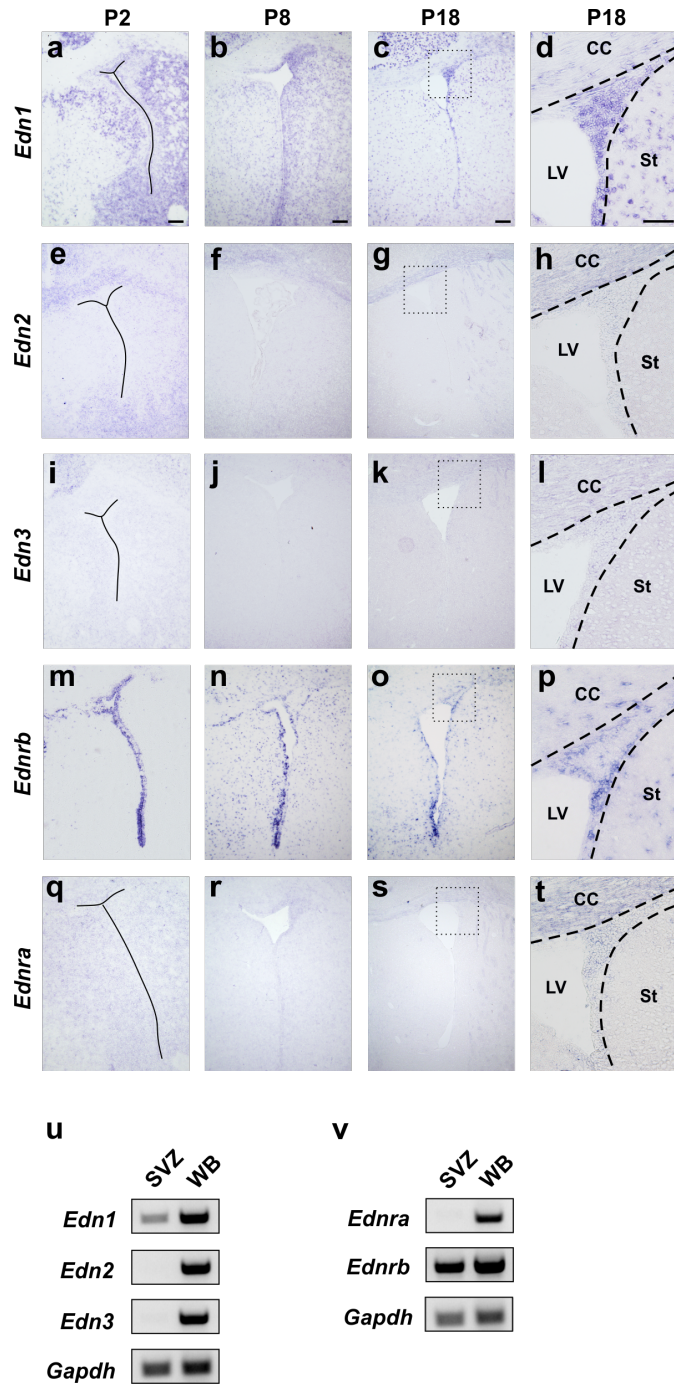


Supplementary Information for:

