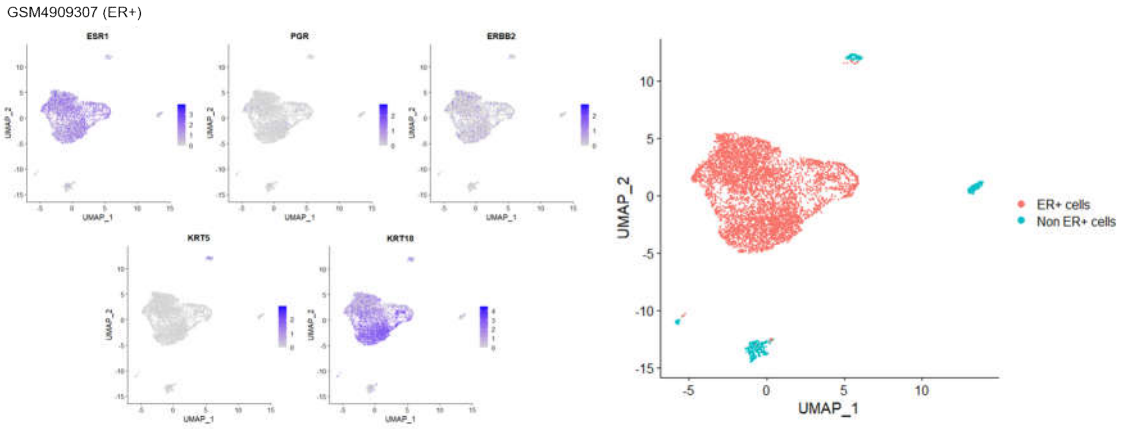
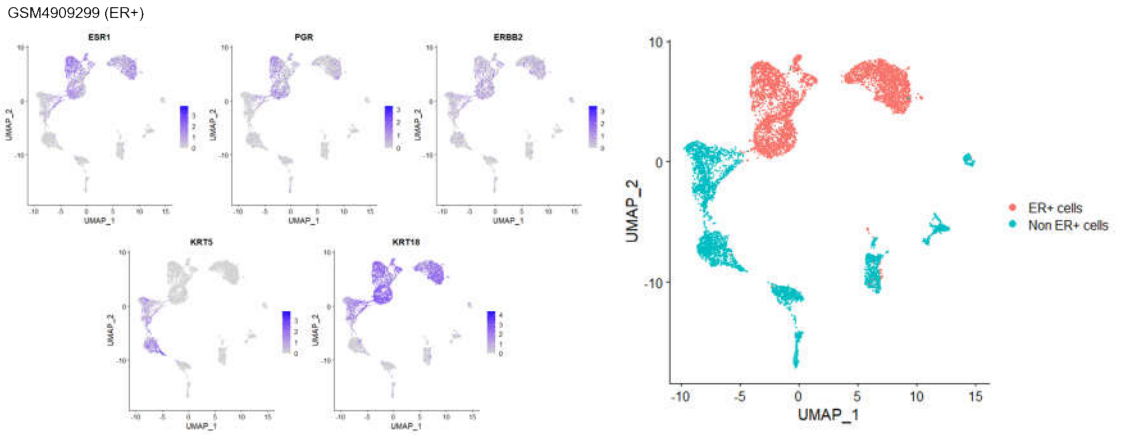
Supplementary Figures

