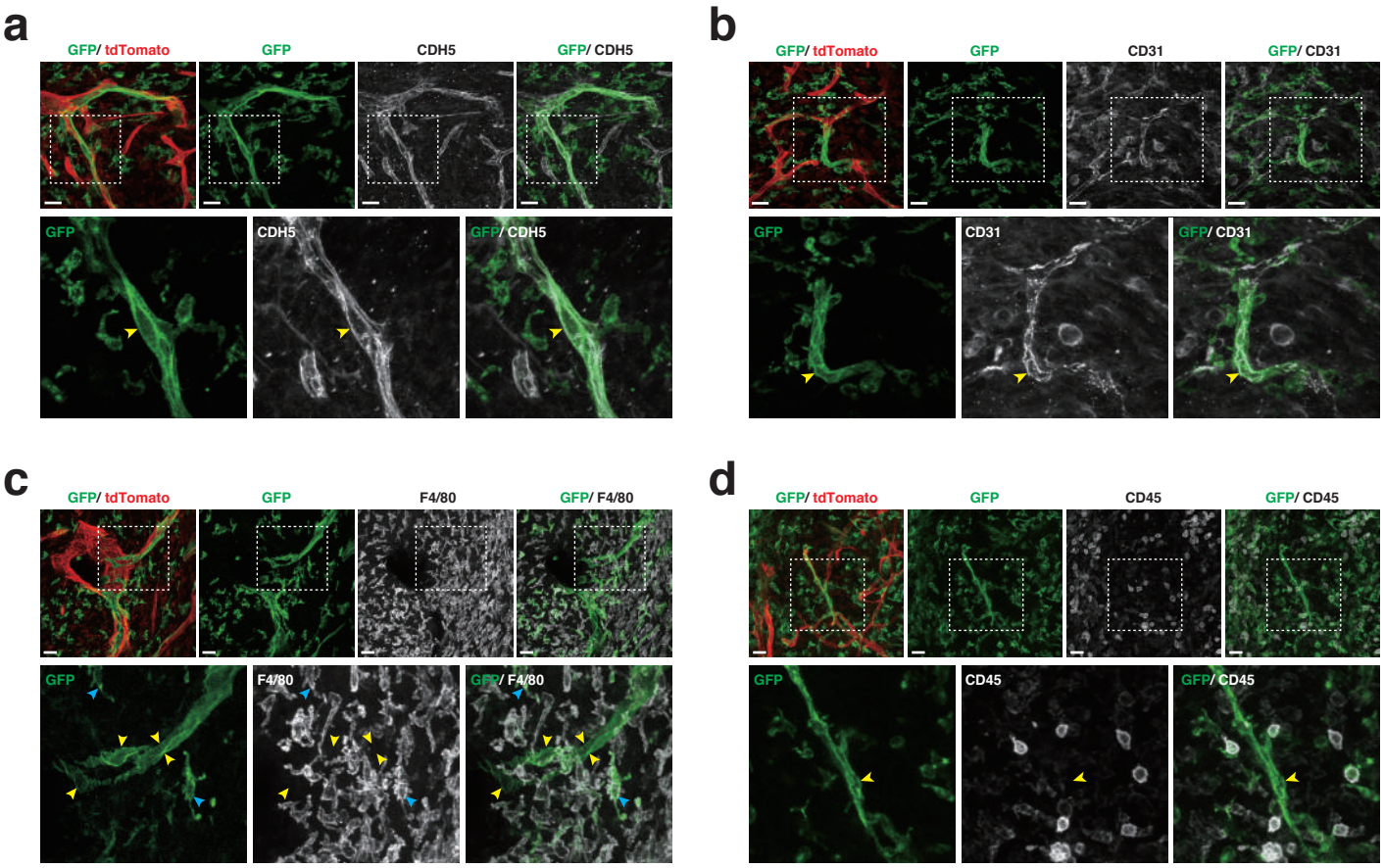
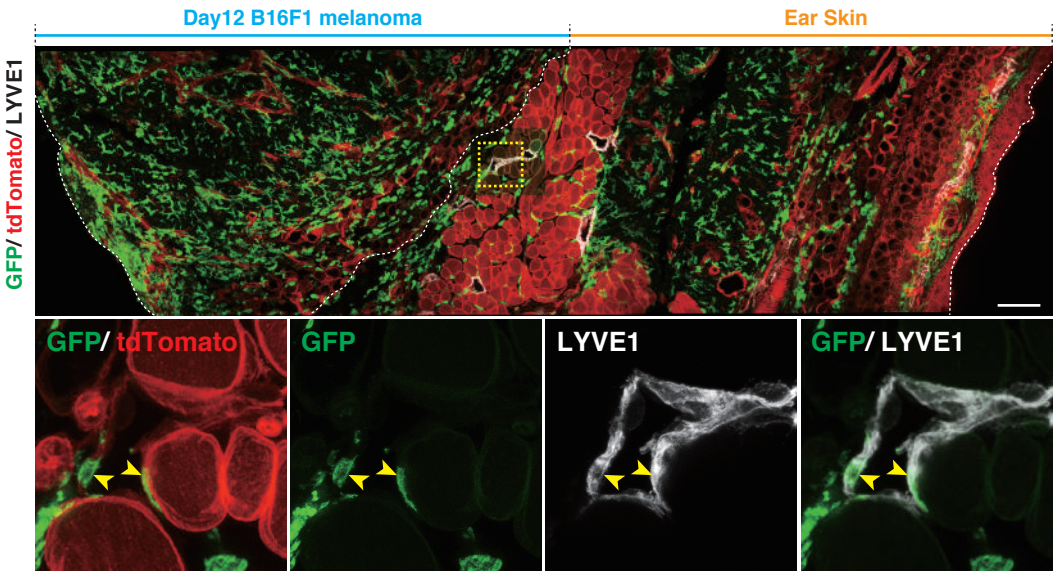
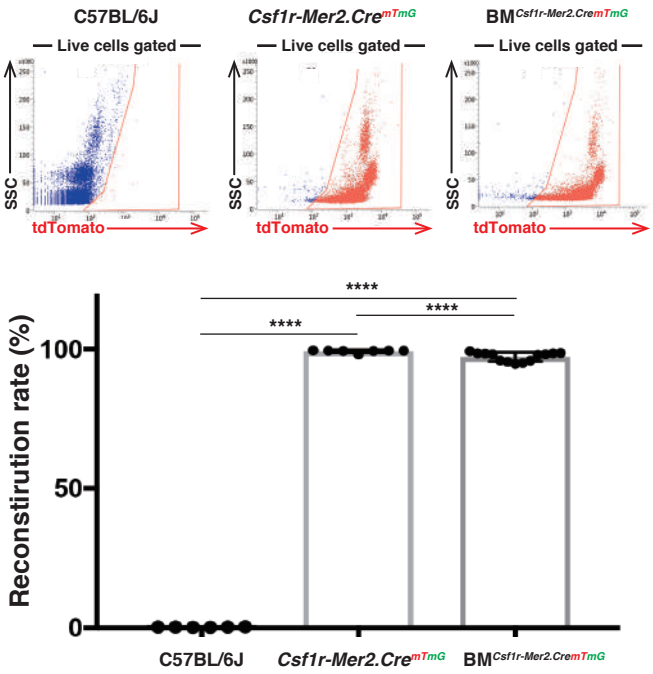


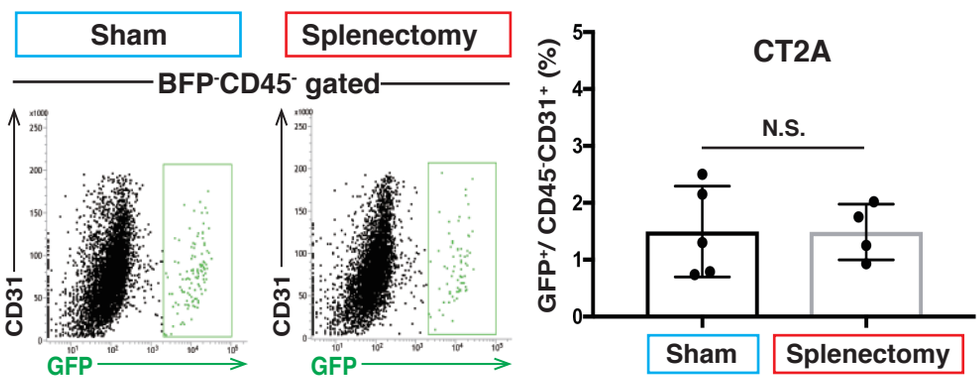
Extended Data Fig. 1: CLECs in mouse glioma express endothelial cell markers, but lack macrophage and myeloid cell markers. Counterstaining on PFA-fixed 4 weeks CT2A glioma sections of *Csf1r-Mer2.Cre*^{mTmG} with indicated antibodies. Lower panels show the detail images of outlined squares in upper panels.Yellow arrowheads, CLECs; blue arrowheads, macrophages. Scale bar: 25 μm.