**Endothelin-1 signaling maintains glial progenitor proliferation in the postnatal subventricular zone**

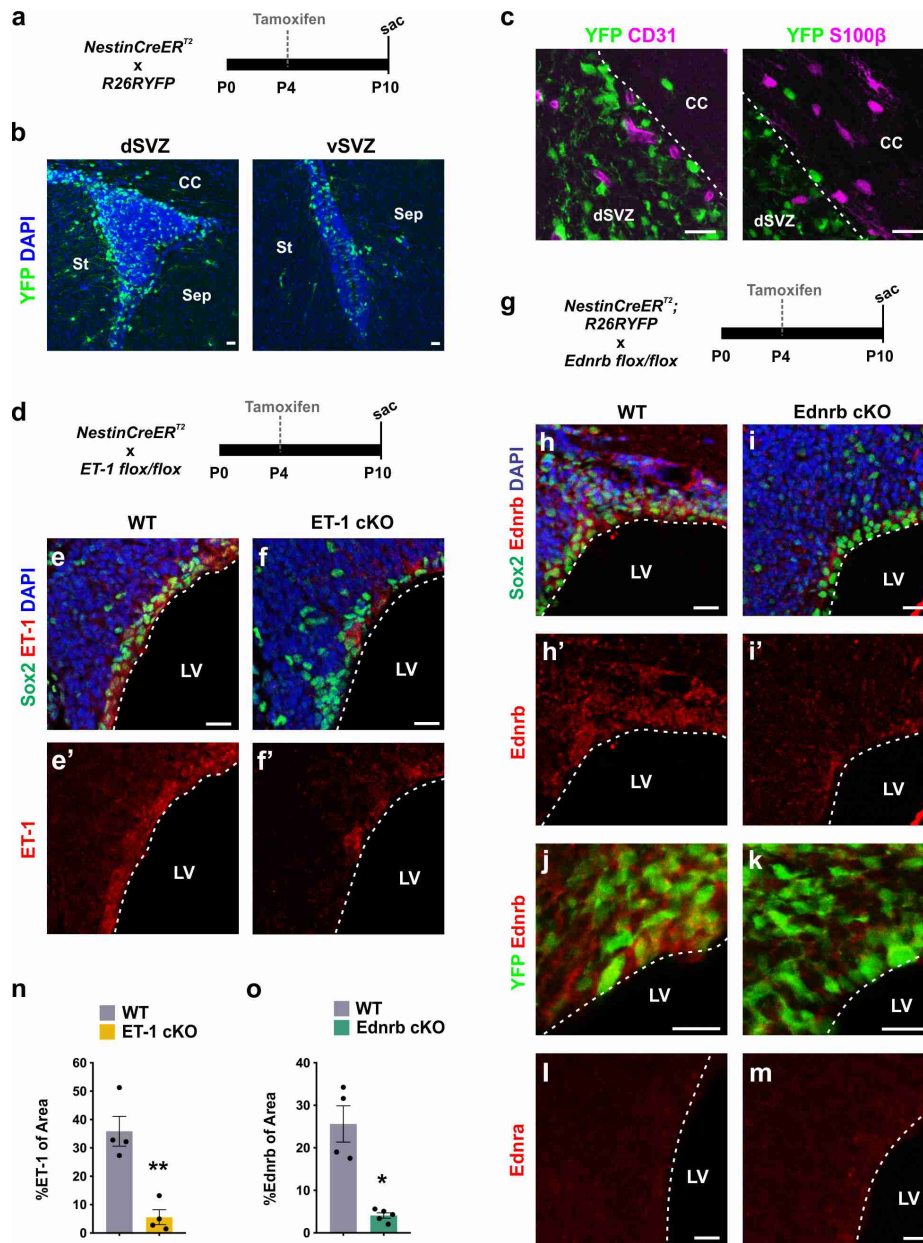
Katrina L Adams<sup>1</sup>, Giulia Riparini<sup>2</sup>, Payal Banerjee<sup>3</sup>, Marjolein Breur<sup>4,5</sup>, Marianna Bugiani<sup>4,5</sup>, and Vittorio Gallo<sup>1\*</sup>.



**Supplementary Figure 1. Expression profile of Endothelin pathway proteins in the postnatal mouse brain.**

(a-d) In situ for *Edn1* expression in WT mouse brain at postnatal day 2 (P2), P8, and P18. Images are focused on the right lateral ventricle (LV). Boxed region in c is magnified in d. Position of LV is drawn in a. Dorsolateral SVZ region is outlined in d. CC = corpus callosum. St = striatum. (e-h)

In situs for *Edn2* expression in WT mouse brain at P2, P8, and P18. Boxed region in g is magnified in h. **(i-l)** In situs for *Edn3* expression in WT mouse brain at P2, P8, and P18. Boxed region in k is magnified in l. **(m-p)** In situs for *Ednrb* expression in WT mouse brain at P2, P8, and P18. Boxed region in o is magnified in p. **(q-t)** In situs for *Ednra* expression in WT mouse brain at P2, P8, and P18. Boxed region in s is magnified in t. In situ images are representative of 3 WT mice. **(u)** RT-PCR for *Edn1*, *Edn2*, *Edn3*, and *Gapdh* using P7 SVZ or whole-brain (WB) derived cDNA. **(v)** RT-PCR for *Ednrb*, *Ednra*, and *Gapdh* using P7 SVZ or WB-derived cDNA. RT-PCR was replicated twice. Scale bars = 100 $\mu$ m for P2, P8, and P18 (c, g, k, o, s). Scale bar = 50 $\mu$ m for P18 (d, h, l, p, t). Source data are provided as a Source Data file.

