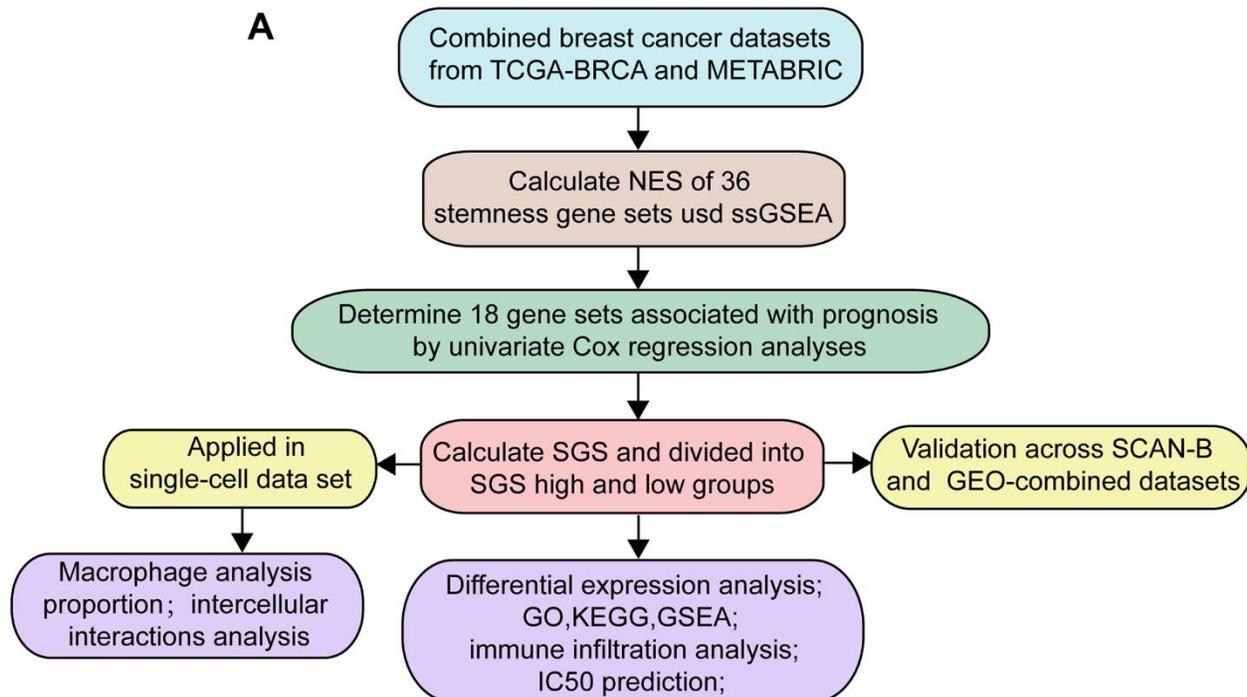
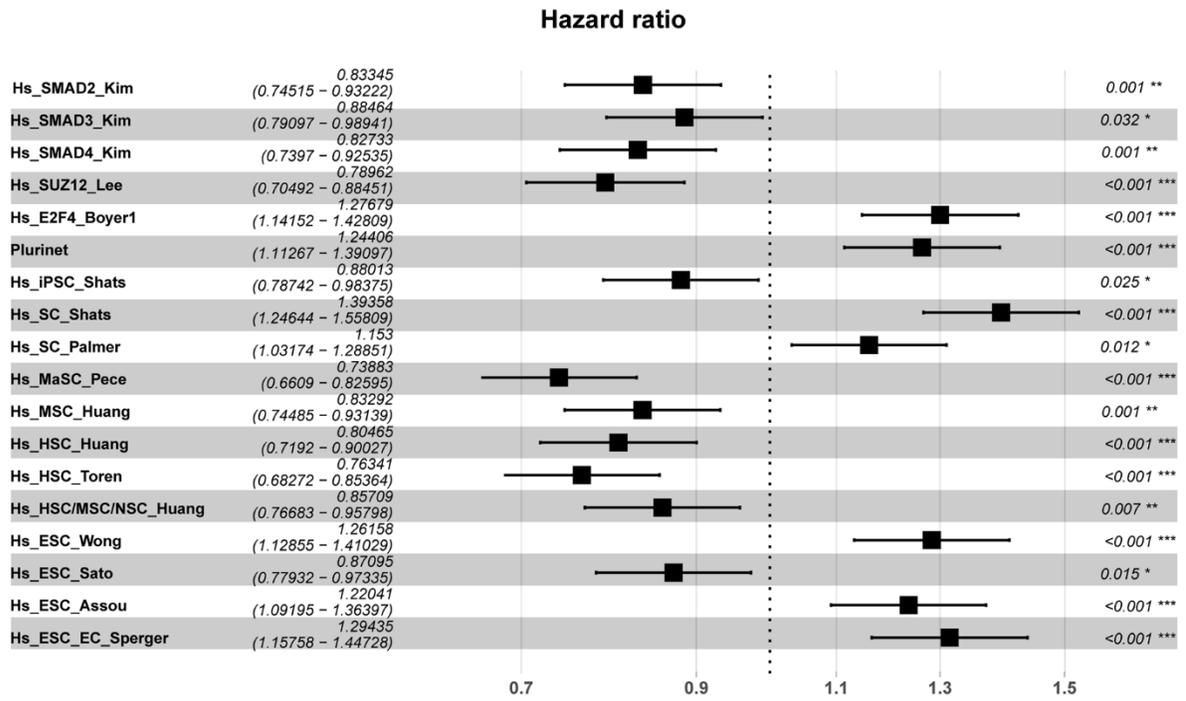