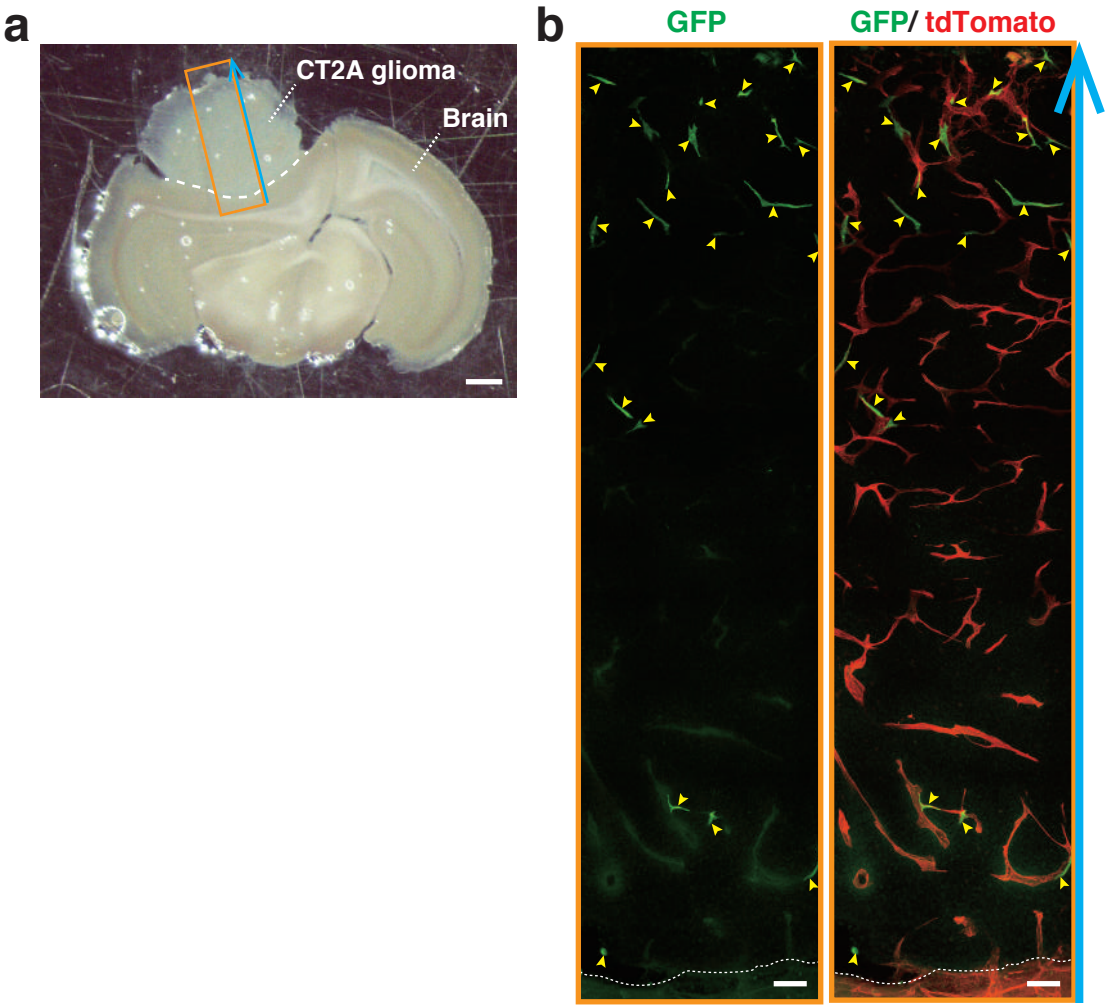
Extended Data Fig. 2: CLECs contribute to lymphatic endothelium in the tumour environment. Fluorescent images of counterstaining on PFA-fixed section of day 12 B16F1 melanoma under ear skin of *Csf1r-Mer2.Cre*^{mTmG} mice using LYVE1 antibody. Lower panel indicates detail image of yellow outlined square in upper panel. Yellow arrow heads, CLECs. Scale bar: 100 μm.