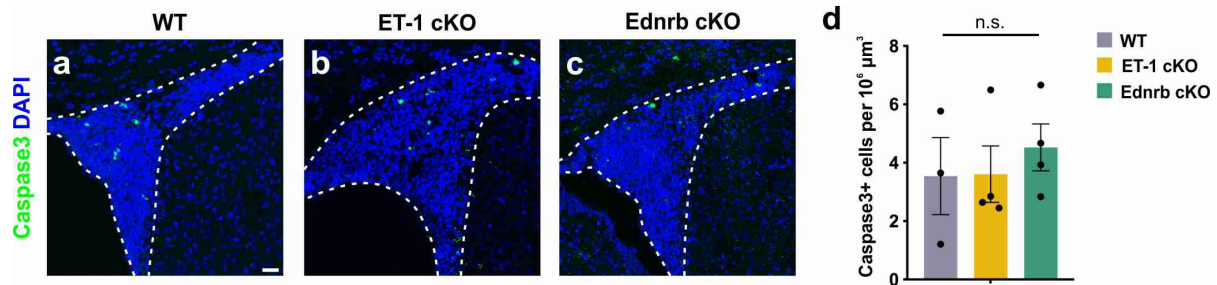


**Supplementary Figure 2. Method and confirmation of ET-1 and EdnrB knockdown in the postnatal SVZ.**

(a) Experimental strategy for images in b and c. (b) Coronal sections of P10 *Nestin::CreER<sup>T2</sup>; R26RYFP* mouse dorsal and ventral SVZ. CC = corpus callosum, dSVZ = dorsal subventricular zone, Sep = septum, St = striatum, vSVZ = ventral subventricular zone. Images are representative of 3 *Nestin::CreER<sup>T2</sup>; R26RYFP* mice. (c) YFP+ recombined cells in *Nestin::CreER<sup>T2</sup>; R26RYFP* mice do not express markers of endothelial cells (CD31) or white matter astrocytes (S100β). Images are representative of 3 *Nestin::CreER<sup>T2</sup>; R26RYFP* mice. (d) Experimental strategy for

