



Figures and figure supplements

Lmx1b is required at multiple stages to build expansive serotonergic axon architectures

Lauren J Donovan et al

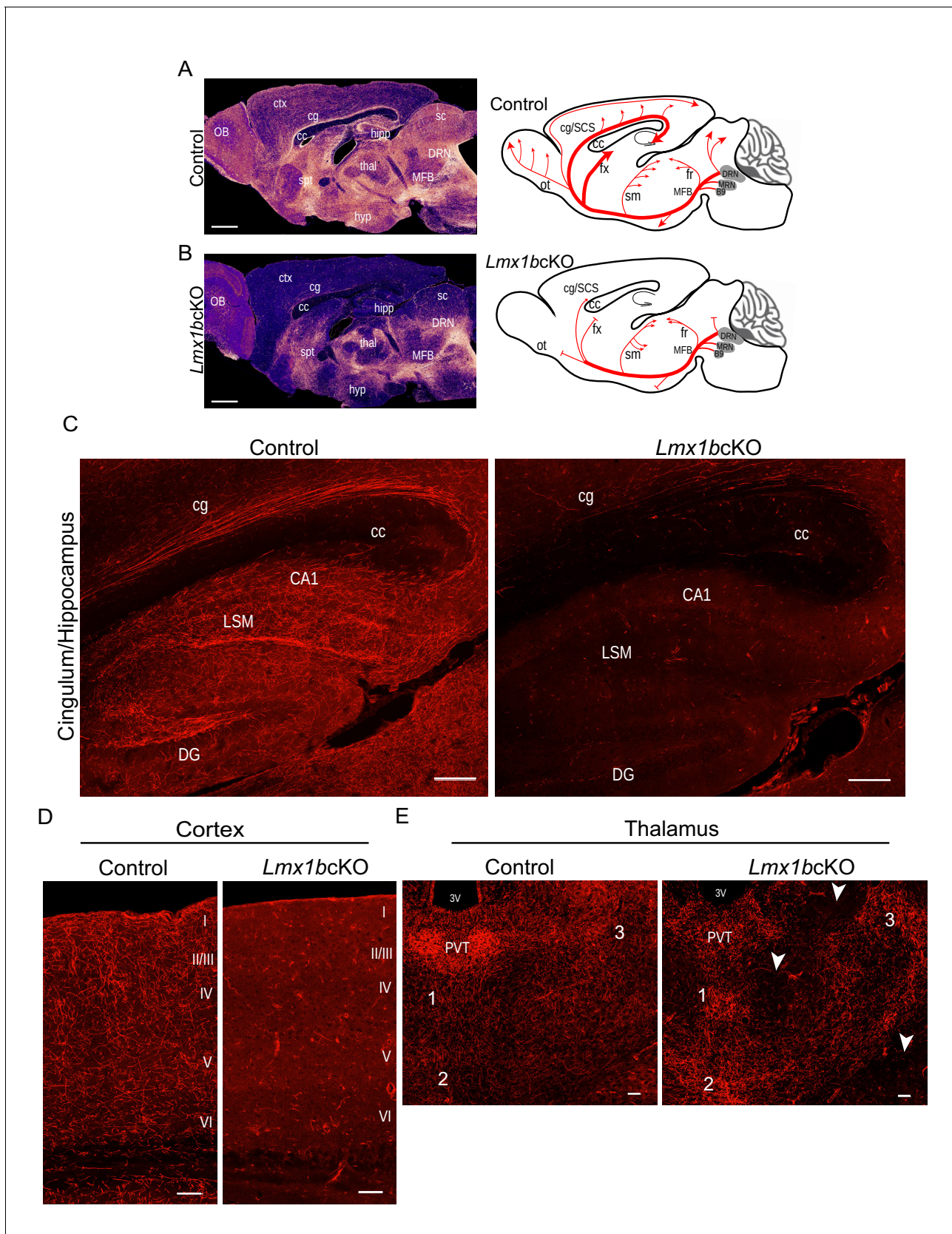


Figure 1. *Lmx1b* is required for the formation of ascending 5-HT axon projection pathways. (A, B) Ascending 5-HT axonal projection system immunolabeled using an anti-RFP antibody to TdTomato in whole sagittal forebrain sections of 3 month old mice displayed by heatmap. *Lmx1bcKO* Figure 1 continued on next page

Figure 1 continued

TdTomato⁺ axons were nearly absent in numerous brain regions (B) compared to controls (A) (n = 6, controls; n = 7, *Lmx1bcKO* adult mice). Right, schematics depicting 5-HT axon trajectories in *Lmx1bcKO* vs. control brains. Scale bars, 1000 μ m. OB, olfactory bulb; ctx, cortex; cg, cingulum; cc, corpus callosum; hipp, hippocampus; spt, septum; hyp, hypothalamus; thal, thalamus; sc, superior colliculus; MFB, medial forebrain bundle; DRN, dorsal raphe nucleus. Schematic (right): ot, olfactory tract; cg/SCS, cingulum/supracallosal stria; fx, fornix; sm, stria medularis; fr, fasciculus retroflexus. (C) Confocal images of TdTomato⁺ axons in sagittal sections. *Lmx1bcKO* axons failed to fill cingulum bundles or innervate the hippocampus. Scale bars, 200 μ m. cg, cingulum; cc, corpus callosum; LSM, lacunosum moleculare; DG, dentate gyrus; CA1 of hippocampus. (D) Coronal sections of cortex show near complete lack of *Lmx1bcKO* TdTomato⁺ axons. Scale bars, 50 μ m. (E) Coronal view of altered patterns of TdTomato⁺ axons in *Lmx1bcKO* thalamus. Arrowheads indicate areas devoid of axons in *Lmx1bcKO* thalamus. Numbers correspond to areas of axon clumping in *Lmx1bcKO* thalamus. See **Figure 1—figure supplement 2** for high magnification images. Scale bars, 100 μ m. PVT, paraventricular nucleus of the thalamus; 3V, third ventricle.

DOI: <https://doi.org/10.7554/eLife.48788.002>

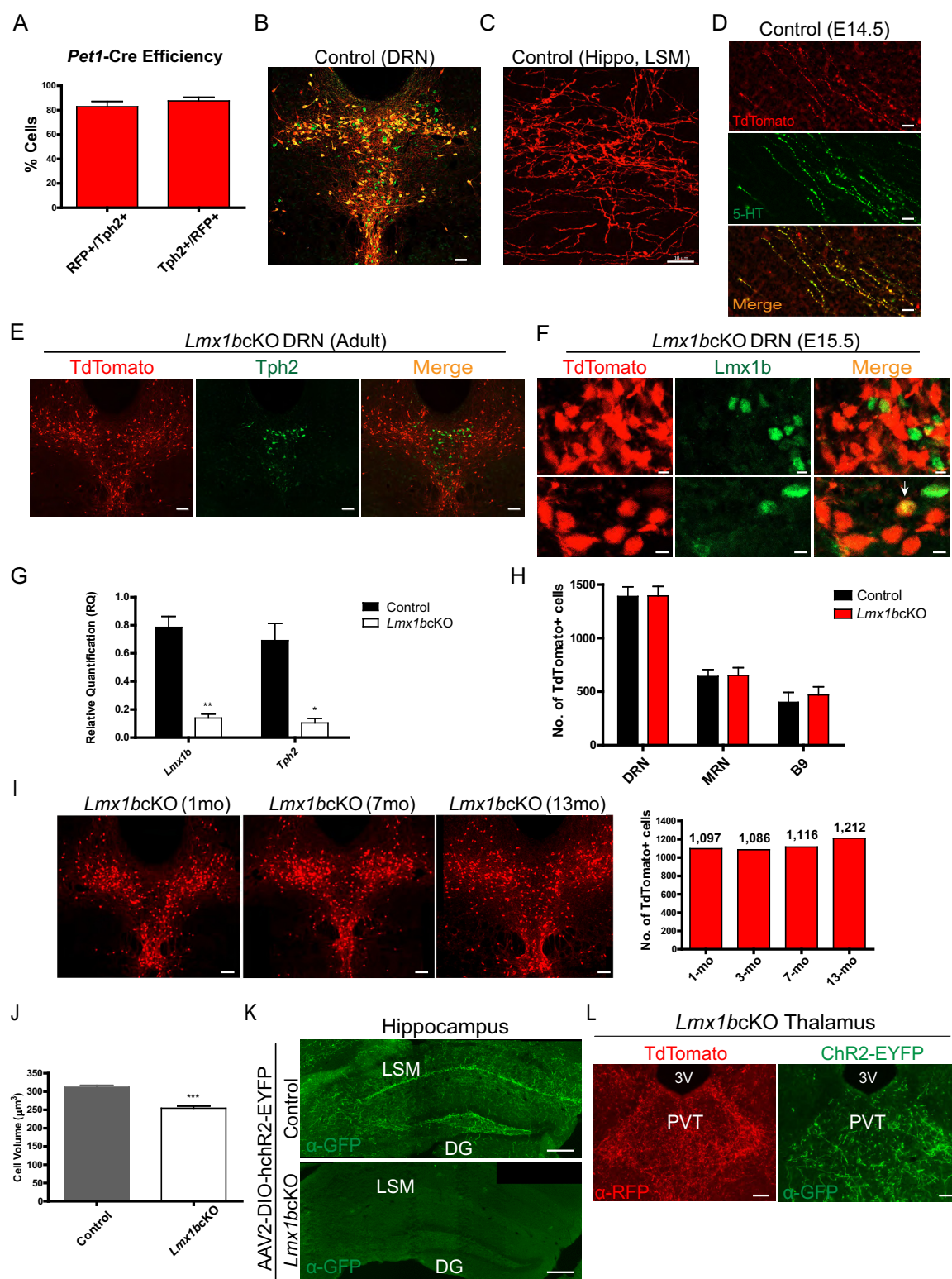


Figure 1—figure supplement 1. Surrogate marking of 5-HT cell bodies and axons and *Lmx1b* conditional targeting. (A) *Pet1-Cre* efficiency: 82% Tph2 + cells expressed TdTomato+ (RFP+/Tph2+) and 88% of TdTomato+ cells expressed Tph2 (Tph2+/RFP+) (n = 2 control mice). Data are represented as Figure 1—figure supplement 1 continued on next page

Figure 1—figure supplement 1 continued

mean \pm SEM. (B) TdTomato+ cells co-labeled with serotonergic marker Tph2 in the DRN. Immunofluorescence of Tph2 (green) and TdTomato (red). Scale bars, 100 μ m. (C) TdTomato+ axons were found throughout the adult brain. Lacunosum moleculare layer (LSM) of hippocampus shown here. Scale bars, 10 μ m. (D) Co-immunolabeled axons at embryonic day (E) 14 with anti-5-HT and anti-RFP antibodies. Scale bars, 20 μ m. (E) A majority of TdTomato+ *Lmx1bcKO* mutant cells did not co-localize with Tph2 ($n = 6$, control; $n = 7$, *Lmx1bcKO*; 2.5–3.5 month old mice). Scale bars, 100 μ m. (F) A majority of TdTomato+ *Lmx1bcKO* mutant cells did not co-localize with Lmx1b protein (E15.5 shown). A small number of cells were TdTomato+ and Lmx1b+ (bottom row, arrow). Scale bars, 5 μ m. (G) RT-qPCR of *Lmx1b* and *Tph2* in flow sorted YFP+ cells from control and *Lmx1bcKO* E17.5 embryos ($n = 4$, control; $n = 4$, *Lmx1bcKO* embryos). Unpaired t-test with Welch's correction, $*p < 0.05$, $**p < 0.001$, and $***p < 0.0001$. Data are represented as mean \pm SEM. (H) Counts of TdTomato+ cells in *Lmx1bcKO* mice did not differ from controls. Every 4th section counted throughout DRN/MRN/B9 raphe nuclei ($n = 3$ mice/genotype). Data are represented as mean \pm SEM. (I) *Lmx1bcKO* cell bodies survive at least up to 13 months. Counts of TdTomato+ neurons in 6 matched sections for each animal (right) ($n = 1$ animal per time point; 1mo, 3mo, 7mo, 13mo). Scale bars, 100 μ m. (J) *Lmx1bcKO* cell bodies survive at least up to 13 months. Counts of TdTomato+ neurons in 6 matched sections for each animal (right) ($n = 1$ animal per time point; 1mo, 3mo, 7mo, 13mo). Scale bars, 100 μ m. (K) Volume of *Lmx1bcKO* cell bodies were significantly smaller than controls ($n = 587$ control cells; $n = 442$ *Lmx1bcKO* cells). Unpaired t-test with Welch's correction, $*p < 0.05$, $**p < 0.001$, and $***p < 0.0001$. Data are represented as mean \pm SEM. (K, L) Expression of a YFP tagged channel rhodopsin by AAV2 viral injection to DRN/MRN of *Lmx1bcKO* and control mice. No YFP expression was found in *Lmx1bcKO* hippocampus (K) while YFP-labeled axons co-localized with TdTomato in the *Lmx1bcKO* thalamus (L). Scale bars, 200 μ m (K), 50 μ m (L).

