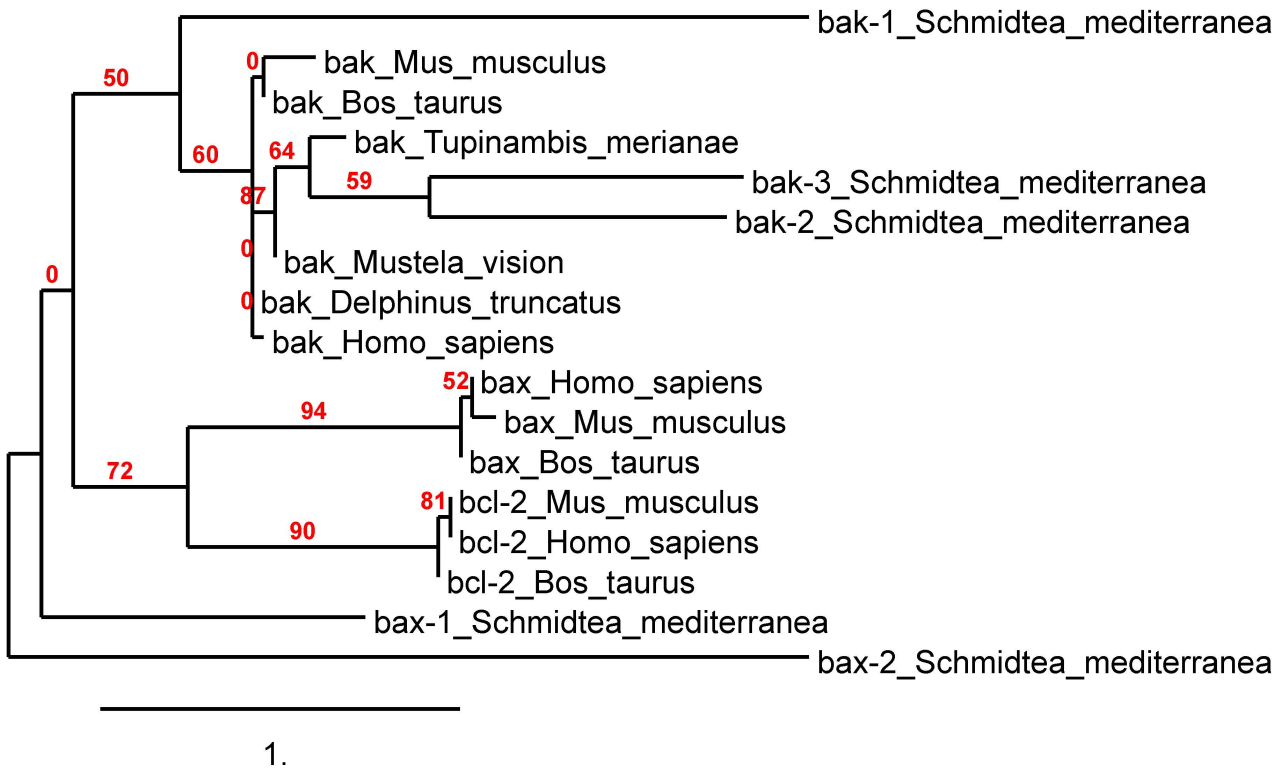
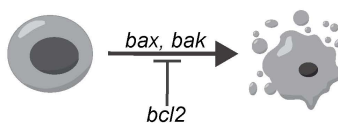
domain, light green = E1 domain, dark green = E2 domain, blue = pleckstrin homology, pink =

APP C terminus, light orange = beta-amyloid peptide, gray = transmembrane predicted regions.



Supplementary Figure 7: *lmo1/3-1* and *app-L1* do not affect the PNS or PhNS. A) Inverted grayscale FISH images showing either TH^+ cells in regenerated tails 10 days post trunk amputation (top) or uninjured tails (bottom) after knockdown of *lmo1/3-1* or *app-L1* compared to control. B-C) Quantification of A. One-way ANOVA with Dunnett's multiple comparisons test. B) N = 9 (control, *lmo1/3-1*), 11 (*app-L1*) C) N = 10 (*app-L1*), 11 (*lmo1/3-1*), 12 (control). D) FISH images showing TH^+ cells (top, inverted grayscale) in regenerated pharynges (marked with *laminin*, bottom, red) 13 dpa (days post amputation) after knockdown of *app-L1* compared to control. E) Quantification of TH^+ cells in D normalized to pharynx size. Unpaired t-test. N = 7 (*app-L1*), 12 (control). F) FISH images showing TH^+ cells (top, inverted grayscale) in maintained pharynges (marked with *laminin*, bottom, red) after knockdown of *app-L1* compared to control. N = 9 (*app-L1*), 10 (control). G) Quantification of TH^+ cells in F normalized to pharynx size. Unpaired t-test with Welch's correction. H-K) Validation of cell death inhibition. H) Inverted grayscale TUNEL staining in the uninjured head for either control, *bak-1,2,3*(RNAi), or *bax-1,2*(RNAi). I) Quantification of H measuring TUNEL⁺ cells/300 μm^2 region in the head. Brown-Forsythe and Welch One-way ANOVA with Dunnett's T3 multiple comparisons test. Control vs *bax-1,2*(RNAi) P = 0.0023. N = 10 (*bak-1,2,3*), 11 (control, *bax-1,2*). J) TUNEL staining in either control or animals dosed with 80 μM M50054 for 18.5 hours. K) Quantification of J measuring the total TUNEL⁺ cells in the animal, with respect to body size. Unpaired t-test with Welch's correction. P = 0.0239. N = 10 (M50054), 12 (control). L) Inverted grayscale FISH showing TH^+ staining in the CNS in either control or *lmo1/3-1*(RNAi) animals with and without M50054 treatment. M) Quantification of L. Two-way ANOVA, Šidák's multiple comparisons test. *GFP*(RNAi) Control P < 0.001; *GFP*(RNAi) M50054 treatment P = 0.0050. N = 9 (*lmo1/3-1* control), 10 (*GFP* M50054), 11 (*GFP* control, *lmo1/3-1* M50054). Scale bars = 200 μm (J),

100 μm (F), 50 μm (A, D, H, L). Bars depict mean and standard deviation. See Source Data File for more information.