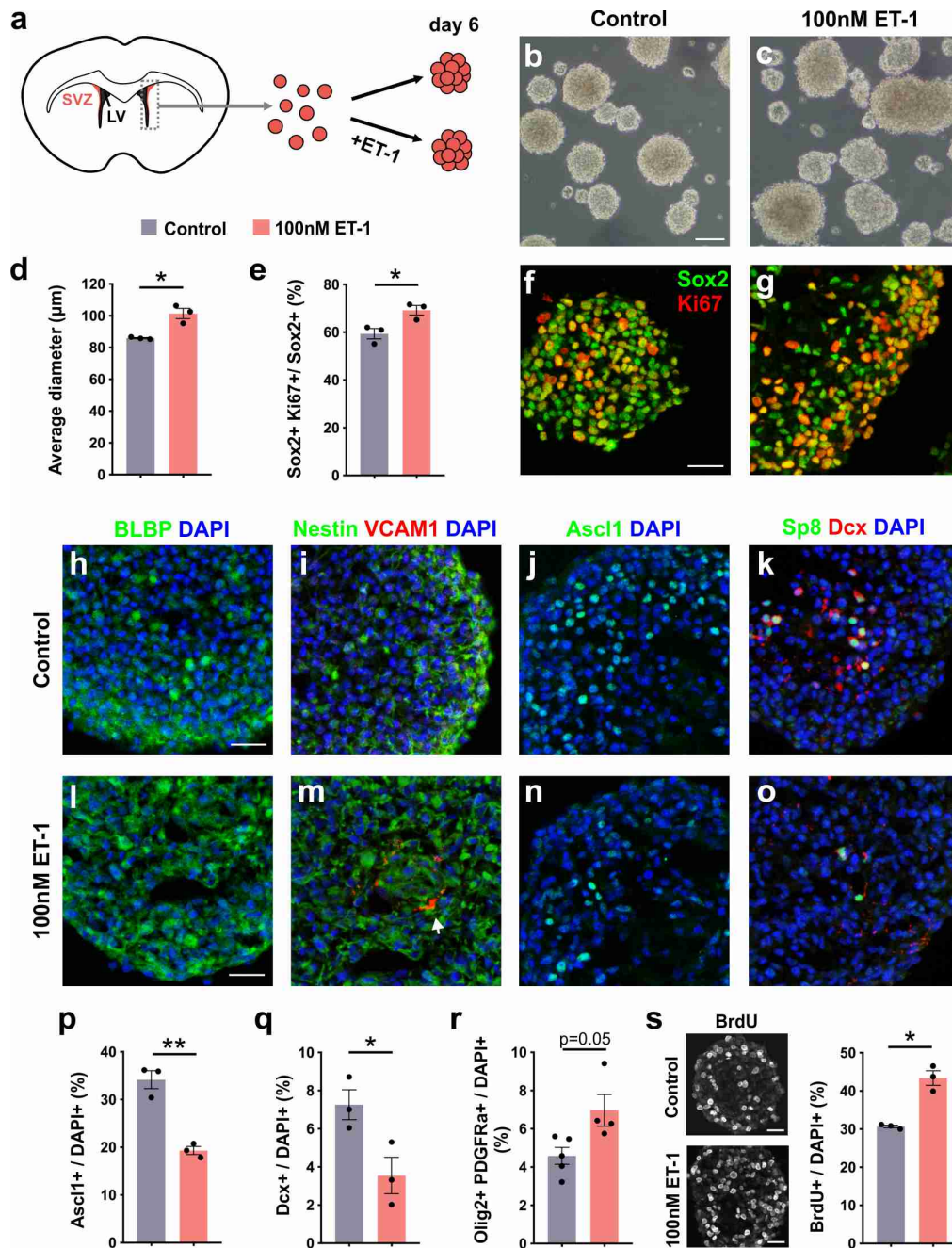


ET-1 ablation in the developing postnatal SVZ. **(e-f)** ET-1 protein is reduced in Sox2+ progenitors lining the lateral ventricle (LV) of P10 ET-1 cKO mice (f), compared to WT controls (e). e' and f' show single channel images for ET-1 staining. Images are representative of 4 WT and ET-1 cKO mice. **(g)** Experimental strategy for Ednrb ablation in the developing postnatal SVZ. **(h-i)** Ednrb protein is reduced in Sox2+ progenitors lining the LV of P10 Ednrb cKO mice (i), compared to WT controls (h). h' and i' show single channel images for Ednrb staining. **(j-k)** Ednrb protein is reduced in YFP+ recombined cells in the SVZ of Ednrb cKO mice (k), compared to WT controls (j). **(l-m)** Ednra protein is not expressed at detectable levels within the SVZ of WT (l) and Ednrb cKO mice (m). Images are representative of 4 WT and 5 Ednrb cKO mice. **(n)** Quantification of percentage of ET-1+ pixels per area in the SVZ in WT and ET-1 cKO mice at P10 (n=4 mice both groups). \*\*p-value = 0.0052 (Welch's t test). **(o)** Quantification of percentage of Ednrb+ pixels per area in the SVZ in WT and Ednrb cKO mice at P10 (n=4 WT, 5 Ednrb cKO mice). \*p-value = 0.0140 (Welch's t test). All scale bars = 25µm. LV = lateral ventricle. Data are presented as mean values +/- SEM. Source data are provided as a Source Data file.



**Supplementary Figure 3. Ablation of *ET-1* or *Ednrb* in the SVZ does not affect cellular apoptosis.**

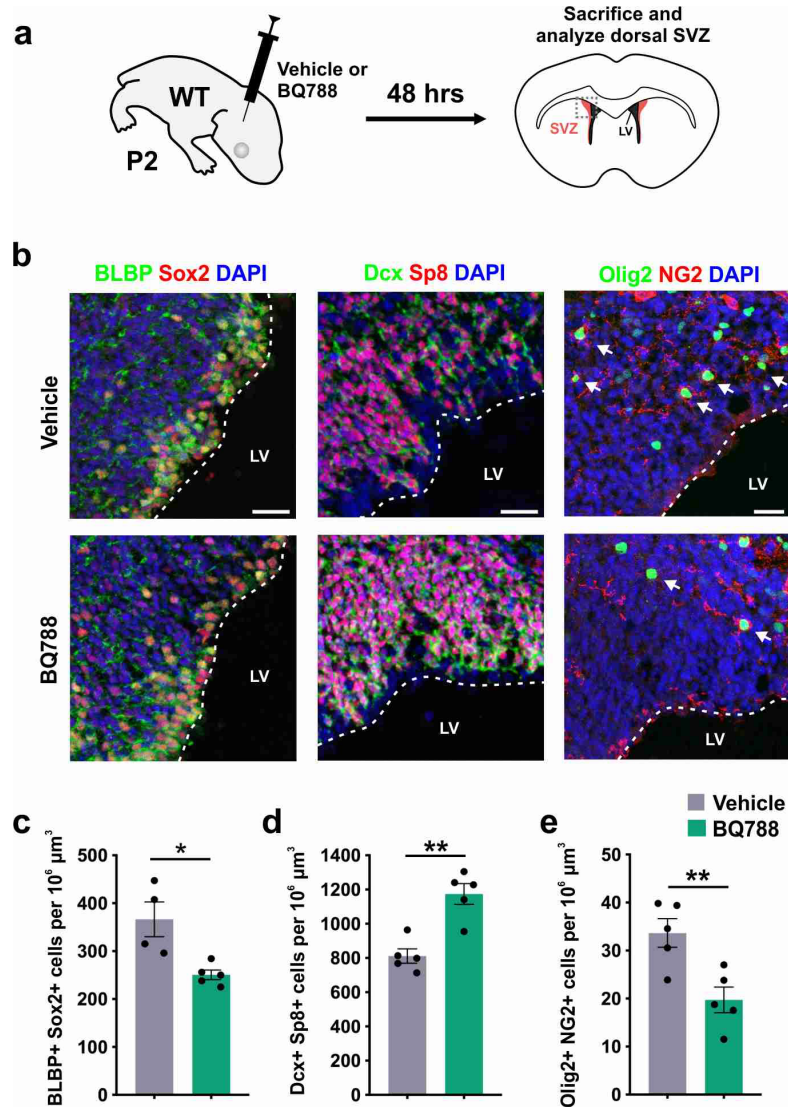
(a-c) Coronal sections of the dorsal SVZ (outlined in white) in WT (a), ET-1 cKO (b), and Ednrb cKO (c) mice at P10. Scale bars = 25μm. (d) Quantification of the number of Caspase3+ cells in the SVZ, normalized to area (n=3 WT, 4 ET-1 cKO, 4 Ednrb cKO mice). n.s. = not significant (One-way ANOVA with Tukey's multiple comparisons test). Data are presented as mean values +/- SEM. Source data are provided as a Source Data file.