DOI: <https://doi.org/10.7554/eLife.48788.003>

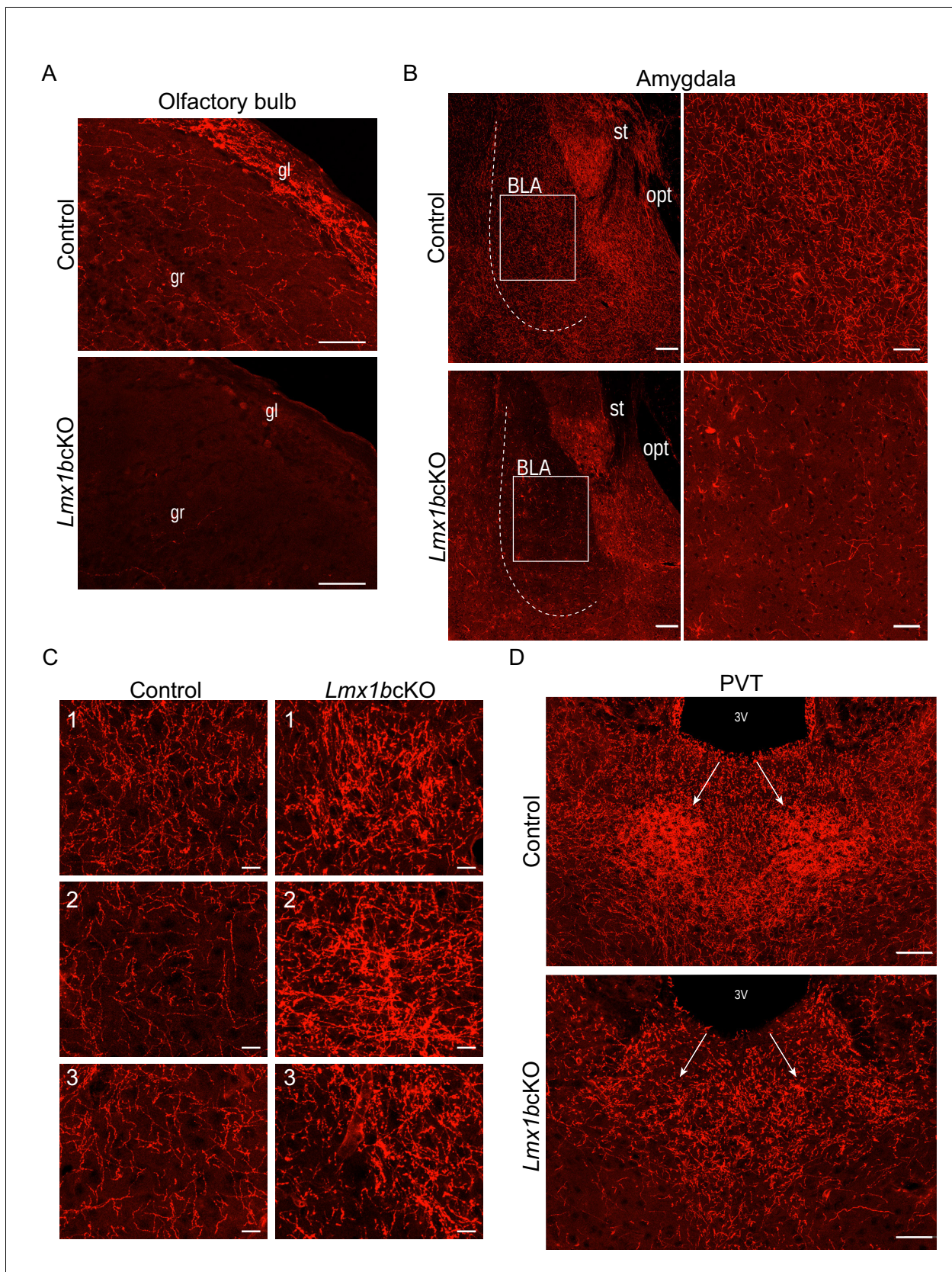


Figure 1—figure supplement 2. *Lmx1b* deficiency disrupts 5-HT axon patterns in the forebrain. (A) Sagittal sections of olfactory bulb show near complete lack of *Lmx1bcKO* TdTTomato+ axons. Scale bars, 50 μm. gl, glomerular layer; gr, granule layer. (B) TdTTomato+ axons severely reduced in the amygdala. (C) High-magnification views of axon patterns in three different regions (1, 2, 3) for control and *Lmx1bcKO* mice. The control images show a dense network of axons, while the *Lmx1bcKO* images show a significant reduction in axon density. (D) Sagittal sections of the paraventricular thalamus (PVT) show a significant reduction in axon density in *Lmx1bcKO* mice. Scale bars, 50 μm. 3v, third ventricle.

Figure 1—figure supplement 2 continued on next page

Figure 1—figure supplement 2 continued

throughout *Lmx1bcKO* amygdala compared to controls (BLA, shown right). Scale bars, 100 μm . BLA, basolateral amygdala; st, stria terminalis; opt, optic tract. (C) High magnification showing areas of clumping (correlate to numbers in **Figure 1E**) found in *Lmx1bcKO* thalamus compared to controls. Scale bars, 20 μm . (D) Lack of TdTomato+ axons in the PVT of *Lmx1bcKO* mice. Scale bars, 50 μm . 3V, third ventricle; PVT, paraventricular nucleus of the thalamus.

DOI: <https://doi.org/10.7554/eLife.48788.004>

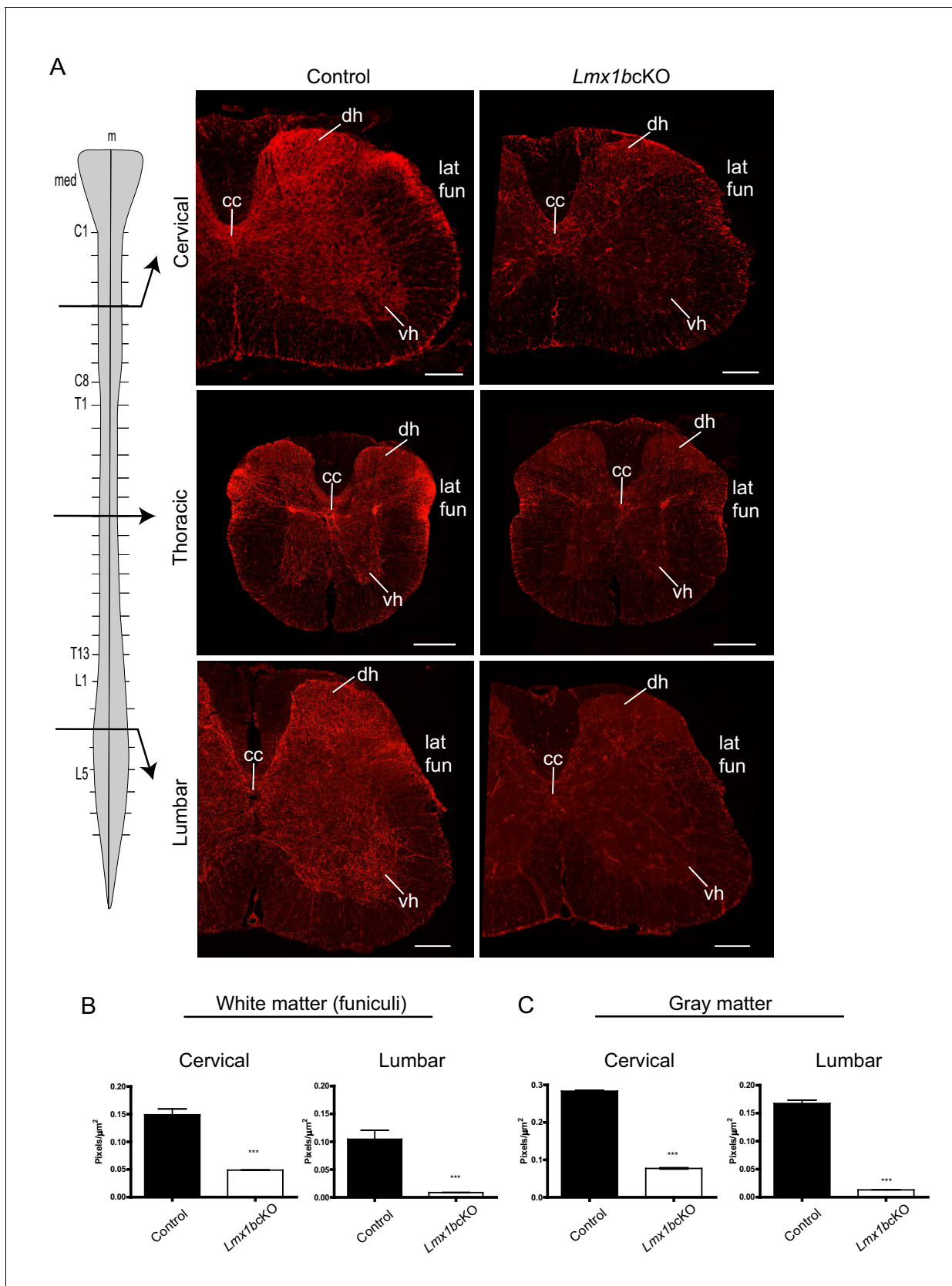


Figure 2. *Lmx1b* is required for the formation of descending 5-HT axon projection pathways. (A) Coronal sections taken at cervical (C4), thoracic (T6), and lumbar (L3) levels of the spinal cord (diagram, left). Immunolabeling for TdTomato shows *Lmx1bcKO* axons were severely reduced at every level of Figure 2 continued on next page

Figure 2 continued

the cord in both gray and white matter compared to controls. Scale bars, 200 μm . m, *midline*; med, *medulla*; cc, *central canal*; dh, *dorsal horn*; vh, *ventral horn*; lat fun, *lateral funiculi*. (B, C) Quantification of total TdTomato⁺ axons (pixels/ μm^2) in white (B) and gray (C) matter at cervical and lumbar levels (n = 3, control; n = 3 *Lmx1bc*KO mice). Two-way ANOVA with Welch's correction, *p<0.05, **p<0.001, and ***p<0.0001. Data are represented as mean \pm SEM.