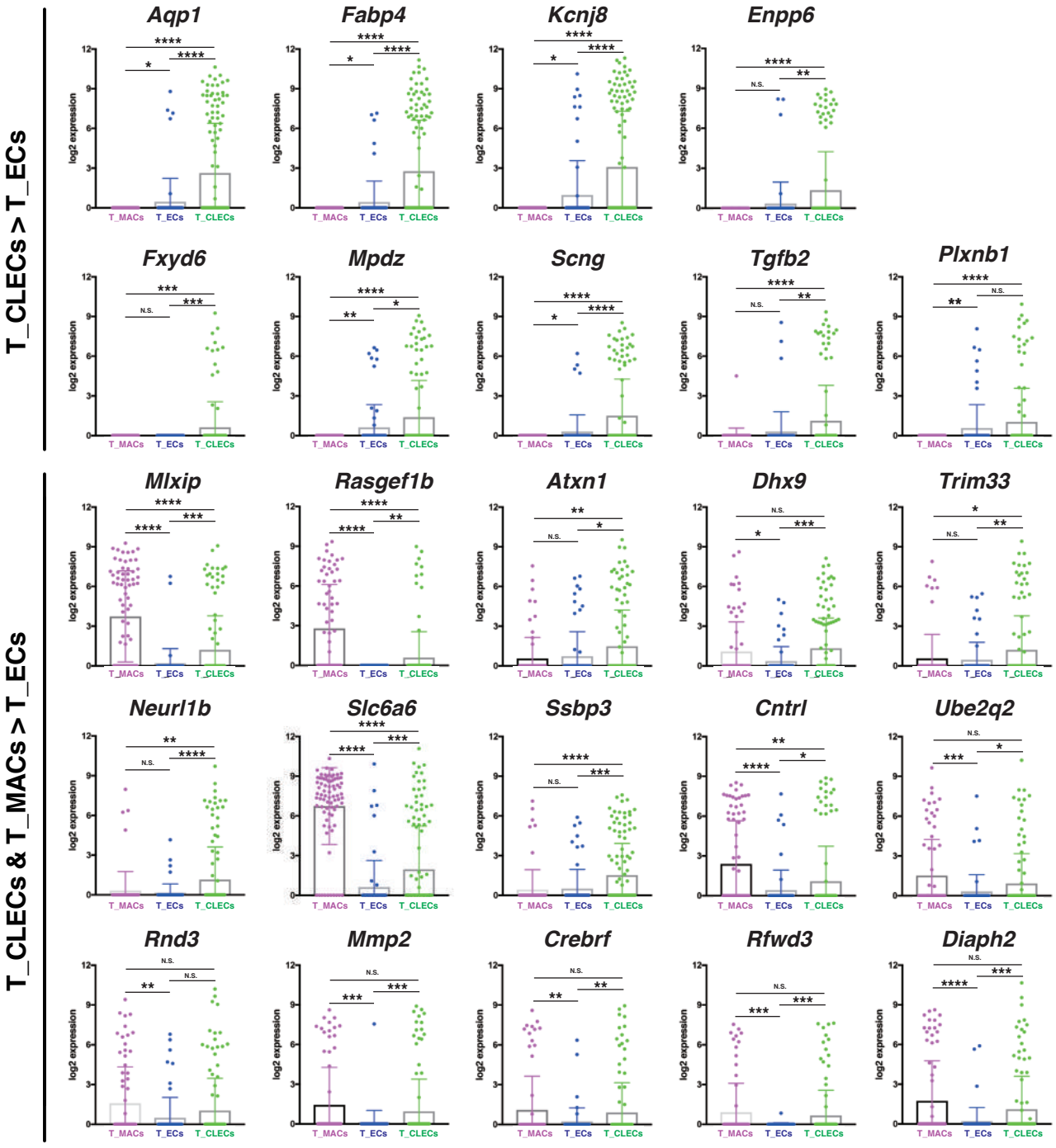
Extended Data Fig. 3: Reconstitution rate in bone marrow chimeras. Reconstitution rate was determined in peripheral blood 8 weeks after bone marrow transplantation. TdTomato-positive cells in blood of: C57BL/6J (0.3 ± 0.1%, n= 6), *Csf1r-Mer2.Cre*^{mTmG} (99.2 ± 0.5%, n= 7), BM$^{Csf1r\text{-}Mer2.CremTmG}$ (97.3 ± 1.6%, n= 13). Bars represent mean ± s.d. ****P<0.0001. Two-tailed unpaired Mann-Whitney' s U test.