**Supplementary Figure 4. ET-1 promotes RGC maintenance and blocks differentiation in neurospheres.**

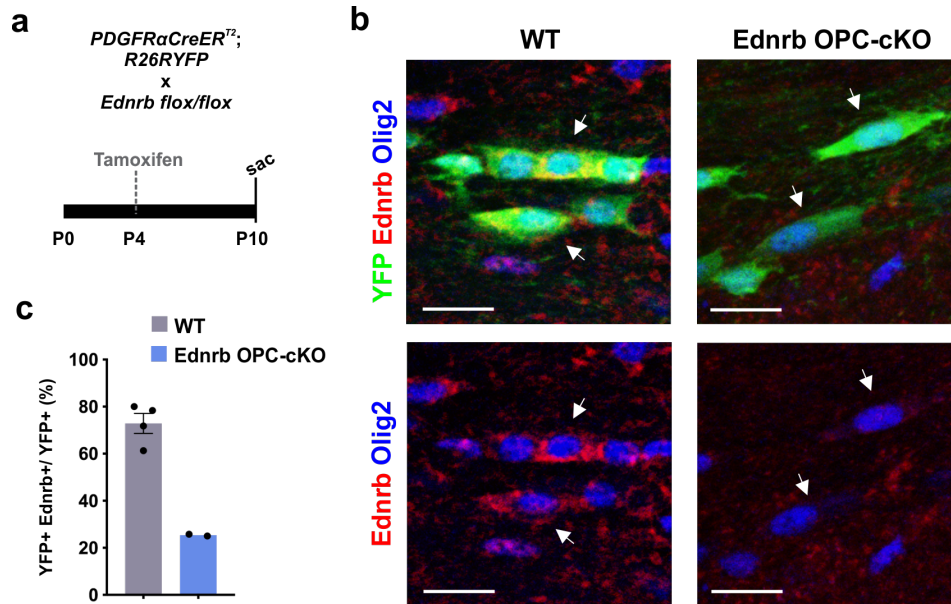
(a) Experimental strategy. (b-c) Representative images of control (b) and ET-1 treated (c) neurospheres 6 days after dissociation. Scale bar = 100µm. (d) Quantification of the average diameter of control and ET-1 treated neurospheres (n=3 independent batches). \*p-value = 0.0399 (Welch's t test). (e) Quantification of the percentage of proliferating Sox2+ progenitors in control

and ET-1 treated neurospheres (n=3 independent batches). \*p-value = 0.0288 (Welch's t test). **(f-o)** Sections of control (f, h-k) and ET-1 treated (g, l-o) neurospheres stained for makers of RGCs and neural progenitors. The arrow in m points to the presence of VCAM1+ cells. Scale bar = 25µm. **(p)** Quantification of the percentage of Ascl1+ cells in control and ET-1 treated neurospheres (n=3 independent batches). \*\*p-value = 0.0071 (Welch's t test). **(q)** Quantification of the percentage of Dcx+ NPCs in control and ET-1 treated neurospheres (n=3 independent batches). \*p-value = 0.0416 (Welch's t test). **(r)** Quantification of the percentage of OPCs in control and ET-1 treated neurospheres (n=5 control, 4 ET-1 treated batches). p-value = 0.0557 (Welch's t test). **(s)** BrdU was administered to neurospheres 20 minutes after the last ET-1 treatment and the cells were collected for analysis 4 hours later. Representative images of BrdU staining in control and ET-1 treated neurospheres. Scale bars = 25µm. Quantification of the percentage of BrdU+ cells in control and ET-1 treated neurospheres (n=3 independent batches). \*p-value = 0.0194 (Welch's t test). Images are representative of 3 independent neurosphere batches. Data are presented as mean values +/- SEM. Source data are provided as a Source Data file.



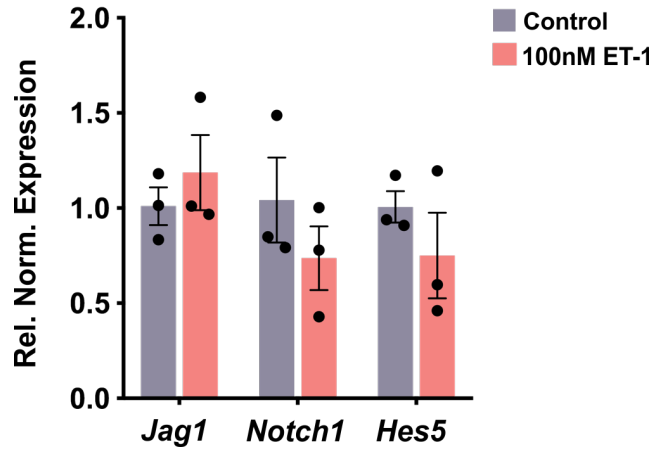
**Supplementary Figure 5. Pharmacological inhibition of *Ednrb* receptor in the SVZ recapitulates the *Ednrb* cKO mouse phenotype.**

(a) Experimental strategy. (b) Coronal images of the dorsal SVZ, labeling different progenitor populations in WT pups 48 hours after injection of vehicle or BQ788. LV = lateral ventricle. Arrows point to Olig2+ NG2+ OPCs. Scale bars = 25μm. (c) Quantification of the total number of BLBP+ Sox2+ RGCs in the dorsal SVZ, normalized to area (n=4 vehicle, 5 BQ788 injected mice). \*p-value = 0.0449 (Welch's t test). (d) Quantification of the total number of Dcx+ Sp8+ NPCs in the dorsal SVZ, normalized to area (n=5 both groups). \*\*p-value = 0.0016 (Welch's t test). (e) Quantification of the total number of Olig2+ NG2+ OPCs in the dorsal SVZ, normalized to area (n=5 both groups). \*\*p-value = 0.0084 (Welch's t test). Data are presented as mean values +/- SEM. Source data are provided as a Source Data file.