DOI: <https://doi.org/10.7554/eLife.48788.005>

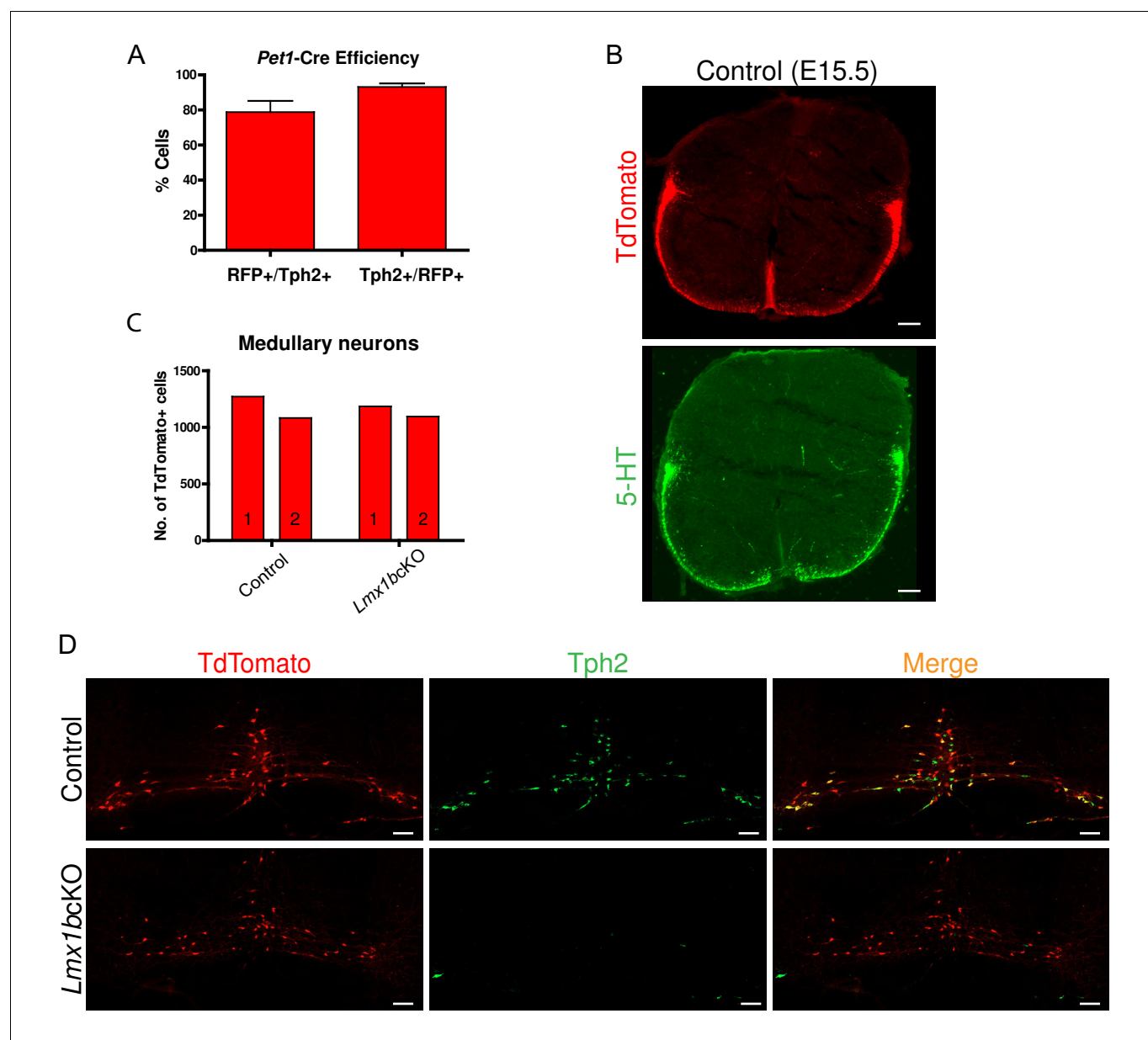


Figure 2—figure supplement 1. Conditional targeting of *Lmx1b* in the descending 5-HT projection pathway. (A) *Pet1-Cre* efficiency: 80% of Tph2+ cells expressed TdTomato+ (RFP+/Tph2+); 92% of TdTomato+ cells expressed Tph2 (Tph2+/RFP+) in medullary nuclei ($n = 2$ control mice). Data are represented as mean \pm SEM. (B) TdTomato+ axon patterns in funiculi of the developing spinal cord aligned with 5-HT labeled axon patterns at E15.5 in controls (coronal view). Scale bars, 100 μ m. (C) Comparable numbers of TdTomato+ medullary cells in *Lmx1bcKO* and control mice ($n = 2$ mice/genotype). (D) Few *Lmx1bcKO* TdTomato+ cell bodies expressed Tph2, a downstream target of *Lmx1b*. Scale bars, 100 μ m.

DOI: <https://doi.org/10.7554/eLife.48788.006>

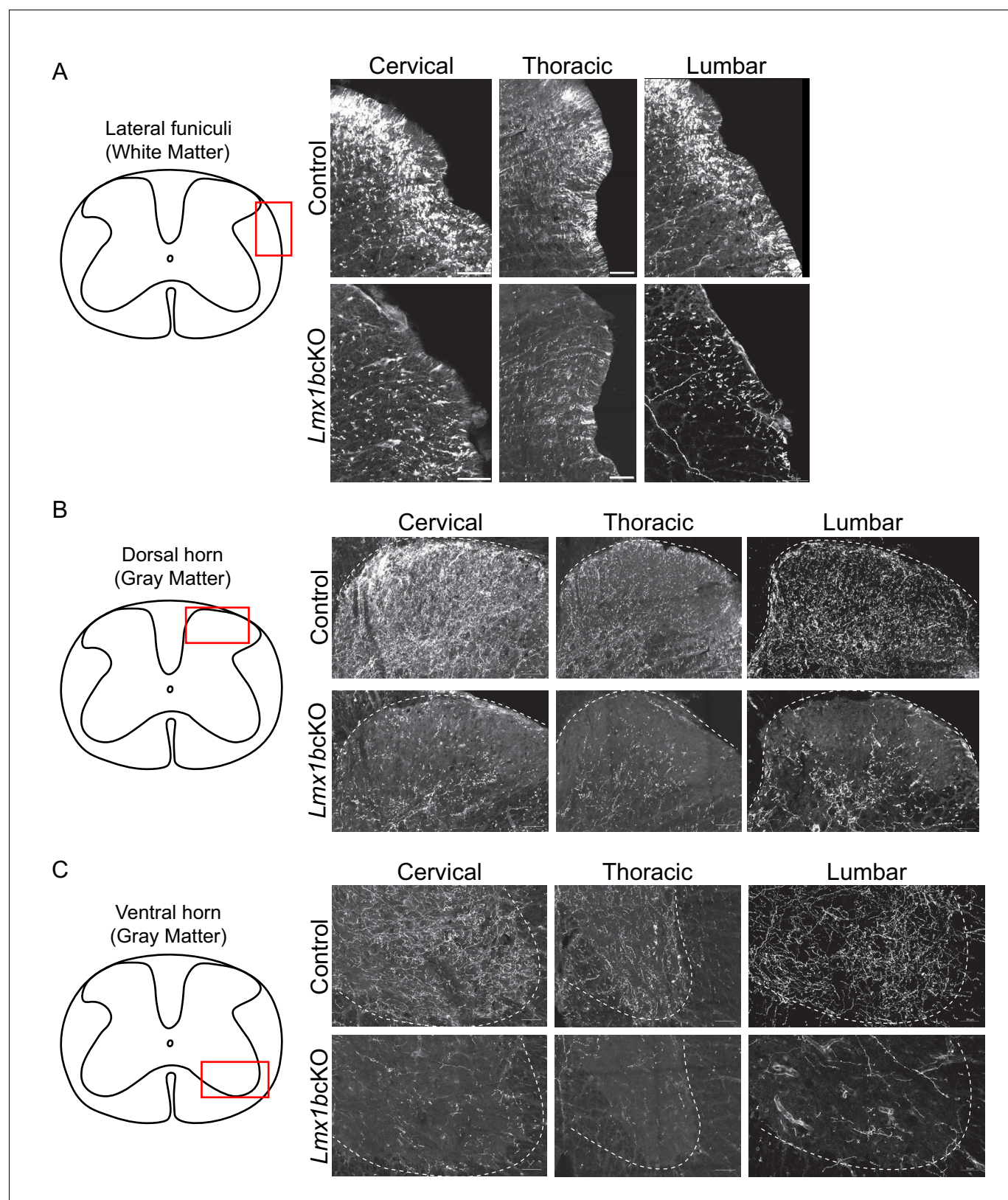


Figure 2—figure supplement 2. Progressive deficits of 5-HT axon fibers in *Lmx1b* deficient spinal cord white and gray matter. (A–C) Coronal sections immunolabeled using an anti-RFP antibody to TdTomato. *Lmx1b*KO TdTomato⁺ axon deficits in spinal cord white matter funiculi (A), gray matter dorsal (B), and ventral (C) horns. Red box in diagram outlines area imaged (right). (n = 3, control; n = 3 *Lmx1b*KO mice). Scale bars, 50 μ m.

DOI: <https://doi.org/10.7554/eLife.48788.007>

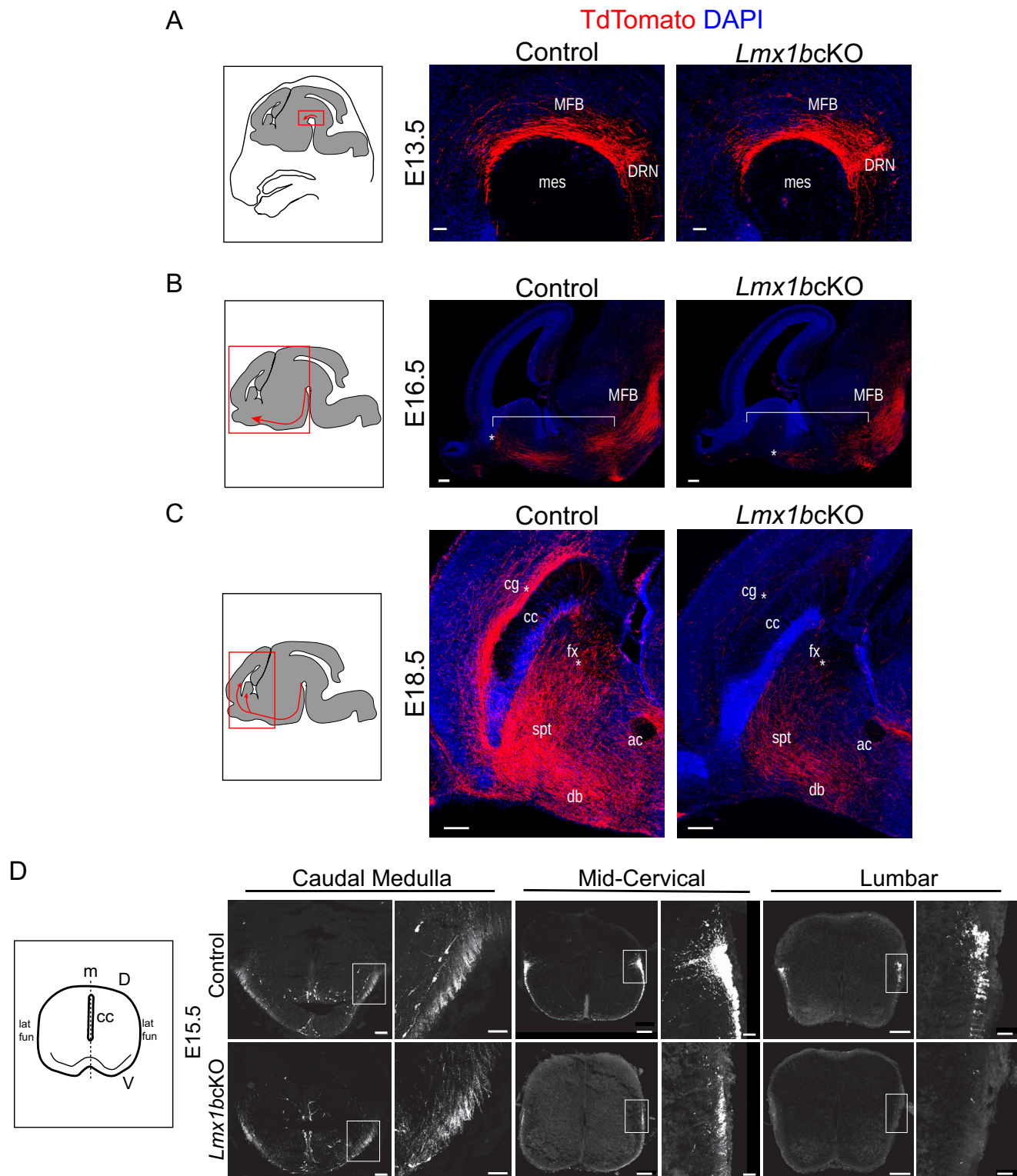


Figure 3. Initial axon outgrowth is delayed and selective pathway routing fails in *Lmx1b* deficient 5-HT neurons. (A–C) Immunolabeled TdTomato⁺ ascending axons in sagittal slices at different embryonic stages. Diagrams (left) show area of image (red box) presented for each time point. Arrows
 Figure 3 continued on next page

Figure 3 continued

indicate direction of growing axons. E13.5 *Lmx1bcKO* axons exhibited similar ascending trajectories and densities as controls (A). E16.5 *Lmx1bcKO* axons did not extend as far (asterisk) and were less abundant (under bracket) compared to control axons (B). E18.5 *Lmx1bcKO* axons failed to fill multiple axon tracts (cg, fx; asterisks) compared to controls (C). Scale bars, 50 μm (A), 200 μm (B,C). DRN, dorsal raphe nucleus; MFB, medial forebrain bundle; mes, mesencephalic flexure; cg, cingulum bundle; fx, fornix; ac, anterior commissure; spt, septum; db, diagonal band; cc, corpus callosum. (D) Diagram (left) depicting coronal section of an embryonic spinal cord. TdTomato⁺ descending axons at E15.5 in control vs *Lmx1bcKO* embryos. *Lmx1bcKO* axons exit caudal medulla similar to controls but were severely reduced in funiculi at lower levels of the cord (mid-cervical and lumbar). Boxed region of lateral funiculi enlarged to the right of each image. Scale bars, 100 μm (low magnification), 50 μm (high magnification-medulla), 20 μm (high magnification- cervical/lumbar insets). Lat fun, lateral funiculi; cc, central canal; m, midline; D, dorsal; V, ventral.

