

Table S1 Pyroptosis-related genes

Gene	Type
<i>CASP6</i>	Pyroptosis
<i>GPX4</i>	Pyroptosis
<i>GSDMD</i>	Pyroptosis
<i>IL18</i>	Pyroptosis
<i>AIM2</i>	Pyroptosis
<i>CASP8</i>	Pyroptosis
<i>GSDMA</i>	Pyroptosis
<i>GSDMC</i>	Pyroptosis
<i>NLR4</i>	Pyroptosis
<i>NLRP2</i>	Pyroptosis
<i>NLRP6</i>	Pyroptosis
<i>NOD1</i>	Pyroptosis
<i>PJK</i>	Pyroptosis
<i>PRKACA</i>	Pyroptosis
<i>SCAF11</i>	Pyroptosis
<i>TNF</i>	Pyroptosis
<i>BAK1</i>	Pyroptosis
<i>CASP1</i>	Pyroptosis
<i>CHMP2A</i>	Pyroptosis
<i>CHMP3</i>	Pyroptosis
<i>CHMP4B</i>	Pyroptosis
<i>CHMP6</i>	Pyroptosis
<i>CYCS</i>	Pyroptosis
<i>HMGB1</i>	Pyroptosis
<i>IRF1</i>	Pyroptosis
<i>TP53</i>	Pyroptosis
<i>CASP5</i>	Pyroptosis
<i>ELANE</i>	Pyroptosis
<i>GSDME</i>	Pyroptosis
<i>IL1B</i>	Pyroptosis
<i>CASP3</i>	Pyroptosis
<i>CASP9</i>	Pyroptosis
<i>GSDMB</i>	Pyroptosis
<i>IL6</i>	Pyroptosis
<i>NLRP1</i>	Pyroptosis
<i>NLRP3</i>	Pyroptosis
<i>NLRP7</i>	Pyroptosis
<i>NOD2</i>	Pyroptosis
<i>PLCG1</i>	Pyroptosis
<i>PYCARD</i>	Pyroptosis
<i>TIRAP</i>	Pyroptosis
<i>GZMA</i>	Pyroptosis
<i>BAX</i>	Pyroptosis
<i>CASP4</i>	Pyroptosis
<i>CHMP2B</i>	Pyroptosis
<i>CHMP4A</i>	Pyroptosis
<i>CHMP4C</i>	Pyroptosis
<i>CHMP7</i>	Pyroptosis
<i>GZMB</i>	Pyroptosis
<i>IL1A</i>	Pyroptosis
<i>IRF2</i>	Pyroptosis
<i>TP63</i>	Pyroptosis

