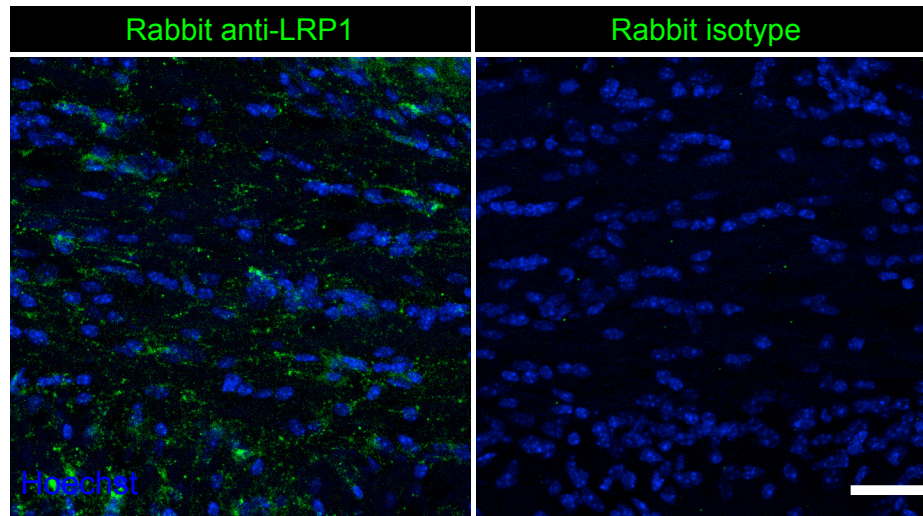


a



b

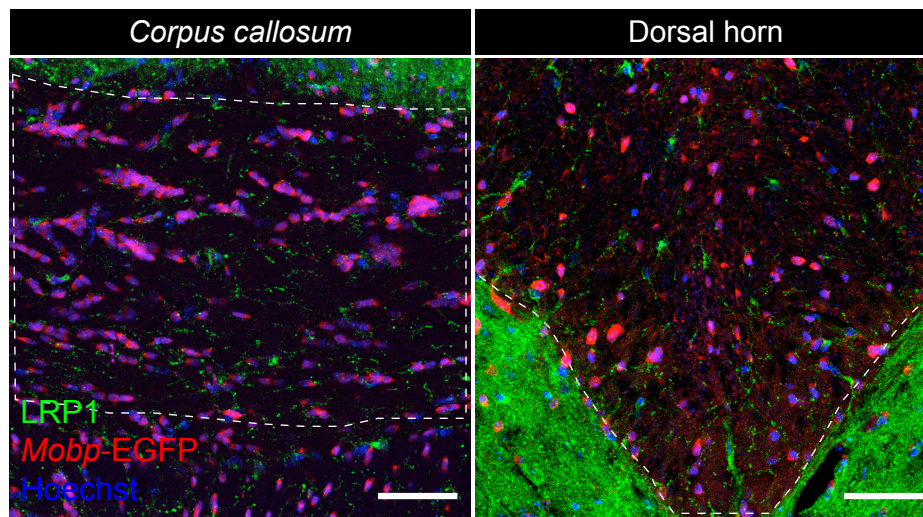


Fig. S1 LRP1 expression in mature oligodendrocytes (a) *Corpus callosum* staining with rabbit anti-LRP1 antibody and rabbit isotype control. Scale bar 30 μ m. (b) Brain (*corpus callosum*) and spinal cord (dorsal horn) slices from *Mbp-EGFP* reporter mice stained for LRP1. Dashed lines demarcate white matter borders. Scale bars 50 μ m.