DOI: <https://doi.org/10.7554/eLife.48788.008>

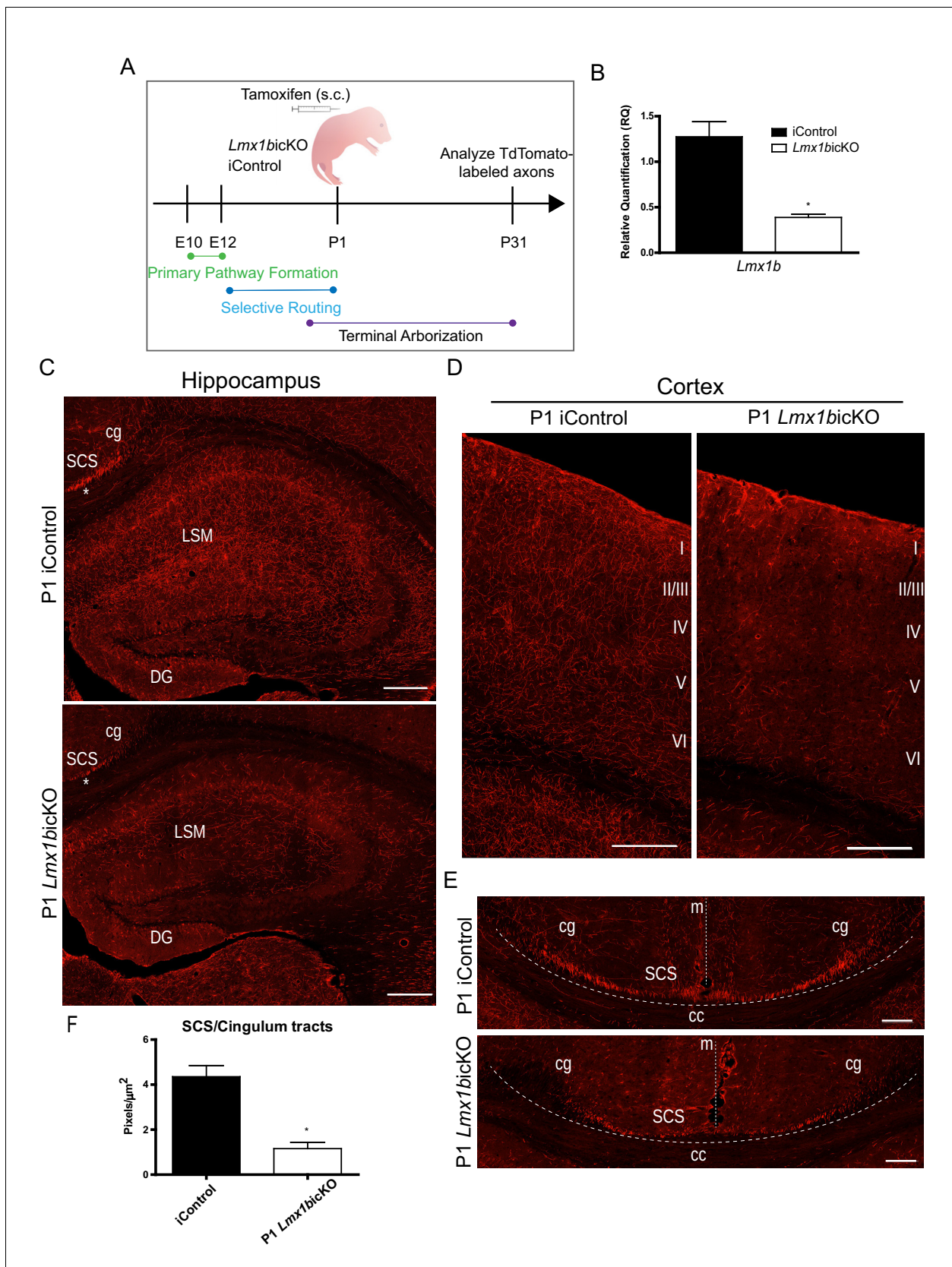


Figure 4. *Lmx1b* is temporally required for 5-HT projection pathway formation. (A) Schematic of tamoxifen-inducible approach to target *Lmx1b* at postnatal day (P)1. (B) RT-qPCR of flow sorted TdTomato⁺ neurons from postnatal targeted mice (n = 3, iControl; n = 4, *Lmx1bicKO* mice). Unpaired t-
Figure 4 continued on next page

Figure 4 continued

test with Welch's correction, $*p < 0.05$. Data are represented as mean \pm SEM. (C) Coronal sections of P1 targeted *Lmx1bicKO* hippocampus compared to iControls analyzed at P31. *, incomplete formation of SCS and cingulum in P1 targeted *Lmx1bicKO* brain. Scale bars, 200 μm . (D) Coronal sections of P1 targeted *Lmx1bicKO* cortex compared to iControls analyzed at P31. Scale bars, 200 μm . (E) Coronal sections at level of corpus callosum showing incomplete formation of major 5-HT axon routes, SCS and cingulum, in P1 targeted *Lmx1bicKO* forebrain compared to iControls (above dotted line). Scale bars, 100 μm . cg, cingulum; SCS, supracallosal stria; cc, corpus callosum; m, midline. (F) Quantification of axons within SCS and cingulum tracts ($n = 3$, iControl; $n = 3$, *Lmx1bicKO* mice). Unpaired t-test with Welch's correction, $p = 0.0112$. Data are represented as mean \pm SEM.

DOI: <https://doi.org/10.7554/eLife.48788.009>

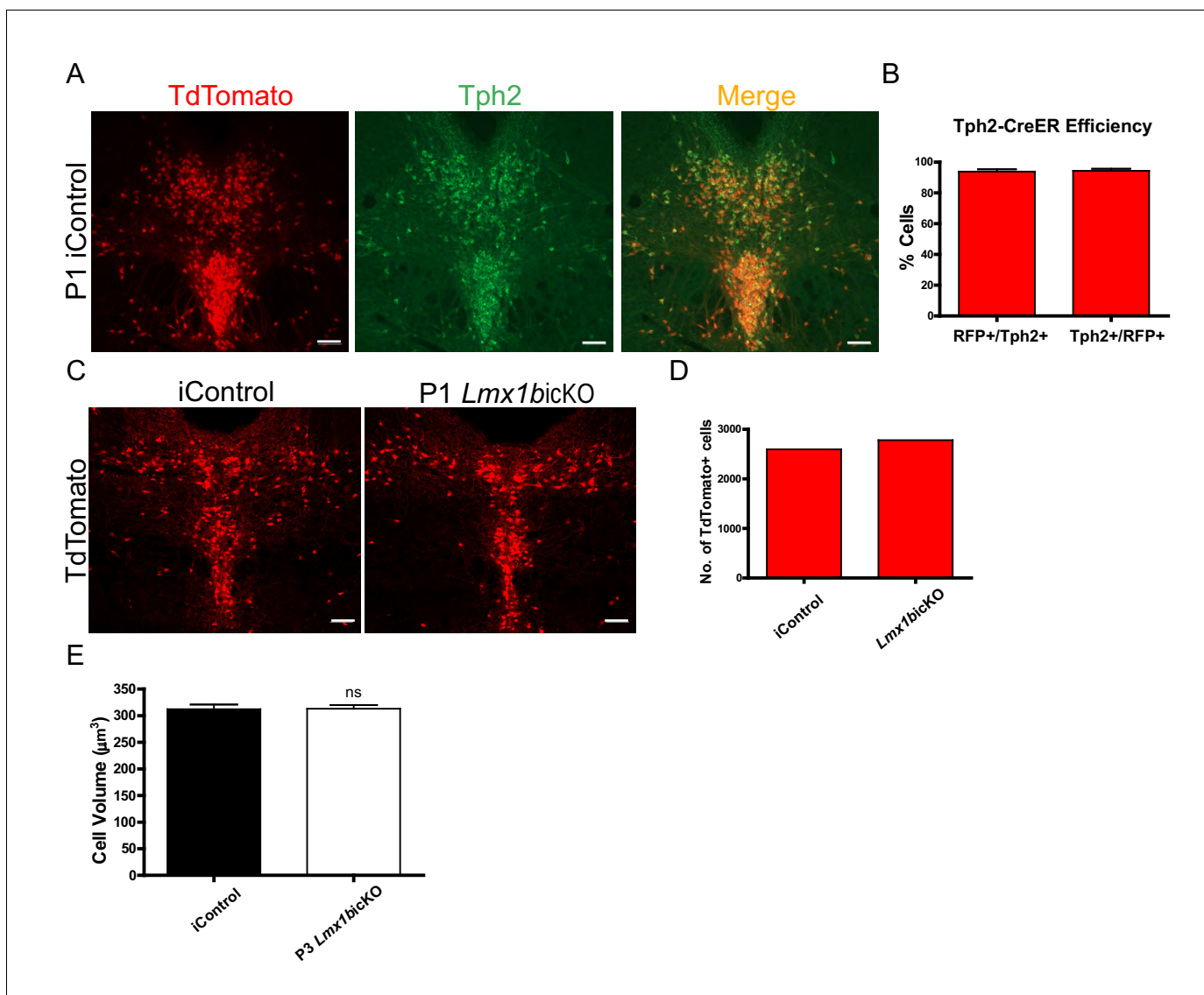


Figure 4—figure supplement 1. Efficiency of postnatal tamoxifen inducible targeting of *Lmx1b*. (A) TdTomato⁺ cells co-localized with serotonergic marker Tph2 in the DRN of iControl mice. Scale bars, 100 μm . (B) *Tph2-CreER* efficiency: 94% of TdTomato⁺ cells expressed Tph2 (Tph2⁺/RFP⁺) and 94% of Tph2⁺ cells expressed TdTomato⁺ (RFP⁺/Tph2⁺) in DRN/MRN/B9 nuclei ($n = 4$, iControl mice). Data are represented as mean \pm SEM. (C) DRN of P1 targeted *Lmx1bicKO* and iControl mice. Scale bars, 100 μm . (D) Cell counts confirmed comparable numbers of TdTomato⁺ cells in *Lmx1bicKO* and iControl mice. (E) Normal cell body volume in postnatal targeted *Lmx1bicKO* mice ($n = 464$, control cells; $n = 651$, P3 *Lmx1bicKO* cells; $p=0.9353$). Unpaired t-test with Welch's correction. Data are represented as mean \pm SEM.