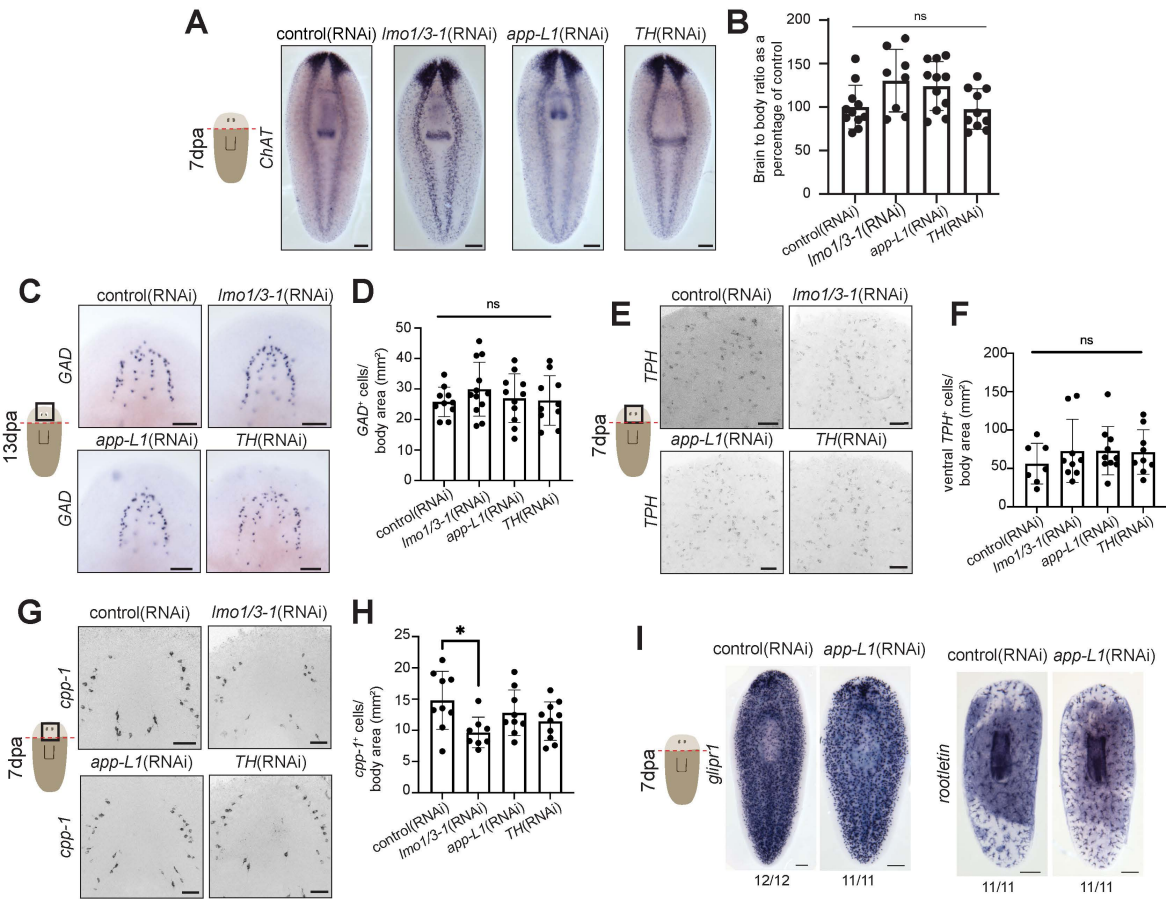


100aa

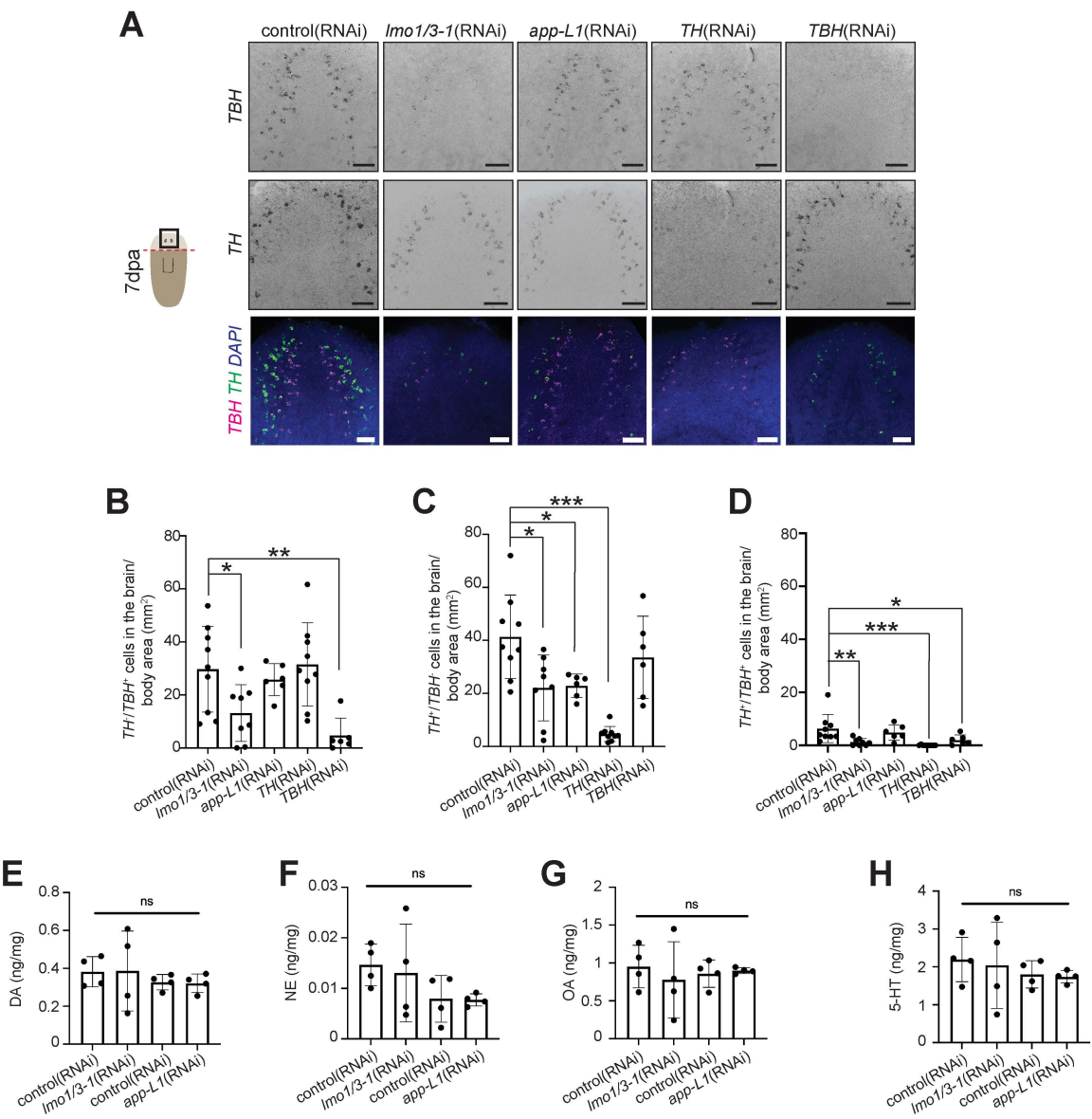
- *bcl-2* apoptosis regulator
- *bcl-2*-like apoptosis regulator
- *bcl-2* inhibitors of programmed cell death
- *bcl-2* BH1-3 domains
- *bcl-2* BH4 domain
- intrinsically disordered region