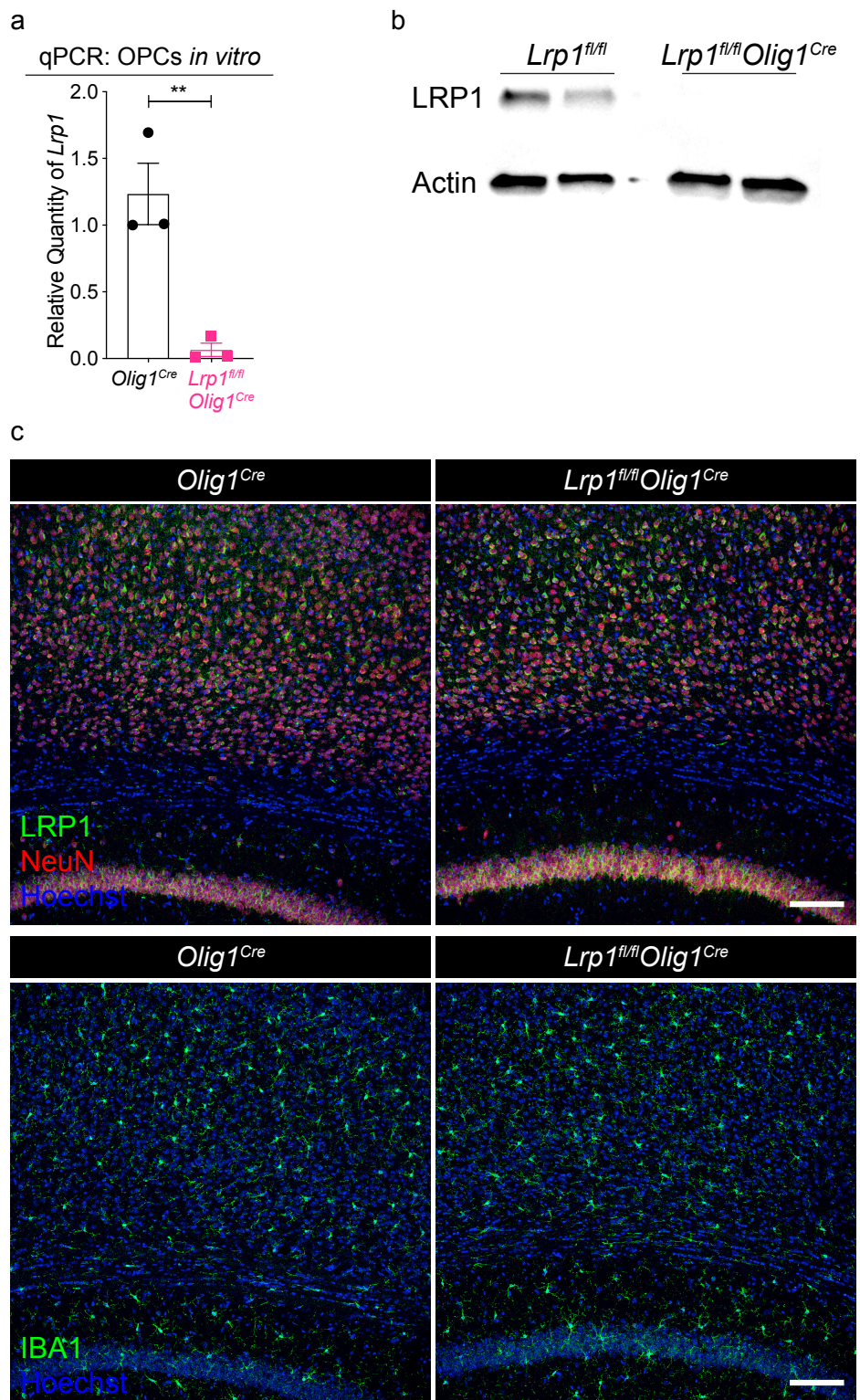


Fig. S2 Silencing of LRP1 in OPCs does not affect neuronal and myeloid compartments (a) qPCR for *Lrp1* from cultured OPCs (unpaired t-test, ** $p=0.0077$; $n=3$ mice per genotype; error bars represent \pm SEM). (b) Western blot for LRP1 and actin from cultured OPCs (2 mice per genotype). (c) Cortical slices stained for LRP1 and NeuN from *Olig1^{Cre}* and *Lrp1^{fl/fl}Olig1^{Cre}* mice (upper panels). IBA1 staining in cortical slices from *Olig1^{Cre}* and *Lrp1^{fl/fl}Olig1^{Cre}* mice (lower panels). Scale bar 100 μ m.

