

Figure S1. Acidic glycoprotein content is elevated in high fibrosis regions and associates with aggression in breast tumors. **A-C.** Representative images of staining of all breast cancer subtypes. Scale bar represents 100 μ m. **D.** Representative images of Alcian blue staining with or without sialidase pretreatment. In the adjacent plot, each point represents one field of view from a HER2+ tumor. The mean is plotted and the error bars represent one standard deviation. **E.** Plots of % area Alcian blue in low and high fibrosis regions by breast cancer subtype.

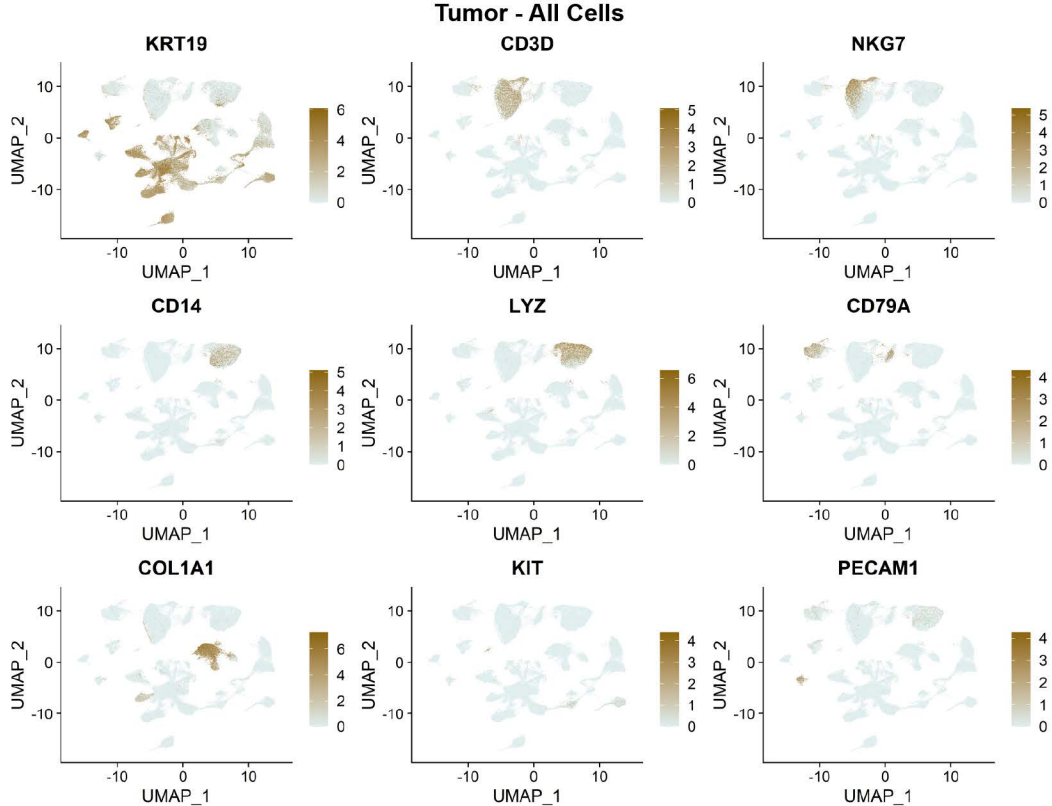
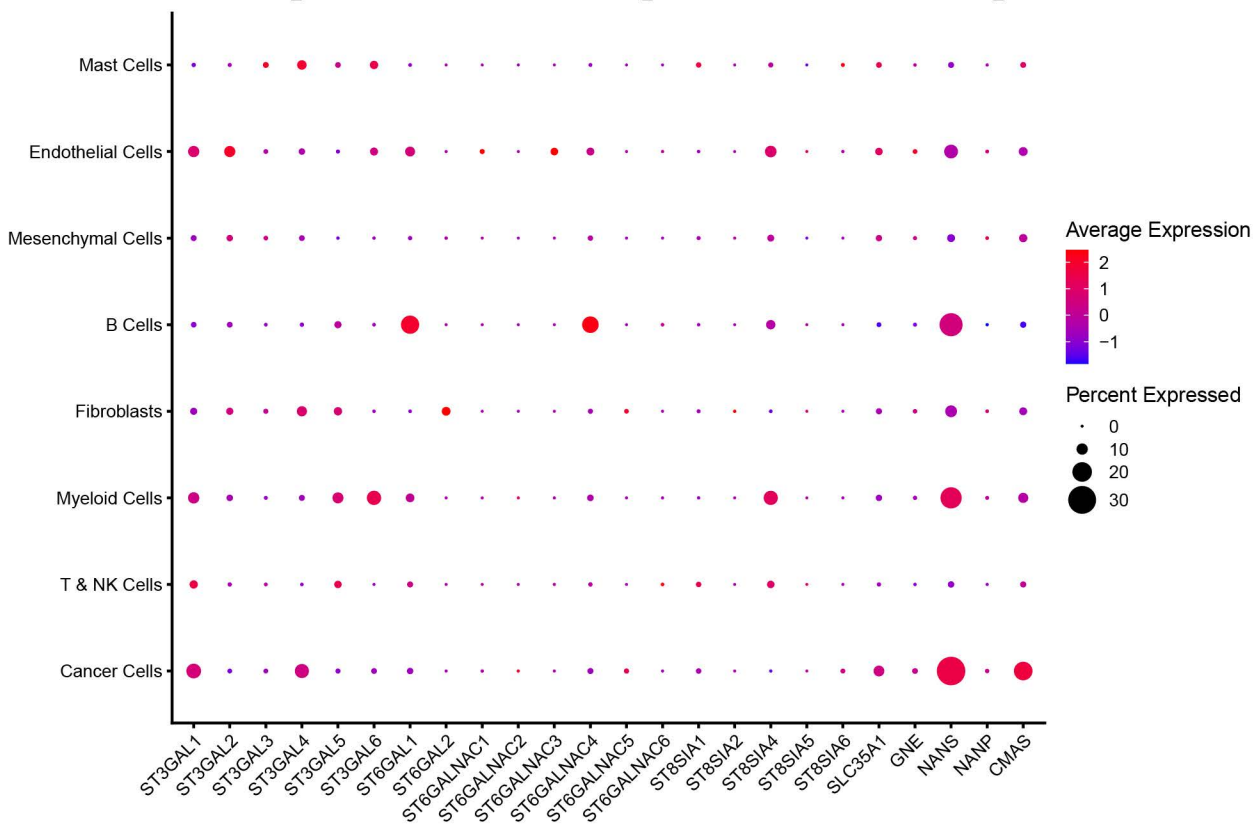
A**B**