DOI: <https://doi.org/10.7554/eLife.48788.010>

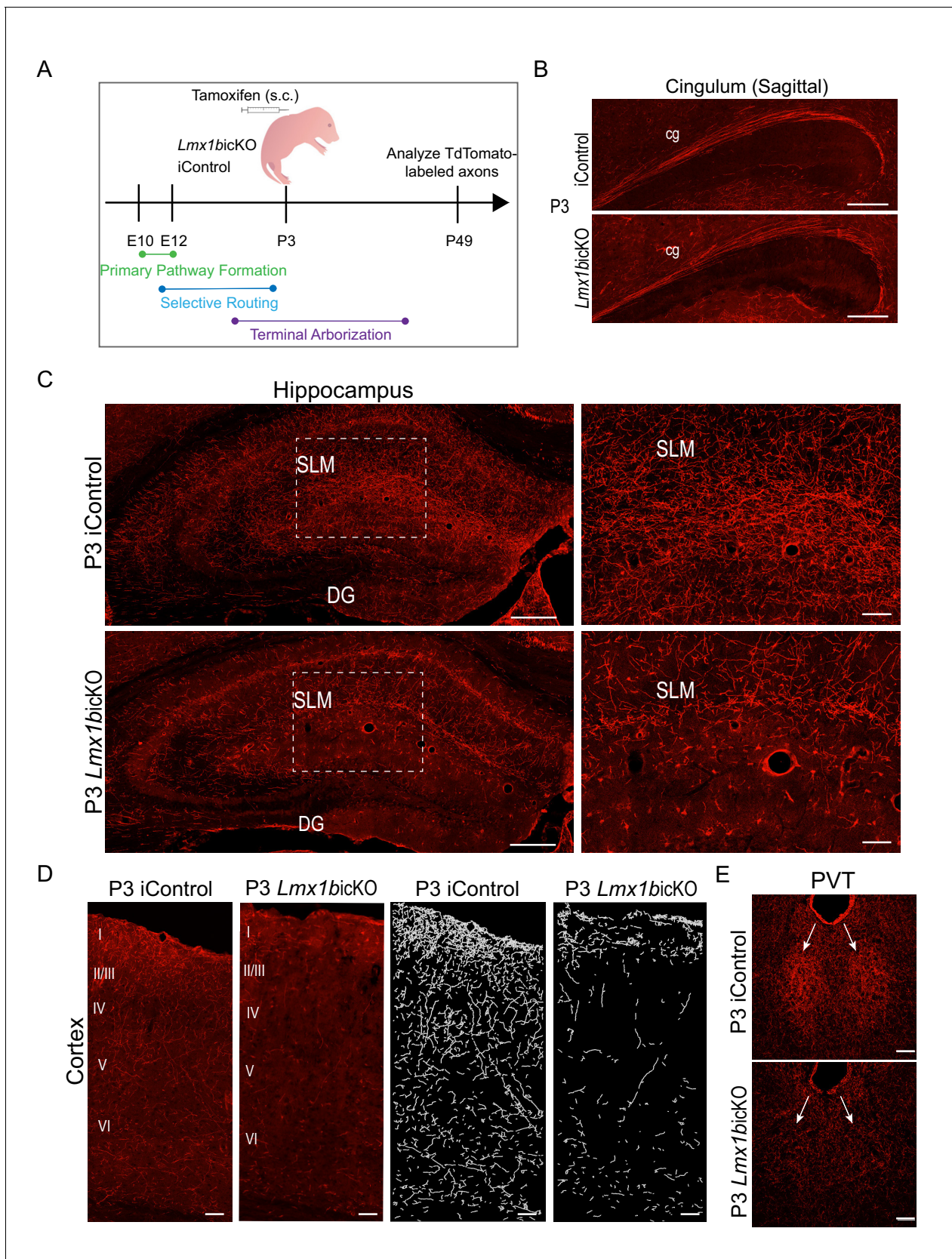


Figure 5. *Lmx1b* temporally controls postnatal 5-HT terminal arborization. (A) Schematic of tamoxifen inducible targeting of *Lmx1b* at postnatal day (P) 3. (B) Sagittal view of cingulum shows fully formed long-range axon routes in P3 targeted *Lmx1bicKO* mice compared to iControls. Scale bars, 200 μ m. Figure 5 continued on next page

Figure 5 continued

(C) Coronal sections of hippocampus in P3 targeted *Lmx1bicKO* mice compared to iControls. Dashed boxed region: higher magnification image at right highlighting reduced TdTomato⁺ axons in *Lmx1bicKO* SLM. Scale bars, 200 μm (low magnification), 50 μm (high magnification). SLM, *stratum lacunosum moleculare*; DG, *dentate gyrus*. (D) Coronal sections of cortex of P3 targeted *Lmx1bicKO* mice compared to iControls. Imaris tracing; *right panels*. Scale bars, 100 μm . (E) Decreased TdTomato⁺ arbors detected in P3 targeted *Lmx1bicKO* PVT compared to iControls (arrows). Scale bars, 50 μm .

DOI: <https://doi.org/10.7554/eLife.48788.011>

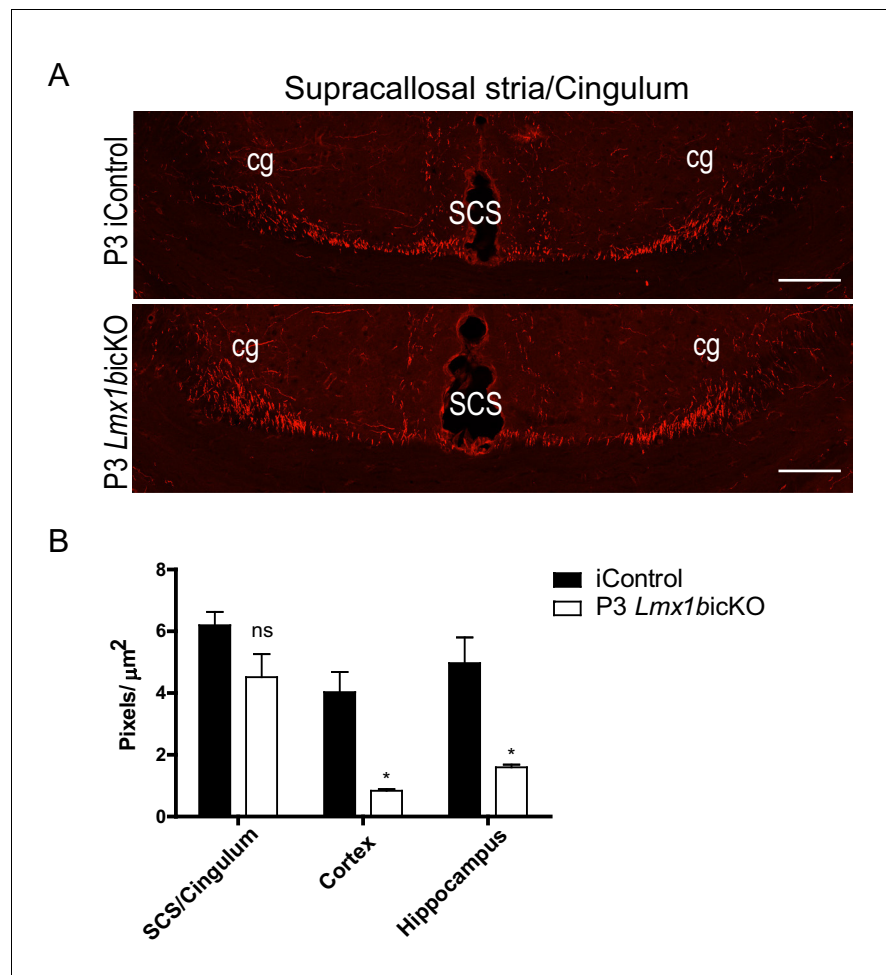


Figure 5—figure supplement 1. P3 targeted *Lmx1bicKO* mice display normal 5-HT axon routing but decreased 5-HT terminal arbors. (A) Coronal view of SCS and cingulum demonstrating complete formation of long-range axon routes in P3 targeted *Lmx1bicKO* mice compared to iControls. Scale bars, 100 μm. (B) Quantification of axons within SCS and cingulum tracts, cortex, and hippocampus of postnatal targeted P3 iControls and P3 *Lmx1bicKO* mice (n = 3, iControl; n = 3, *Lmx1bicKO* mice). Unpaired t-test with Welch's correction; axon tracts, p=0.1474; cortex, p=0.04; hippocampus, p=0.0277. Data are represented as mean ± SEM.

DOI: <https://doi.org/10.7554/eLife.48788.012>

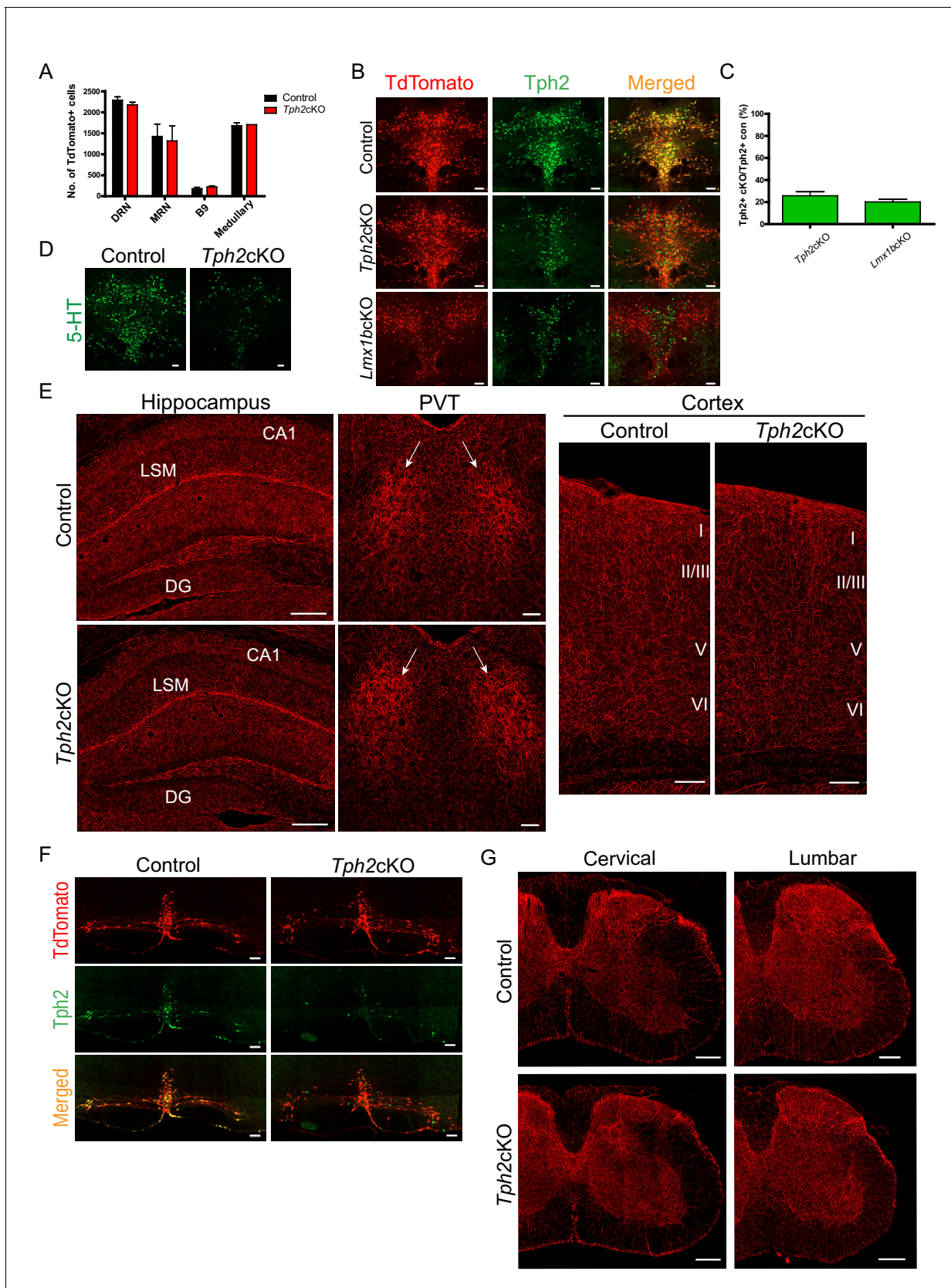


Figure 6. Specific targeting of 5-HT synthesis does not alter 5-HT arborization patterns. (A) Counts of TdTomato+ cells in each raphe nucleus of *Tph2cKO* mice did not differ from controls ($n = 2$ mice/genotype). Data are represented as mean \pm SEM. (B) Comparable Tph2 knock-down in Figure 6 continued on next page

Figure 6 continued

*Tph2*cKO and *Lmx1bc*KO mice. Scale bars, 100 μ m. (C) Cell counts of residual *Tph2*⁺ neurons in *Tph2*cKO and *Lmx1bc*KO mice expressed as a percentage (*n* = 2 mice/genotype). Data are represented as mean \pm SEM. (D) Immunolabeling shows 5-HT was severely reduced in *Tph2*cKO mice. Scale bars, 100 μ m. (E) Coronal forebrain sections showing no deficits of TdTomato⁺ axon densities in *Tph2*cKO hippocampus, PVT, and cortex (*n* = 3 mice/genotype). LSM, lacunosum moleculare; DG, dentate gyrus; CA1 of hippocampus. Scale bars, 100 μ m (PVT, cortex); 200 μ m (hippocampus). (F) Co-immunolabeling for *Tph2* and TdTomato in medullary neurons. *Tph2* expression was severely reduced in medullary neurons of *Tph2*cKO mice. Scale bars, 50 μ m. (G) No deficits of TdTomato⁺ axons were present throughout the *Tph2*cKO spinal cord (*n* = 3 mice/genotype). Scale bars, 200 μ m.