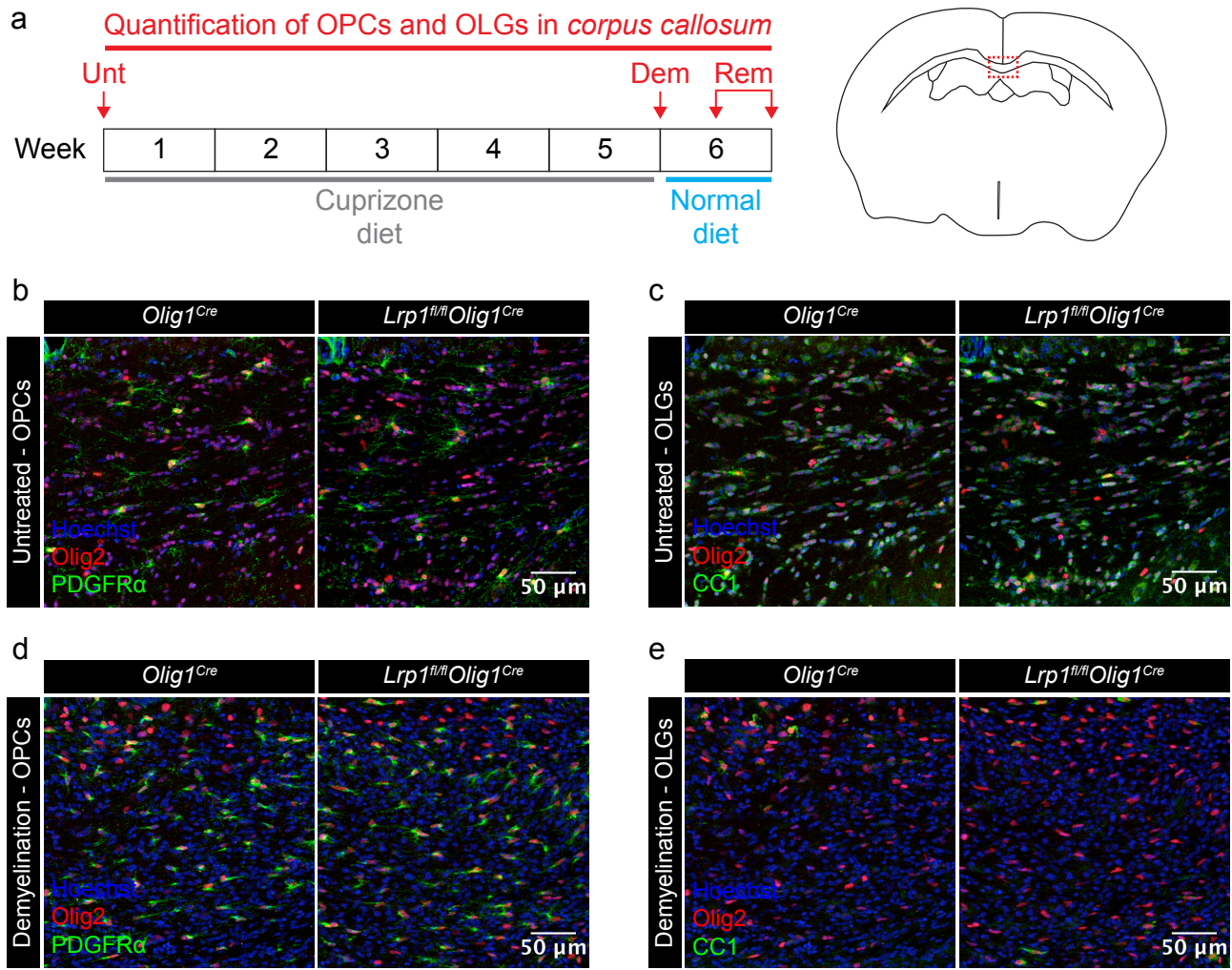


Fig. S3 OPCs and oligodendrocytes in the naïve and demyelinating *corpus callosum* (a) Schematic illustrating the cuprizone diet timeline and the timepoints at which the *corpus callosum* was imaged in *Olig1^{Cre}* and *Lrp1^{fl/fl}Olig1^{Cre}* mice. (b) Representative images of OPCs and (c) mature oligodendrocytes in the untreated *corpus callosum*. (d) Representative images of OPCs and (e) mature oligodendrocytes in the demyelinating *corpus callosum*.