Supplementary Figure 8: BAX and BAK phylogeny and domain analysis Top – phylogeny:

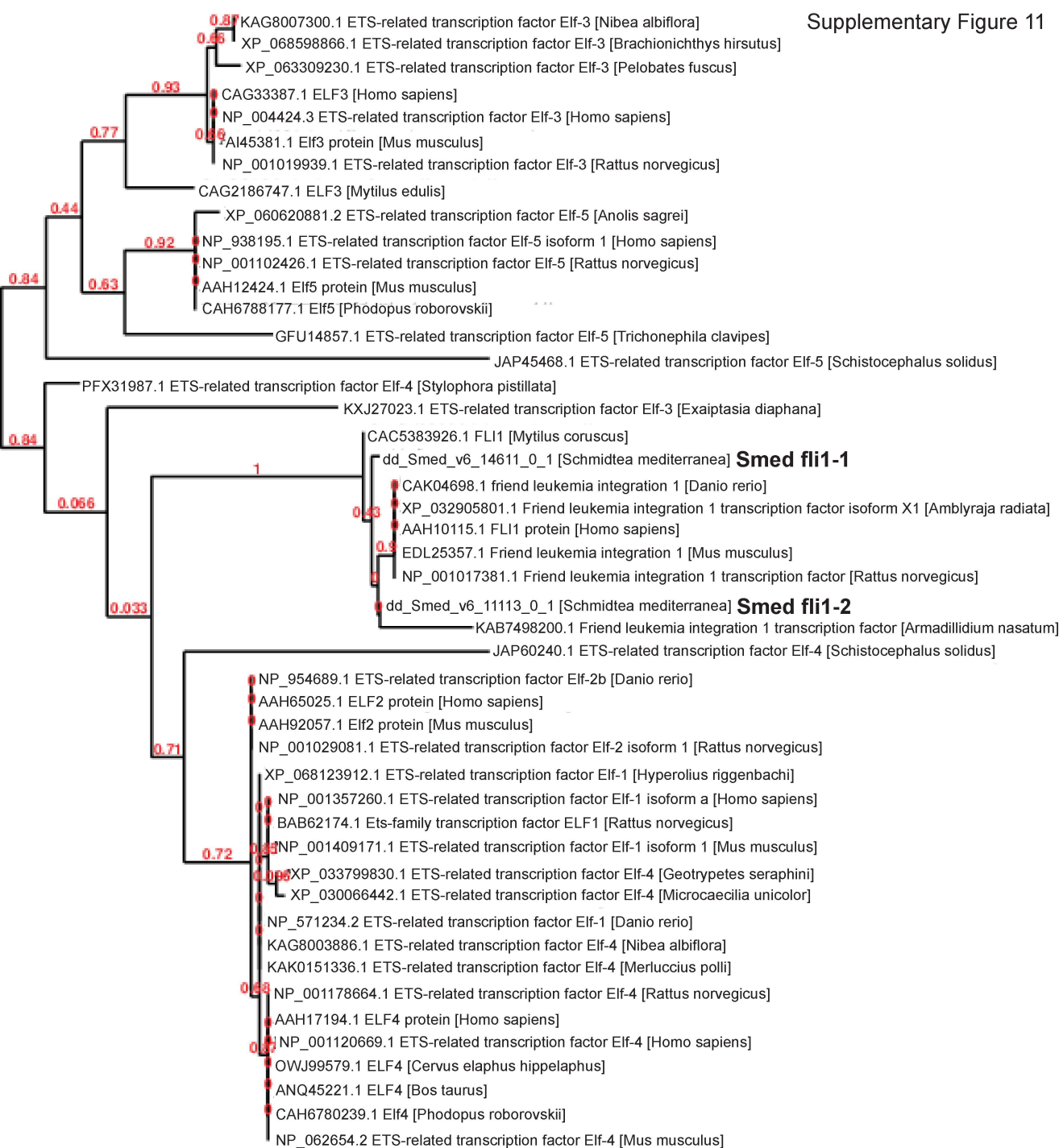
Numbers in red denote bootstrap percentages. Scale indicates substitutions per site. Bottom – domains: Ovals denote protein domains. Red = bcl-2 apoptosis regulator (hallmark of bcl-2 proteins), green = bcl-2-like apoptosis regulator, purple = bcl-2 inhibitors of programmed cell death, blue = bcl-2 BH1-3 domains, pink = bcl-2 BH4 domain (hallmark of bcl-2 proteins), yellow = intrinsically disordered region. Scale indicates 100aa (amino acids).