DOI: <https://doi.org/10.7554/eLife.48788.013>

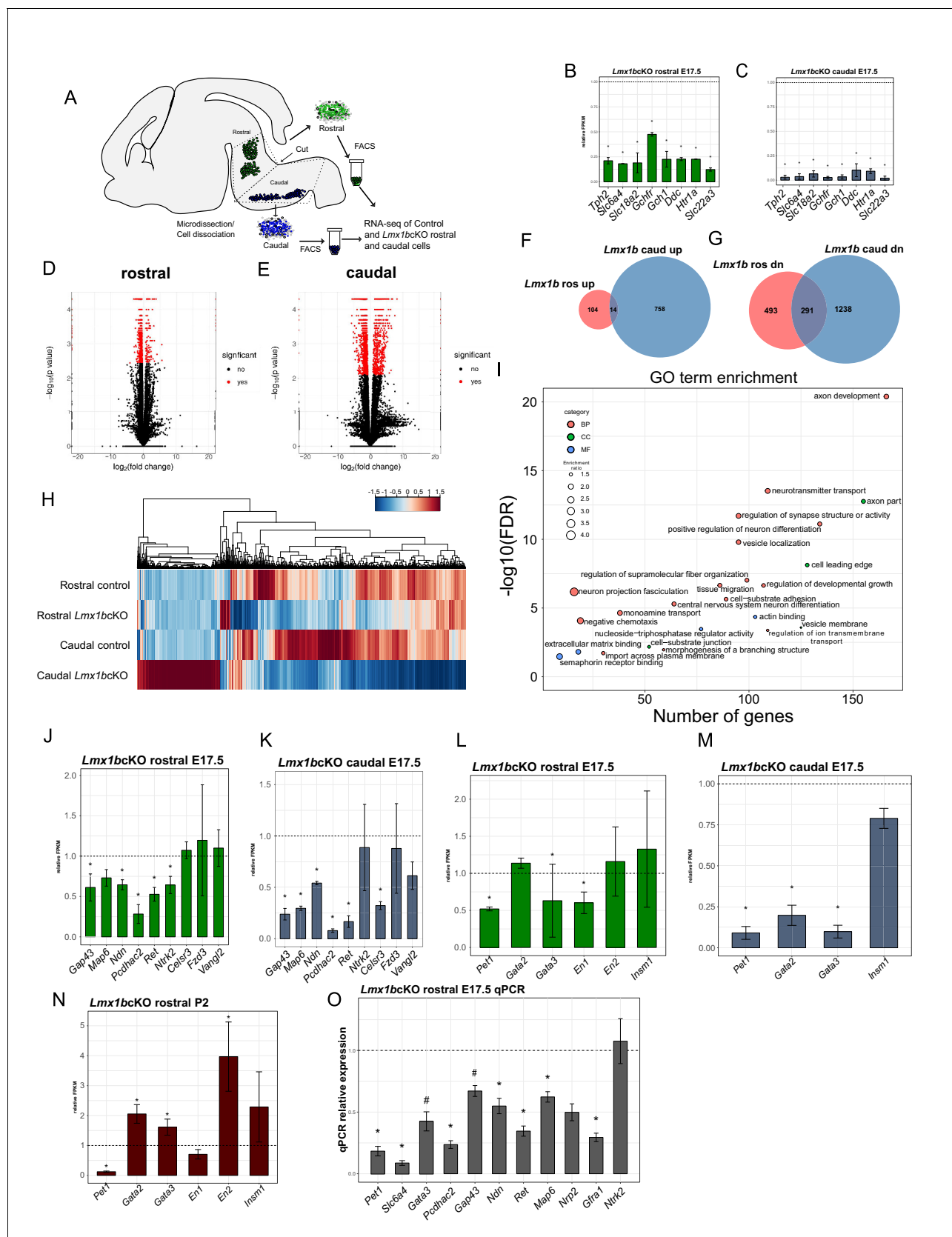


Figure 7. Ascending and descending *Lmx1b* regulated transcriptomes. (A) Schematic for dissection of E17.5 brain to isolate rostral and caudal 5-HT neurons genetically labeled by *Pet1-EYFP*. After dissection, EYFP⁺ neurons were flow-sorted separately and prepared for RNA-sequencing (n = 3, Figure 7 continued on next page

Figure 7 continued

controls; $n = 2$ *Lmx1bcKO* embryos). (B) Relative expression level of 5-HT pathway genes in rostral control versus *Lmx1bcKO* 5-HT neurons. Control gene expression levels were normalized to one. * indicates $FDR \leq 0.05$. Data are represented as mean \pm SEM. (C) Relative expression level of 5-HT pathway genes in caudal control versus *Lmx1bcKO* 5-HT neurons. Control gene expression levels were normalized to one. * indicates $FDR \leq 0.05$. Data are represented as mean \pm SEM. (D) Volcano plot for rostral control versus *Lmx1bcKO* differential expression. Significantly altered genes are in red with $\geq \log_2(1.5X)$ and $FDR \leq 0.05$. (E) Volcano plot for caudal control versus *Lmx1bcKO* differential expression. Significantly altered genes are in red with $\geq \log_2(1.5X)$ and $FDR \leq 0.05$. (F) Venn diagram of genes upregulated in rostral and caudal *Lmx1bcKO* 5-HT neurons. (G) Venn diagram of genes downregulated in rostral and caudal *Lmx1bcKO* 5-HT neurons. (H) Heatmap of differentially-expressed genes in rostral and caudal *Lmx1bcKO* 5-HT neurons. (I) GO term enrichment of *Lmx1b* regulated genes. BP = biological process, CC = cellular component, MF = molecular function. GO terms were enriched with $FDR \leq 0.05$. (J) Relative expression (FPKMs) of known 5-HT neuron axon-related genes in rostral *Lmx1bcKO* 5-HT neurons. Data are represented as mean \pm SEM. (K) Relative expression (FPKMs) of known 5-HT neuron axon-related genes in caudal *Lmx1bcKO* 5-HT neurons. Data are represented as mean \pm SEM. (L) Relative expression (FPKMs) of 5-HT GRN transcription factors in rostral *Lmx1bcKO* 5-HT neurons. Data are represented as mean \pm SEM. (M) Relative expression (FPKMs) of 5-HT GRN transcription factors in caudal *Lmx1bcKO* 5-HT neurons. Data are represented as mean \pm SEM. (N) Relative expression (FPKMs) of 5-HT GRN transcription factors in flow sorted TdTomato⁺ rostral *Lmx1bcKO* 5-HT neurons at postnatal day 2 ($n = 3$, controls; $n = 4$, *Lmx1bcKO* mice). Data are represented as mean \pm SEM. (O) RT-qPCR verification of 5-HT GRN transcription factors and known axon-related genes from flow sorted rostral YFP⁺ *Lmx1bcKO* 5-HT neurons relative to control levels ($n = 4$ mice/genotype). * indicates $p\text{-value} \leq 0.05$, # indicates $p < 0.1$, t-test with Welch's correction. Data are represented as mean \pm SEM.

DOI: <https://doi.org/10.7554/eLife.48788.014>

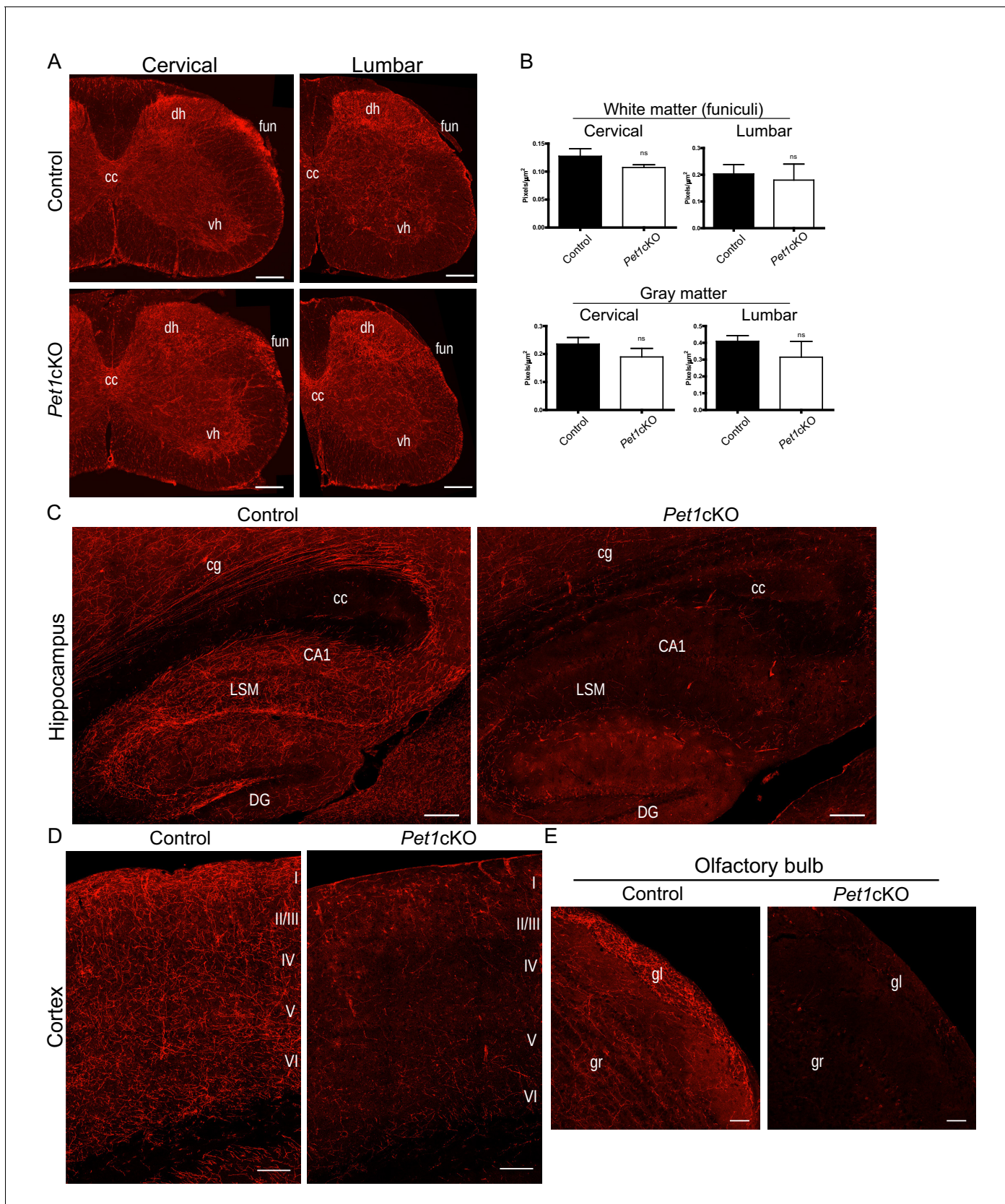


Figure 8. Distinct transcription factor requirements in the formation of ascending and descending 5-HT projection pathways. **(A)** TdTomato⁺ axon innervation in *Pet1cKO* vs control spinal cords in 3 month old mice. Coronal semi-section views of cervical and lumbar levels. Scale bars, 200 μ m. cc, Figure 8 continued on next page