**Supplementary Figure 6. Confirmation of *Ednrb* knockdown in OPCs.**

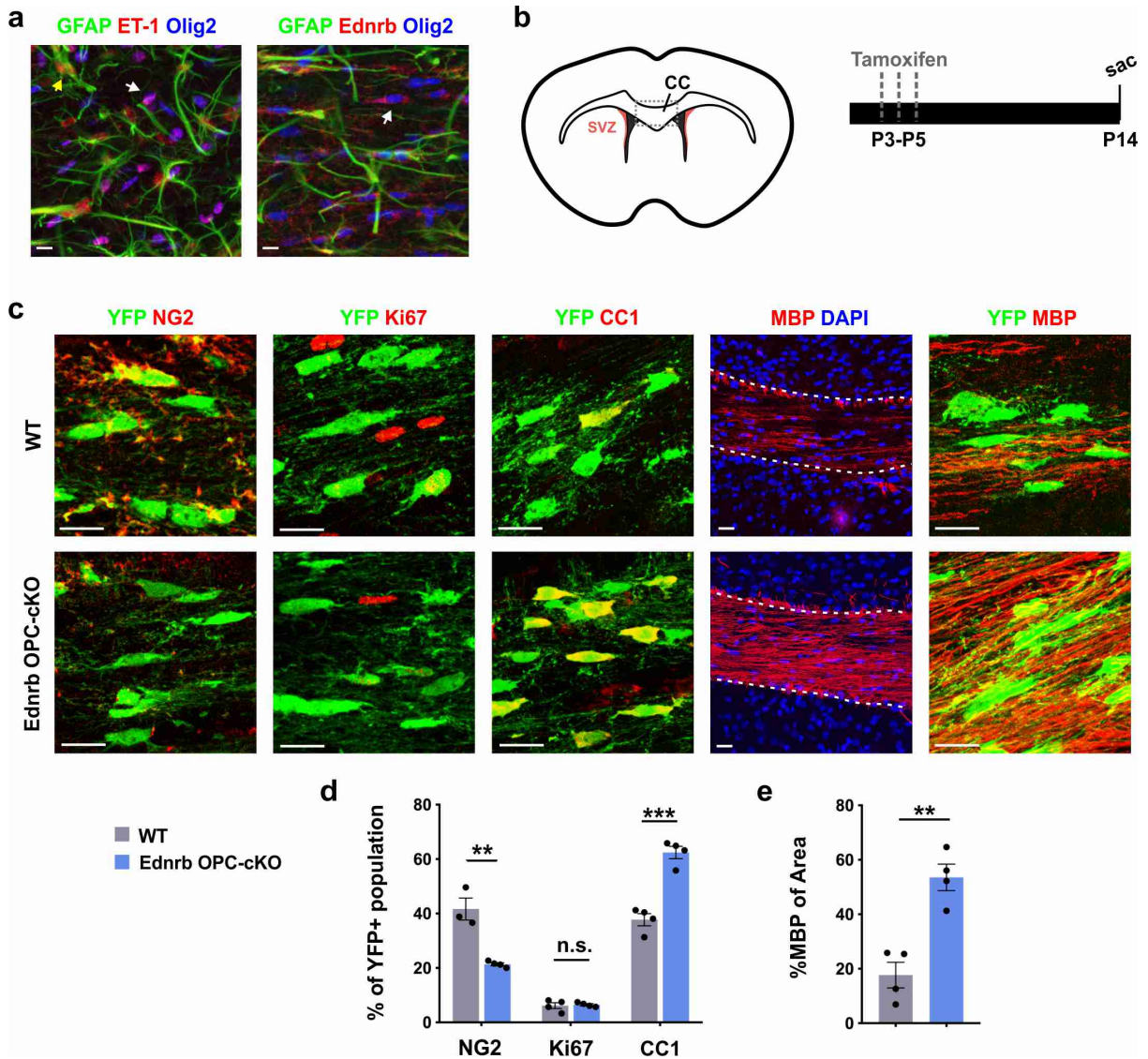
(a) Experimental strategy for *Ednrb* ablation in OPCs. (b) *Ednrb* expression in YFP+ Olig2+ cells is reduced in *Ednrb* OPC-cKO mice, compared to WT controls. Scale bars = 25µm. (c) Quantification of the percentage of *Ednrb*+ YFP+ cells in the SVZ and CC at P10 (n=4 WT, 2 *Ednrb* OPC-cKO mice). Data are presented as mean values +/- SEM. Source data are provided as a Source Data file.



