

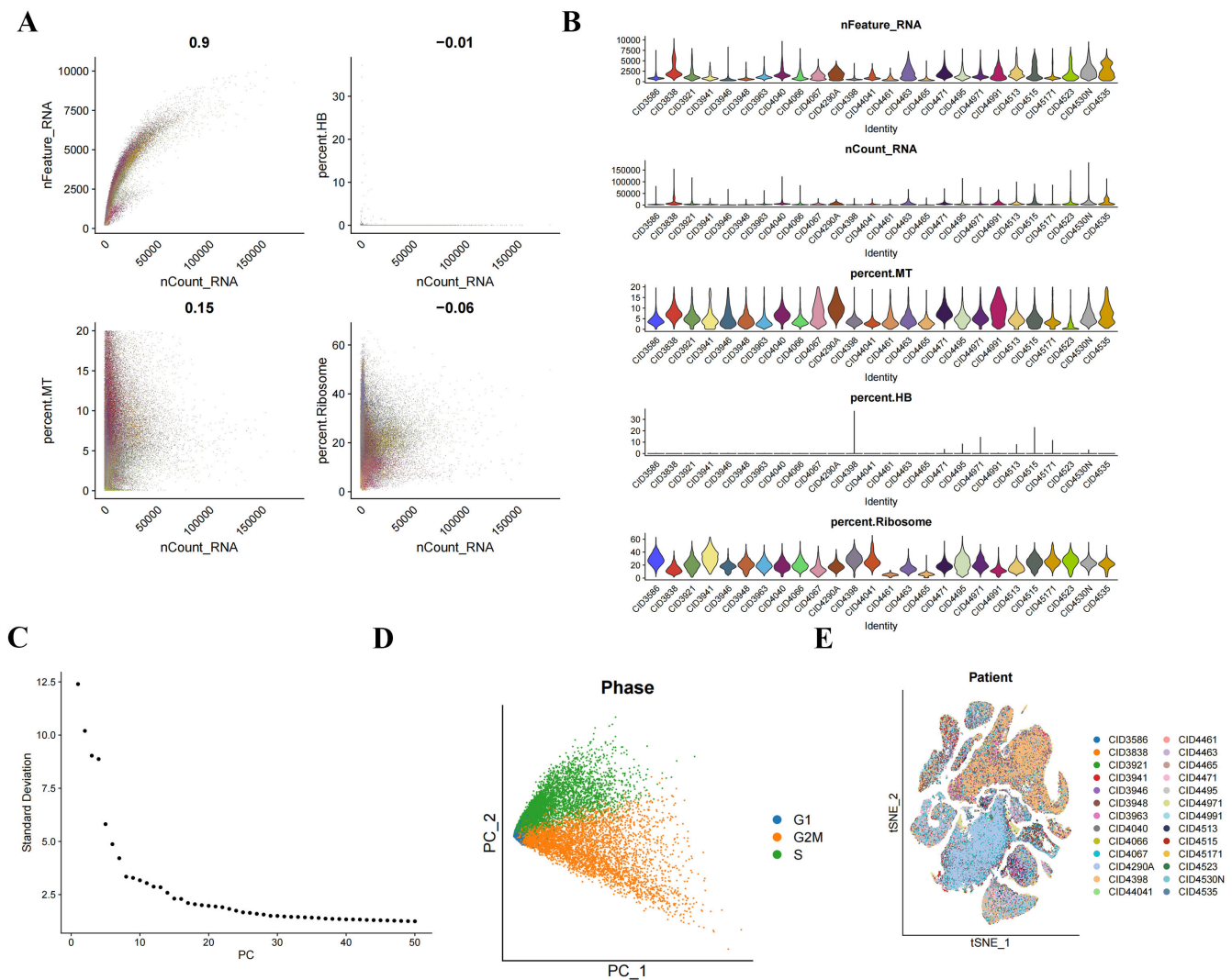


Figure S1 Quality control and normalization of the scRNA-seq Profiling. (A-C) Quality control of the scRNA-seq data from the BRCA samples in the GSE176078 cohort. (D) Cells were colored according to the cell cycle phase inferred from scRNA-seq data. (E) t-SNE visualization of single-cell transcriptomes colored by patient identity. Each dot represents an individual cell.

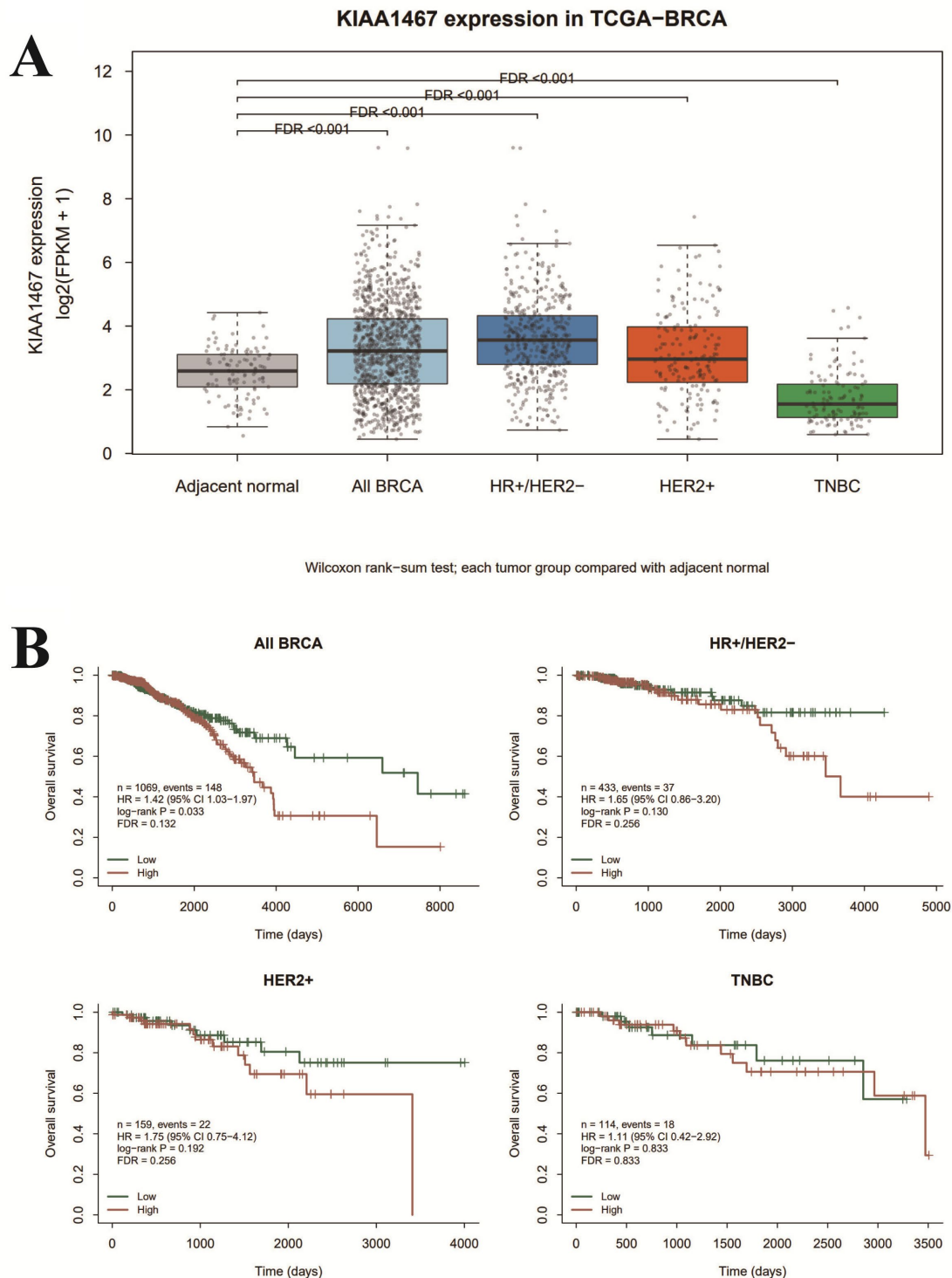
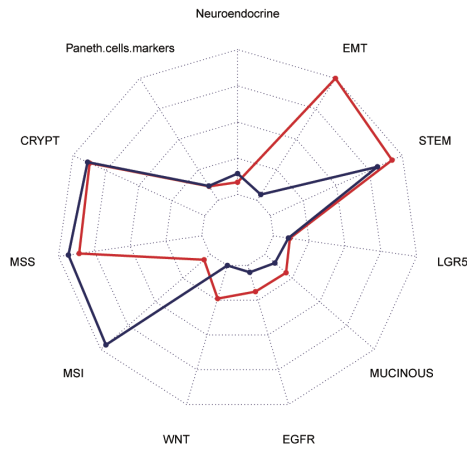