Figure 8 continued

central canal; dh, dorsal horn; vh, ventral horn; fun, funiculi. (B) Quantification of TdTomato⁺ axons (pixels/ μm^2) in cervical and lumbar spinal cords ($n = 3$, controls; $n = 3$, *Pet1cKO* animals; Two-way ANOVA; white matter: cervical $p=0.1372$; lumbar $p=0.6764$; gray matter: cervical $p=0.4440$; lumbar $p=0.1995$). Data are represented as mean \pm SEM. (C) Decreased TdTomato⁺ arbors detected in *Pet1cKO* hippocampus compared to controls at 3 months of age. Scale bars, 200 μm , sagittal view. (D) Decreased TdTomato⁺ arbors detected in *Pet1cKO* cortex compared to controls at 3 months of age. Scale bars, 100 μm , coronal view. (E) Decreased TdTomato⁺ arbors detected in *Pet1cKO* olfactory bulb compared to controls at 3 months of age. Scale bars, 50 μm , sagittal view. cg, cingulum; cc, corpus callosum; LSM, lacunosum moleculare; DG, dentate gyrus; CA1 of hippocampus; gr, granule layer; gl, glomerular layer.

DOI: <https://doi.org/10.7554/eLife.48788.015>

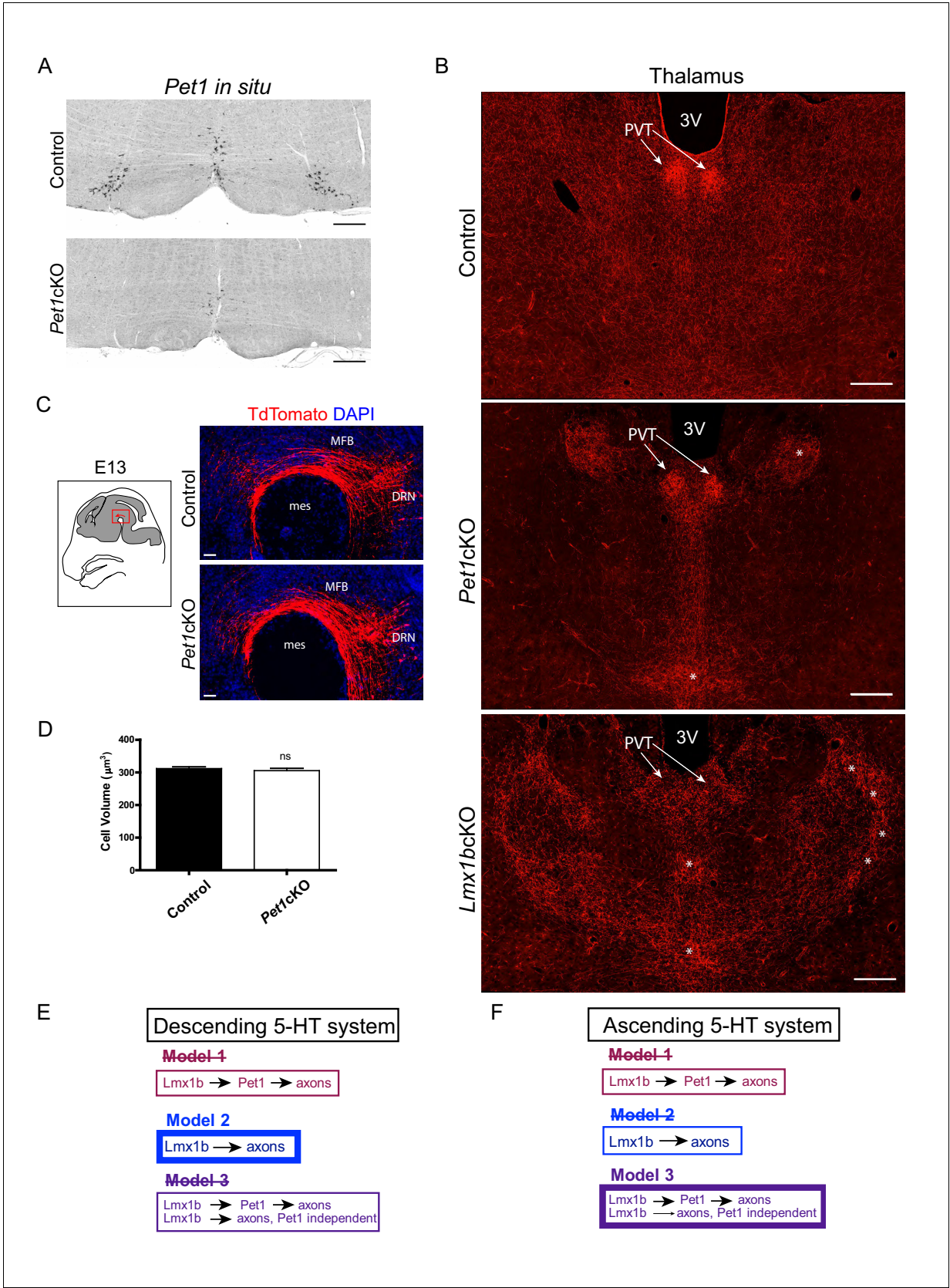


Figure 8—figure supplement 1. *Pet1*cKO and *Lmx1*bckO mice exhibit distinct axon defects in thalamus. (A) *Pet1* ISH shows *Pet1* was targeted in medullary neurons of *Pet1*cKO mice. Scale bars, 200 μm . (B) Distinctly different clumping pattern in *Pet1*cKO thalamus (asterisks) compared to control. (C) TdTomato and DAPI staining of E13 thalamus. (D) Bar graph of cell volume. (E) Descending 5-HT system models. (F) Ascending 5-HT system models. Figure 8—figure supplement 1 continued on next page

Figure 8—figure supplement 1 continued

Lmx1bcKO thalamus. Patterning in the PVT was normal in *Pet1cKO* mice (arrows). Scale bars, 200 μm . (C) No differences in early embryonic (E13.5) primary growth through the MFB in *Pet1cKO* embryos. Scale bars, 50 μm . (D) Cell volume analysis in *Pet1cKO* DRN revealed no significant difference in cell body size ($n = 587$ control cells; $n = 549$ *Pet1cKO* cells, $p=0.4745$). Compare to *Lmx1bcKO* cell volume, see **Figure 1—figure supplement 1J**. Unpaired t-test with Welch's correction. Data are represented as mean \pm SEM. (E) Scheme illustrating evidence-supported model for control of descending 5-HT axon development (Model 2). (F) Scheme illustrating evidence-supported model for control of ascending 5-HT axon development (Model 3).

DOI: <https://doi.org/10.7554/eLife.48788.016>

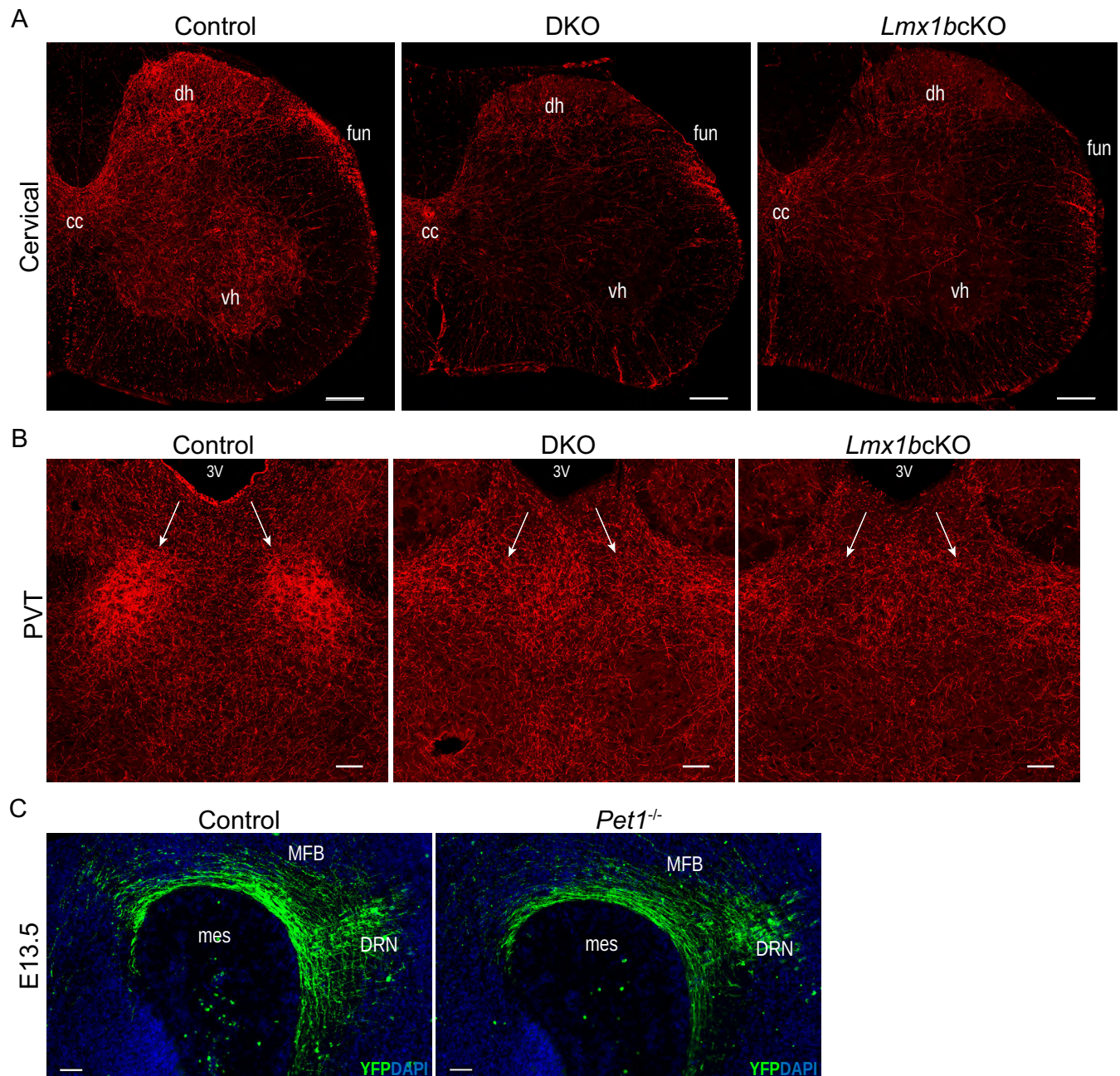


Figure 8—figure supplement 2. DKO and *Pet1^{-/-}* analyses. (A) Similar 5-HT axons defects in spinal cord of DKO and *Lmx1bcKO* mice (n = 3 mice/genotype). Scale bars, 200 μ m. cc, central canal; dh, dorsal horn; vh, ventral horn; fun, funiculi. (B) DKO PVT was unarborized similar to *Lmx1bcKO* PVT (n = 3 mice/genotype). Scale bars, 100 μ m. PVT, paraventricular nucleus of the thalamus; 3V, third ventricle. (C) Immunolabeled YFP+ axons in *Pet1^{-/-}* embryos at E13.5 showed no deficit in primary ascending axon growth through the MFB (n = 2 mice/genotype). Scale bars, 50 μ m. MFB, medial forebrain bundle; mes, mesencephalic flexure.