A



B



C

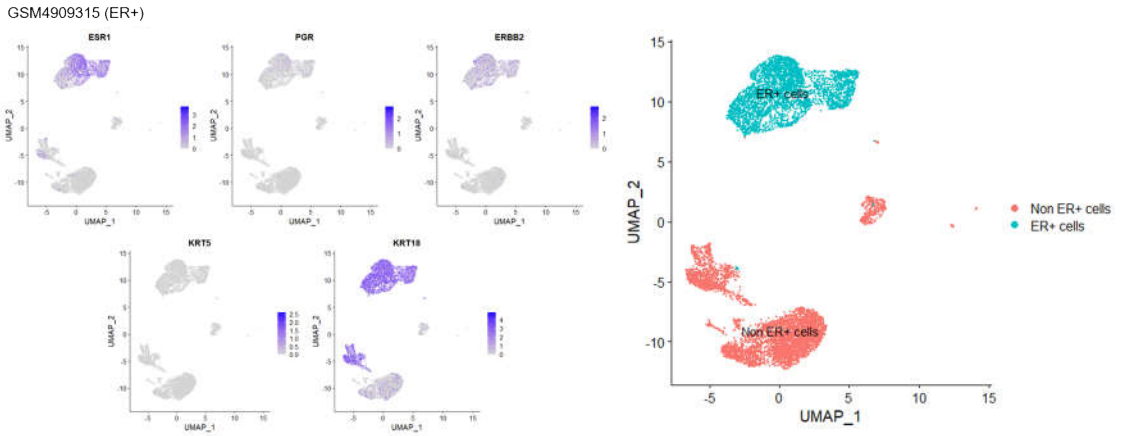


Figure S1 Segmentation of ER⁺ breast cancer cells from single cell data with patients.

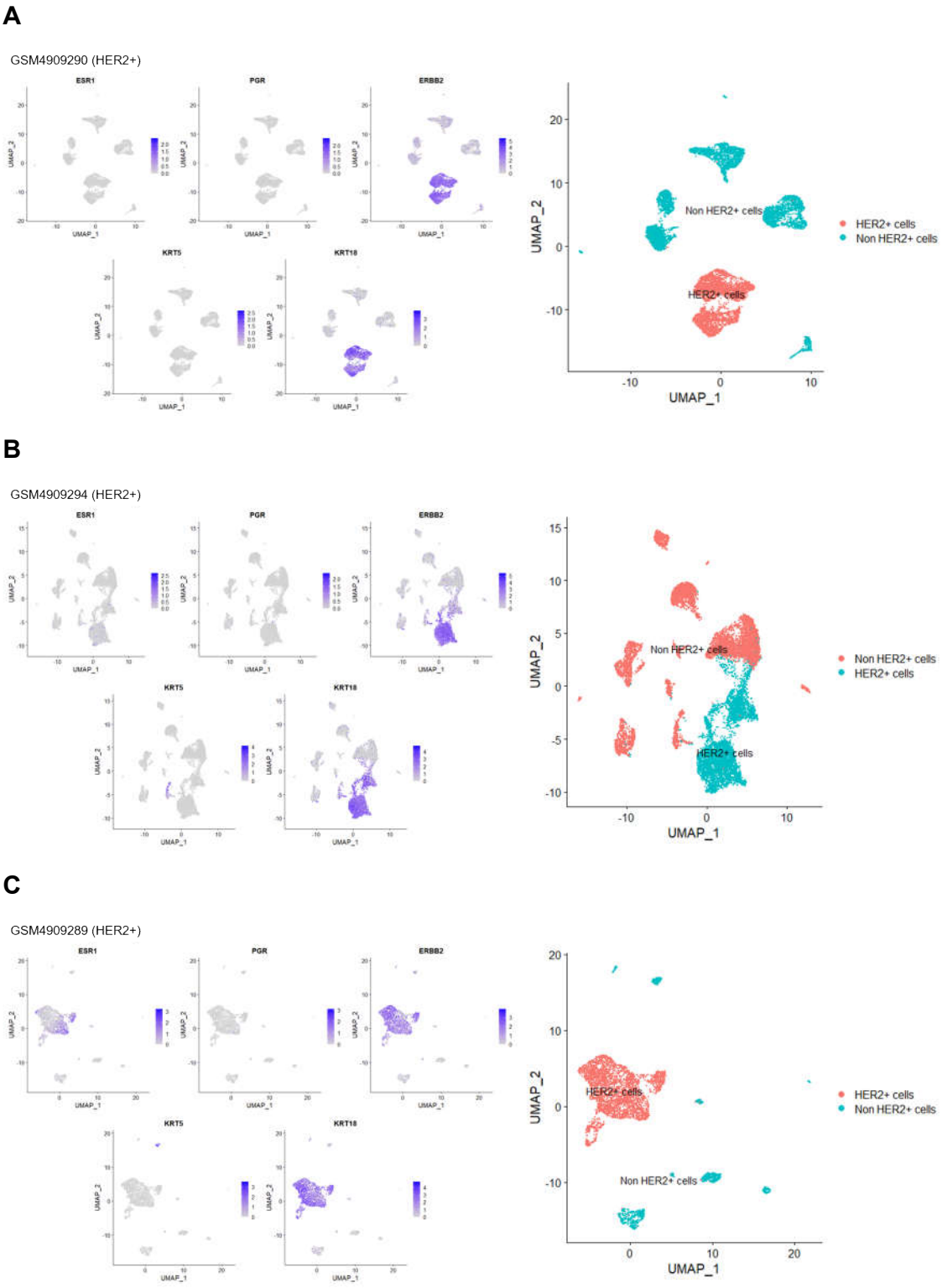


Figure S2 Segmentation of HER$^+$ breast cancer cells from single cell data with patients.