Figure S2 KIAA1467 expression and survival analysis based on the TCGA-BRCA cohort. (A) Compare KIAA1467 expression between adjacent normal tissues and distinct BRCA subtypes. (B) Kaplan-Meier survival analysis for overall survival stratified by KIAA1467 expression status across all BRCA, HR⁺/HER2⁻, HER2⁺ and TNBC subgroups.

A



B

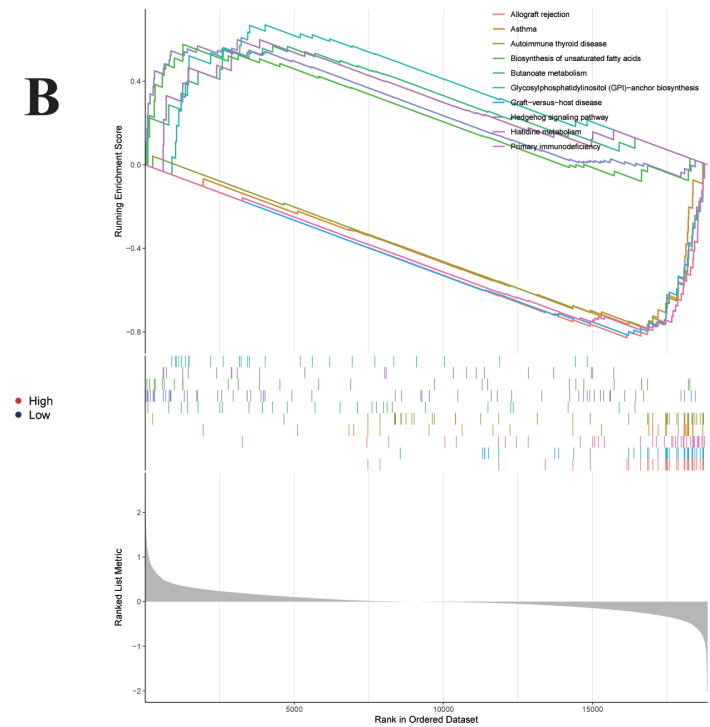


Figure S3 The potential functions of KIAA1467 in BRCA. (A) SSEA analysis of KIAA1467 in BRCA based on GSE176078 dataset. The red line indicates high expression of KIAA1467, and the blue line indicates low expression of KIAA1467. (B) GSE176078 dataset-based single gene GSEA analysis to show KIAA1467-related pathways.