Figure S2. Analysis of scRNAseq of 34 tumor samples from Pal et al., EMBO 2021. **A.** Feature plots for cluster assignments. **B.** Dot plot of sialic acid biosynthetic gene expression for each cell type.

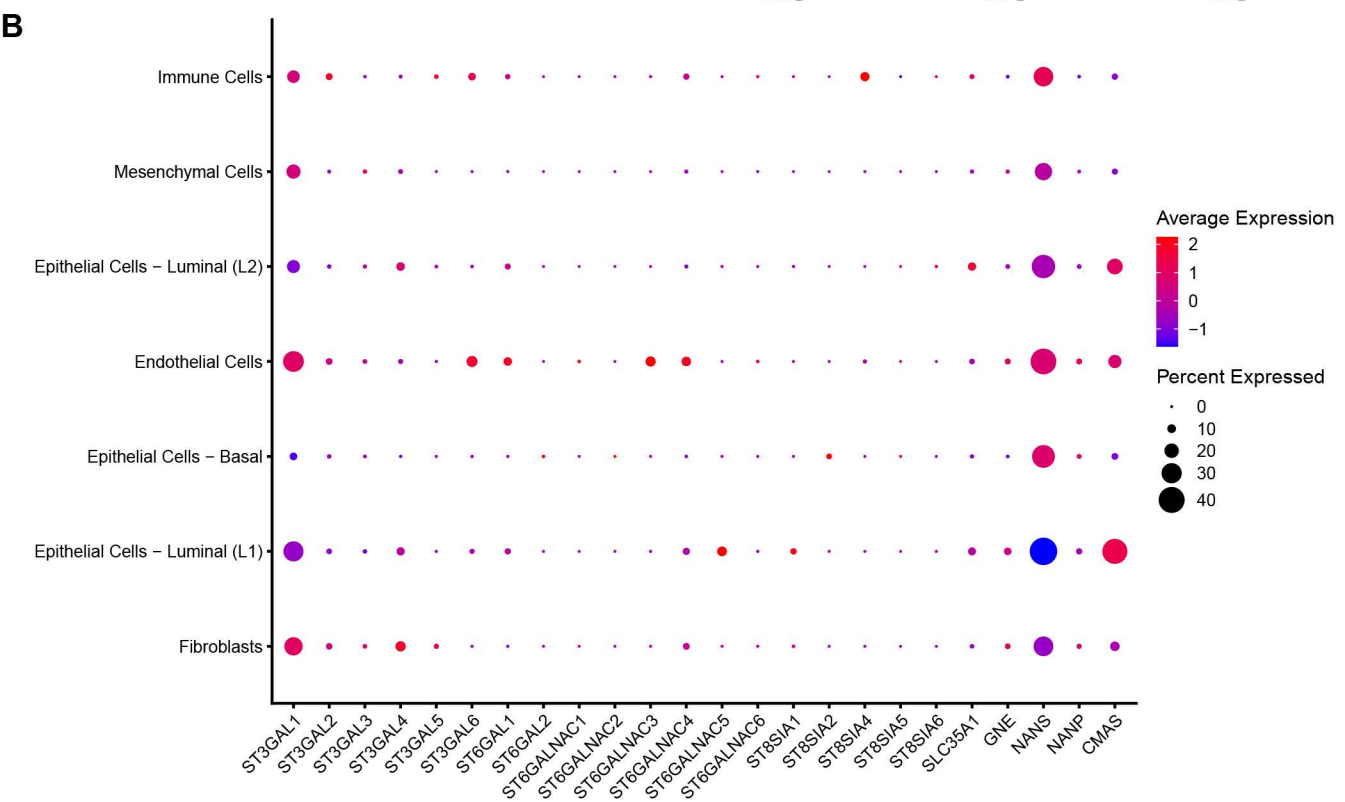
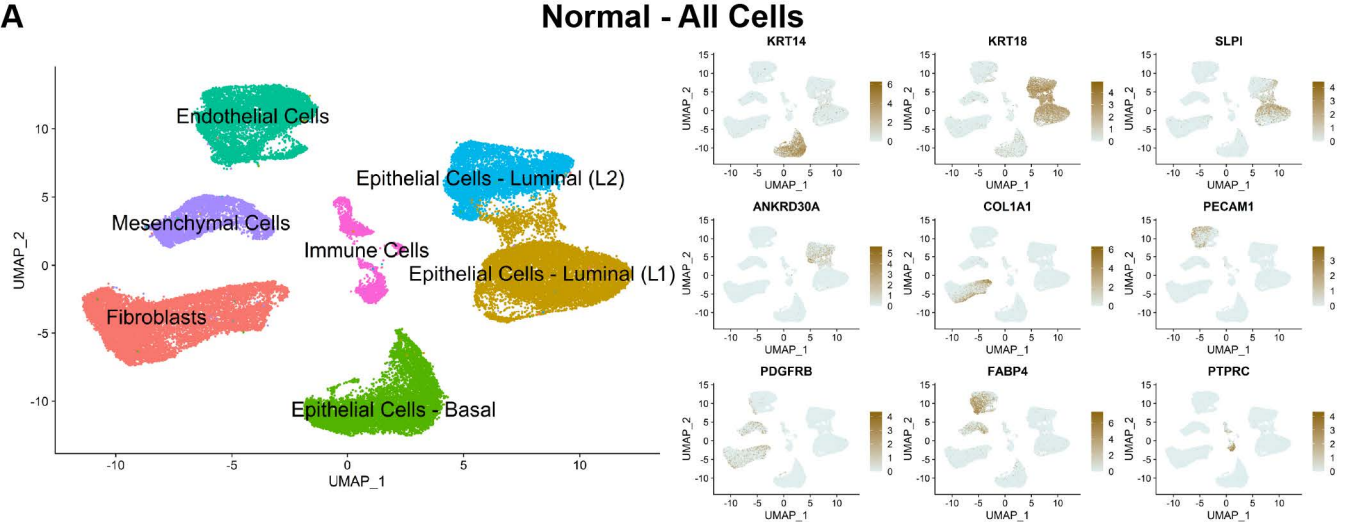


Figure S3. Clustering of normal breast samples from Pal et al., EMBO 2021.