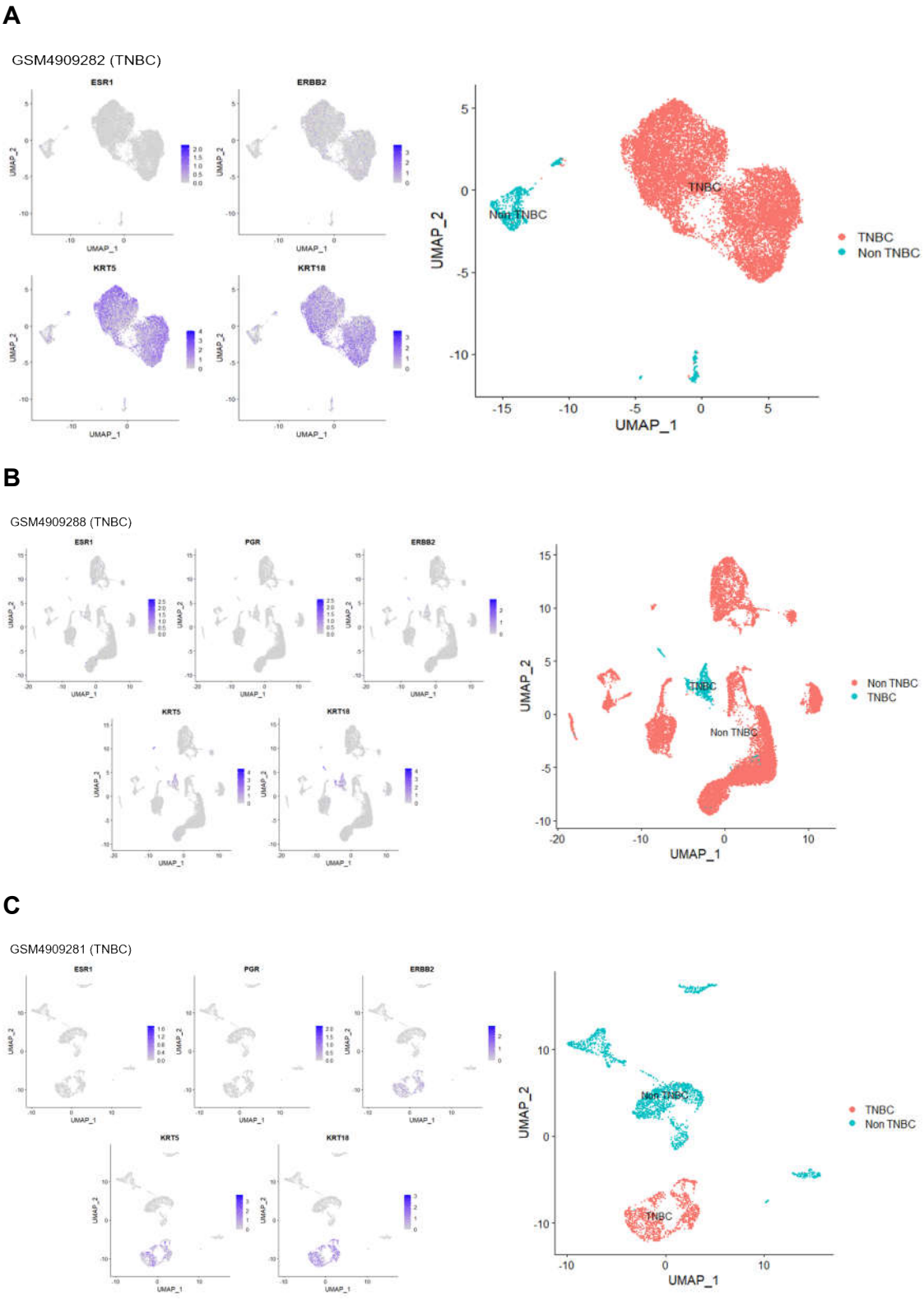


Figure S3 Segmentation of TN breast cancer cells from single cell data with patients.