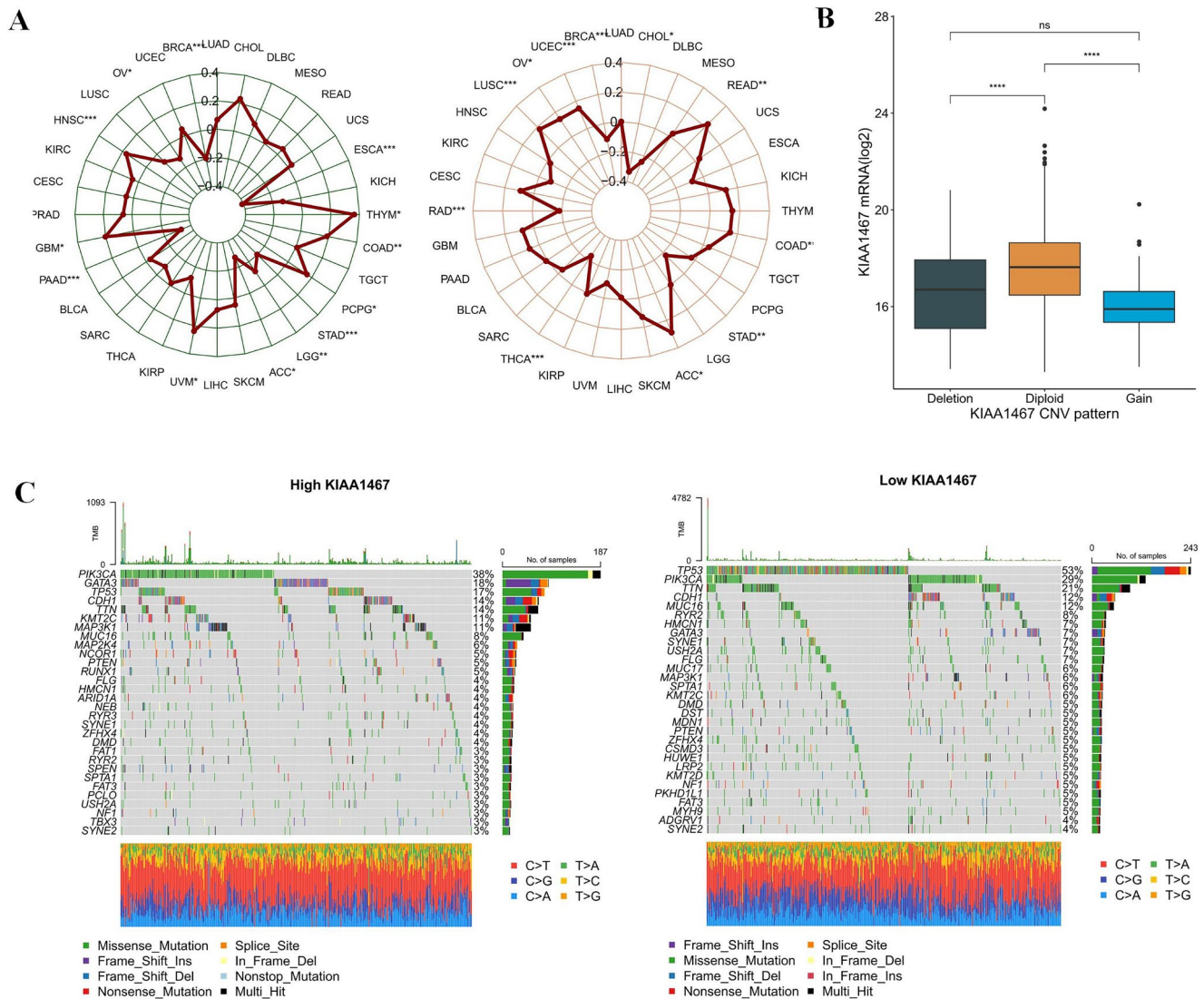


Figure S4 Correlations between KIAA1467 and TMB or MSI and multi-omics analysis of KIAA1467 in BRCA. (A) Pan-cancer correlations between KIAA1467 expression and TMB (left panel) or MSI (right panel). Data are retrieved from TCGA. (B) KIAA1467 mRNA expression by different CNV patterns (deletion, diploid, gain). (C) Top thirty mutational genes in high and low Siglec15 group. The upper barplot revealed the TMB, and mutation frequency was denoted as the number on the right side. The right barplot indicated the percentage of variant types, and the legend was placed at the bottom. * $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$, **** $P < 0.0001$.

KIAA1467/FAM234B vs immune infiltration by TP53 status

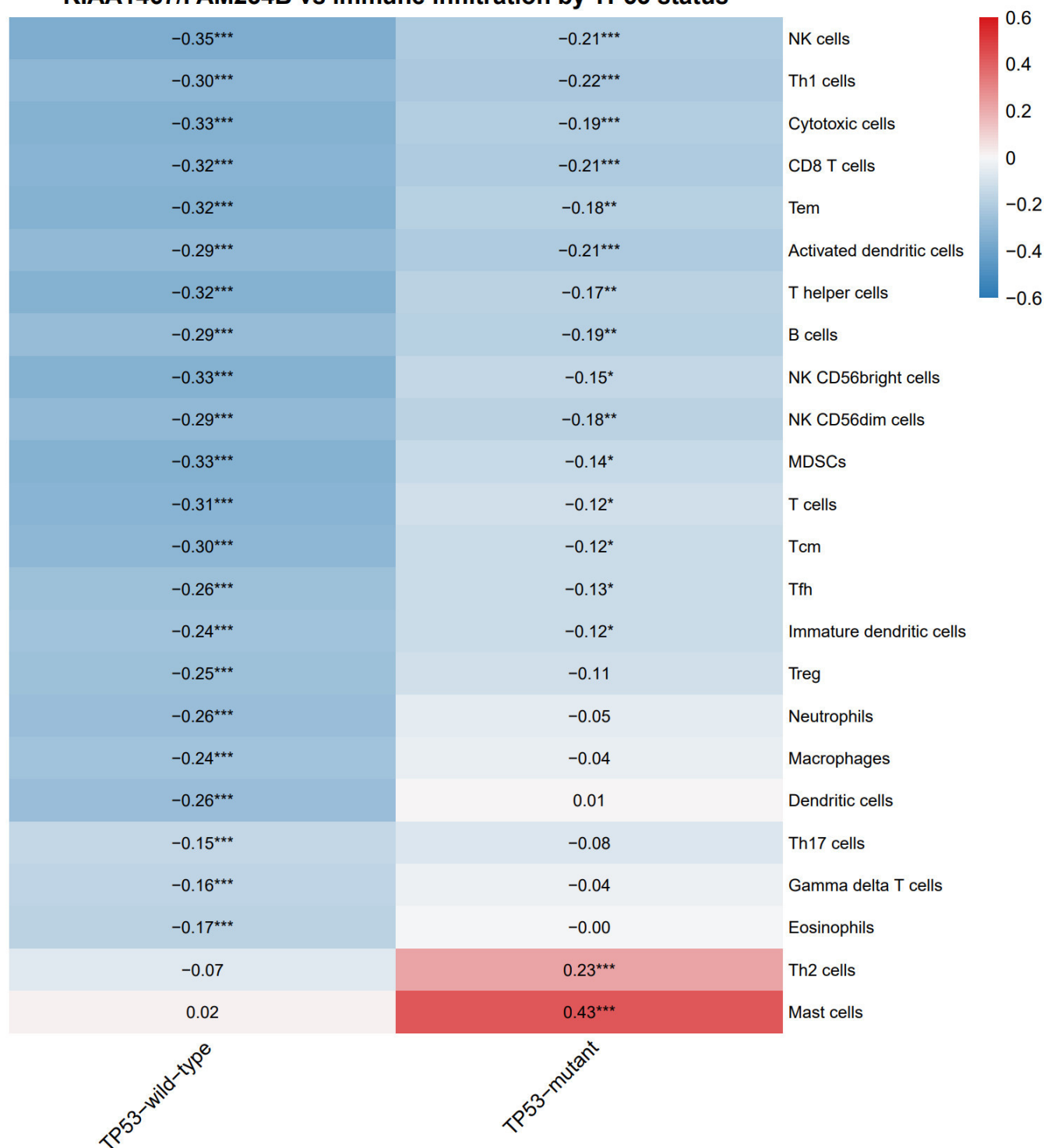


Figure S5 Spearman correlation between KIAA1467 expression and ssGSEA-derived immune-cell infiltration scores stratified by TP53 mutation status; *, ** and *** indicate FDR < 0.05, 0.01 and 0.001.

