**Integrated single-cell and bulk RNA sequencing identifies SERPING1 as a biomarker of immune infiltration and prognosis in Triple-negative breast cancer**



**Supplementary Fig. 1** Kaplan-Meier survival curve of OS for TNBC based on GSE103091. OS, overall survival. TNBC, triple-negative breast cancer.



**Supplementary Fig. 2** Box plots of SERPING1 protein expression in normal tissues and breast cancer subtype using the UALCAN tool.



**Supplementary Fig. 3** Immune infiltration analysis of TNBC using (A) EPIC, (B) mcpcounter and (C) CIBERSORT-ABS algorithms. The difference between groups was analyzed using the Wilcox test. Two-sided *P*-values < 0.05 were considered to be statistically significant. \**P*-value < 0.05, \*\**P*-value < 0.01, \*\*\**P*-value < 0.001, ns = not significant. TNBC, triple-negative breast cancer.



**Supplementary Fig. 4** Identification of 9 cell types and 8 CAFs clusters in TNBC based on single cell RNA sequencing data. (A) Expression levels of marker genes for each cell type in GSE176078. (B) UMAP plot for the dimension reduction and visualization of 8 cell clusters of CAFs in GSE176078. (C) Violin plots of HLA-DRA, HLA-A, HLA-B and HLA-C in each CAFs subtype. UMAP, uniform manifold approximation and projection; TNBC, triple negative breast cancer; CAFs, cancer-associated fibroblasts; apCAFs, antigen-presenting CAFs; iCAFs, inflammatory CAFs; myCAFs, myofibroblastic CAFs; vCAFs, vascular CAFs.



**Supplementary Fig. 5** GO enrichment analysis of SERPING+ apCAFs and SERPING1-KRT8+ CAFs. GO, gene ontology; BP, biological processes; CC, cellular component; MF, molecular function.