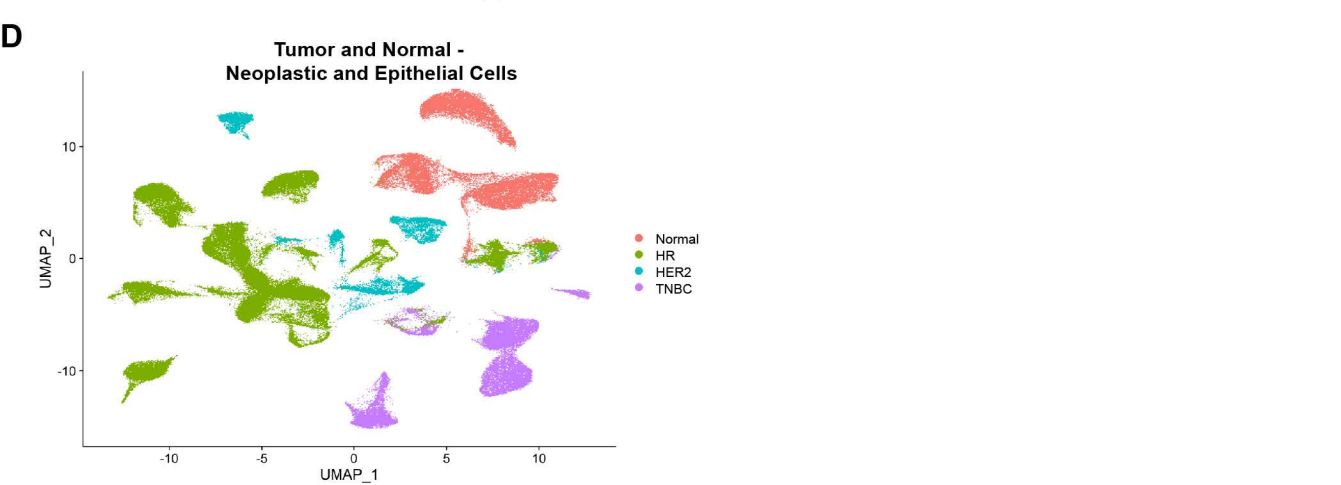
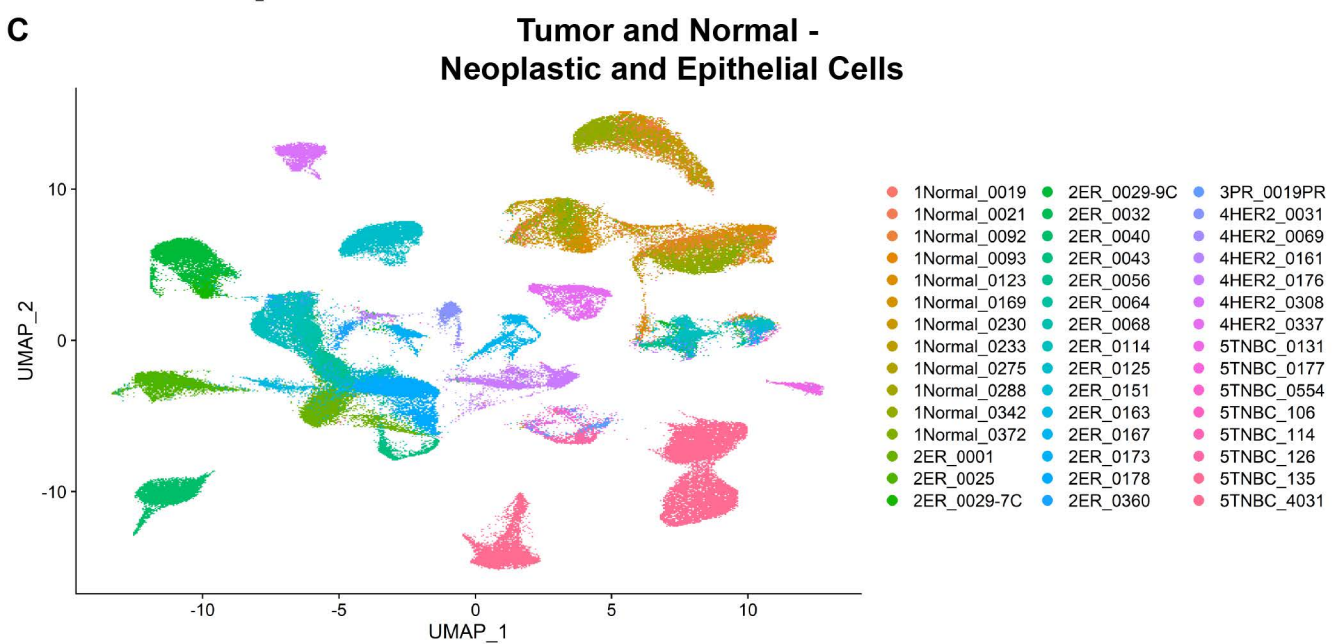