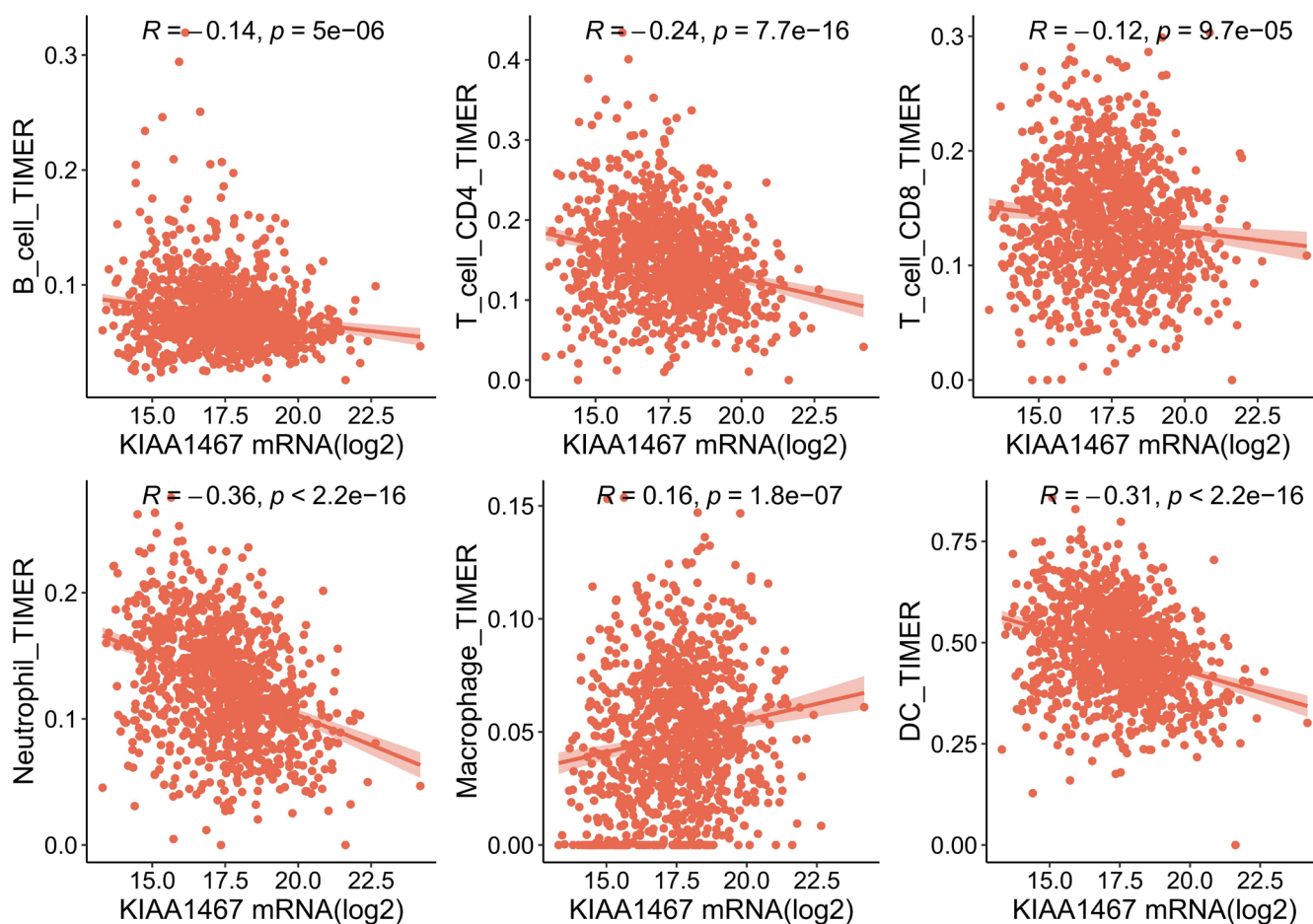


Figure S6 Spearman correlation analysis of KIAA1467 expression and TIICs based on the TIMER algorithm.

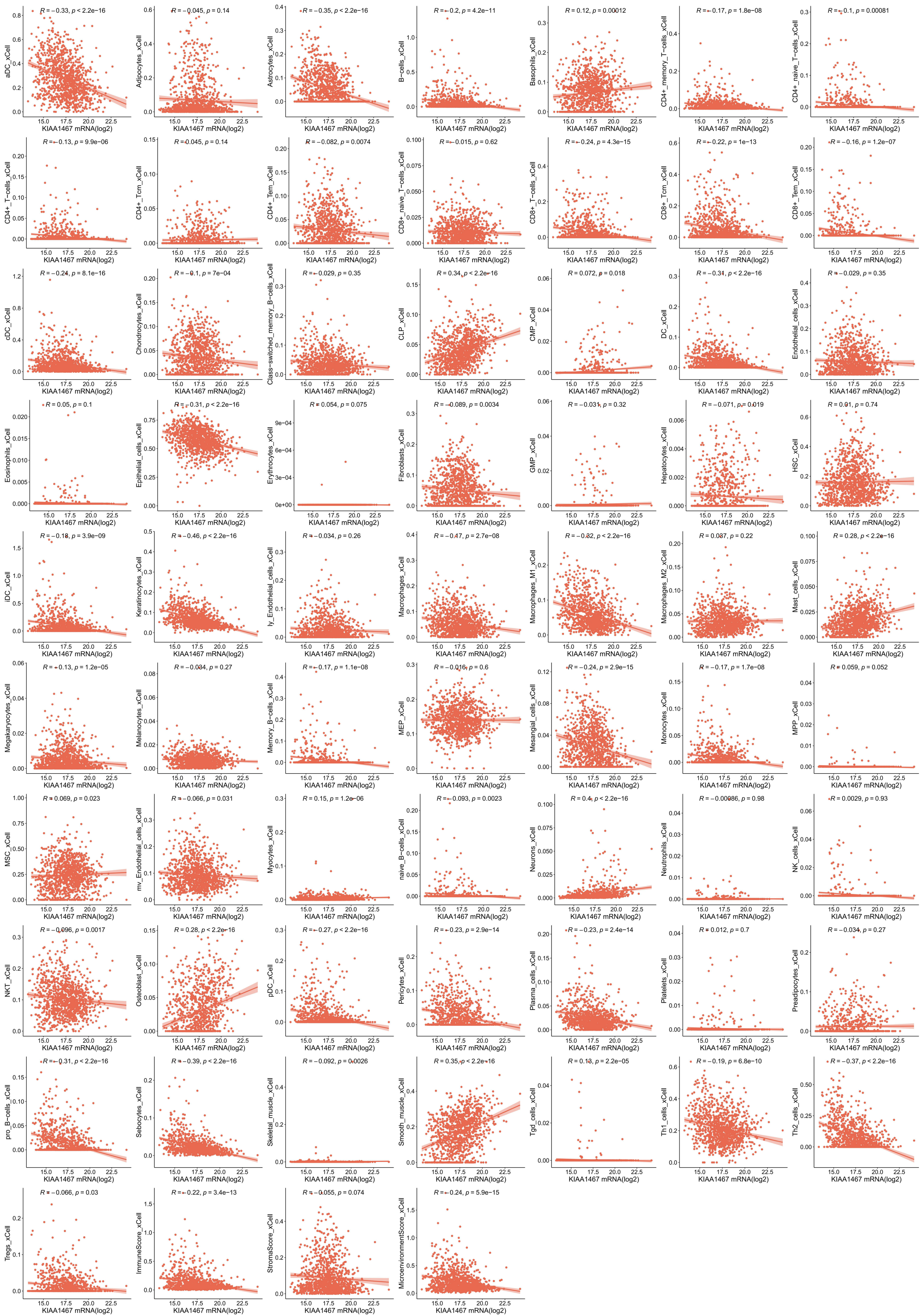


Figure S7 Spearman correlation analysis of KIAA1467 expression and TIICs based on the xCell algorithm.