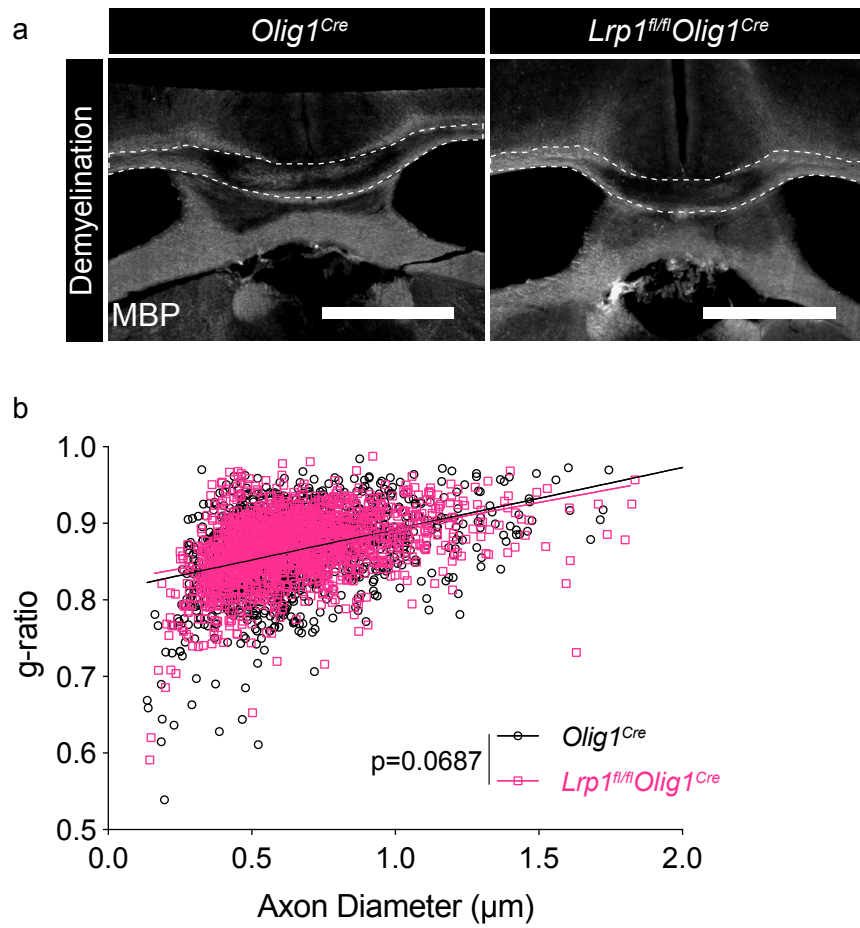


Fig. S4 MBP staining during demyelination and G-ratio analysis in the remyelinating corpus callosum (a) MBP immunofluorescence staining at 4 weeks of cuprizone treatment in the corpus callosum of *Olig1^{Cre}* and *Lrp1^{fl/fl}Olig1^{Cre}* mice. Scale bars 1000 μm . (b) Calculated g-ratios from axons in the remyelinating (0.5 Wk Rem) corpus callosum of *Olig1^{Cre}* and *Lrp1^{fl/fl}Olig1^{Cre}* mice (linear regression analysis with slopes comparison).