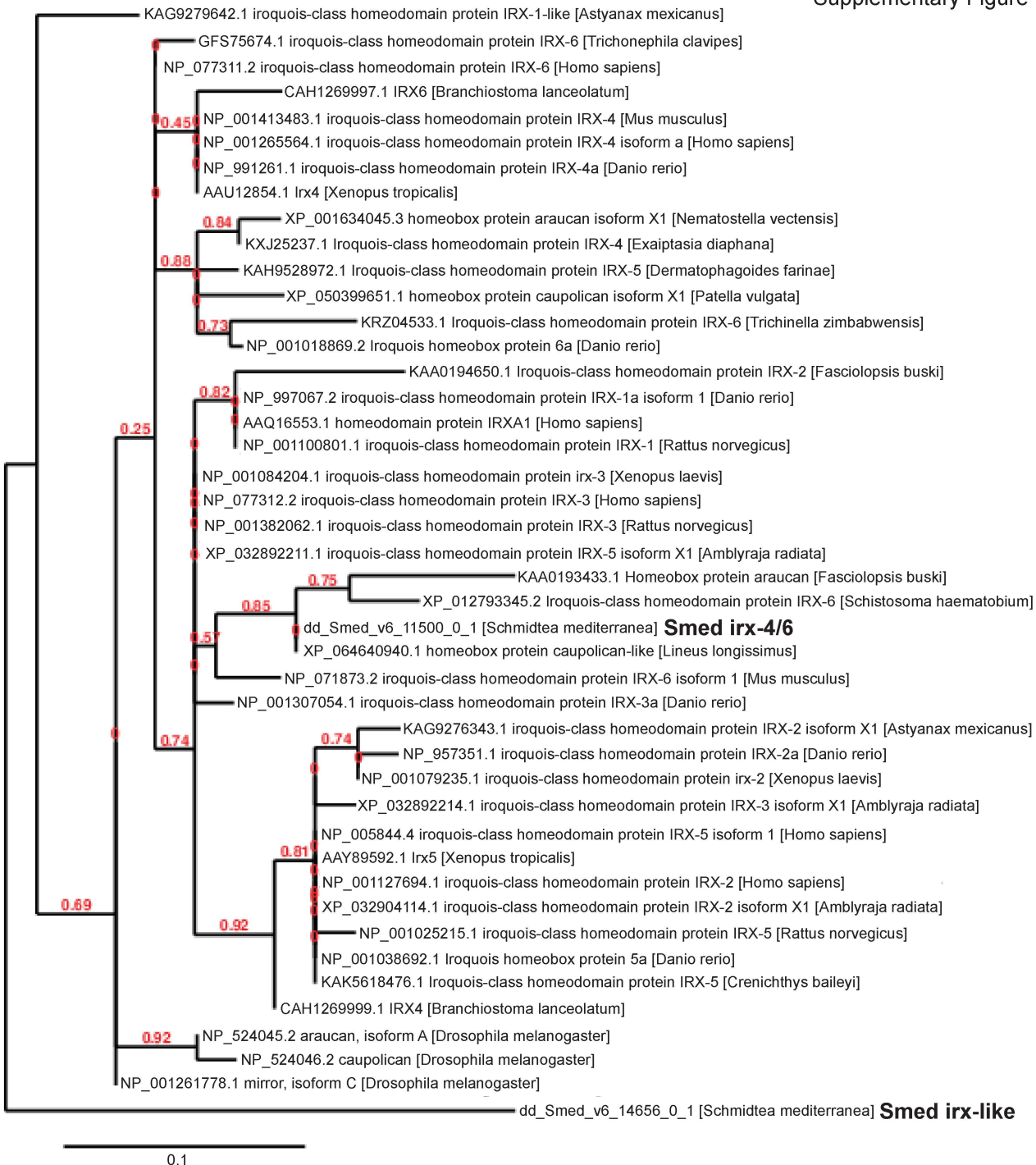
Supplementary Figure 9: Specificity of *lmo1/3-1* and *app-L1*. A) Colorimetric ISH showing regenerated brain size (marked with *ChAT*⁹³) 7 dpa (days post amputation) after knockdown of either *lmo1/3-1*, *app-L1*, or *TH* compared to control. B) Quantification of A. One-way ANOVA and Dunnett's multiple comparisons test. N = 8 (*lmo1/3-1*), 10 (*TH*), 11 (control, *app-L1*). C) Colorimetric ISH showing *GAD*⁺ cells in 13 dpa regenerated heads after knockdown of *lmo1/3-1*, *app-L1*, or *TH* compared to control. Animals were allowed 13 days to regenerate to ensure that *GAD*⁺ cells were present. D) Quantification of C. One-way ANOVA, Dunnett's multiple comparisons test. N = 10 (control, *TH*), 11 (*app-L1*), 12 (*lmo1/3-1*). E) Inverted grayscale FISH images showing *TPH*⁺ cells in 7 dpa regenerated heads after knockdown of *lmo1/3-1*, *app-L1*, or *TH* compared to control. F) Quantification of E. One-way ANOVA and Dunnett's multiple comparisons test. N = 7 (control), 9 (*lmo1/3-1*, *TH*), 10 (*app-L1*). G) Inverted grayscale FISH images showing *cpr-1*⁺ cells in 7 dpa regenerated heads after knockdown of *lmo1/3-1*, *app-L1*, or *TH* compared to control. H) Quantification of G. One-way ANOVA and Dunnett's multiple comparisons test. One-way ANOVA and Dunnett's multiple comparisons test. P = 0.0155. N = 8 (*lmo1/3-1*), 9 (*app-L1*, control), 10 (*TH*). I) Colorimetric ISH showing either *glpr-1*⁺ or *rootletin*⁺ cells in animals 7 days into head regeneration and after knockdown of *app-L1* compared to control. Scale bars = 200 μ m (A, I), 50 μ m (C, E, G). Bars depict mean and standard deviation. See Source Data File for more information.



