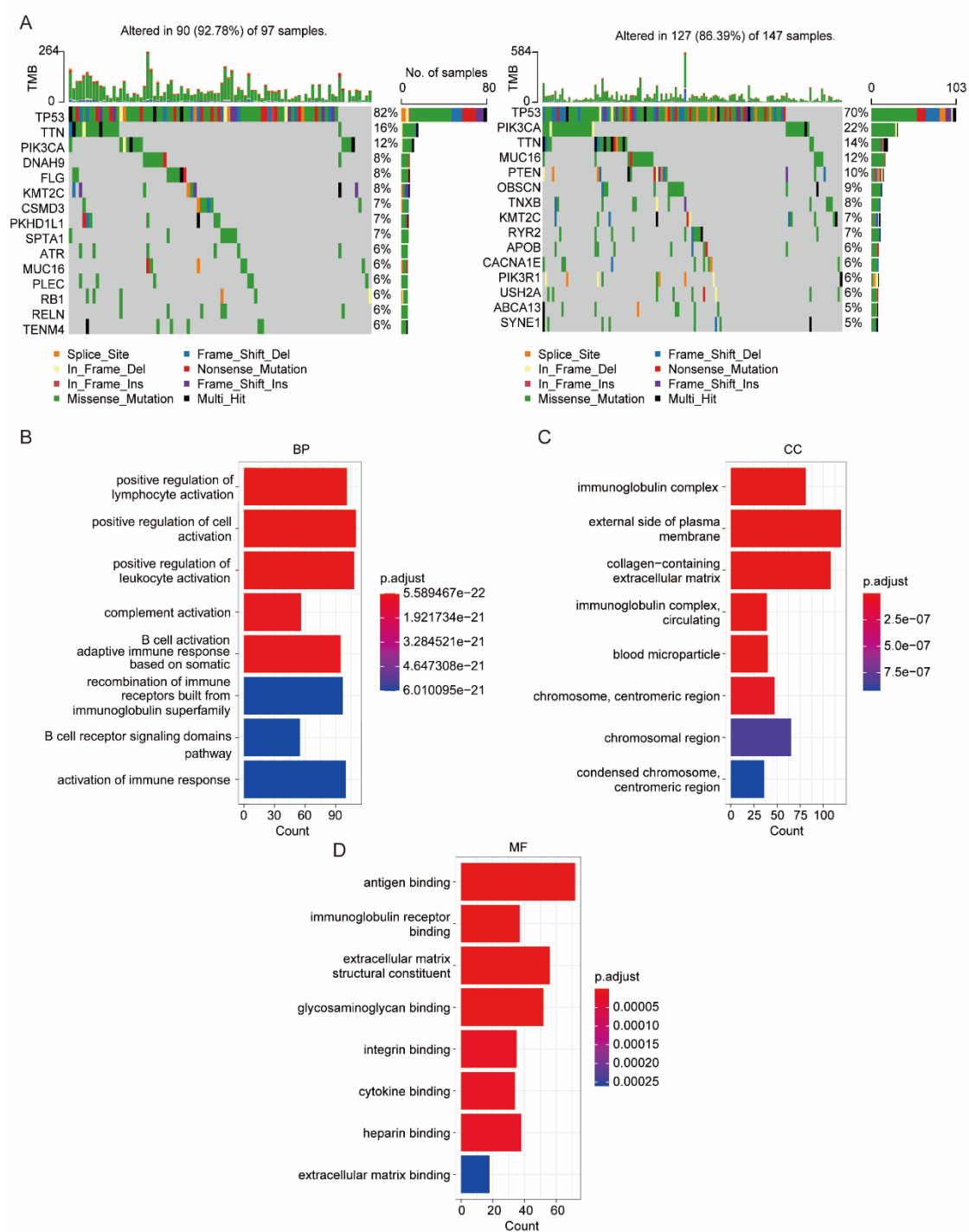
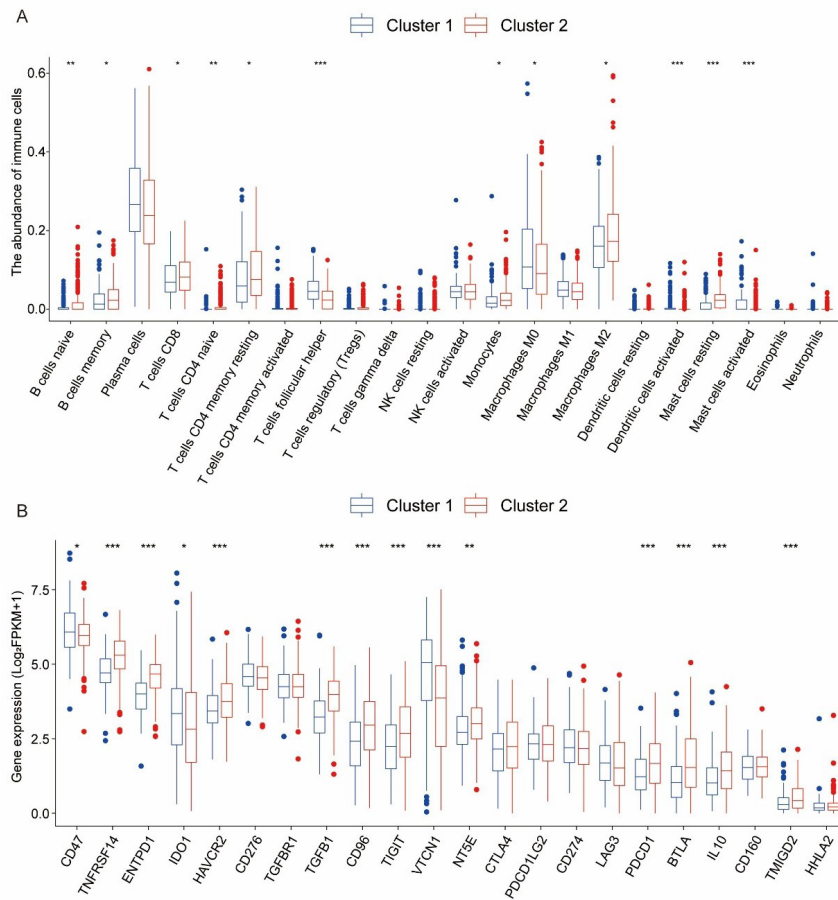