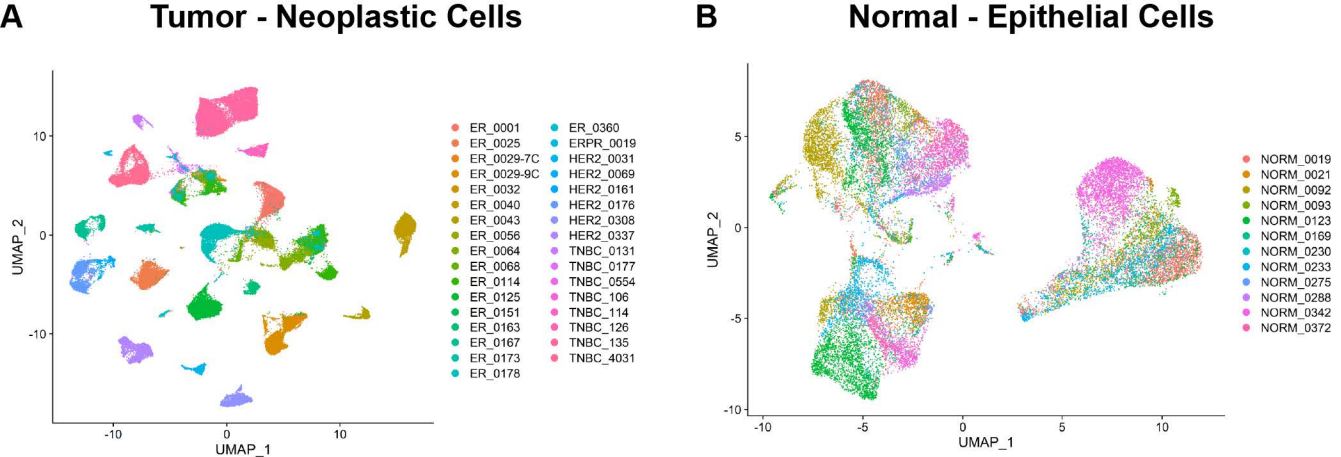