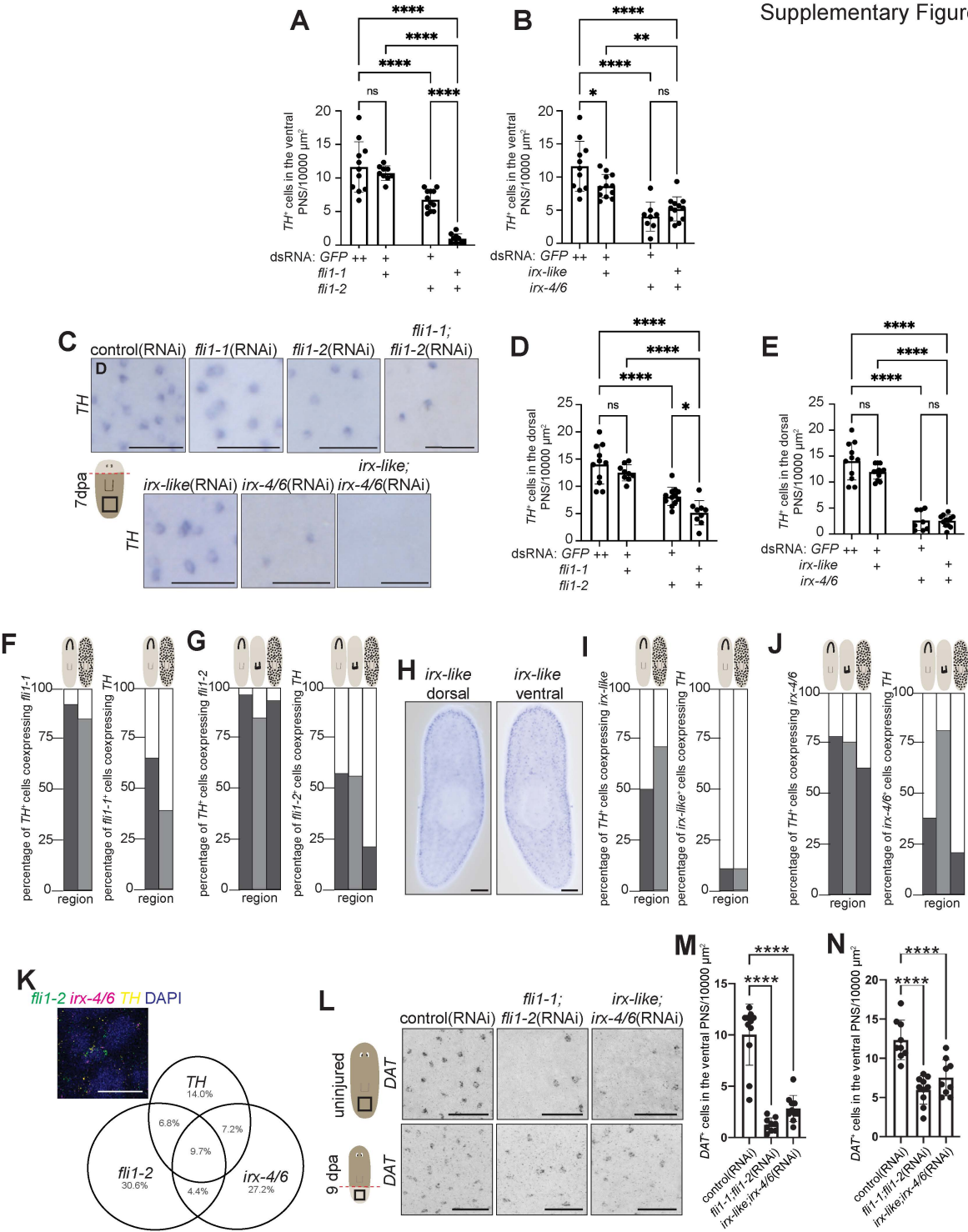
Supplementary Figure 10: Specificity of *lmo1/3-1* and *app-L1*, continued. A) FISH images showing either *TBH* (top – inverted grayscale), *TH* (middle – inverted grayscale), or both (bottom - *TBH* magenta, *TH* green, DAPI blue) in regenerated heads after knockdown of *lmo1/3-1*, *app-L1*, *TH*, or *TBH* compared to control, 7 dpa (days post amputation). B-D) Quantification of A. B) Brown-Forsyth and Welch ANOVA with Dunnett's T3 multiple comparisons. Control vs *lmo1/3-1*(RNAi) P = 0.0384; control vs *TBH*(RNAi) P = 0.0026. C-D) One-way ANOVA with Dunnett's multiple comparisons test. *TH*⁺/*TBH*⁺ cells control vs *lmo1/3-1*(RNAi) P = 0.0488; control vs *app-L1*(RNAi) P = 0.0280; control vs *TH*(RNAi) P = 0.0003. *TH*⁺/*TBH*⁺ cells control vs *lmo1/3-1*(RNAi) P = 0.0054; control vs *TH*(RNAi) P = 0.0004; control vs *TBH*(RNAi) P = 0.0355. N = 6 (*app-L1*, *TBH*), 8 (*lmo1/3-1*), 9 (control, *TH*). E-H) Amount of dopamine, norepinephrine, octopamine, and serotonin detected after control, *lmo1/3-1* knockdown, or *app-L1* knockdown. Two separate unpaired t-tests - *lmo1/3-1* versus control used unpaired t-test with Welch's correction. N = 4 homogenized samples of 12 animals/condition. Scale bars = 50 μ m. Bars depict mean and standard deviation. See Source Data File for more information.



Supplementary Figure 11: FLI phylogeny Numbers in red denote bootstrap values. Scale at the bottom indicates substitutions per site.