## SUPPLEMENTARY FIGURES

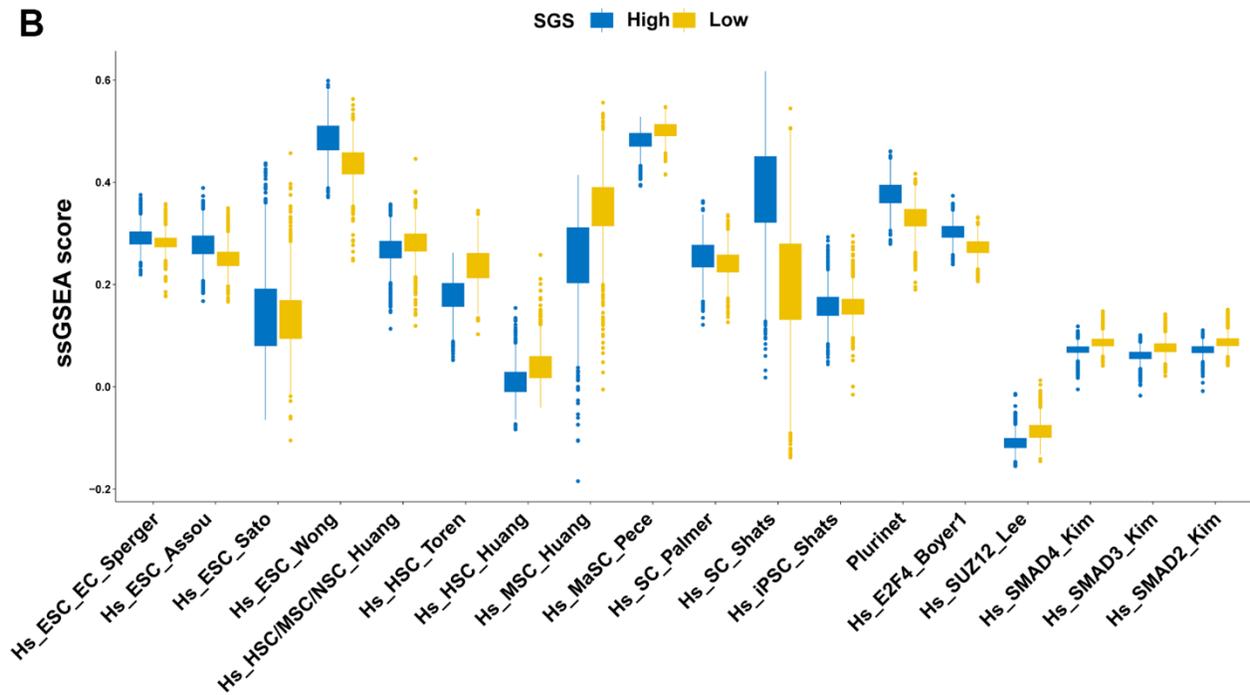


Supplementary Figure 1. Workflow of this study.