***Supplementary Figure 7. Notch signaling is not activated in OPCs following ET-1 treatment.***

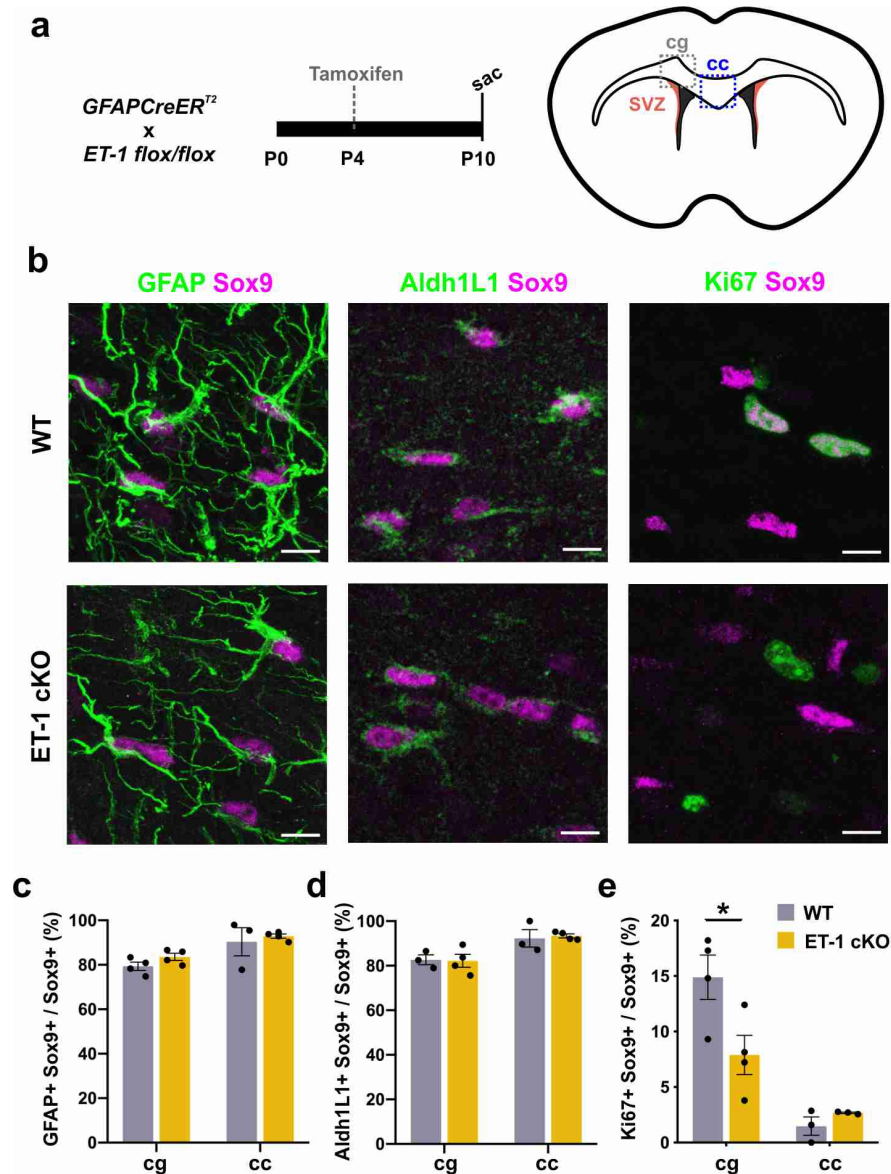
QPCR for Notch pathway components 24 hours after ET-1 treatment of primary SVZ OPCs (n=3 independent batches). No significant differences ( $p < 0.05$ ) were detected (Multiple t tests with Holm-Sidak multiple comparisons correction). Data are presented as mean values  $\pm$  SEM. Source data are provided as a Source Data file.





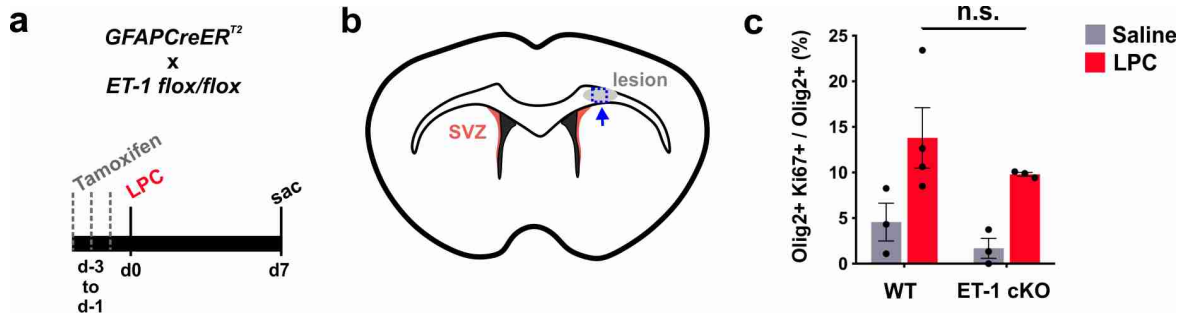
**Supplementary Figure 8. OPC-specific Ednrb ablation promotes OL maturation in the CC.**