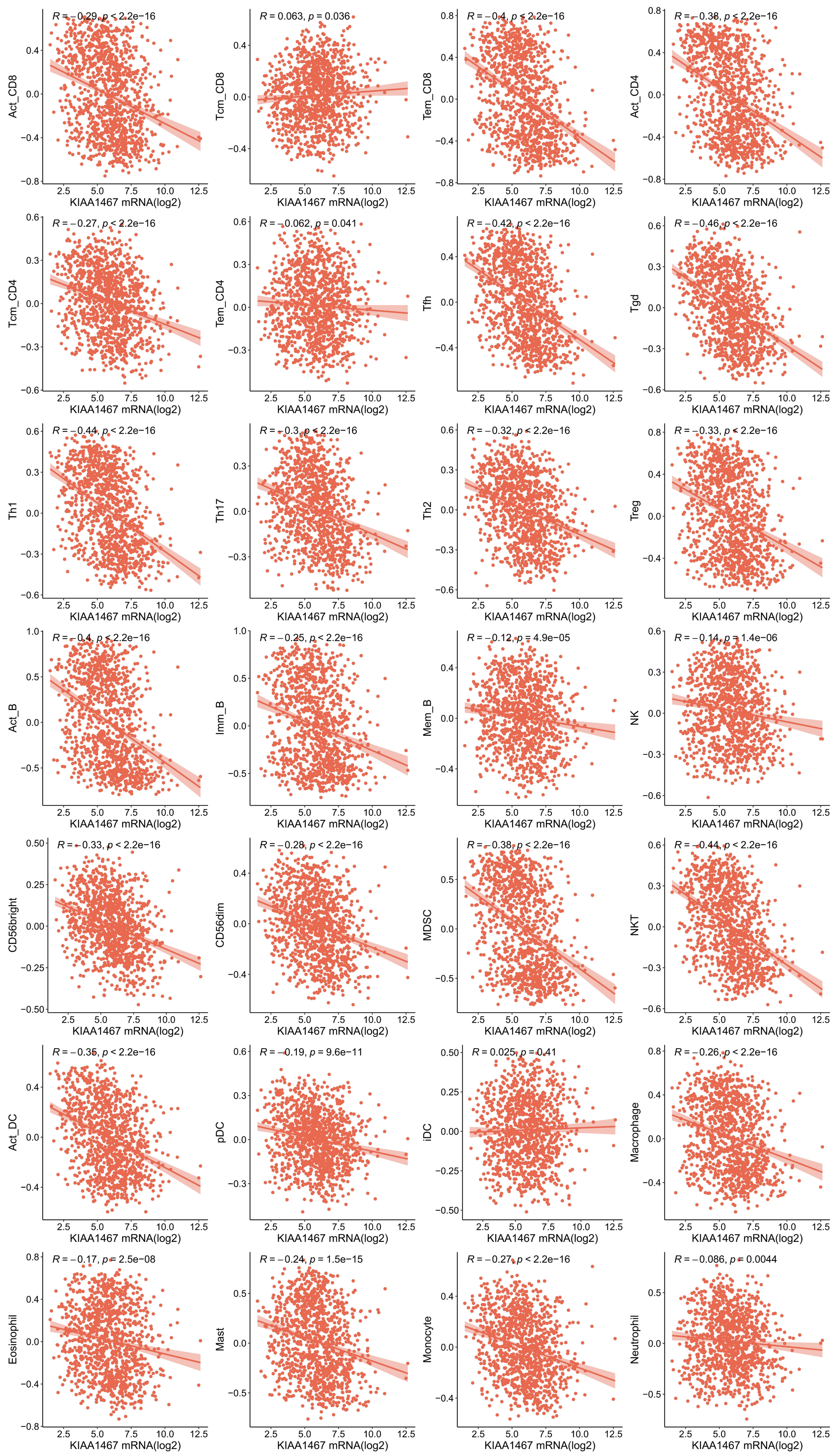


Figure S8 Spearman correlation analysis of KIAA1467 expression and TIICs based on the TISIDB algorithm.

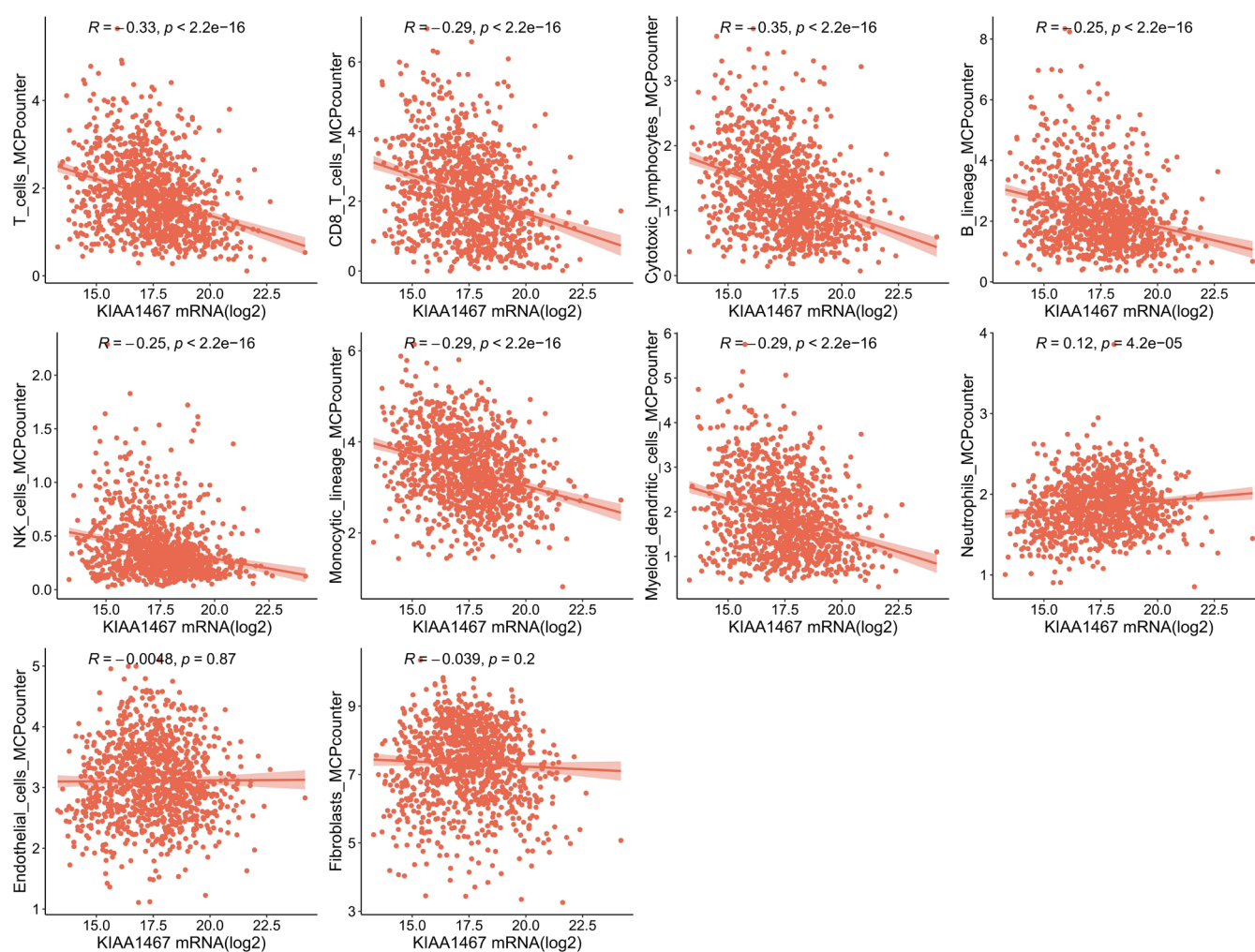


Figure S9 Spearman correlation analysis of KIAA1467 expression and TIICs based on the MCP-counter algorithm.