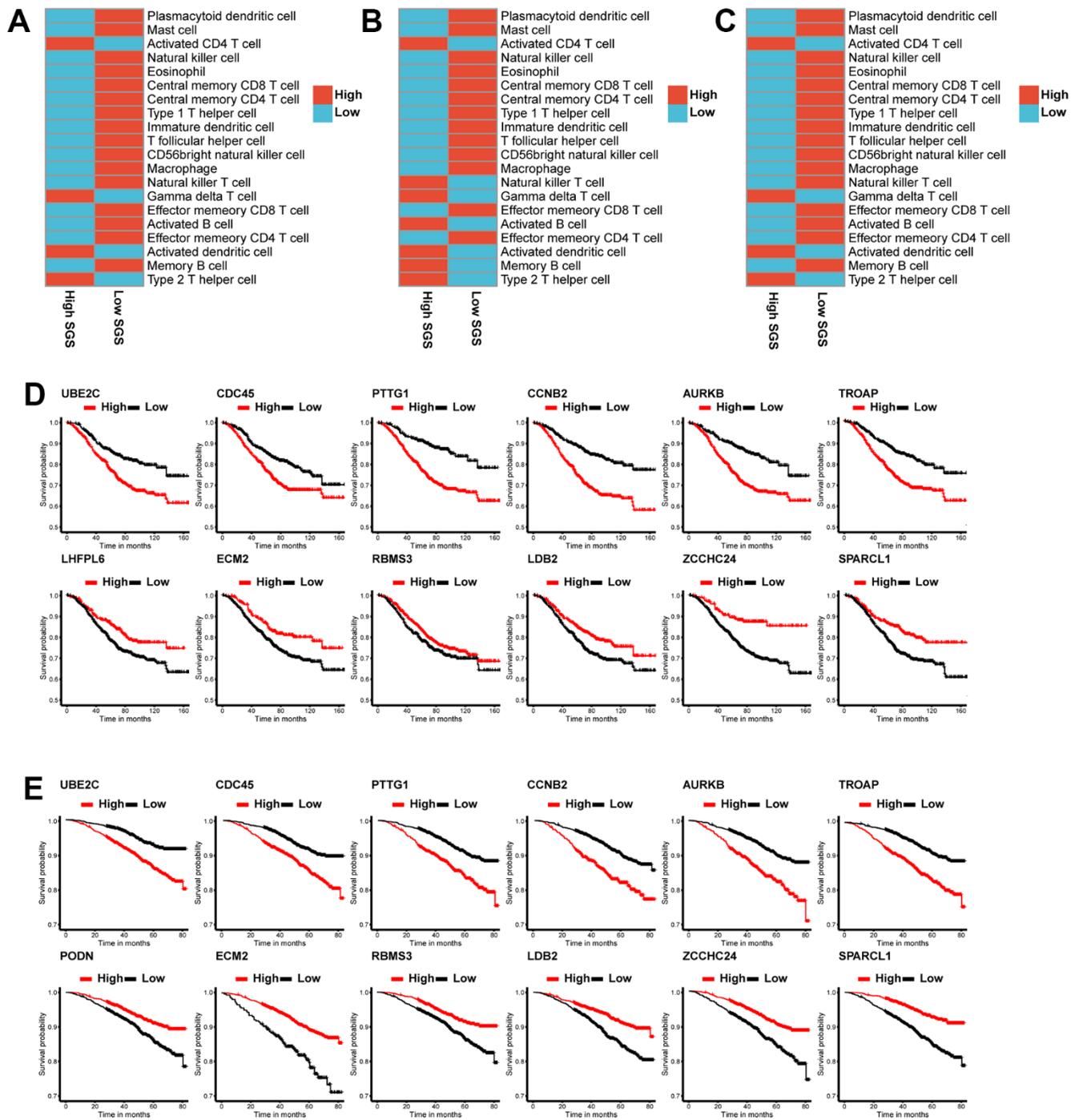
**A**



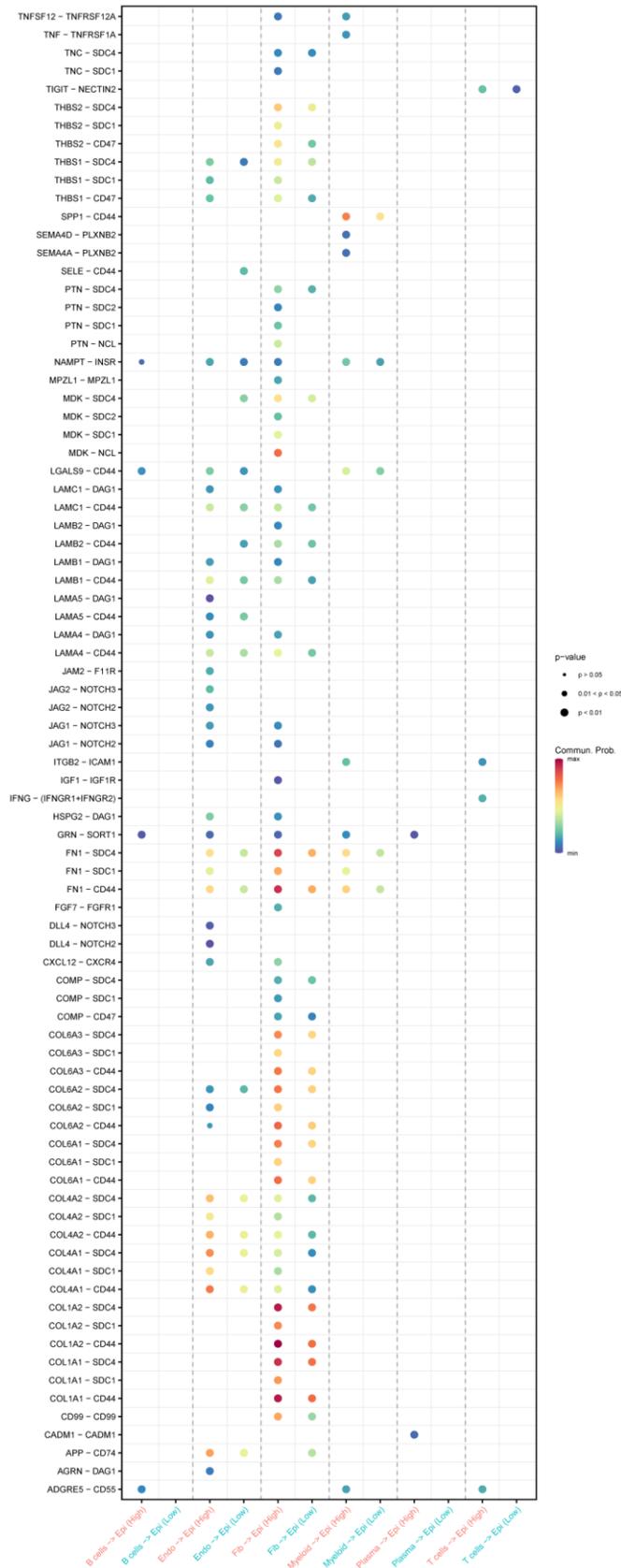
**B**



**Supplementary Figure 2.** (A) Univariate COX regression analysis of ssGSEA scores and OS for prognosis-related stemness gene sets. (B) ssGSEA scores of 18 prognosis-associated stemness gene sets.



**Supplementary Figure 3.** (A–C) Immune infiltration analysis of TCGA and METABRIC combined dataset (A) GEO-combined dataset (B) and SCAN-B dataset (C). (D, E) KM survival analysis of top6 up-and down-regulated genes in the GEO -combined dataset (D) and SCAN-B dataset (E).



**Supplementary Figure 4. Dot plot with ligand-receptor interactions between stromal cells and endothelial cells.** Point size indicates P value. Color indicates the strength of the interaction.