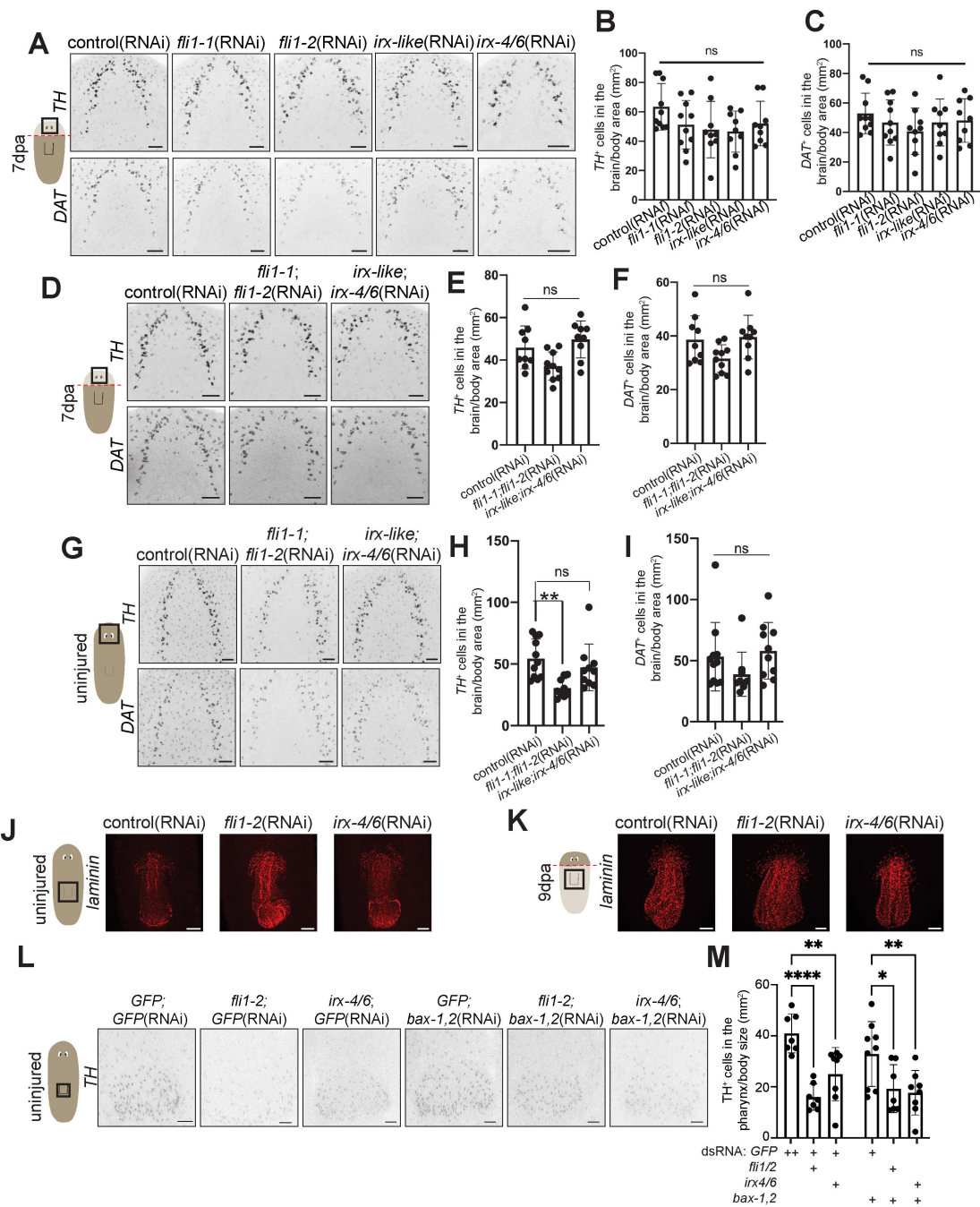


Supplementary Figure 12: IRX phylogeny Numbers in red denote bootstrap values. Scale at the bottom indicates substitutions per site.



Supplementary Figure 13: *FLI* and *IRX* genes are required for regeneration and maintenance of PNS dopaminergic neurons. A-B) Data from Fig. 3B repeated, showing the results of a Two-way ANOVA with Tukey's comparisons, comparing single knockdowns to their respective double knockdowns. A) *FLI* genes vs. control - Source of variation: Interaction 7.079% P = 0.0011; *fli1-1*(RNAi) 13.21% P < 0.0001; *fli1-2*(RNAi) 63.63% P < 0.0001. **** P < 0.0001. B) *IRX* genes vs. control – Source of variation: Interaction 7.7392%, P = 0.0110; *irx-like* 1.460%, P = 0.2424; *irx-4/6* 52.30% P < 0.0001. control vs *irx-like*(RNAi) P = 0.0330; *irx-like*(RNAi) vs *irx-like;irx-4/6*(RNAi) P = 0.0092. C) Post-pharyngeal insets of colorimetric ISH imaged on the dorsal side showing *TH*⁺ cells in the maintained tail 7 dpa (days post [head] amputation) after knockdown of *fli1-1*, *fli1-2*, *fli1-1;fli1-2*, *irx-like*, *irx-4/6*, or *irx-like;irx-4/6* compared to control. D-E) Quantification of dorsal PNS *TH*⁺ cell number. Two-way ANOVA with Tukey's comparisons test comparing the single knockdowns to their respective double knockdowns. D) *FLI* genes vs. control - Source of variation: Interaction 0.772%, P = 0.3423; *fli1-1*(RNAi) 7.291% P = 0.0055; *fli1-2*(RNAi) 62.42% P < 0.0001. *fli1-2*(RNAi) vs *fli1-1;fli1-2*(RNAi) P = 0.0395. E) *IRX* genes vs. control – Source of variation: Interaction 0.7877%, P = 0.1463; *irx-like* 0.8764%, P = 0.1260; *irx-4/6* 82.92% P < 0.0001. F-G) Extended quantification of co-expression from Fig. 3C-D. Schematics above the bars denote the region of the nervous system being quantified. H) Colorimetric ISH showing the polarized expression of *irx-like* in the same worm, dorsal (left) and ventral (right). I-J) Extended quantification of co-expression from Fig. 3E-F. Schematics above the bars denote the region of the nervous system being quantified. K) Top: Triple FISH showing co-expression of *TH* (yellow), *fli1-2* (green), *irx-4/6* (magenta) and DAPI (nuclei - blue) in the uninjured tail. Bottom: Euler diagram showing overlap of expression between genes with percentage of co-expressed cells listed. A total of 60 cells per

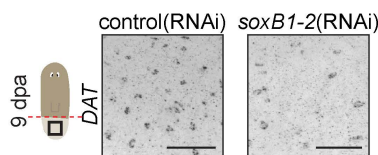
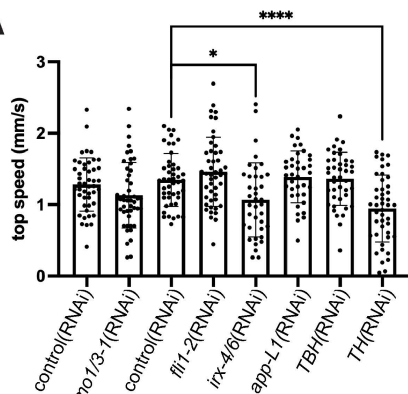
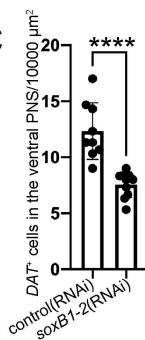
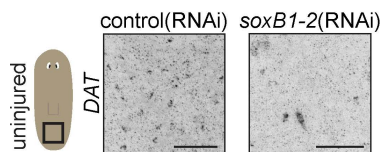
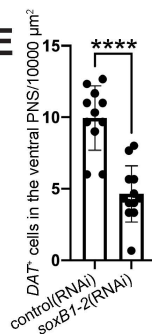
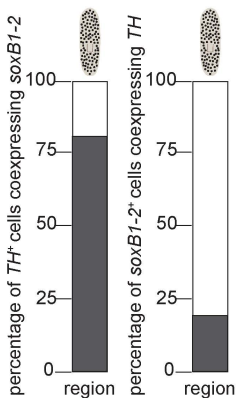
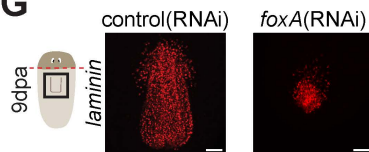
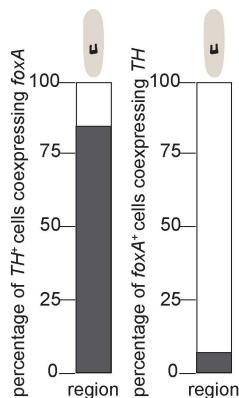
animal in 7 animals was measured. L) Inverted grayscale FISH images showing *DAT*⁺ cells in the maintained tail (top) or regenerated tail 7 dpa (bottom) after double knockdown of *fli1-1;fli1-2* or *irx-like;irx-4/6* compared to control. M) Quantification of PNS *DAT*⁺ cell number in maintained tail tissue. One-way ANOVA with Dunnett's multiple comparisons test. Control vs. *fli1-1;fli1-2*(RNAi) $P < 0.0001$; control vs. *irx-like;irx-4/6*(RNAi) $P < 0.0001$. $N = 9$ (*fli1-1;fli1-2*), 10 (*irx-like;irx-4/6*), 11 (control). N) Quantification of PNS *DAT*⁺ cell number in 7 dpa tail tissue. One-way ANOVA with Dunnett's multiple comparisons test. Control vs. *fli1-1;fli1-2*(RNAi) $P < 0.0001$; control vs. *irx-like;irx-4/6*(RNAi) $P < 0.0001$ $N = 9$ (all conditions). Scale bars = 200 μm (H), 50 μm (C, K). Bars depict mean and standard deviation. See Source Data File for more information.