DOI: <https://doi.org/10.7554/eLife.48788.017>

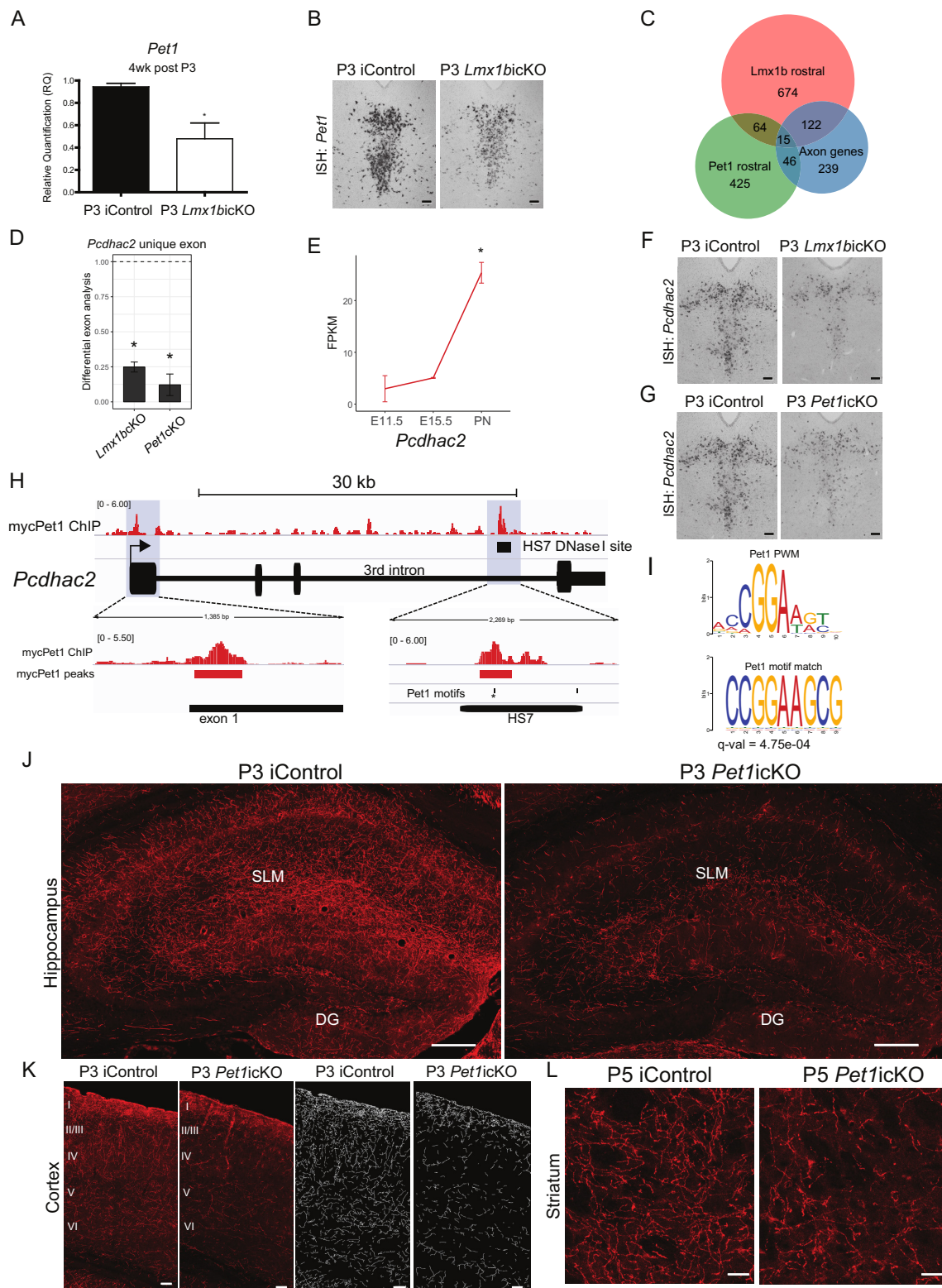


Figure 9. An ascending specific *Lmx1b*→*Pet1* cascade controls stage specific 5-HT gene expression and postnatal terminal arborization. (A) RT-qPCR analysis of *Pet1* expression in flow sorted TdTomato⁺ neurons 4 weeks post P3 tamoxifen treatment (n = 3, iControl; n = 4, P3 *Lmx1bicKO*). Figure 9 continued on next page

Figure 9 continued

mice). Unpaired t-test with Welch's correction, $*p < 0.05$. Data are represented as mean \pm SEM. (B) *Pet1* in situ hybridization in P3 targeted *Lmx1b*icKO mice. Scale bars, 100 μ m. (C) Venn diagram showing overlap of rostral *Lmx1b* and *Pet1* regulated genes and the axon-related gene dataset. *Lmx1b* rostral: genes controlled by *Lmx1b* in rostral 5-HT neurons; *Pet1* rostral: genes controlled by *Pet1* in rostral 5-HT neurons; Axon genes: *Lmx1b* regulated rostral and caudal axon-related genes. (D) Relative expression of the unique *Pcdhac2* exon in rostral *Lmx1b*icKO and *Pet1*icKO 5-HT neurons. * indicates $FDR \leq 0.05$. Data are represented as mean \pm SEM. (E) Developmental expression profile of *Pcdhac2* in 5-HT neurons from E11.5 to early postnatal (PN). * indicates $FDR \leq 0.05$. Data are represented as mean \pm SEM. (F) *Pcdhac2* in situ hybridization at postnatal day 14 in P3 targeted *Lmx1b*icKO mice. Representative image from $n = 3$ mice/genotype. Scale bars, 100 μ m. (G) *Pcdhac2* in situ hybridization at postnatal day 14 in P3 targeted *Pet1*icKO mice. *ISH* experiments done in parallel, iControl section is the same section in (F) and (G) to compare icKOs at the same tissue level. Representative image from $n = 3$ *Pet1*icKO mice. Scale bars, 100 μ m. (H) Visualization of the *Pcdhac2* gene locus showing mycPet1 ChIP peaks at the TSS and 3rd intron (shaded) and matches to the known *Pet1* motif. Zoomed regions of the significant mycPet1 binding sites are shown at the bottom. (I) The mycPet1 binding region located within the 3rd *Pcdhac2* intron DNase I hypersensitivity site (HS7) contains a significant match to the known *Pet1* position-weight matrix. TOMTOM q-value = 4.75×10^{-04} . (J) Decreased TdTomato⁺ arbors detected in P3 targeted *Pet1*icKO hippocampus compared to iControl mice. Scale bars, 200 μ m. (K) Decreased TdTomato⁺ arbors detected in all layers of P3 targeted *Pet1*icKO cortex (Imaris tracing; right panels) compared to iControl mice. Scale bars, 50 μ m. (L) Decreased TdTomato⁺ arbors in striatum of P5 targeted *Pet1*icKO mice. Scale bars, 20 μ m. See also **Figure 9—figure supplement 1F**.

DOI: <https://doi.org/10.7554/eLife.48788.018>

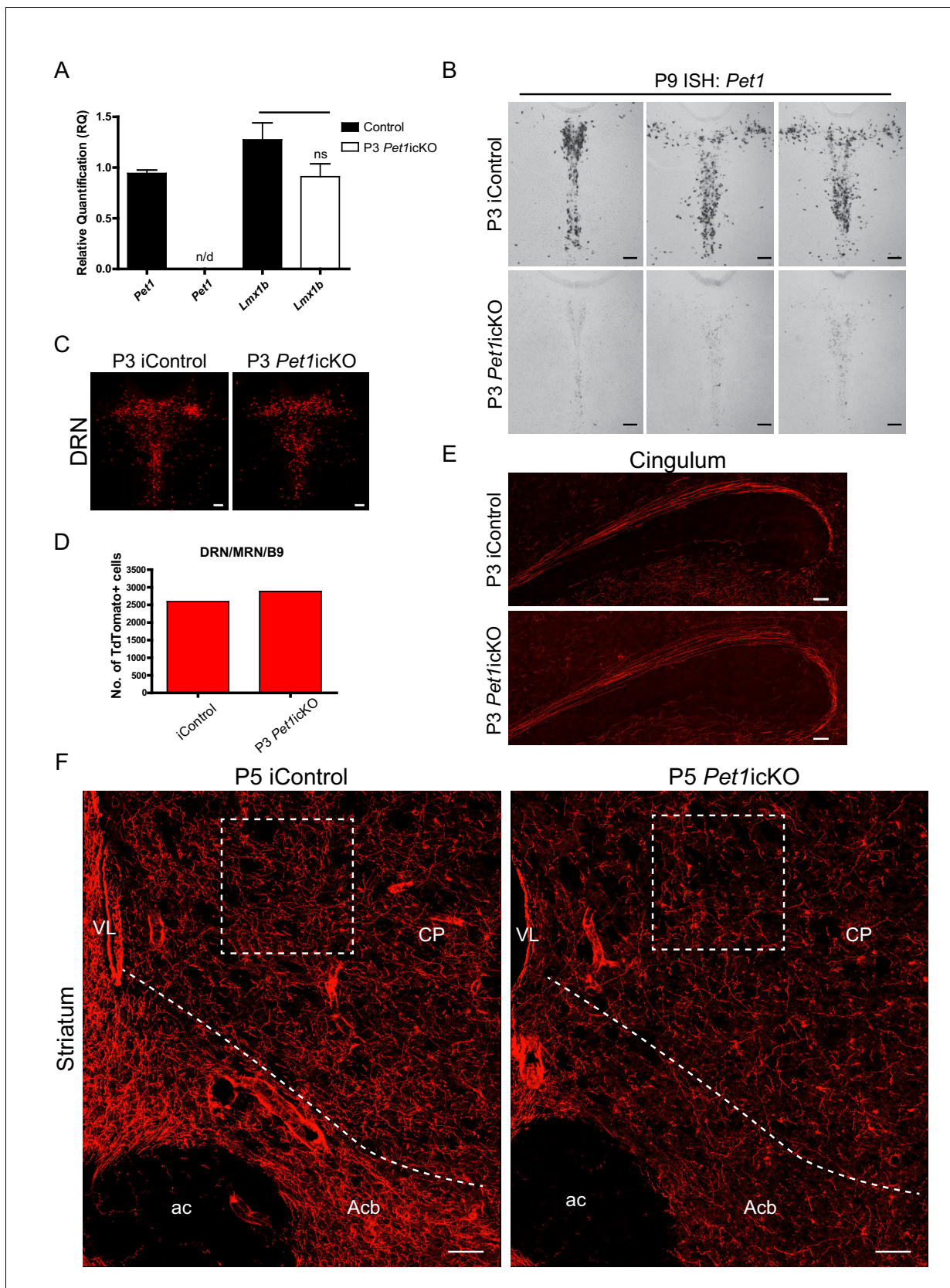


Figure 9—figure supplement 1. *Lmx1b*→*Pet1* cascade acts postnatally to control 5-HT terminal arborization. (A) RT-qPCR of flow sorted TdTomato⁺ cells in P3 targeted *Pet1icKO* mice at 4 weeks of age. *Pet1* was not detected by qPCR in flow sorted cells. *Lmx1b* was not significantly regulated by

Figure 9—figure supplement 1 continued on next page

Figure 9—figure supplement 1 continued

Pet1 ($p=0.1791$) ($n = 3$, iControl; $n = 3$, *Pet1*icKO mice). Unpaired t-test with Welch's correction, $*p<0.05$. Data are represented as mean \pm SEM. (B) *Pet1* ISH confirmed *Pet1* targeting in the DRN. Scale bars, 100 μm . (C, D) Similar numbers of TdTomato⁺ cells were counted in P3 *Pet1*icKO and P3 iControl mice. Scale bars, 100 μm . (E) Long-range cingulum route was fully formed in P3 targeted *Pet1*icKO mice. Scale bars, 100 μm . (F) Analysis of TdTomato⁺ arbors in P5 targeted *Pet1*icKO mice revealed continuing requirement for *Pet1* late-stage arborization in the striatum. Boxed regions presented in **Figure 8L**. Scale bars, 50 μm . CP, caudate putamen; Acb, nucleus accumbens; ac, anterior commissure; VL, lateral ventricle.

DOI: <https://doi.org/10.7554/eLife.48788.019>