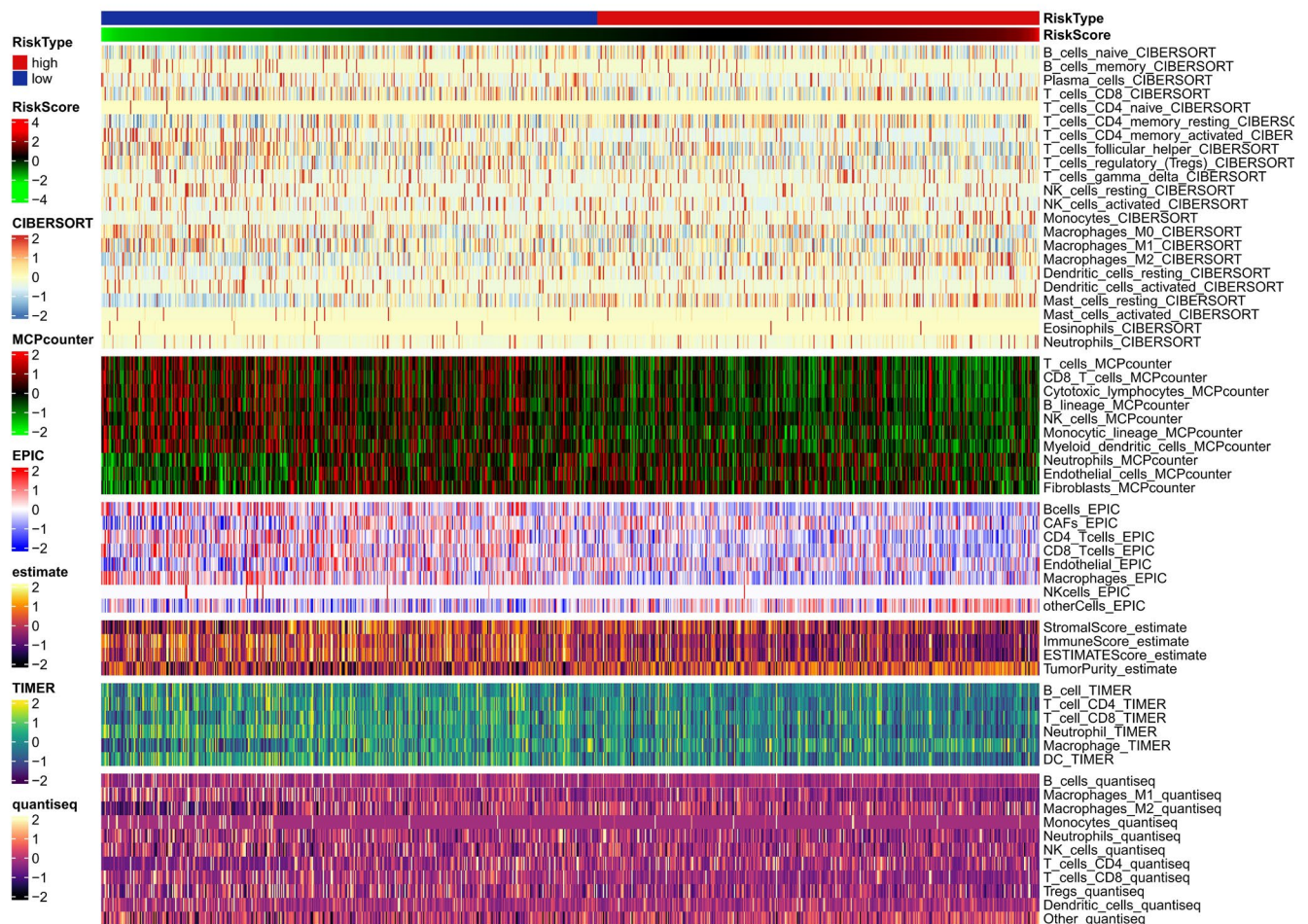


Figure S12 A heatmap to show the association of KIAA1467 expression and immune cells in BRCA based on CIBERSORT, MCPcounter, EPIC, estimate, TIMER, and quantiseq algorithms.