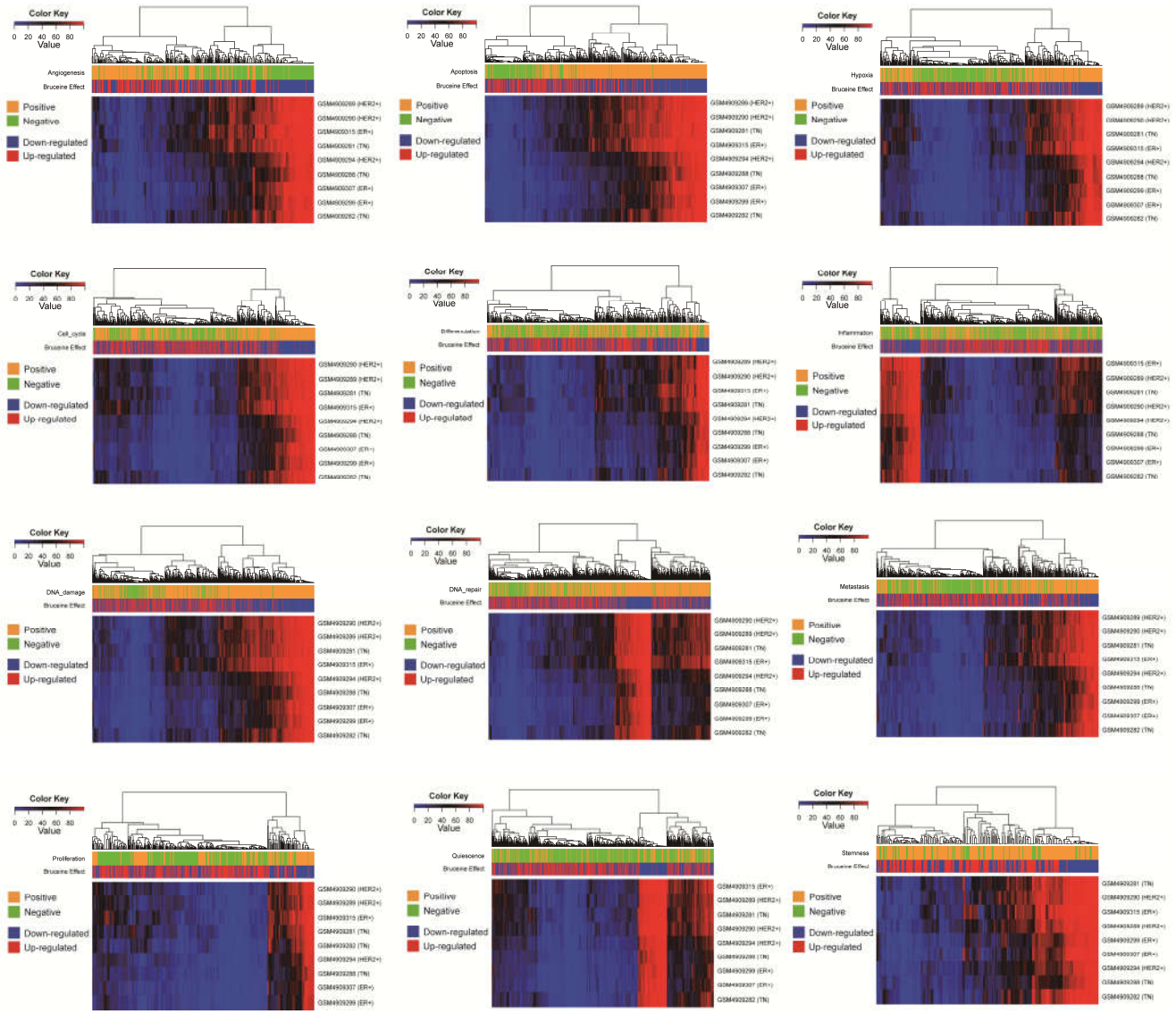


Figure S4 Heatmap of proportion of positive cells within segmented tumor cells from scRNA-seq with 12 different functional states of cancer cells and gene expression status by BD treated or not.