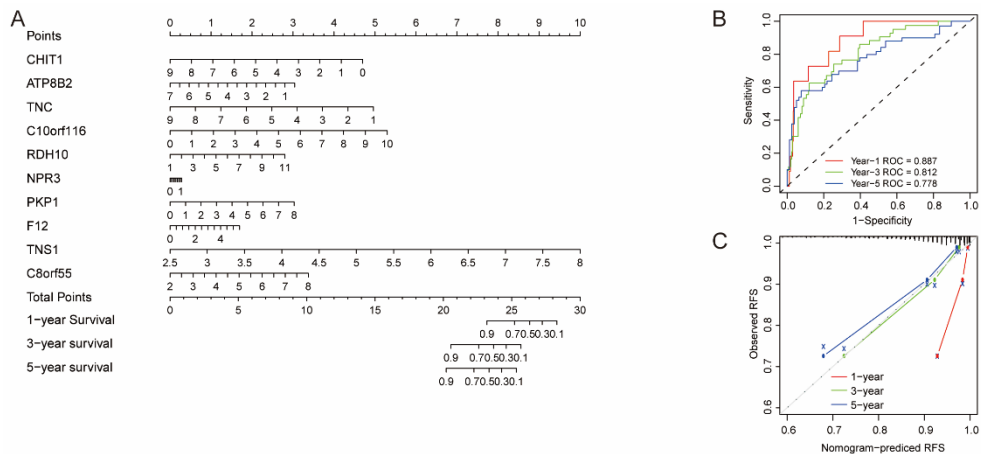
**Figure S1** TNBC molecular subtype consensus clustering of disulfidptosis. (A) Determining the best number of clusters for TNBC involves identifying the point where the rate of decrease slows down. (B) Principal component analysis (PCA) reveals a significant variation in DRGs expression between the two clusters.



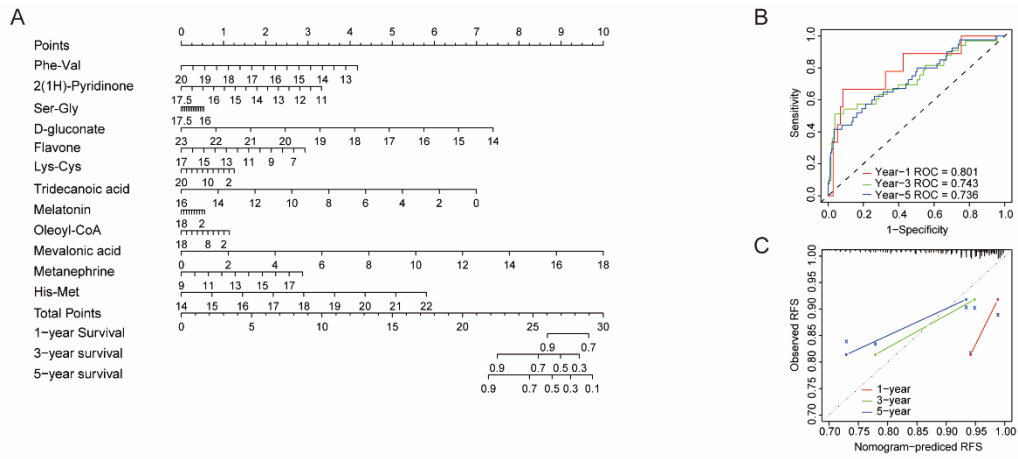
**Figure S2** The biological characterization of two disulfidptosis-related clusters. (A) Gene mutational patterns of two disulfidptosis-related clusters. Waterfall plot of the top 15 gene mutations in cluster 1 (Left) and 2 (Right). (B-D) BP (B), CC (C) and MF (D) enrichment analysis of differential gene among between.



**Figure S3** Immune characteristics of two disulfidptosis-related clusters. (A) CIBERSORT immune cell infiltration analysis in two clusters. (B) The mRNA expression of immune checkpoints in two clusters. Data are presented as the mean  $\pm$  SEM. Statistical significance was determined by Student's *t*-test. \*,  $P < 0.05$ ; \*\*,  $P < 0.01$ ; \*\*\*,  $P < 0.001$ .



**Figure S4** Visualization and validation prediction models based on disulfidptosis related genes. (A) Prediction nomogram integrated the predictors selected, including 10 disulfidptosis related genes. (B) The time-ROC curves for 1, 3 and 5 years of the model. (C) Calibration plots for 1, 3 and 5 years of the model.



**Figure S5** Visualization and validation prediction models based on disulfidptosis related metabolites. (A) Prediction nomogram integrated the predictors selected, including 12 disulfidptosis related metabolites. (B) The time-ROC curves for 1, 3 and 5 years of the model. (C) Calibration plots for 1, 3 and 5 years of the model.