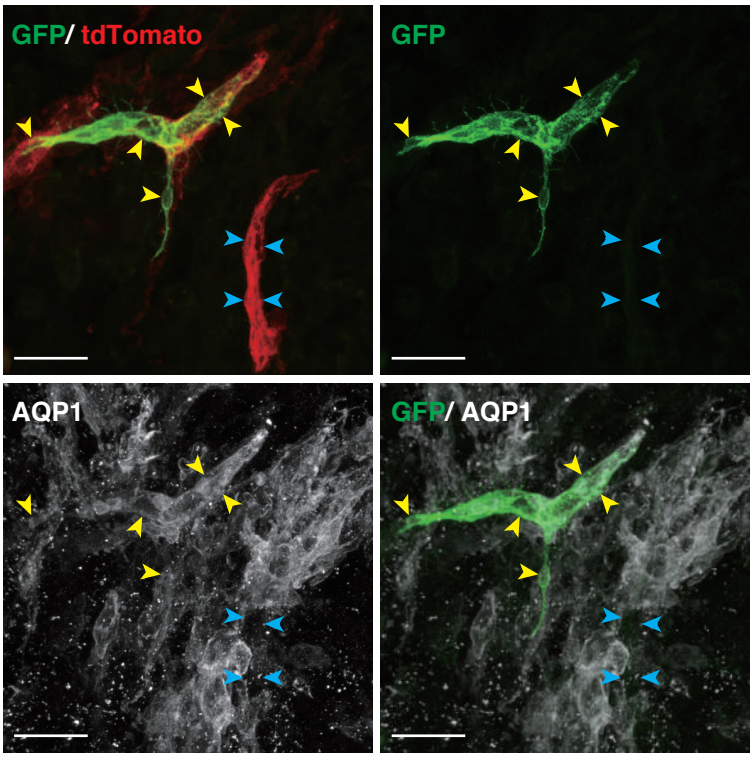
Extended Data Fig. 4: CLECs do not originate from spleen. Surgical removal of spleen (splenectomy) was performed 3 weeks before glioma injection. CLECs isolated from CT2A glioma of sham control *Csf1r-Mer2.Cre*^{mTmG} mice (n= 5) constitute 1.5 ± 0.8 % of total tumour endothelial cell population, compared to 1.5 ± 0.5% found in *Csf1r-Mer2.Cre*^{mTmG} with splenectomy (n= 4). Bars represent mean ± s.d. Two-tailed unpaired Mann-Whitney' s U test.



