Supplementary material

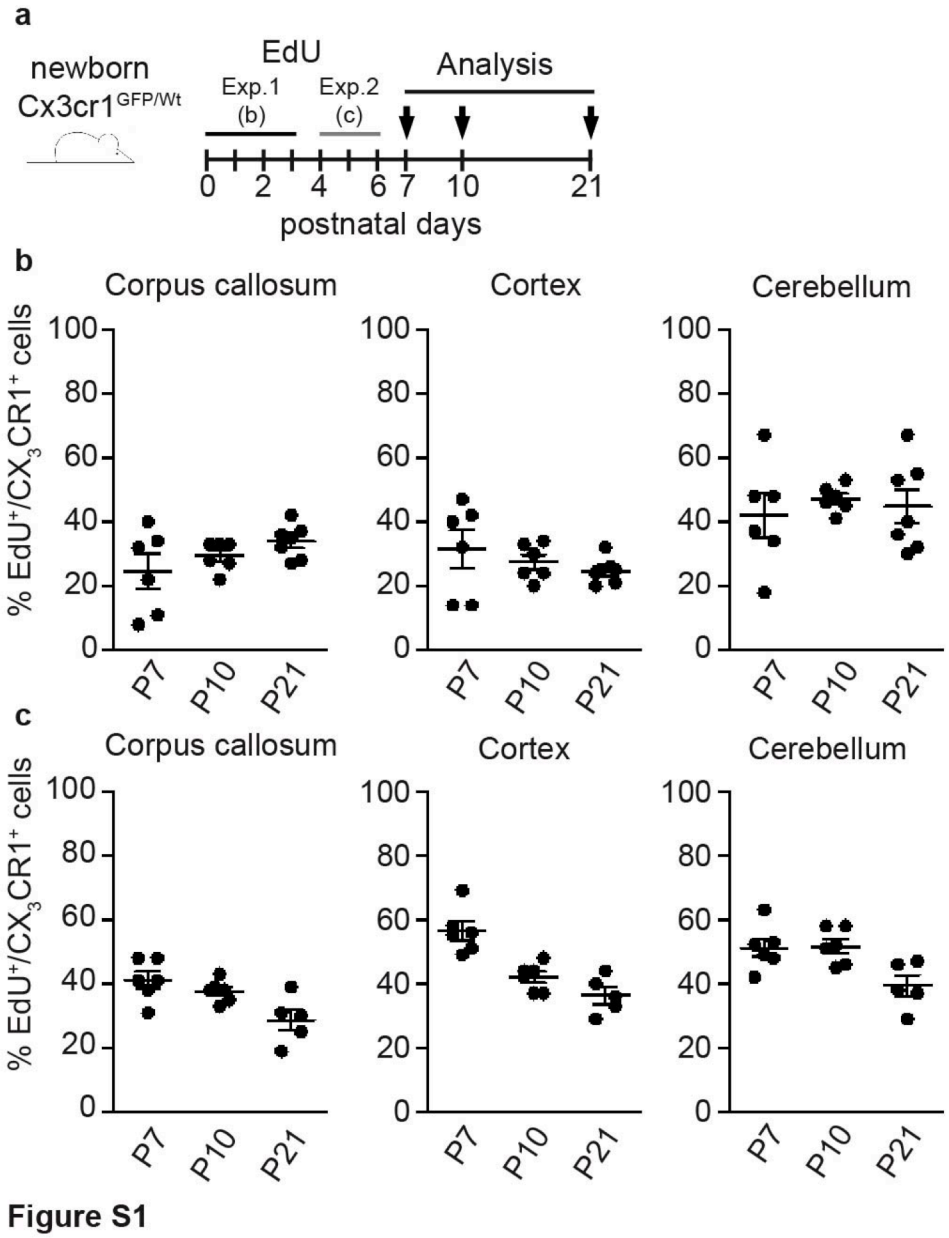

Figure S1

Figure S1 (related to Fig. 1): High proliferation rate of postnatal microglia. (a) Scheme of experimental setup. *Cx3cr1* $^{GFP/Wt}$ mice were intraperitoneally injected (i.p.) with 5-Ethynyl-2′-deoxyuridine (EdU) at P0-P3 or P4-P6. Analysis was performed on day P7, P10, and P21. (b) Quantification of EdU^+/CX_3CR1^+ microglia in the corpus callosum, cortex, and cerebellum at the indicated time points. EdU was applied at P0-P3. Each symbol represents one mouse. Mean ± SEM are shown. (c) Quantification of EdU^+/CX_3CR1^+ microglia in the corpus callosum, cortex, and cerebellum at the indicated time points. EdU was applied at P4-P6. Each symbol represents one mouse. Mean ± SEM are shown

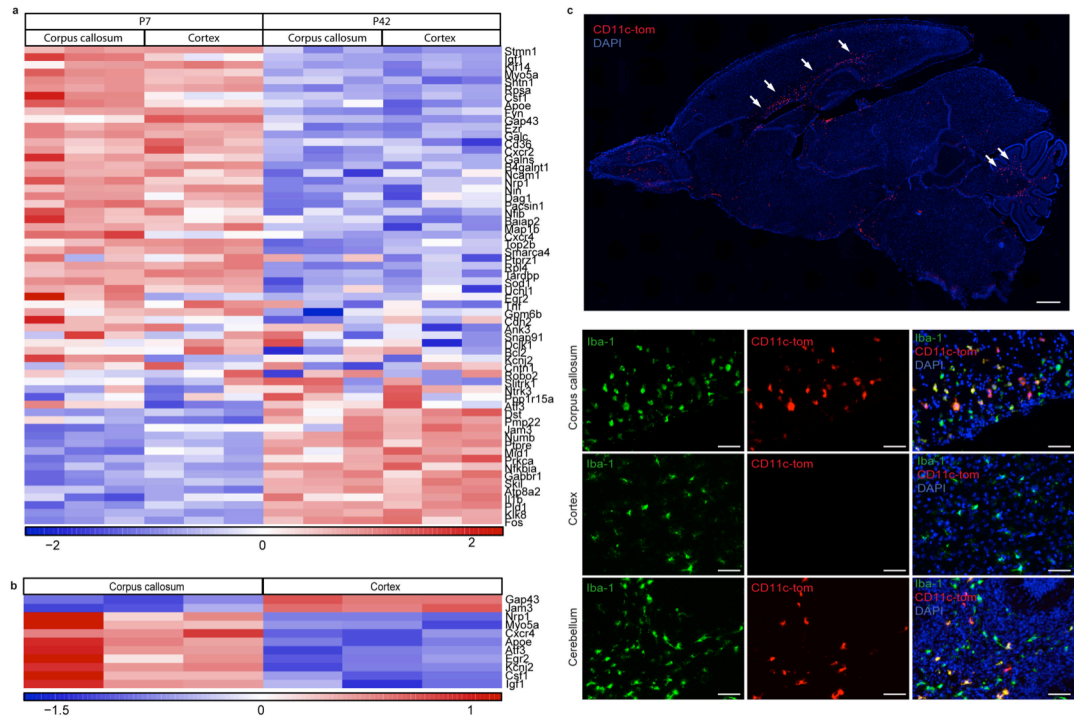

Figure S2

Figure S2 (related to Fig. 1): Genes related to myelination and axogenesis are highly upregulated in the postnatal brain. (a)(b) Hierarchical clustering created on the most significantly differentially expressed genes (cut off adjusted to p value < 0.01) related to the GO-terms myelination and axogenesis between microglia from the corpus callosum and cortex at postnatal day 7 and at P42 (adult) (a) or between microglia from the corpus callosum and cortex only at postnatal day 7 (b). Heat map displays row z-score values from red to blue via white. (c) Immunofluorescent images of a P8 *Cd11c* ^{CreER}*:R26-tomato* mouse injected with tamoxifen at P3-P7. Representation of the accumulation of CD11c^{+} (red) Iba-1^{+} microglia (green) specifically in white matter regions (corpus callosum and cerebellum; indicated by arrows). Scale bar = 200 μm upper image, 50 μm: lower images