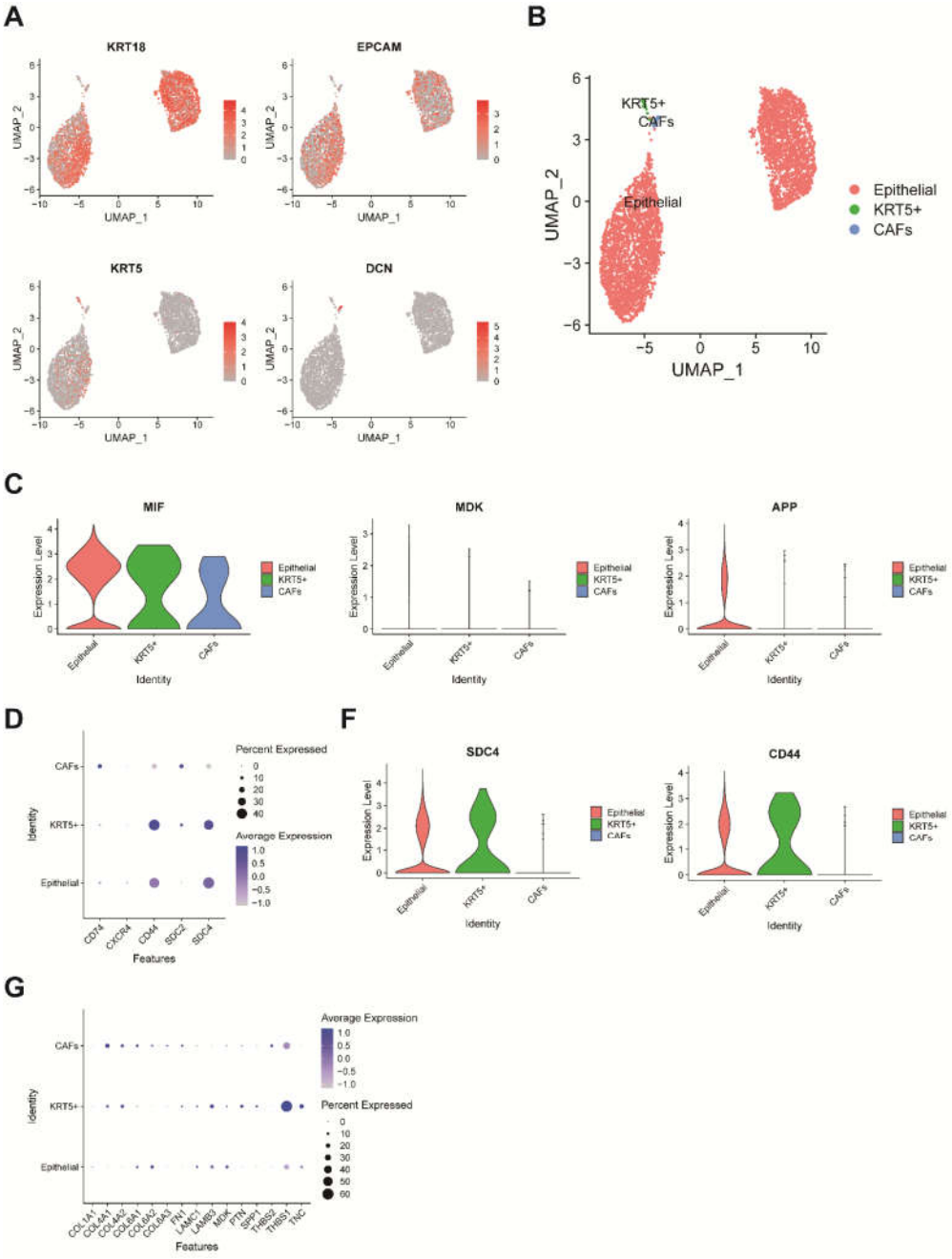


Figure S5 Analysis of normal scRNA-seq data (GSM4909262) which is paired with GSM4909313 ER$^+$ BC. (A) Feature plot of the specific markers (KRT18: Luminal, EPCAM: Epithelial, KRT5: basal-like, and DCN: Fibroblast), (B) Feature plot with cluster of cell types according to the specific markers, (C) Violin plot of ligands which were expressed in ER$^+$ sample GSM (GSM4909313), (D) Dot plot with percent of positively expressed and average of expression of ligands which were expressed in ER$^+$ sample GSM (GSM4909313), (E) Violin plot of receptors which were expressed in ER$^+$ sample GSM (GSM4909313) and (G) Dot plot with percent of positively expressed and average of expression of receptors which were expressed in ER$^+$ sample GSM (GSM4909313).