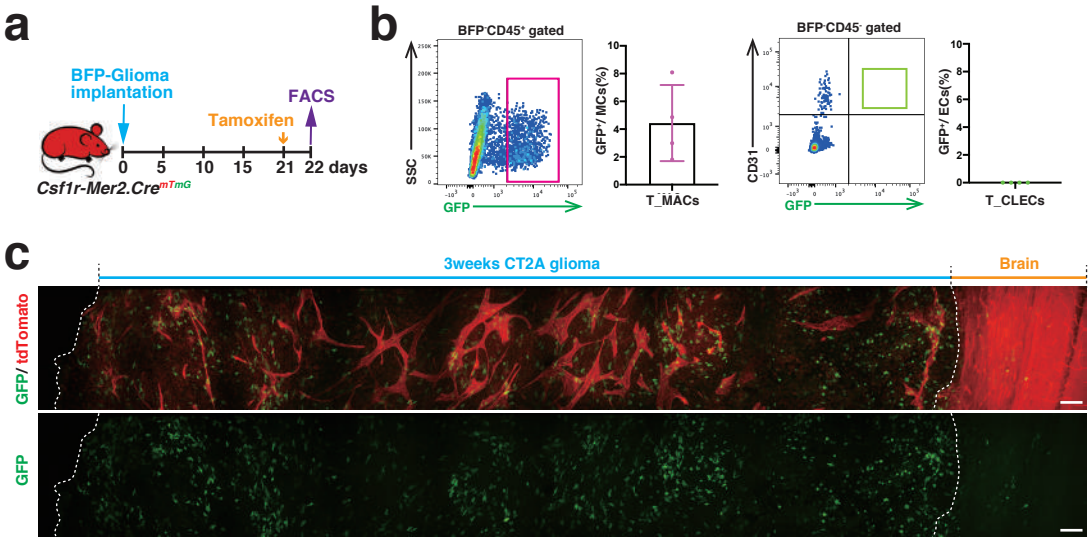
Extended Data Fig. 5: CLECs locate at peripheral area of mouse glioma. a, Vibratome section (200 μm-thick) of 4 weeks CT2A glioma of *Csf1r-Mer2.Cre*^{mTmG}:: BM^{WT} mice. Scale bar: 1 mm. b, Fluorescent images of area outlined in a. Yellow arrowheads, CLECs. Scale bar: 100 μm.



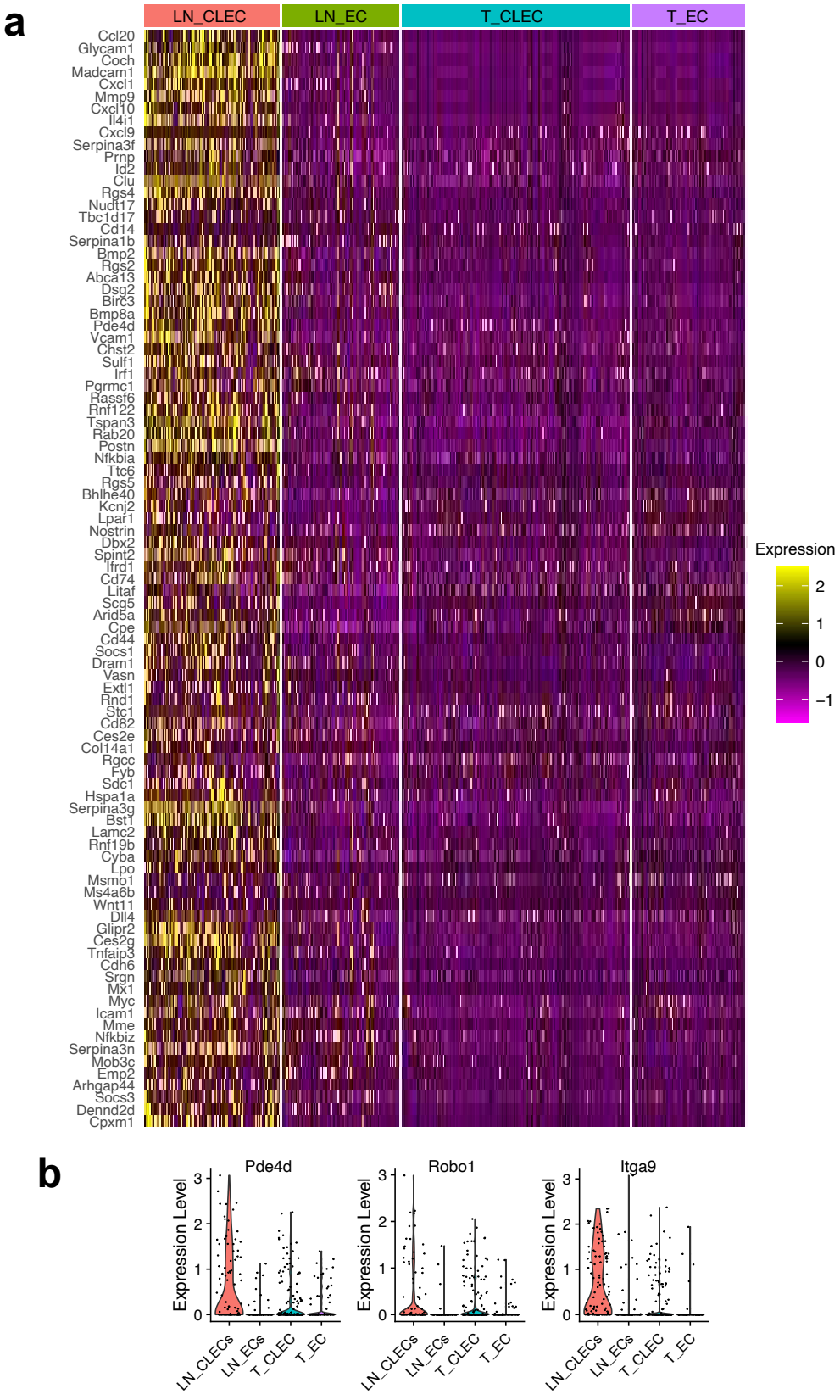
Extended Data Fig. 6: 24 tumour CLECs markers in mouse glioma. SCDE analysis of scRNA-seq data of tumour macrophages (T_MACs: CD45^{+}GFP^{+}, n= 79), tumour endothelial cells (T_ECs: CD45^{-}CD31^{+}GFP^{-}, n= 78), tumour CLECs (T_CLECs: CD45^{-}CD31^{+}GFP^{+}, n= 141) in 4 weeks CT2A glioma in *Csf1r-Mer2.Cre^{mTmG}* mice. Bars represent mean ± s.d. *P<0.05,**P<0.01,***P<0.001, ****P<0.0001. Two-tailed unpaired t-test with Welch correction.