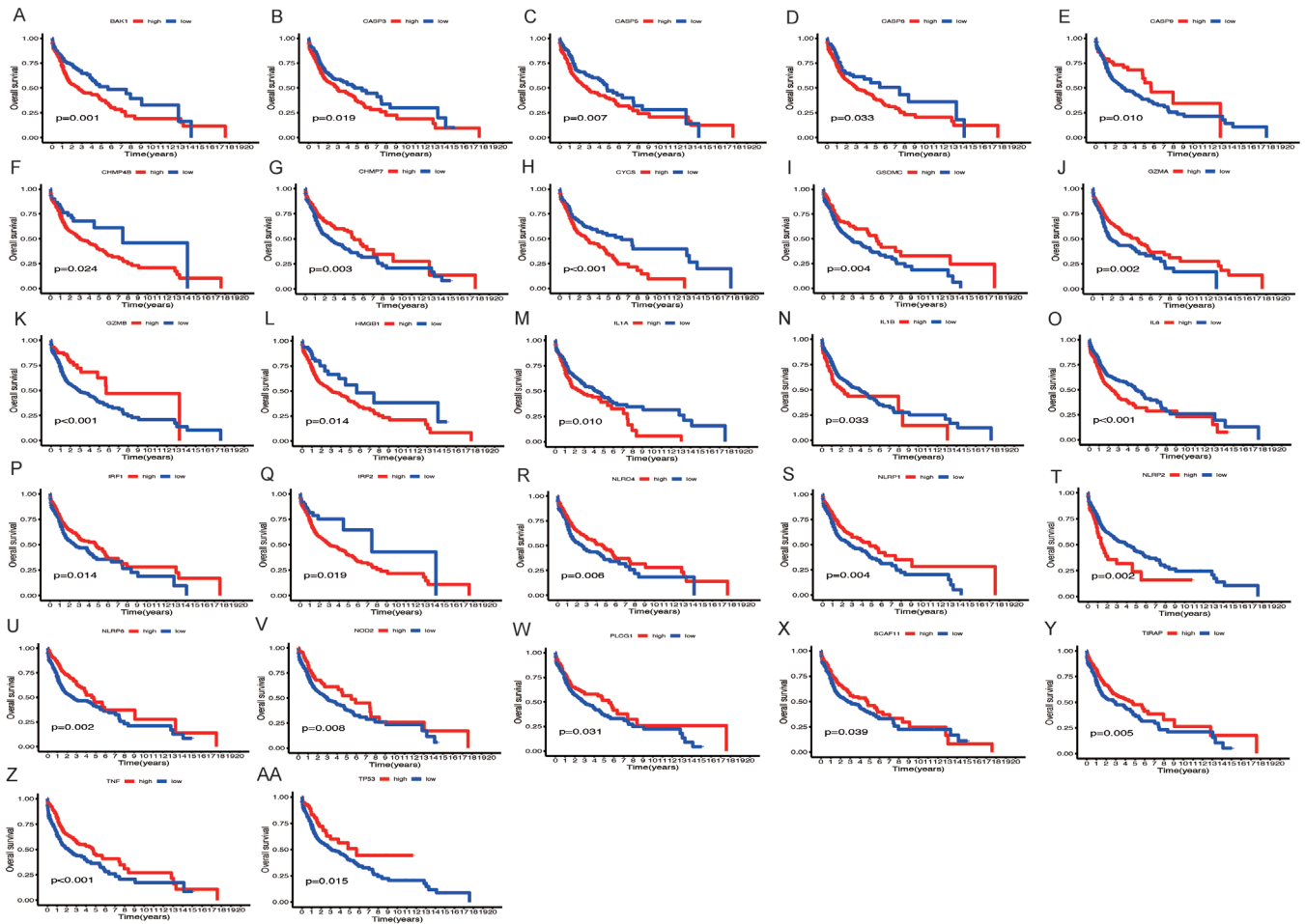


Figure S1 Overall survival curve of pyroptosis-related DEGs. (A-AA) Overall survival curve of pyroptosis-related DEGs in the survival analysis. DEGs, differentially expressed genes.