(a) Coronal sections of the CC in WT mice at P10. White arrows point to Olig2+ cells that express ET-1 or Ednrb. Yellow arrow points to ET-1+ GFAP+ astrocyte. Images are representative of 3 WT mice. (b) Experimental strategy. CC = corpus callosum. (c) Coronal sections of YFP+ recombined OL-lineage cells in the CC of WT and Ednrb OPC-cKO mice at P14. (d) Quantification of YFP+ OLs in the CC at P14 (NG2: n=3 WT, 4 Ednrb OPC-cKO mice. Ki67: n=4 mice both groups. CC1: n=4 mice both groups). \*\*p-value = 0.003904; \*\*\*p-value = 0.000744; n.s. = not significant (Multiple t tests with Holm-Sidak multiple comparisons correction). (e) Quantification of the percentage of MBP+ pixels in the CC at P14 (n=4 mice both groups). \*\*p-value = 0.0018 (Welch's t test). All scale bars = 25µm. Data are presented as mean values +/- SEM. Source data are provided as a Source Data file.



**Supplementary Figure 9. ET-1 ablation reduces astrocyte proliferation in the subcortical white matter.**

(a) Experimental strategy. Cg = cingulum. Cc = corpus callosum. (b) Coronal sections of the cg in WT and ET-1 cKO mice at P10. Scale bar = 10 $\mu$ m. (c) Quantification of the percentage of GFAP+ astrocytes in the cg and cc at P10 (cg: n=4 mice both groups. cc: n=3 WT, 4 ET-1 cKO mice). (d) Quantification of the percentage of Aldh1L1+ astrocytes in the cg and cc at P10 (n=3 WT, 4 ET-1 cKO mice). (e) Quantification of the percentage of proliferating astrocytes in the cg and cc at P10 (cg: n=4 mice both groups. cc: n=3 mice both groups). \*p-value = 0.0337 (Two-way ANOVA with Tukey's multiple comparisons test). Data are presented as mean values +/- SEM. Source data are provided as a Source Data file.



**Supplementary Figure 10. *ET-1* ablation does not alter OPC proliferation within subcortical white matter lesions.**

(a-b) Experimental strategy. LPC = lysolecithin. Arrow in b points to the region quantified in c. (c) Quantification of the percentage of proliferating OPCs within the lesion of WT and ET-1 cKO mice at 7 days post LPC injection (Saline: n=3 mice both groups. LPC: n=4 WT, 3 ET-1 cKO mice). n.s. = not significant (Two-way ANOVA with Tukey's multiple comparisons test). Data are presented as mean values +/- SEM. Source data are provided as a Source Data file.

**Supplementary Table 1.** Quantitative PCR Primers.

<b>Gene</b>	<b>Forward primer</b>	<b>Reverse primer</b>
<i>Edn1</i>	5'-CCCAAAGTACCATGCAGAAAAG-3'	5'-GATGCCTTGATGCTATTGCTG-3'
<i>Ednrb</i>	5'-CAATCCTCTGTATTTGGTGAG-3'	5'-CGTGATCGTTGGCTTTGAAC-3'
<i>Gapdh</i>	5'-CTTTGTCAAGCTCATTTCCTGG-3'	5'-TCTTGCTCAGTGTCCCTTGC-3'
<i>Hes5</i>	5'-CAAGGAGAAAAACCGACTGCG-3'	5'-GCGAAGGCTTTGCTGTGTTT-3'
<i>Jag1</i>	5'-ACACCCGAACTGGACAAATAA-3'	5'-GTGCCCTCAAACCTCTACCTATG-3'
<i>Notch1</i>	5'-GCAACTGTCCTCTGCCATATAC-3'	5'-GTCTTCAGACTCCTTGCATACC-3'

**Supplementary Table 2.** Primers for generating in situ probes.

<b>Gene</b>	<b>Forward primer</b>	<b>Reverse primer</b>
<i>Edn1</i>	5'- GAGAGCCAGGAGATTCC ACA-3'	5'- GAGATTAACCCTCACTAAAGGGAGCATGGCAATGTT TCAGCTA-3'
<i>Edn2</i>	5'- GGGAGACCCCTATGCCT ATC-3'	5'- GAGATTAACCCTCACTAAAGGGATCCCAAAGTGTC CCAAGAG-3'
<i>Edn3</i>	5'- ACCAGGCTGGCTCTTTAC AA-3'	5'- GAGATTAACCCTCACTAAAGGGACCAGACCAGTAGC CTTGAGC-3'
<i>Ednrb</i>	5'- TTCCCATTCCTTAGCCCTG TG-3'	5'- GAGATTAACCCTCACTAAAGGGAAGATCTGGGGCGT CCTTTAT-3'
<i>Ednra</i>	5'- TGGGAGAAAGGAGATGA TGG-3'	5'- GAGATTAACCCTCACTAAAGGGACCTGGCTTTTCCG AACTATG-3'