Figure S4. Analysis of extracted epithelial cells from tumor and normal breast. **A.** UMAP plot of cancer cells colored by patient. **B.** UMAP plot of epithelial cells colored by patient. **C-D.** UMAP plot of epithelial cells from tumors and normal breast colored by **C.** patient and **D.** subtype.

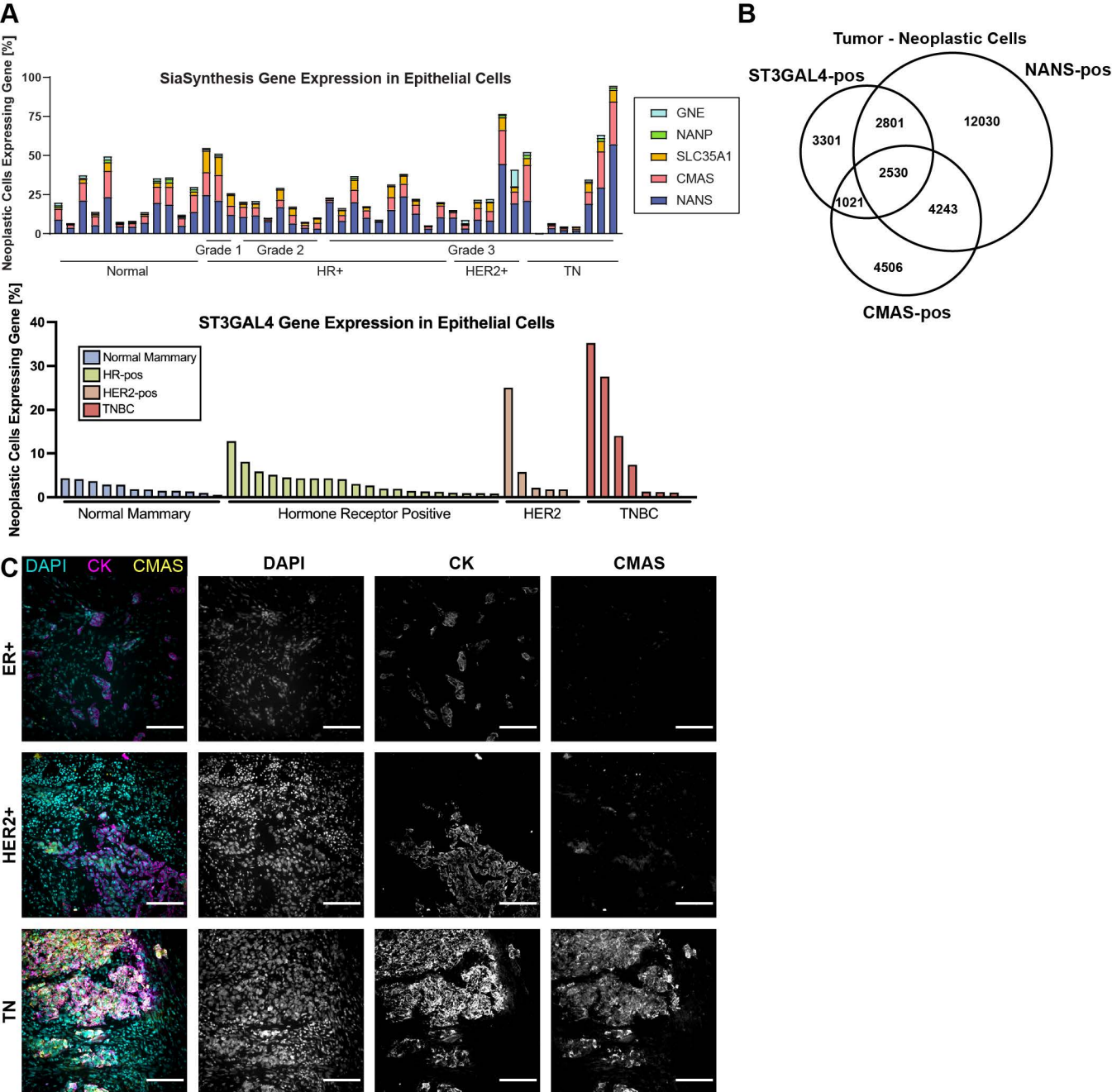


Figure S5. Analysis of sialoglycoprotein biosynthetic gene expression. **A.** Bar plot of (*top*) sialic acid biosynthetic genes and (*bottom*) *ST3GAL4* expression in epithelial cells from breast tumors and normal breast from scRNAseq dataset from Pal, et al., EMBO, 2021. **B.