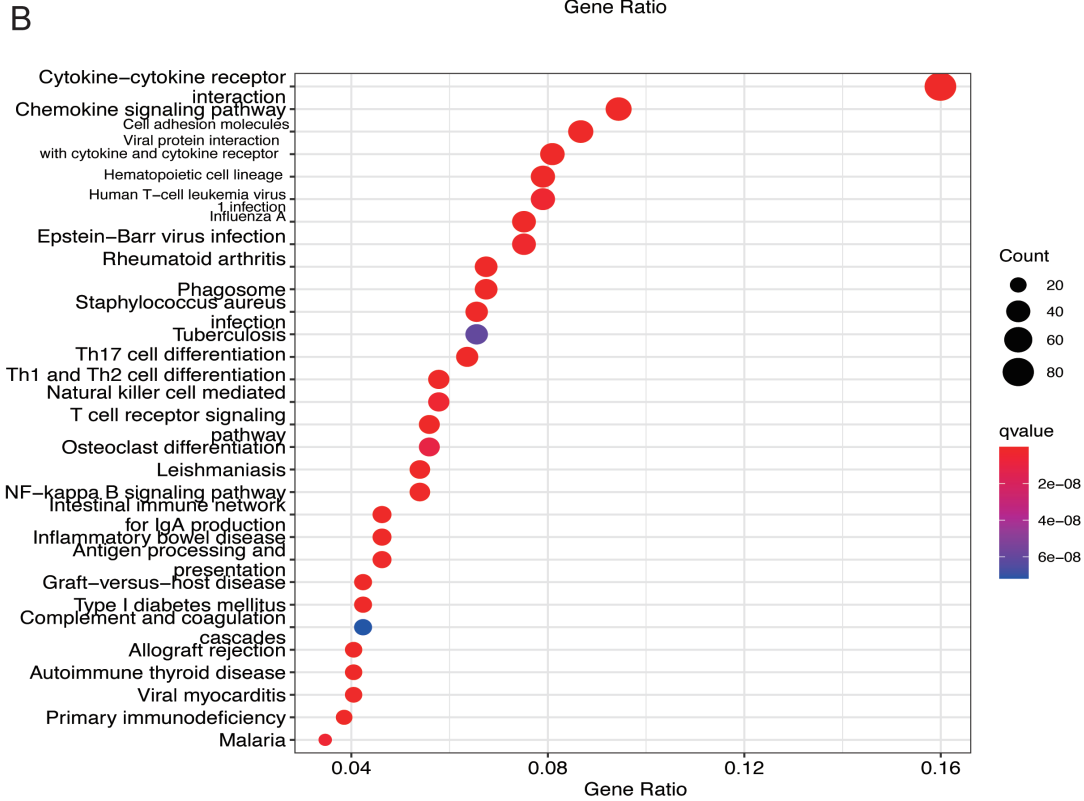
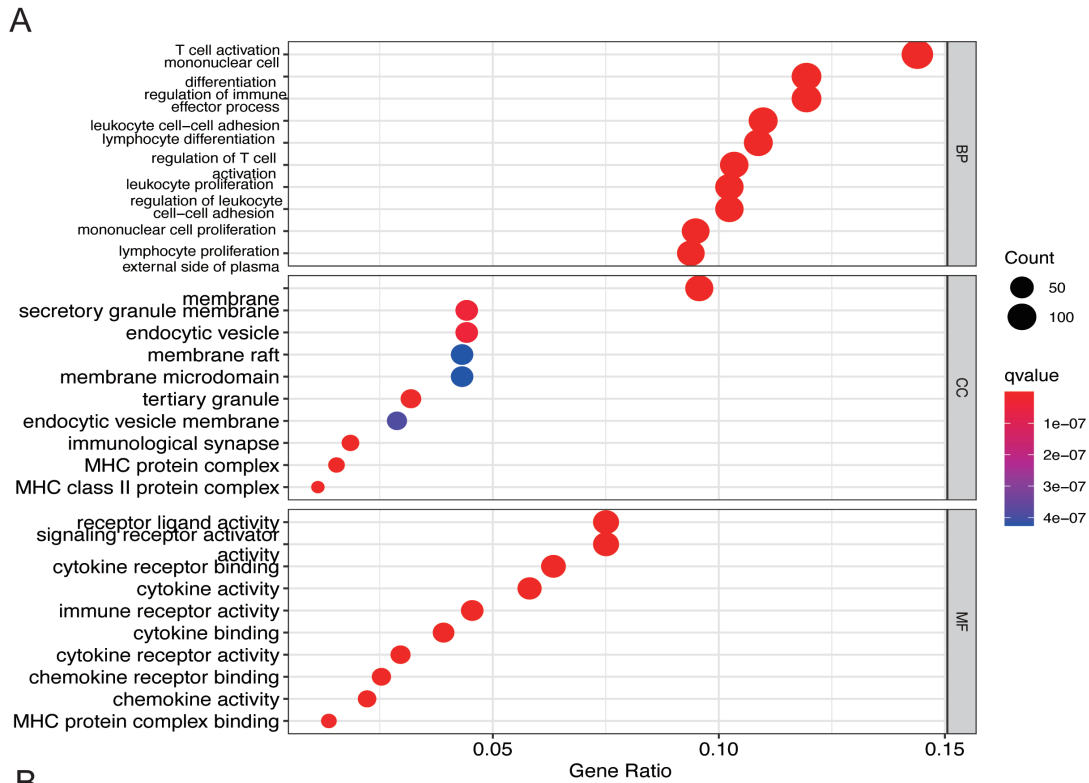


Figure S2 Immunological pathway analysis. (A) Bubble diagram of Gene Ontology (GO) pathways; (B) bubble diagram of Kyoto Encyclopedia of Genes and Genomes (KEGG) pathways.