Supplementary Figure 14: *FLI* and *IRX* genes regulate *TH*⁺ cells and *DAT*⁺ cells in the CNS

and PhNS. A) Inverted grayscale FISH images showing either *TH*⁺ cells (top) or *DAT*⁺ cells (bottom) in the regenerated brain 7 dpa (days post amputation) after knockdown of *fli1-1*, *fli1-2*, *irx-like*, or *irx-4/6* compared to control. B) Quantification of A top. One-way ANOVA with Dunnett's multiple comparisons test. N = 9 (*fli1-2*, *irx-like*, *irx-4/6*), 10 (control, *fli1-2*). C) Quantification of A bottom. One-way ANOVA with Dunnett's multiple comparisons test. N = 9 (*fli1-2*, *irx-like*, *irx-4/6*), 10 (control, *fli1-2*). D) Inverted grayscale FISH images showing either *TH*⁺ cells (top) or *DAT*⁺ cells (bottom) in the regenerated brain 7 dpa after double knockdown of *fli1-1*;*fli1-2* or *irx-like*;*irx-4/6* compared to control. E) Quantification of D, top. One-way ANOVA with Dunnett's multiple comparisons test. N = 9 (control, *irx-like*;*irx-4/6*), 10 (*fli1-1*;*fli1-2*). F) Quantification of D, bottom. One-way ANOVA with Dunnett's multiple comparisons test. N = 9 (control, *irx-like*;*irx-4/6*), 10 (*fli1-1*;*fli1-2*). G) Inverted grayscale FISH images showing either *TH*⁺ cells (top) or *DAT*⁺ cells (bottom) in the maintained brain after double knockdown of *fli1-1*;*fli1-2* or *irx-like*;*irx-4/6* compared to control. H) Quantification of G, top. One-way ANOVA with Dunnett's multiple comparisons test. Control vs. *fli1-1*;*fli1-2*(RNAi) P = 0.0015. N = 9 (*fli1-1*;*fli1-2*), 10 (*irx-like*;*irx-4/6*), 11 (control). I) Quantification of G, bottom. One-way ANOVA with Dunnett's multiple comparisons test. N = 9 (*fli1-1*;*fli1-2*), 10 (*irx-like*;*irx-4/6*), 11 (control). J) FISH images showing *laminin* expression in maintained pharynges after knockdown of *fli1-2* or *irx-4/6* compared to control. K) FISH images showing *laminin* expression in regenerated pharynges 9 dpa after knockdown of *fli1-2* or *irx-4/6* compared to control. L) Inverted grayscale FISH images showing *TH*⁺ cells in the PhNS of uninjured animals in either control or *fli1-2* or *irx-4/6*(RNAi) with and without blocking cell death through *bax-1,2*(RNAi). M) Quantification of L. Two-way ANOVA, Tukey's multiple

comparisons test. *gfp;gfp* vs *fli1-2;gfp* $P < 0.0001$. *gfp;gfp* vs *irx-4/6;gfp* $P = 0.0026$. *gfp;bax* vs *fli1-2;gfp* $P = 0.0105$. *gfp;bax* vs *irx-4/6;gfp* $P = 0.0023$. $N = 7$ (*gfp;gfp*, *fli1-2;gfp*, *fli1-2;bax*), 8 (*irx-4/6;gfp*, *irx-4/6;bax*), 9 (*gfp;bax*). Scale bars = 100 μm (J, L), 50 μm (A, D, G, H, K). Bars depict mean and standard deviation. See Source Data File for more information.

B**A****C****D****E****F****G****H**

Supplementary Figure 15: *soxB1-2* and *foxA* regulate dopaminergic neurons in a location-

specific manner. A) Speed of animals 6 dpa (days post amputation). Analysis for *lmo1/3-*

l(RNAi) and its control using an unpaired t-test. Analysis for all other conditions vs. Control

using one way ANOVA with Dunnett's multiple comparisons test. Control vs *irx-4/6*(RNAi) P =

0.0151; control vs *TH*(RNAi) P < 0.0001. B) Inverted grayscale FISH images showing *DAT*⁺

cells in regenerated tails 9 dpa after knockdown of *soxB1-2* compared to control. C)

Quantification of B. Unpaired t-test. P < 0.0001. N = 9 (control), 10 (*soxB1-2*). D) Inverted

grayscale FISH images showing *DAT*⁺ cells in maintained tail after knockdown of *soxB1-2*