** Venn diagram of individual cell expression of *ST3GAL4*, *NANS*, and *CMAS* from breast tumor scRNAseq data. **C.** Representative images of breast tumors stained with DAPI, anti-pan-cytokeratin (CK), and anti-CMAS.

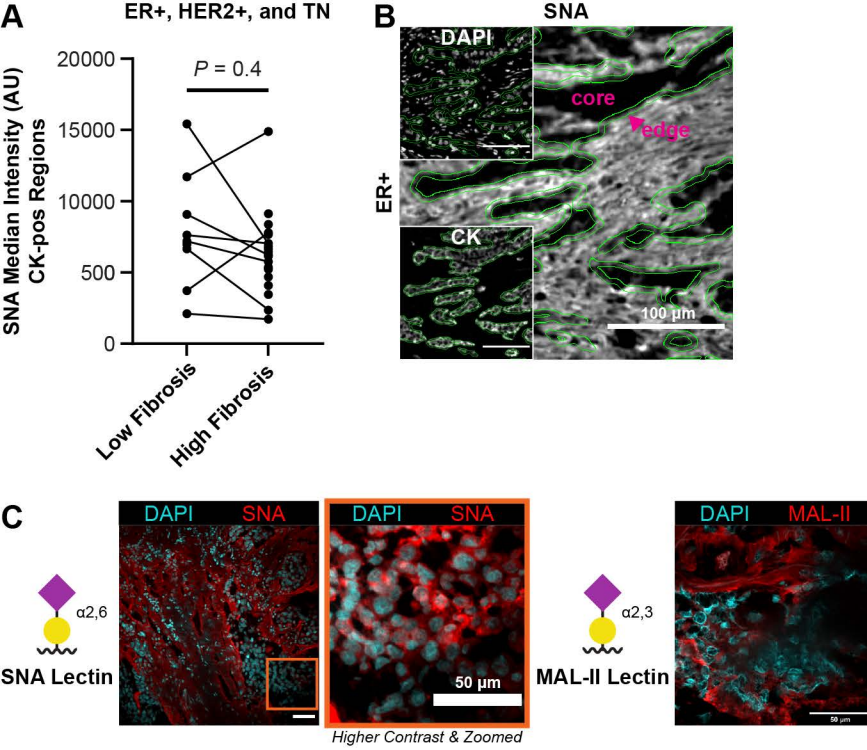


Figure S6. Analysis of lectin staining in breast tumors. **A.** Plot of SNA lectin median intensity staining in anti-pan-cytokeratin-positive regions (CK-pos) by local fibrosis. **B.** Representative IF images used for quantification of SNA lectin staining of cancer cell region edge and core. Cancer cell regions were identified as CK-pos regions. **C.** Representative IF images of SNA lectin and MAL-II lectin.