Extended Data Fig. 7: CLECs in glioma express AQP1. Counterstaining on PFA-fixed CT2A glioma of *Csf1r-Mer2.Cre*^{mTmG}::BM^{WT} mice using AQP1 antibody. Yellow arrowheads, T_CLECs; blue arrowheads, T_ECs. Scale bar: 25 μm.



Extended Data Fig. 8: CLECs in glioma cannot be labelled by GFP within 24 hours after tamoxifen induction. a-b, Tamoxifen induction timing. b, Quantification of the population of tumour macrophagens (T_MACs: $CD45^{+}GFP^{+}$) and tumour CLECs (T_CLECs: $CD45^{-}CD31^{+}GFP^{+}$) by flow cytometric analysis in tumour samples (n=4). Bars represent mean ± s.d. c, Fluorescent images of PFA-fixed 3 weeks CT2A glioma de of *Csf1r-Mer2.Cre*^{mTmG} mice within 24 hours after tamoxifen induction. Scale bar: 100 μm.



Extended Data Fig. 9: CLEC and EC heterogeneity in tumor and lymph node .

a, Heatmap shows the expression of n=91 fLECs markers in LN_CLEC, LN_EC, T_CLEC and T_EC single cells. b, Violin plots show the expression of 3 CLEC markers: Pde4d, Robo1 and Itga9

Matsumoto K et al., Extended Data Figure 9