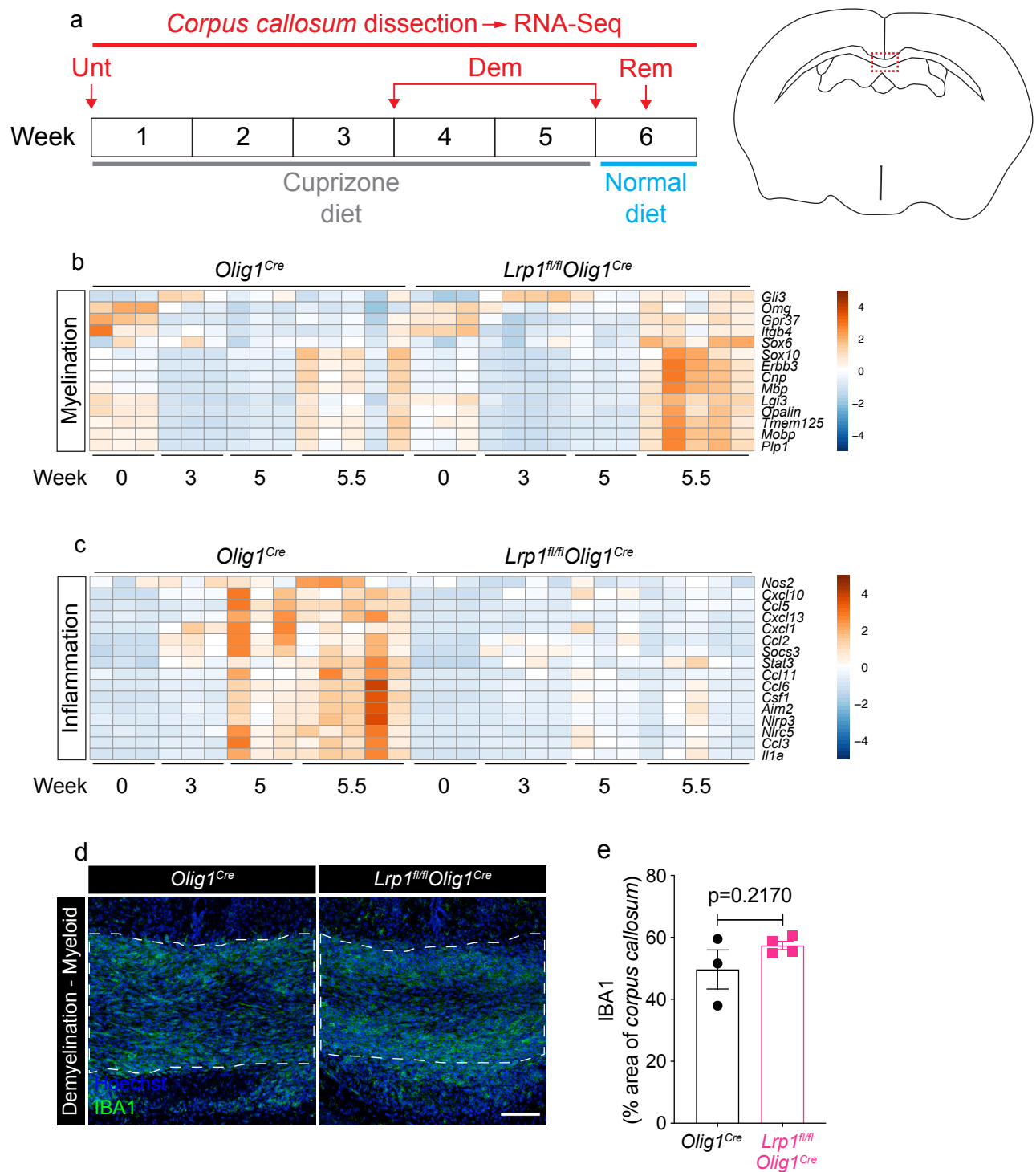


Fig. S5 RNA-seq analysis of the *corpus callosum* over the course of cuprizone treatment (a) Schematic illustrating the cuprizone diet timeline and timepoints at which the *corpus callosum* was dissected and analyzed by RNA-seq. **(b)** Heat map of myelination- and **(c)** inflammation-related genes in *Olig1^{Cre}* and *Lrp1^{fl/fl}Olig1^{Cre}* mice. Heat maps have a normalized count scale with z-score normalization. **(d)** Staining and **(e)** quantification of IBA1 in the *corpus callosum* of *Olig1^{Cre}* and *Lrp1^{fl/fl}Olig1^{Cre}* mice after 5 weeks of cuprizone treatment (unpaired t-test; n=3-4 mice per genotype; error bars represent +/- SEM). Scale bar 50µm.