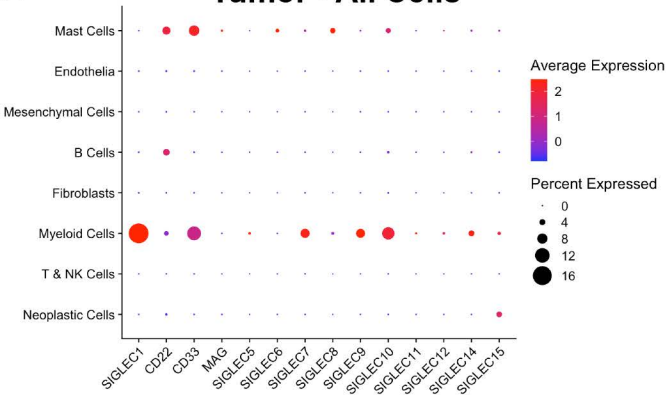
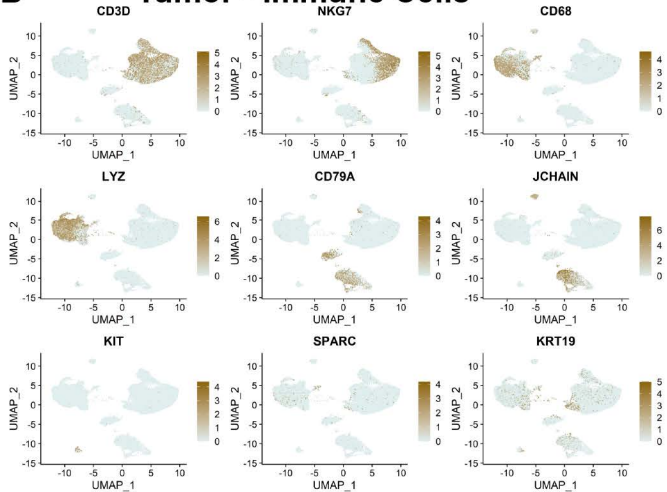
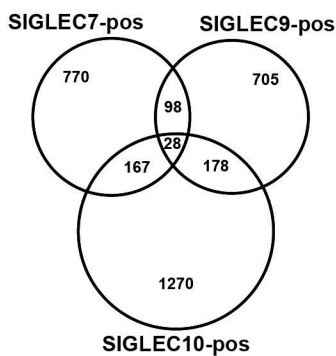
A Tumor - All Cells**B Tumor - Immune Cells****C**

Figure S7. Analysis of *SIGLEC* expression in breast tumors from scRNAseq dataset from Pal et al., EMBO 2021. **A.** Dot plot for all 14 human *SIGLECs*. **B.** Feature plots for cluster assignments. **C.** Venn diagram of individual cell expression of *SIGLEC7*, *SIGLEC9*, and *SIGLEC10*.