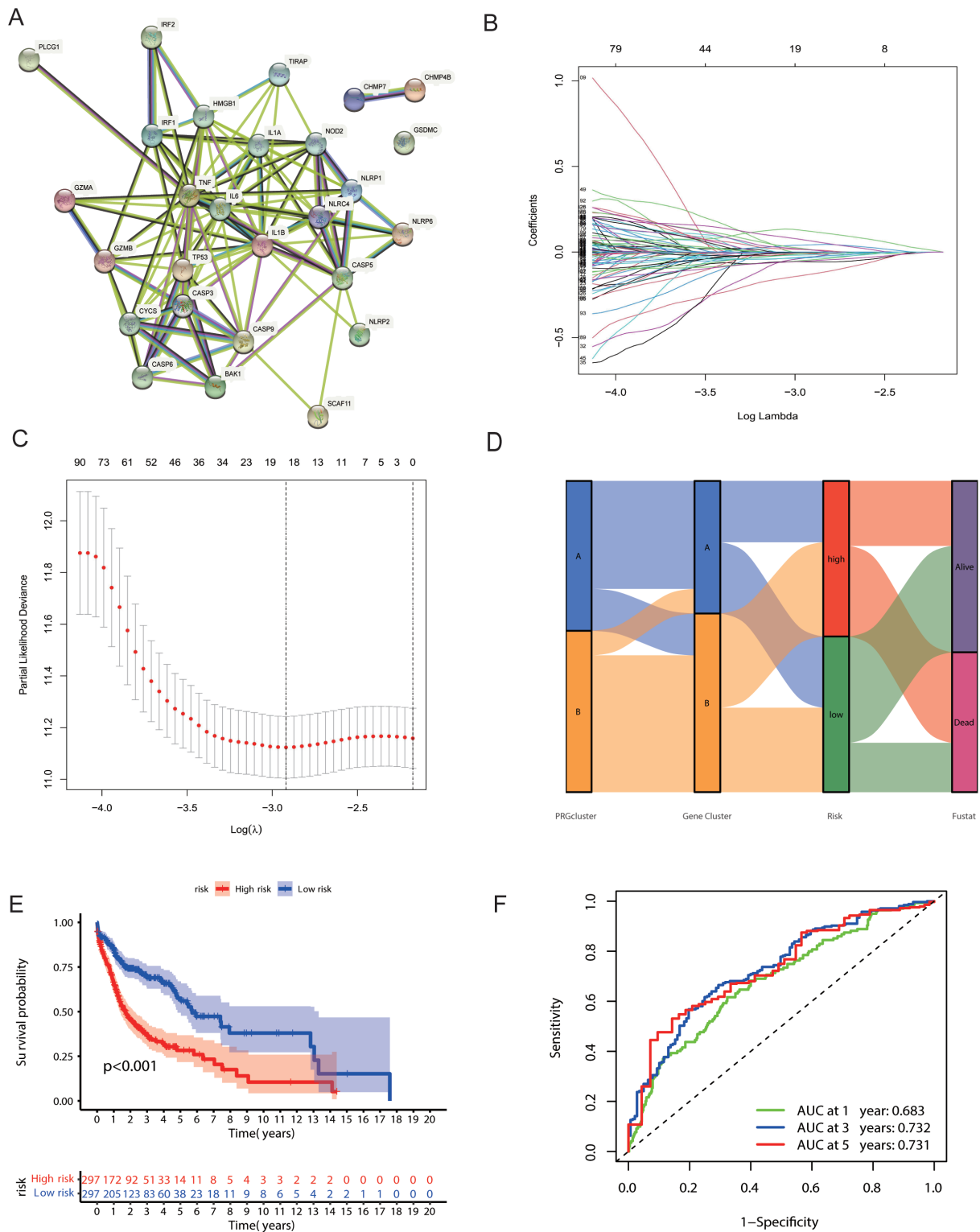


Figure S3 Analysis of prognostic models. (A) Protein-protein interaction (PPI) diagram of prognostic pyroptosis-related differentially expressed genes (DEGs); (B) LASSO regression graph of the prognostic model; (C) Lambda. minimum as the critical value of the prognostic model; (D) Sangqi diagram of the prognostic model; (E) survival curve of all groups; (F) receiver operating characteristic (ROC) curve of all groups. AUC, area under the curve.