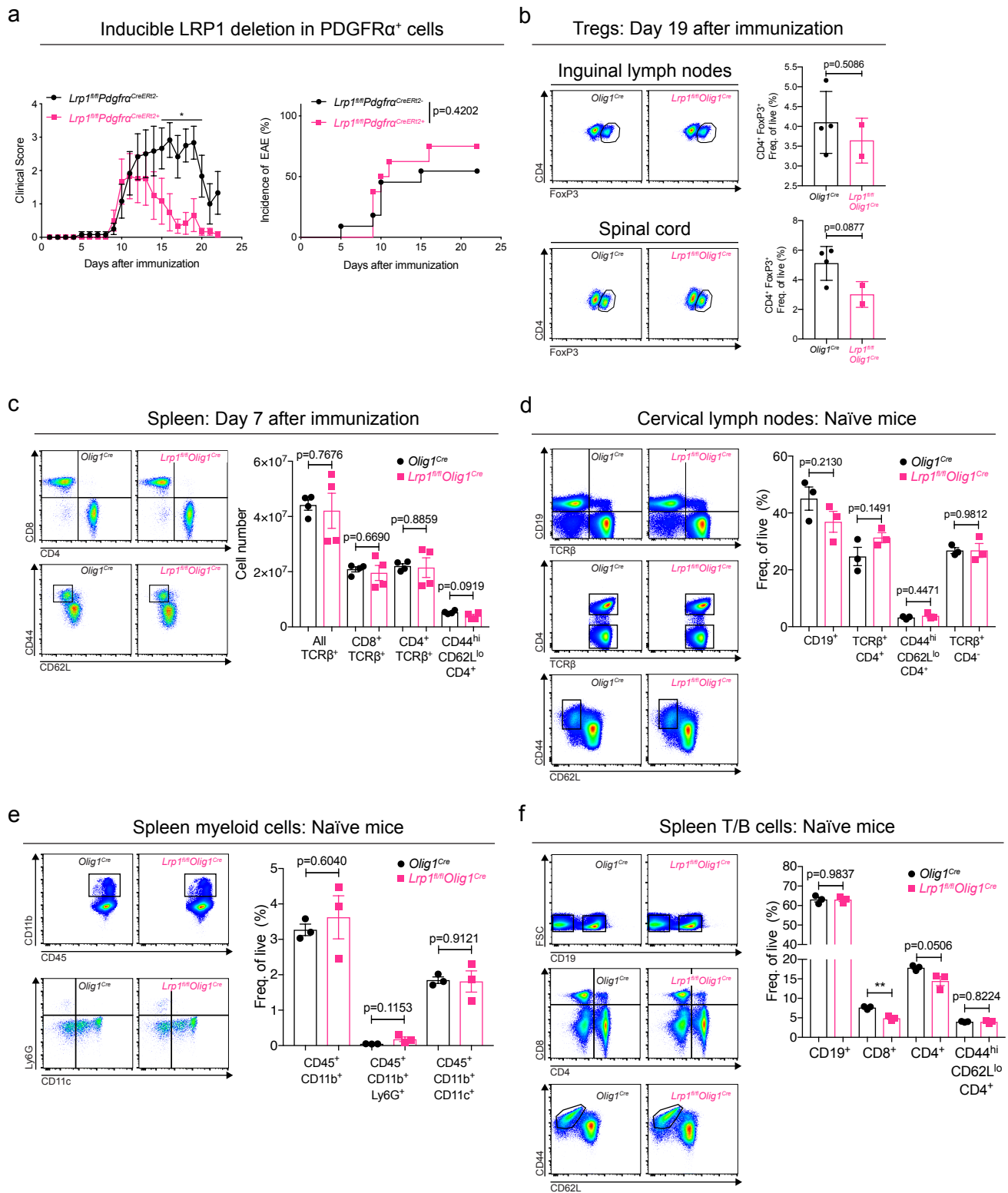


Fig. S6 Inflammatory phenotype in LRP1-deficient mice is not mediated by peripheral immune defects (a) EAE clinical scores and incidence from *Lrp1^{fl/fl}Pdgrfa^{CreERT2}* mice (EAE scores: Mann-Whitney U test, * $p < 0.05$; $n = 6$ mice with disease per genotype; incidence: Log-rank test; $n = 8-11$ total mice per genotype). (b) Flow cytometric analysis of Tregs (TCR β^+ CD4⁺ FoxP3⁺) in the draining lymph nodes (inguinal) and spinal cord during EAE in *Olig1^{Cre}* and *Lrp1^{fl/fl}Olig1^{Cre}* mice (unpaired t-test; $n = 2-4$ mice per genotype). (c) Representative flow plots and quantification of T cell subsets in the spleen 7 days after EAE immunization. (d) T and B cell populations in the cervical lymph nodes of naïve mice. (e) Myeloid cells and (f) T and B cell populations in the spleen of naïve mice (FSC: forward scatter height). Error bars represent \pm SEM.