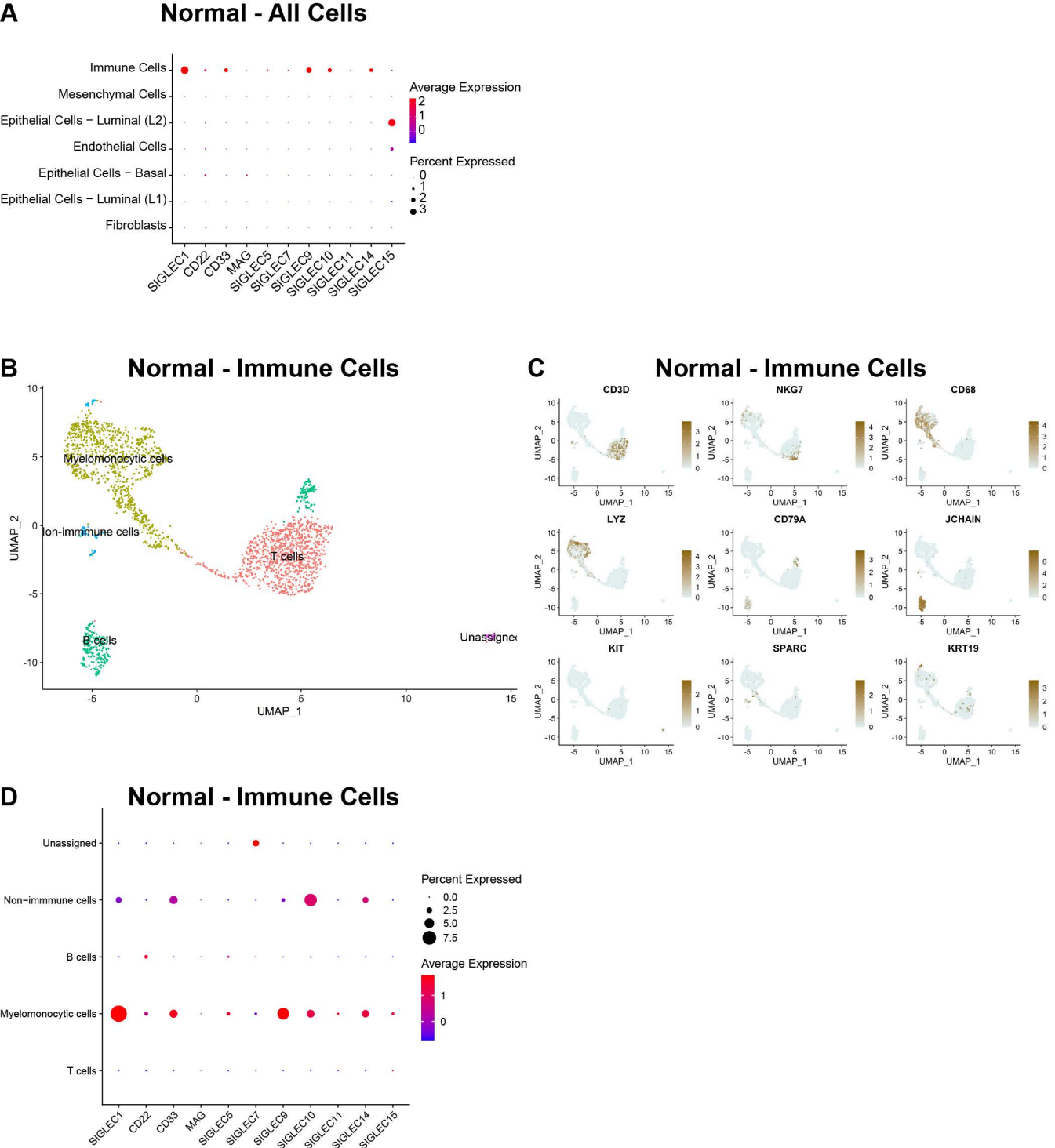


Figure S8. Analysis of *SIGLEC* expression in normal breast tissues from scRNAseq dataset from Pal et al., EMBO 2021. **A.** Dot plot for all 14 human *SIGLECs* in all cell types. **B.** UMAP plot of extracted immune cells. **C.** Feature plots for cluster assignments. **D.** Dot plot for all 14 human *SIGLECs* in immune cell types.

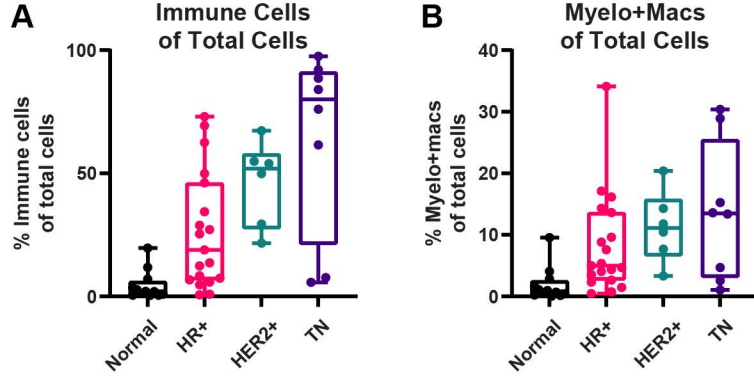


Figure S9. Analysis of inflammation in breast tumors and normal breast tissue from scRNAseq dataset from Pal, et al., EMBO, 2021. **A.** Quantification of percent immune cells of total cells by subtype. **B.** Quantification of percent myelomonocytic cells and macrophages of total cells by subtype.

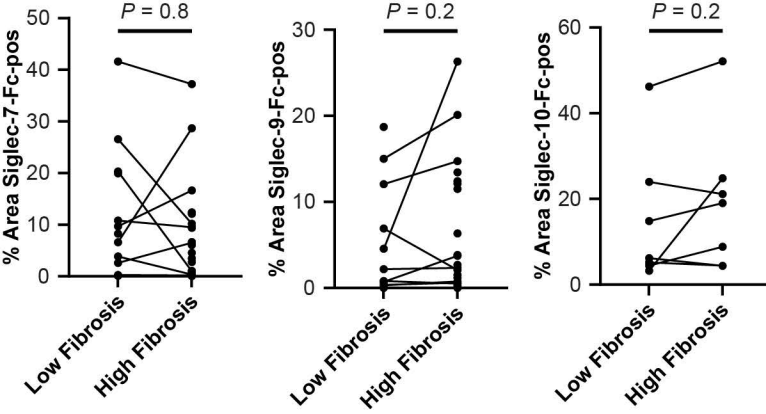


Figure S10. Quantification of Siglec ligand staining percent area in low and high fibrosis regions.