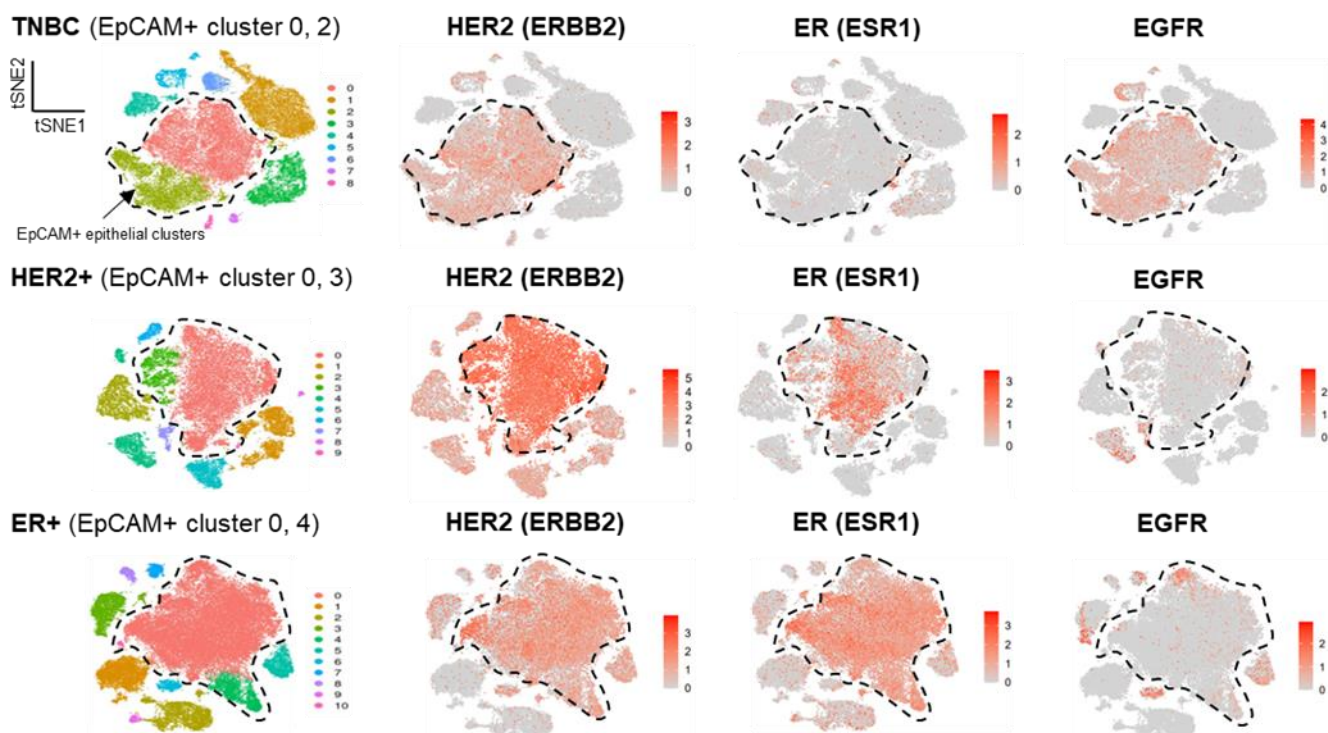
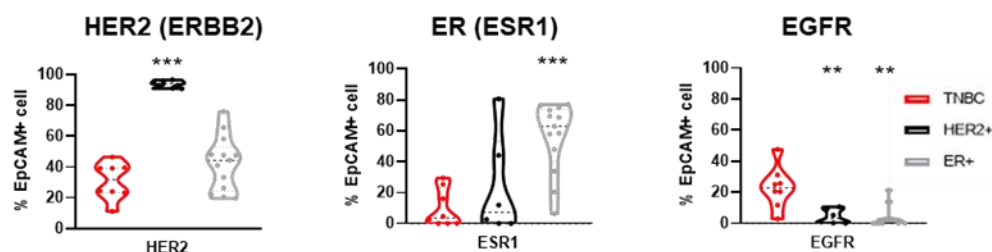


(A)



(B)



### Supplementary Figure 2. Single-cell RNA sequencing analyses of HER2, ER and EGFR in breast cancer.

(A) Dimensionality reduction t-SNE map of combined scRNA-seq transcriptomes of total 150290 cells from 27 untreated primary tumors (TNBC,  $n=8$  samples, 54819 cells; HER2+,  $n=6$  samples, 31917 cells; ER+,  $n=13$  samples, 63554 cells) colored by cell cluster (see Figure 2A and 2B). (B) In the EpCAM+ cells, the expression of HER2 (ERBB2) and ER (ESR1) were evaluated as internal controls for the TNBC subtype. EGFR is only upregulated in EpCAM+ TNBCs, but not in the HER2+ or ER+ samples.  $P$ -values determined by two-tailed unpaired  $t$  test against TNBC subtype.