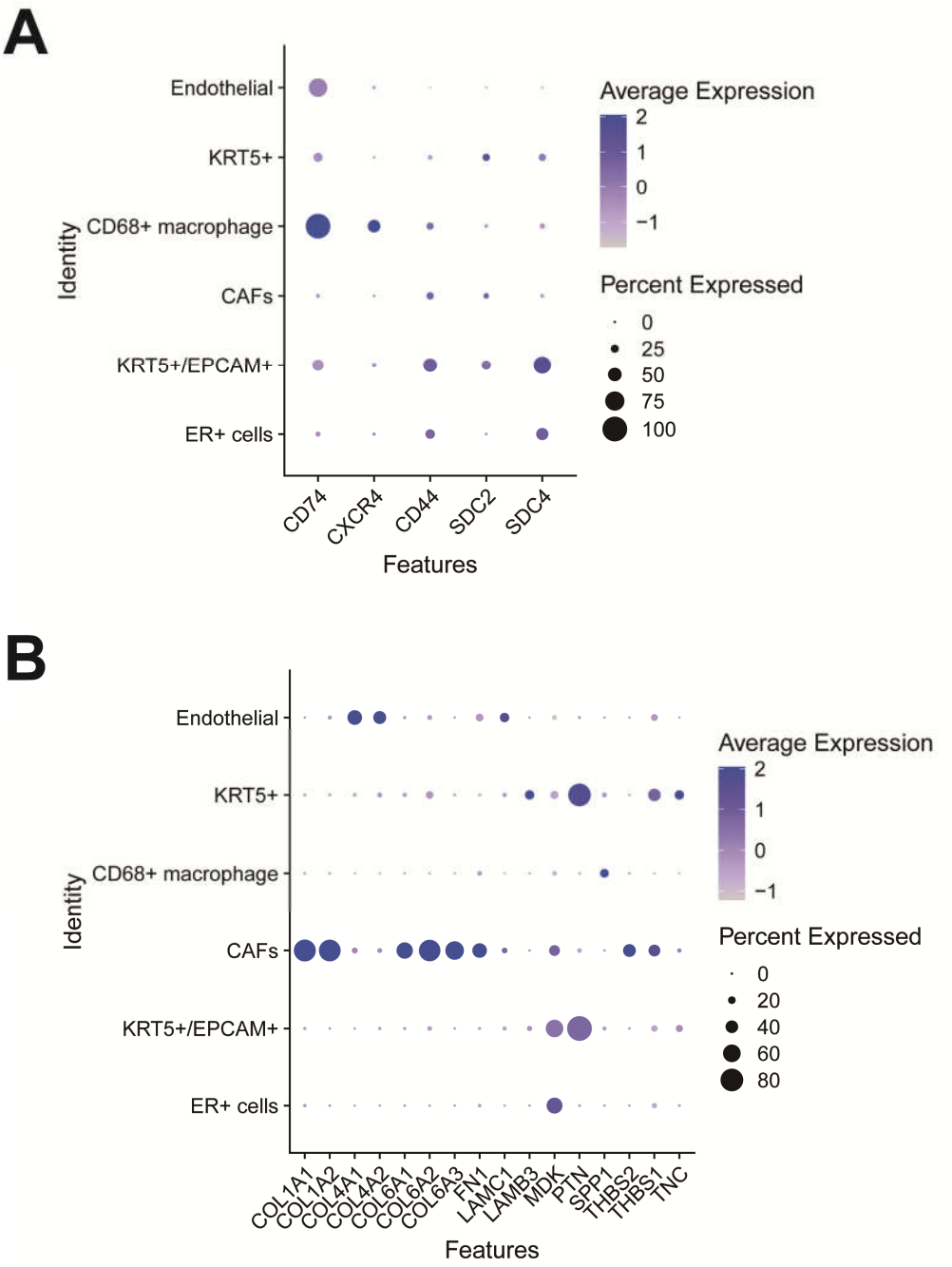


Figure S6 Dot plots of expression of ligands receptor with percent of positively expressed and average of expression in ER⁺ sample GSM (GSM4909313). (A) dot plot of significant ligands from cell-to-cell interaction analysis and (B) dot plot of significant receptors from cell-to-cell interaction analysis.