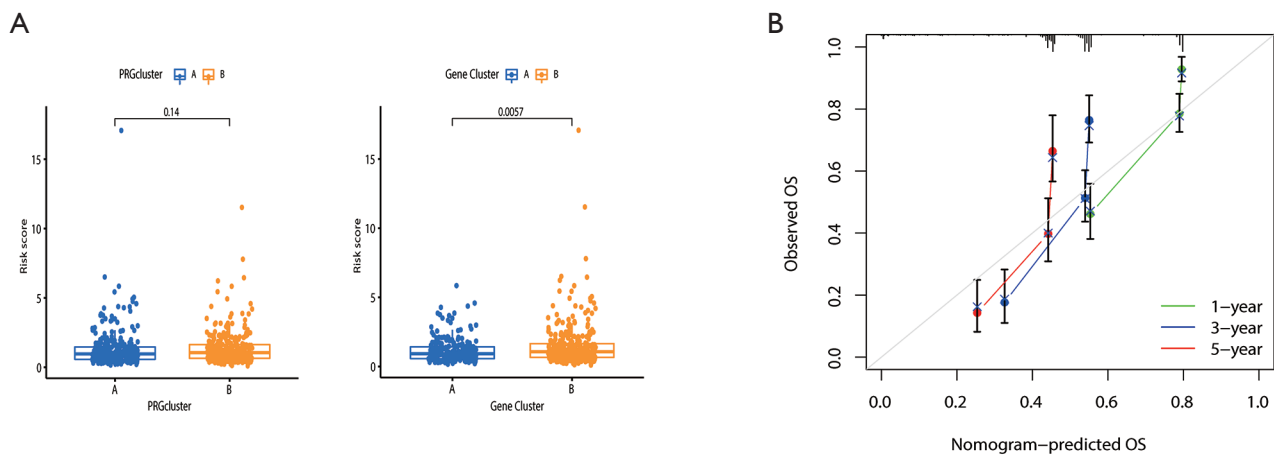


Figure S4 Clinical analysis of the prognostic models. (A) Risk score of the pyroptosis-related-gene (PRG) clusters and gene clusters; (B) predicted 1-, 3-, and 5-year survival calibration curve.

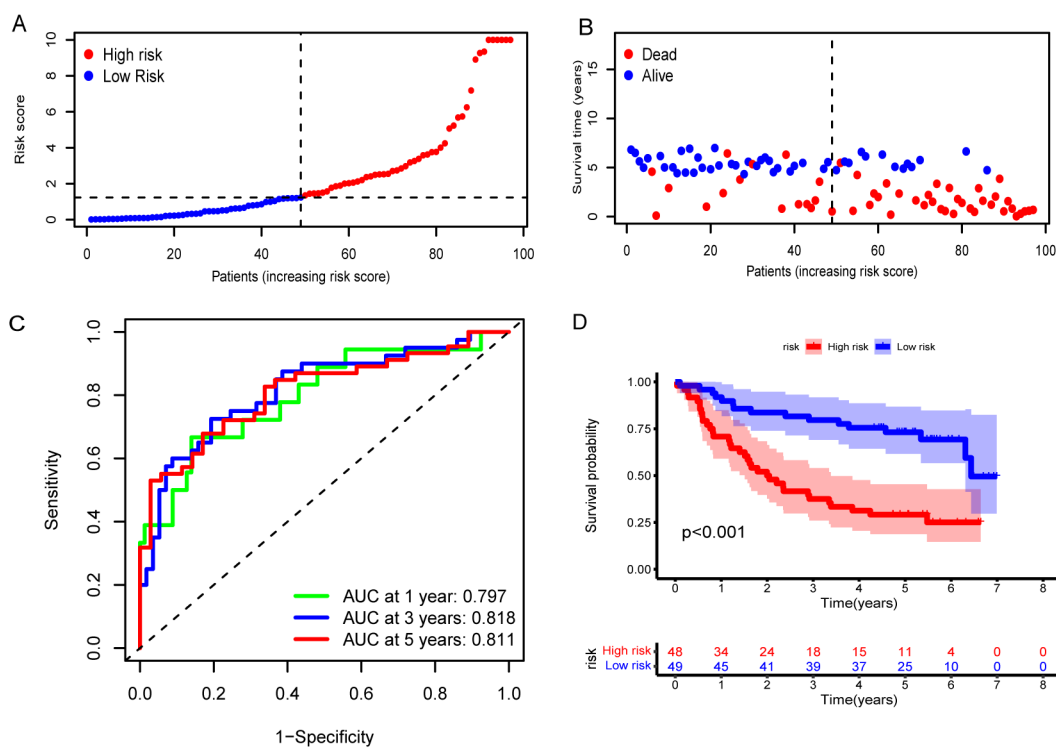


Figure S5 External validation of GEO data. (A) Risk curve of survival-related genes in the validation group; (B) survival state diagram of the survival-related genes in the validation group; (C) ROC curve of the validation group; (D) survival curve of the validation group. AUC, area under the curve; GEO, Gene Expression Omnibus; ROC, receiver operating characteristic.