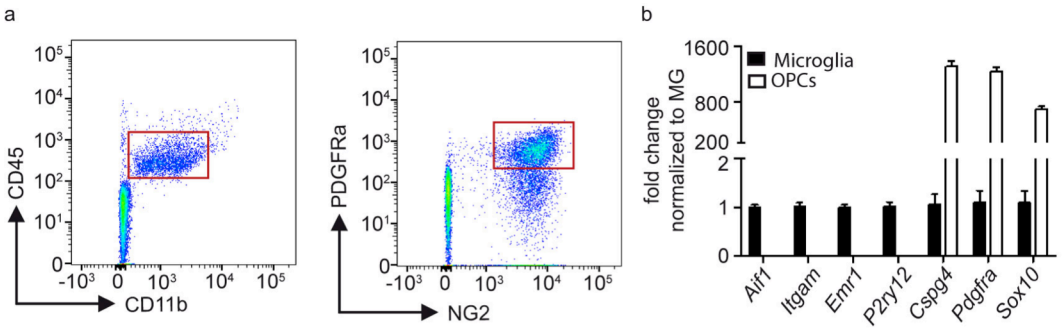

Figure S3

Figure S3 (related to Fig. 3): Purity of sorted microglia and oligodendrocyte progenitors. (a) Representative flow cytometry blots showing the sorting strategy for $CD45^{+}CD11b^{+}$ microglia (left) and $PDGFR\alpha^{+}/NG2^{+}$ oligodendrocyte progenitors (OPCs; right) used for the gene expression analysis in (**b**). Cells were pre-gated on living cells, single cells, and $Gr\text{-}1^{-}$ cells. (b) Quantitative RT-PCR of the genes *allograft inflammatory factor 1 (Aif1), integrin subunit alpha M (Itgam), adhesion G protein-coupled receptor E1 (Emr1), purinergic receptor P2Y12 (p2ry12), chondroitin sulfate proteoglycan 4 (Cspg4), platelet derived growth factor receptor alpha (Pdgfra),* and *SRY-Box 10 (Sox10)*. Data are normalized to *Gapdh* and β-*Actin* and presented normed to microglia. Bars represent mean ± SEM

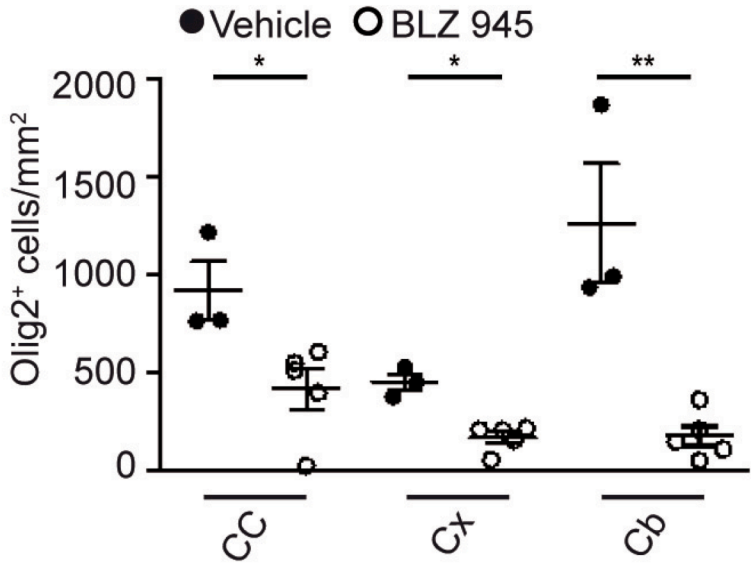

Figure S4

Figure S4 (related to Fig. 3): $Olig2^{+}$ oligodendrocyte numbers upon microglia depletion. Quantification of $Olig2^{+}$ oligodendrocytes in the corpus callosum, cortex, and cerebellum at P8, 1 day after BLZ945-induced depletion of microglia at P2, P4, P6, and P7. n = 3 - 5; samples from two independent experiments. Significant differences were examined by an unpaired *t* test and marked with asterisks ($*P < 0.05$, $**P < 0.01$)