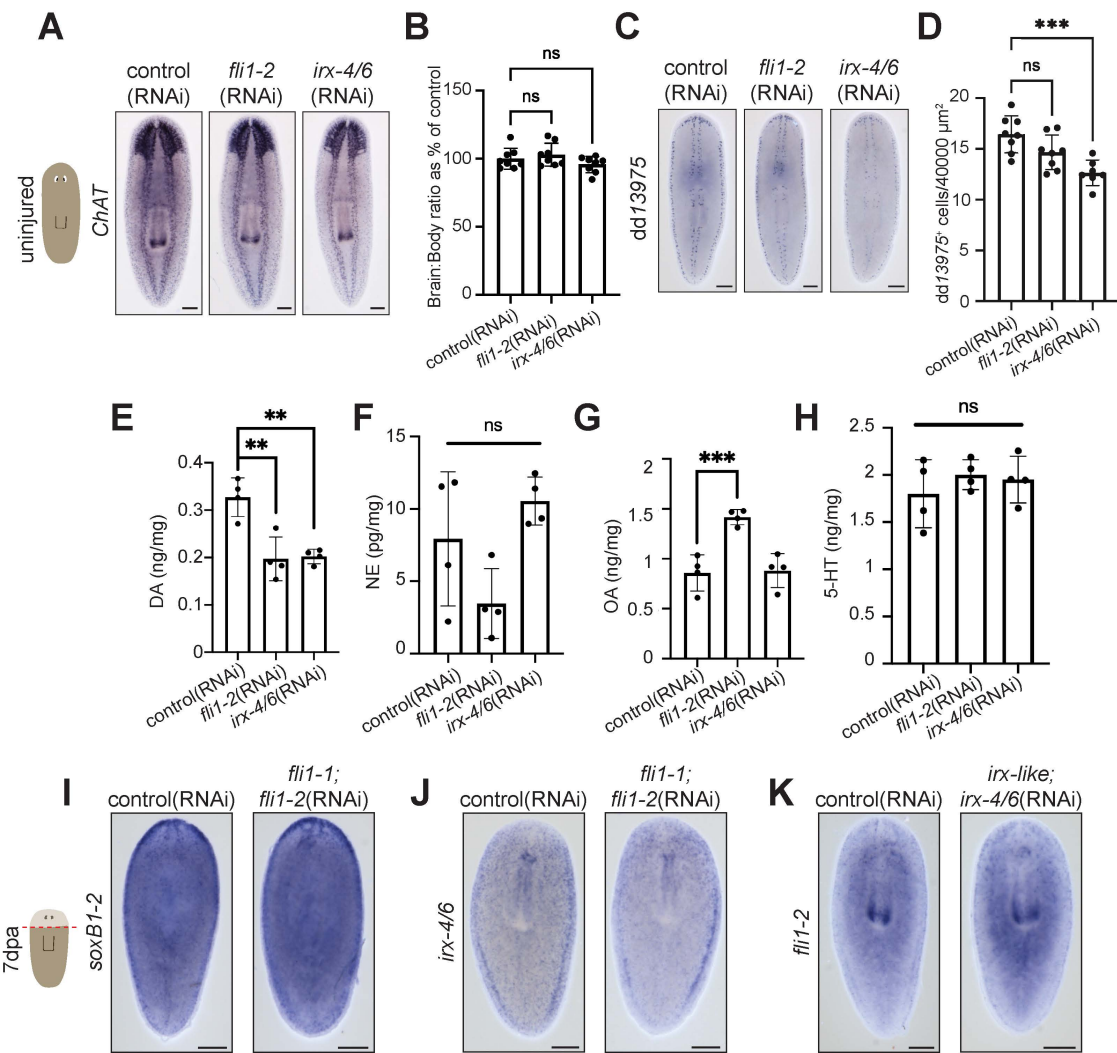
compared to control. E) Quantification of D. Unpaired t-test. P < 0.0001. N = 11 (control), 12

(*soxB1-2*). F) Extended quantification of co-expression shown in Fig. 7G. G) FISH images

showing *laminin* expression in regenerated pharynges 9 dpa after knockdown of *foxA* compared

to control. H) Extended quantification of co-expression shown in Fig. 7J. Scale bars = 50 μ m.

Bars depict mean and standard deviation. See Source Data File for more information.



Supplementary Figure 16: Transcription factor-encoding genes regulate each other and may affect non-dopaminergic neurons.

A) Whole-body colorimetric ISH showing *Chat* expression in uninjured animals after knockdown of either *fli1-2* or *irx-4/6*. B) Quantification of A. One-way ANOVA with Dunnett's multiple comparisons test. N = 8 (all conditions). C) Whole-body colorimetric ISH showing *dd_Smed_v6_19375_0_1* expression in uninjured animals after knockdown of either *fli1-2* or *irx-4/6*. D) Quantification of C. One-way ANOVA with Dunnett's multiple comparisons test. Control vs. *irx-4/6*(RNAi) P = 0.0004. N = 7 (*irx-4/6*), 8 (control and *fli1-2*). E-H) HPLC results showing mass of each neurotransmitter detected in animals 7 dpa (days post [head] amputation) after knockdown of either *fli1-2* or *irx-4/6* compared to control. Each point on the graph represents a single replicate of 9-12 homogenized animals. One-way ANOVA with Dunnett's multiple comparisons test. DA control(RNAi) vs. *fli1-2*(RNAi) P = 0.0048, control(RNAi) vs. *irx-4/6*(RNAi) P = 0.0066; OA control(RNAi) vs. *fli1-2*(RNAi) P = 0.001. I) Whole-body colorimetric ISH showing *soxB1-2* expression 7 days post head amputation after double knockdown of *fli1-1;fli1-2*. J) Whole-body colorimetric ISH showing *irx-4/6* expression 7 days post head amputation after double knockdown of *fli1-1;fli1-2*. K) Whole-body colorimetric ISH showing *fli1-2* expression 7 days post head amputation after double knockdown of *irx-like;irx-4/6*. Scale bars = 200 μ m. Bars depict mean and standard deviation. See Source Data File for more information.

Supplementary Data 1: Primers, Enrichment, and BLAST analysis

Tab 1: All genes used in this study – primer sequences and enrichment in TH^+ clusters for genes from the screen

Tab 2: BLAST analysis used for nomenclature of select genes

Supplementary Data 2: RNAseq results

Tab 1: *fli1-1*; *fli1-2*(RNAi) vs control(RNAi)

Tab 2: *irx-4/6*; *irx-like*(RNAi) vs control(RNAi)

Tab 3: *soxB1-2*(RNAi) vs control(RNAi)

Tab 4: levels of neural genes and genes from the screen across RNAi conditions; yellow highlighted cells indicate a P-value less than 0.05.