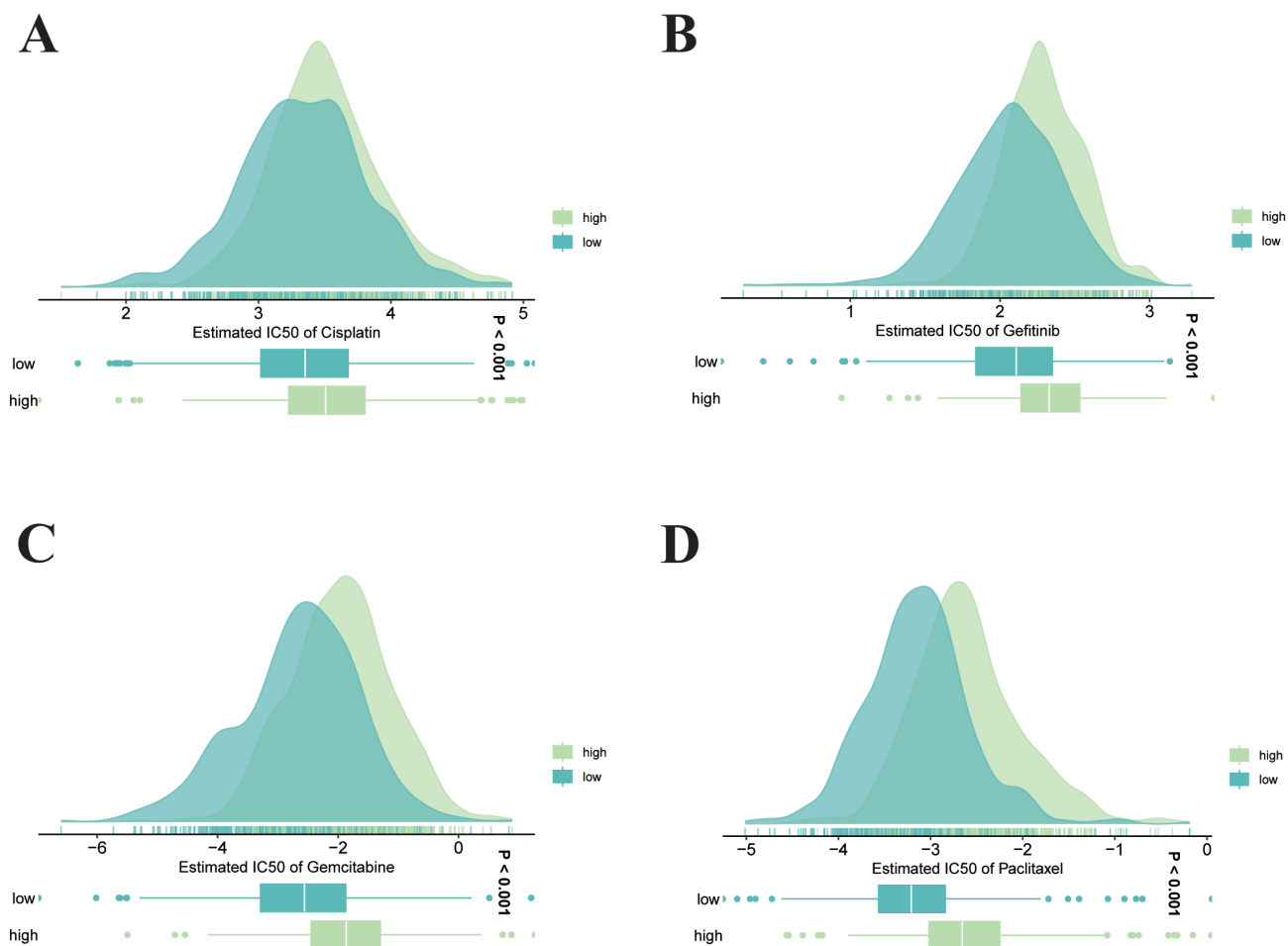


Figure S13 The relationship between KIAA1467 and drug resistance. (A-D) Estimated IC50 of Cisplatin, Gefitinib, Paclitaxel, and Gemcitabine in high or low KIAA1467 group in BRCA tissues based on GDSC analysis.

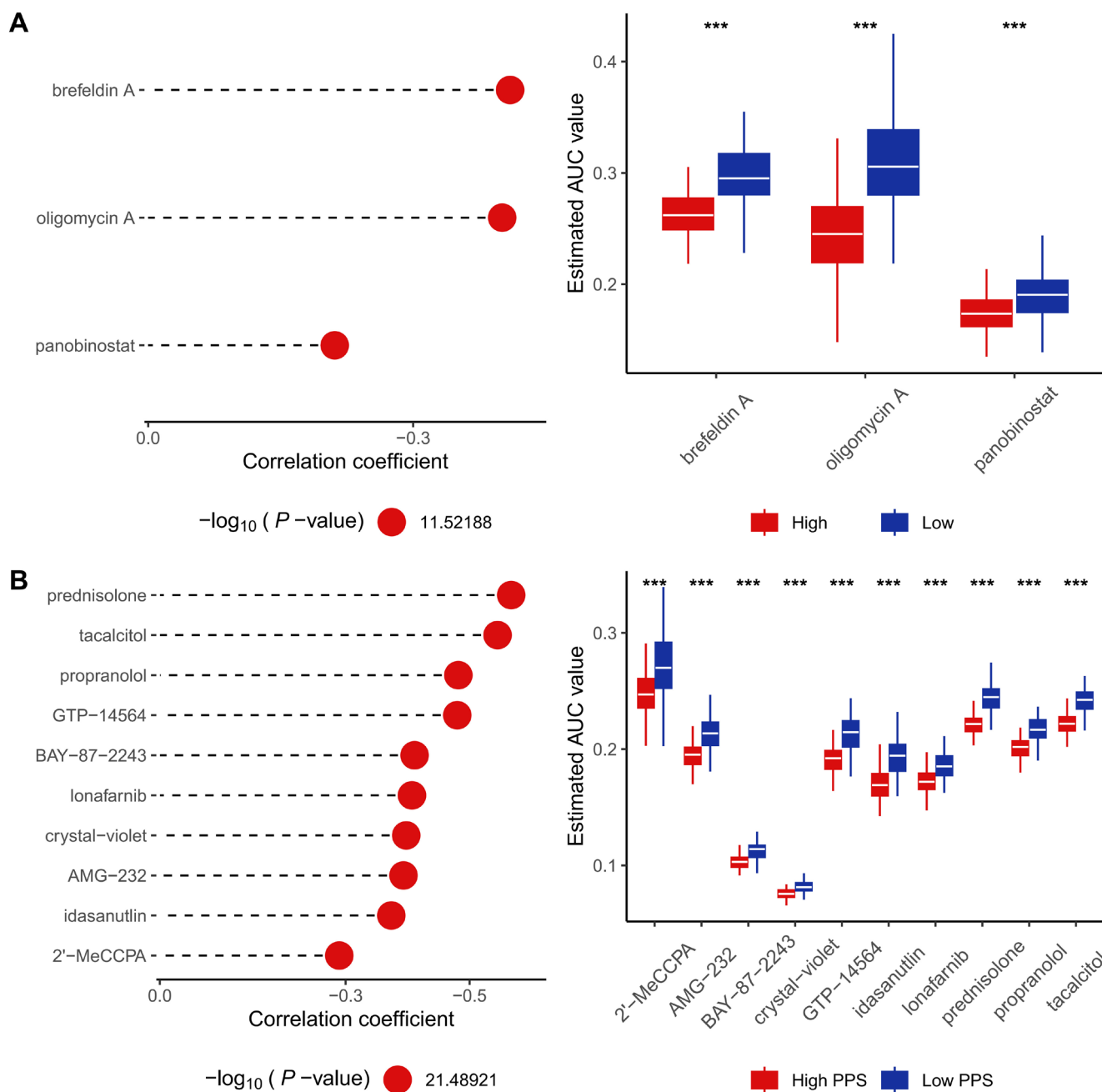


Figure S14 Exploration of potential drugs with high sensitivity in BRCA. (A) Estimated AUC value of different chemotherapeutic agents in high or low PPS groups and correlation coefficient between AUC value and PPS score based on the pharmacogenomics profile databases CTRP. (B) Estimated AUC value of different chemotherapeutic agents in high or low PPS groups and the correlation coefficient between their AUC value and PPS score based on the pharmacogenomics profile databases PRISM.