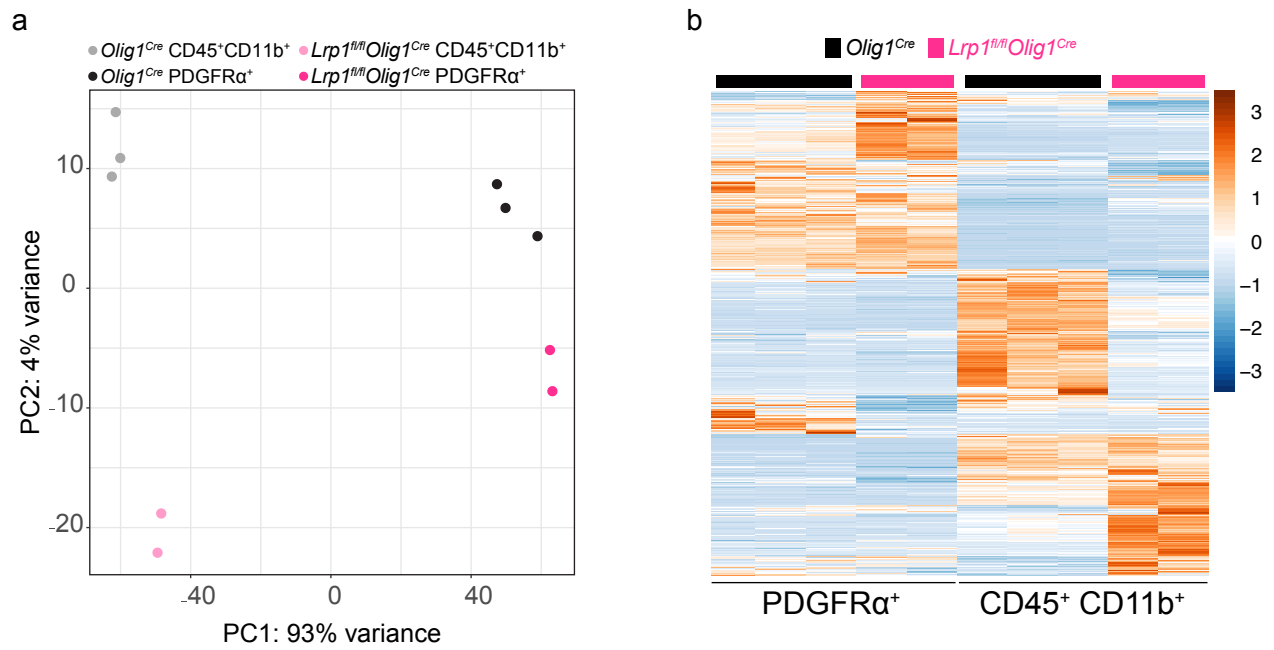


Fig. S7 Transcriptional profiling of the EAE spinal cord (a) Principal component analysis (PCA) plot and (b) heat map of the transcriptomes of sorted cells from EAE spinal cords of *Olig1*^{Cre} and *Lrp1*^{fl/fl}*Olig1*^{Cre} mice. Heat maps have a normalized count scale with z-score normalization.

