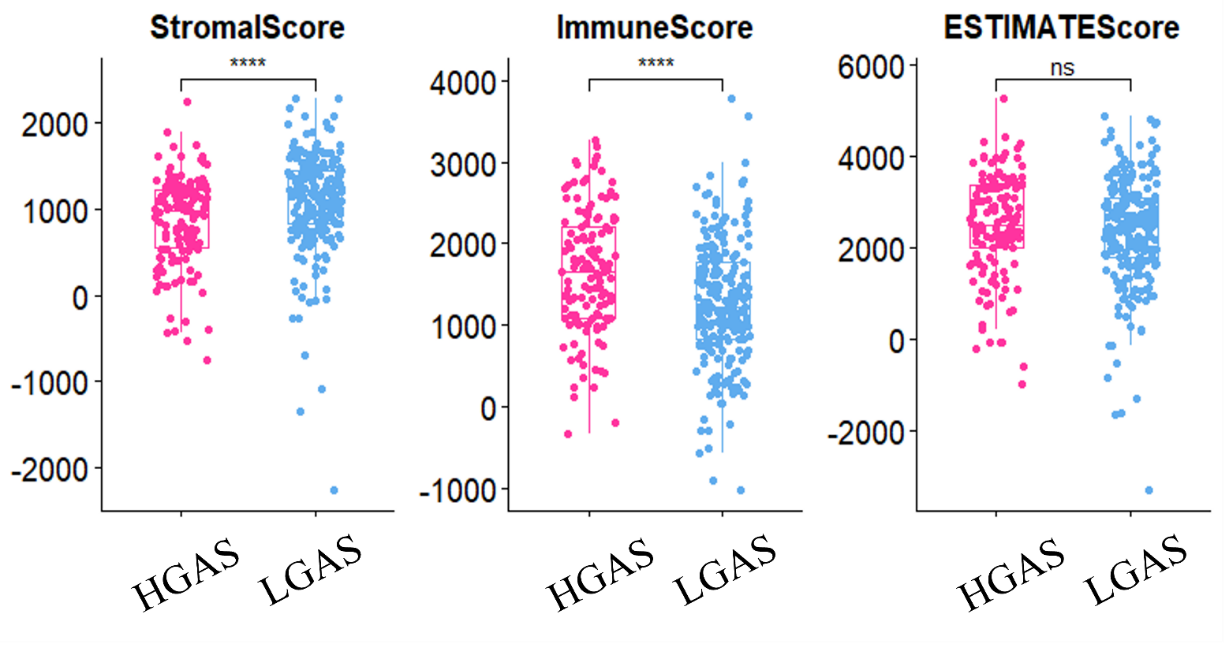
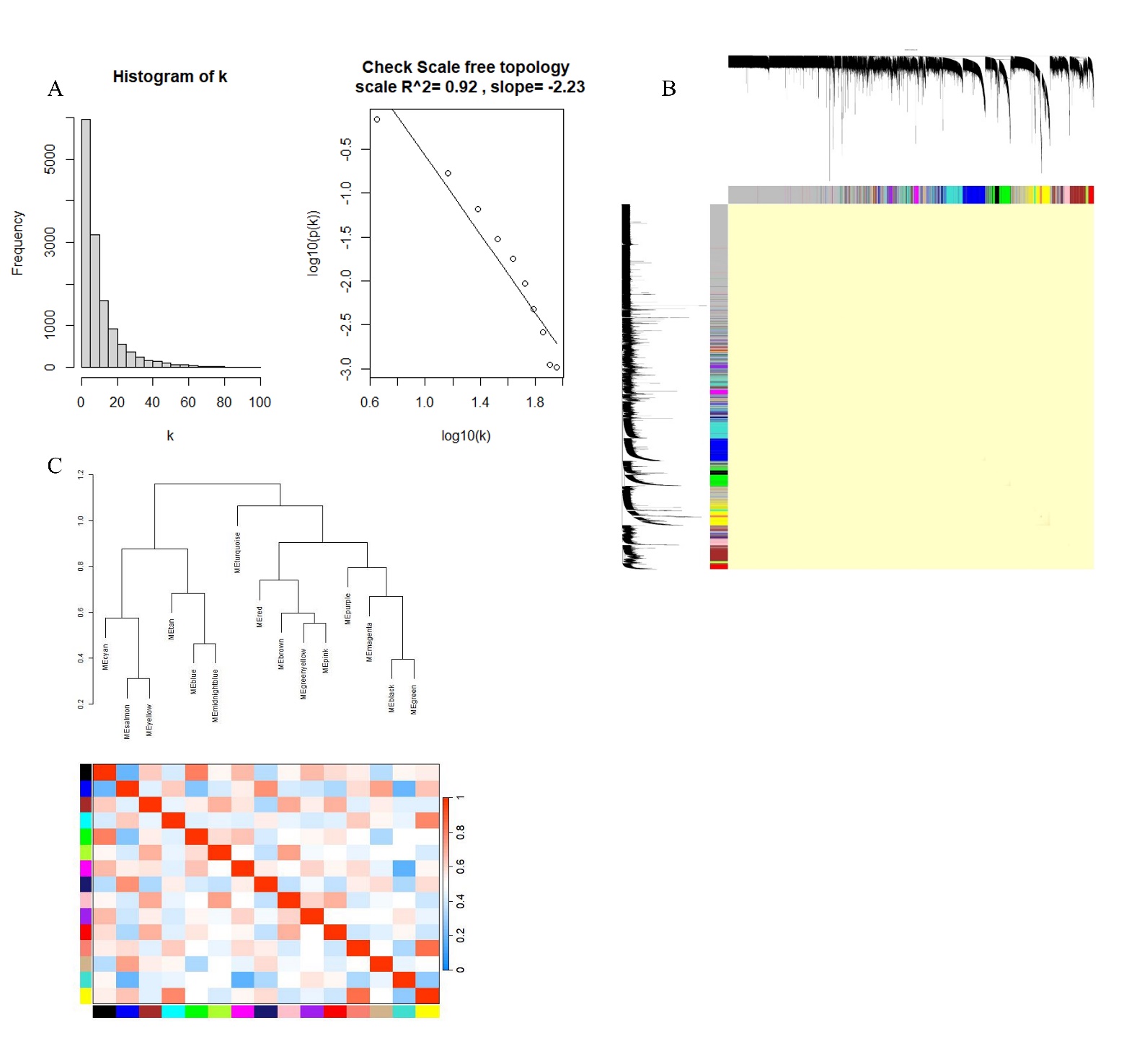


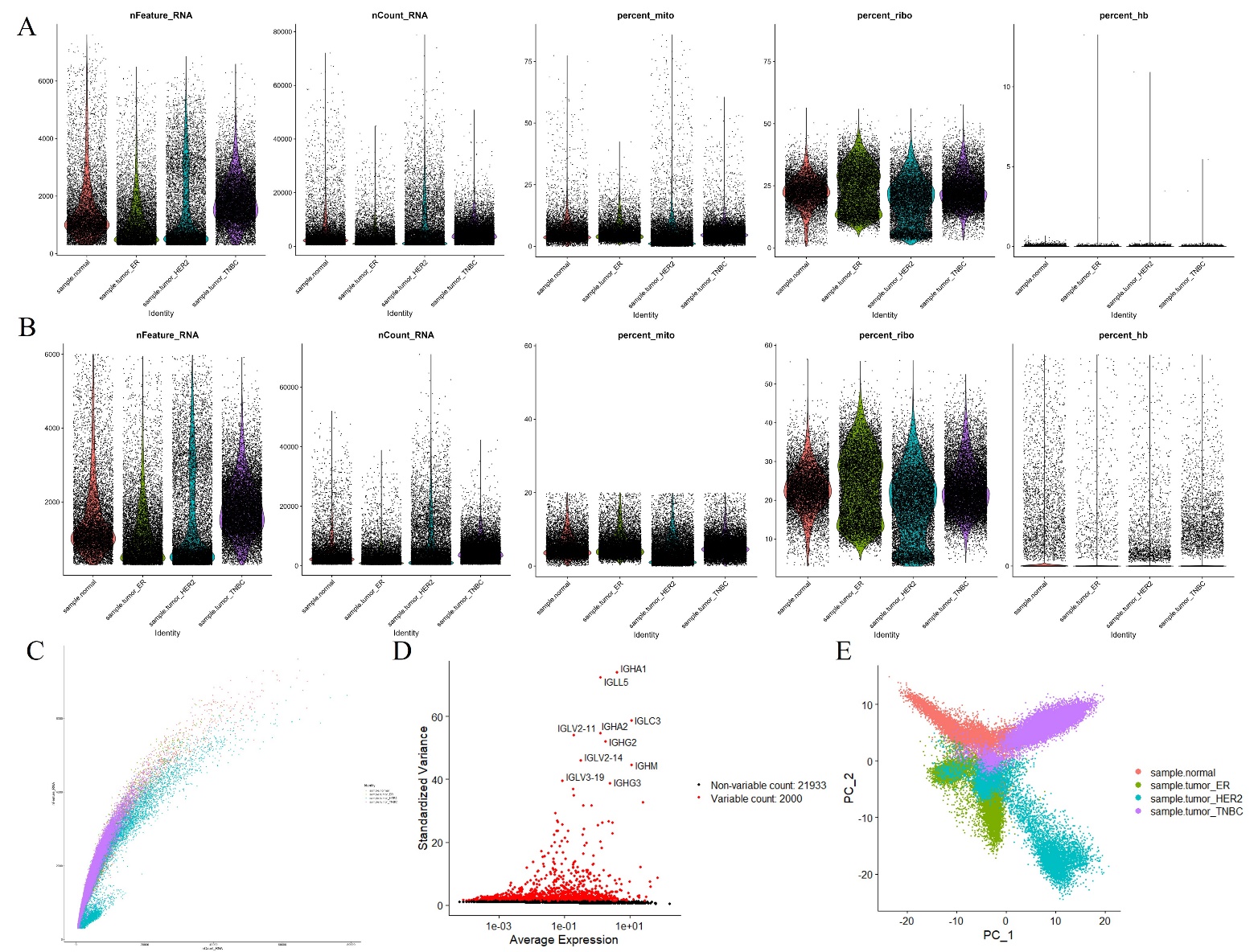
**Supplementary Fig. 1. Principal component analysis (PCA) map before (A) and after batch removal (B); (C) Univariate Cox analysis; (D) CDF curves of consensus matrix for each k (indicated by colors).** CDF, cumulative distribution function.



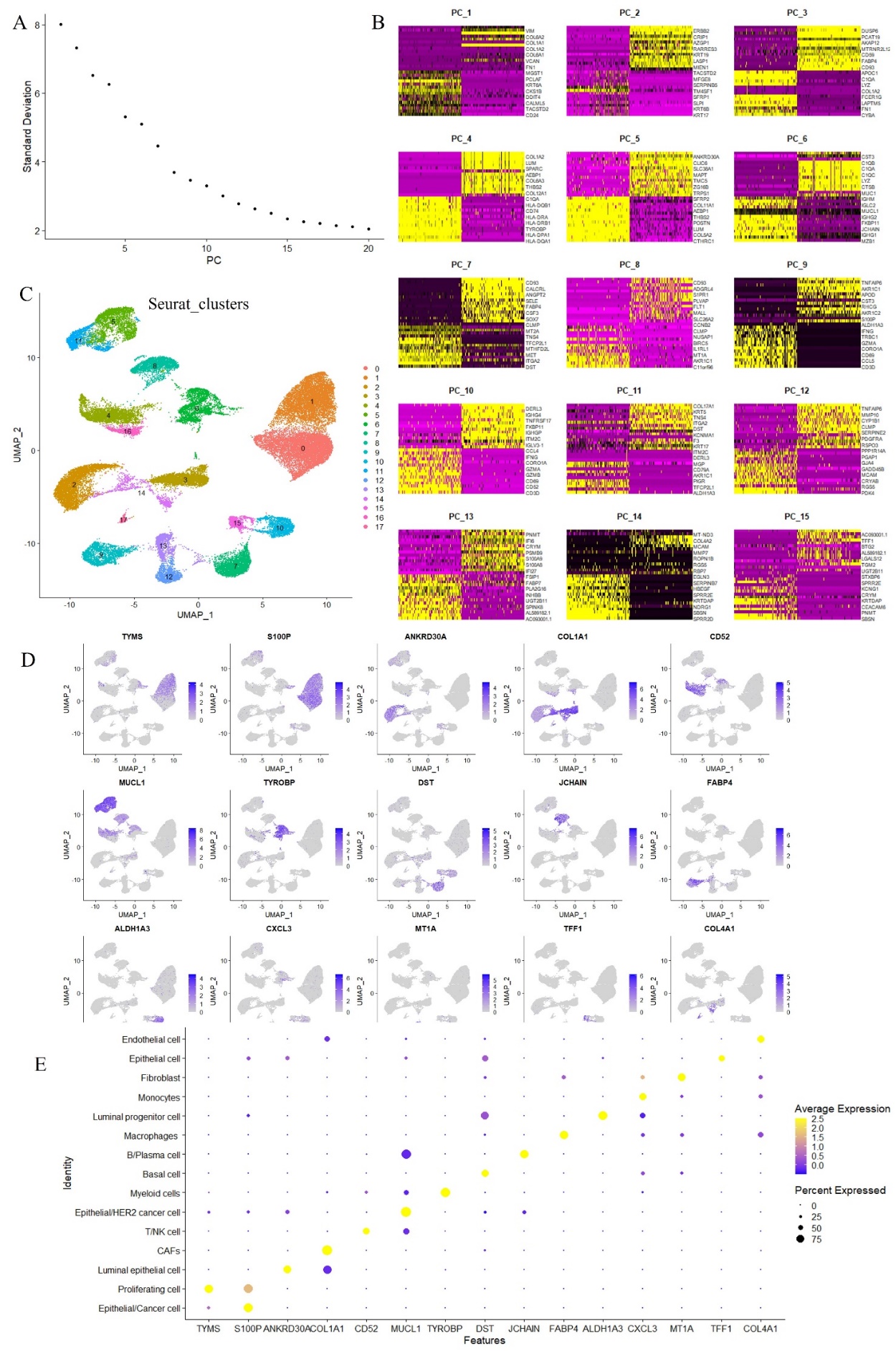