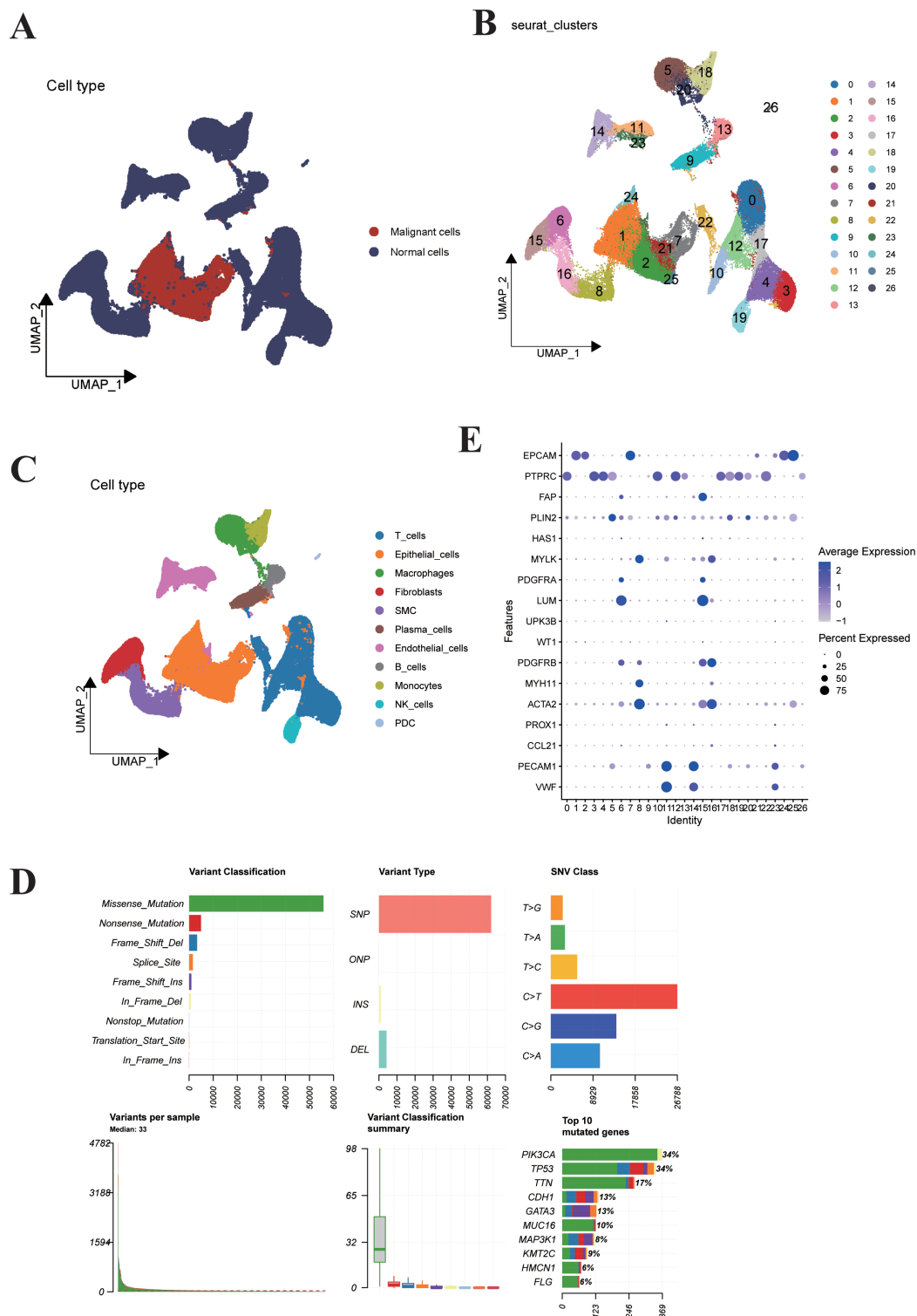


Figure S15 ScRNA-seq analysis of main cell types in BRCA tumor tissues. (A) Identification of malignant cells and normal cells in the UMAP plots. (B) UMAP was used to cluster the cells from 26 primary breast tumors analyzed by scRNA-seq analysis in the GSE176078 cohort. (C) UMAP was used to cluster the cells based on cell lineage. (D) Dot plot of the maker genes of the 26 clusters. (E) Data analysis on mutations.

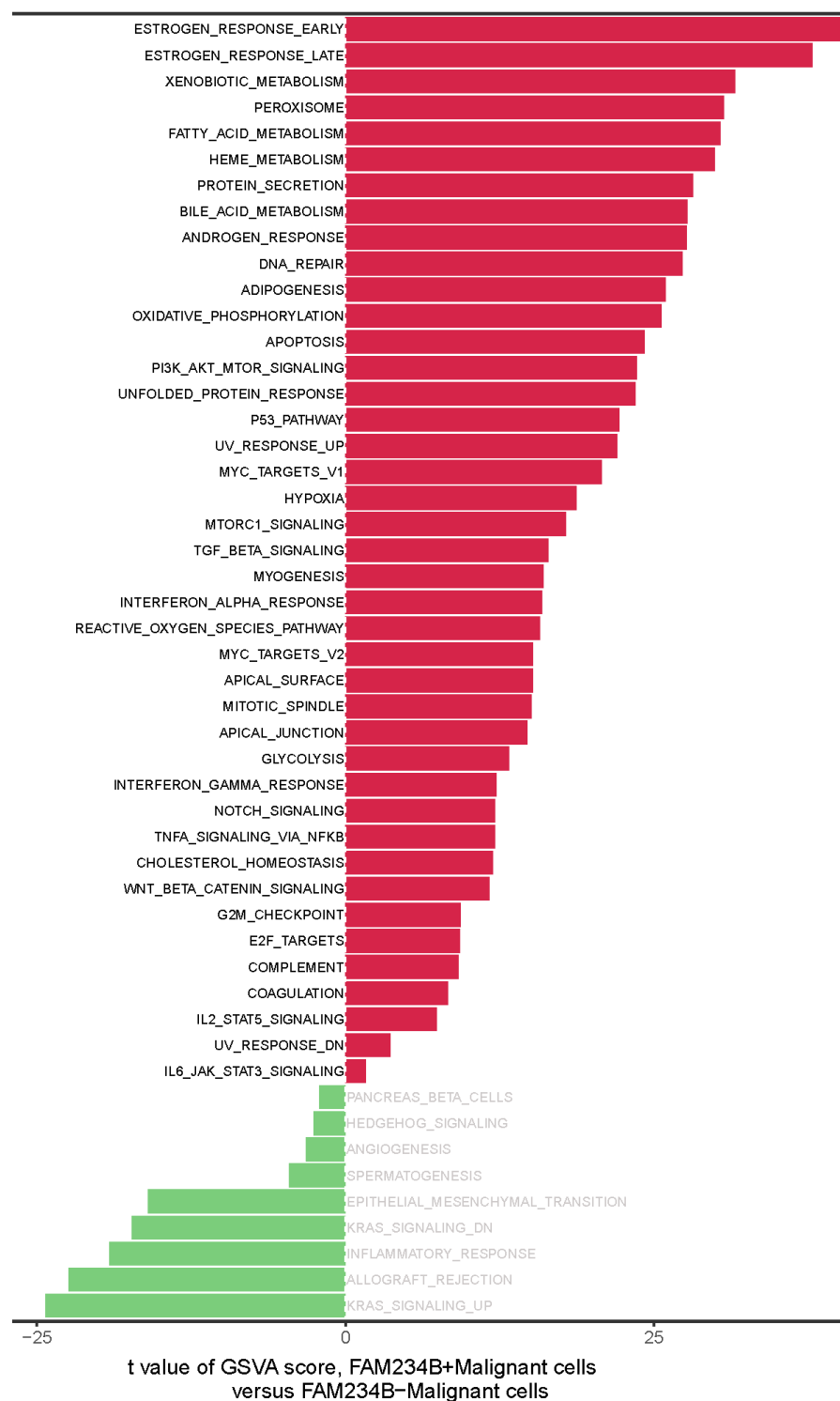


Figure S16 GSVA of enriched pathways in KIAA1467-positive/negative BRCA cells.