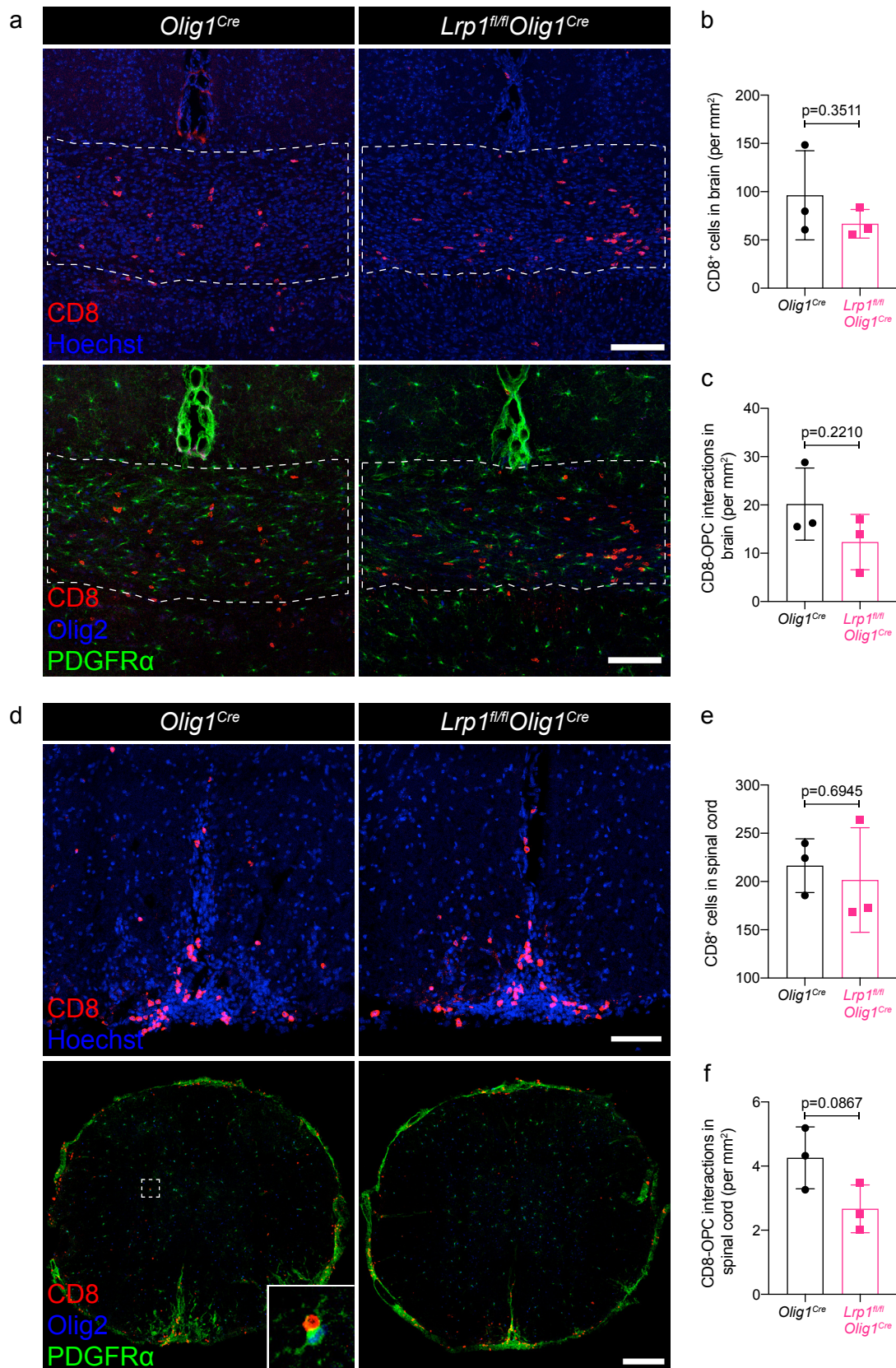


Fig. S8 CD8 cells in the cuprizone brain and EAE spinal cord. (a) Staining for CD8 (top panels), Olig2 and PDGFR α (lower panels) in the remyelinating brain (1 Wk Rem) of *Olig1^{Cre}* and *Lrp1^{fl/fl}Olig1^{Cre}* mice (dashed line outlines the *corpus callosum*). Scale bars 100 μ m. (b) Quantification of CD8 cells and (c) CD8-OPC interactions in remyelinating brains (unpaired t-test; n=3 mice per genotype). (d) Staining for CD8 (top panels), Olig2 and PDGFR α (lower panels) in EAE spinal cords (genotypes have similar disease scores; scale bars 75 μ m and 200 μ m, respectively.). (e) Quantification of CD8 cells and (f) CD8-OPC interactions in chronic EAE spinal cords (unpaired t-test; n=3 mice per genotype). Error bars represent \pm SEM.

Table S1 Ages of mice at experimental endpoints

Figure Panel	Age (weeks)
Fig. 1a,b	8
Fig. 1d	16
Fig. 1e	16
Fig. 2a	35-42
Fig. 2b-d	22
Fig. 2e,f	8
Fig. 3b-e cohort 1	35-42
Fig. 3b-e cohort 2	34
Fig. 3b-e cohort 3	22-25
Fig. 3f-h cohort 1	34
Fig. 3f-h cohort 2	22-25
Fig. 4a,b cohort 1	34
Fig. 4a,b cohort 2	22-25
Fig. 4c,d	17
Fig. 5b-g	16-25
Fig. 6a,b cohort 1	17-22
Fig. 6a,b cohort 2	12-16
Fig. 6c-i	17-24
Fig. 6j,k	26
Fig. 7a-f cohort 1	17-24
Fig. 7a-f cohort 2	27
Fig. 7g-j	14-17