**Supplementary Fig. 2. ESTIMATE analysis for high- and low-glycolytic activity signature groups.** \*\*\*\**p* < 0.001, ns, not significant. HGAS, high glycolytic activity signature; LGAS, low glycolytic activity signature.



**Supplementary Fig. 3. Construction of co-expression modules.** (A) Analysis of network topology for various soft threshold powers. (B) Heatmap depicting the topological overlap matrix among genes based on co-expression modules. (C) Visualization of the gene network.



**Supplementary Fig. 4. Pre-analysis of scRNA-seq data.** (A,B) scRNA-seq quality control before (A) and after (B). (C) Correlation coefficient diagram between mRNA expression level and quantity. (D) The variance diagram shows the variation of gene expression in all cells of BRCA. The red dots represent highly variable genes and the black dots represent non-variable genes. (E) PCA plot shows different sample distribution diagrams. scRNA-seq, Single-cell RNA sequencing; BRCA, Breast invasive carcinoma; PCA, principal component analysis.



**Supplementary Fig. 5. Identification of different cell types.** (A) Elbow plot of Top20 PC. (B) Dimensionality reduction heat map of Top15 PC. (C) UMAP plots showing the cell clusters. (D) UMAP plots showing the expression of marker genes in different cell clusters. (E) Expression levels of marker genes for each cell cluster. PC, principal component； UMAP, Uniform Manifold Approximation and Projection.