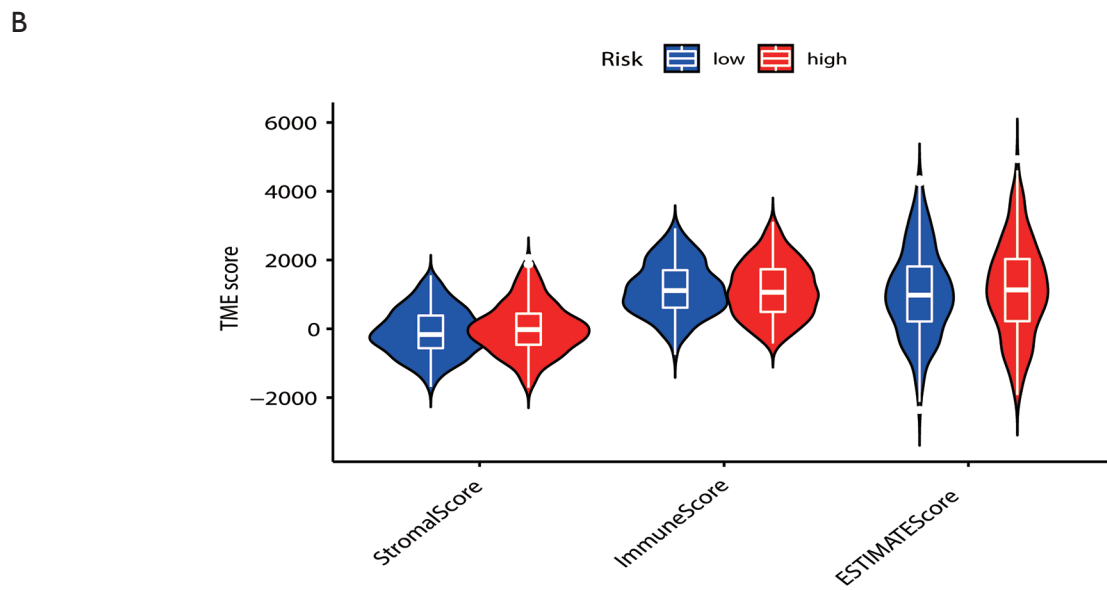
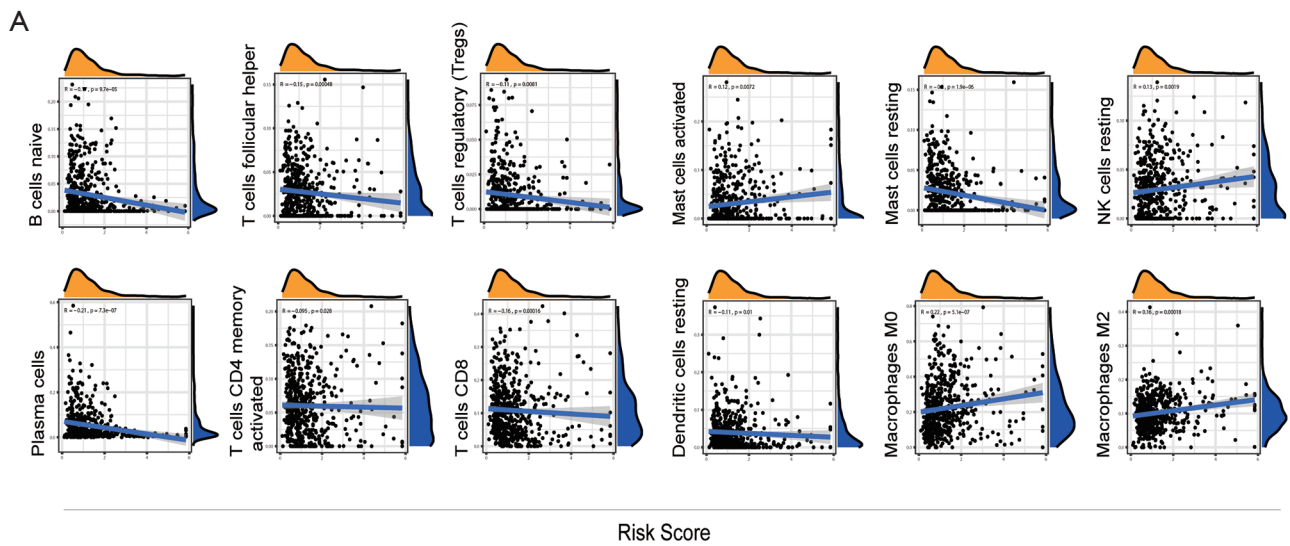


Figure S6 Analysis of the immune microenvironment of the prognostic models. (A) Correlation graph between the risk score and each immune cells; (B) differential analysis of tumor immune microenvironment. TME, tumor microenvironment.

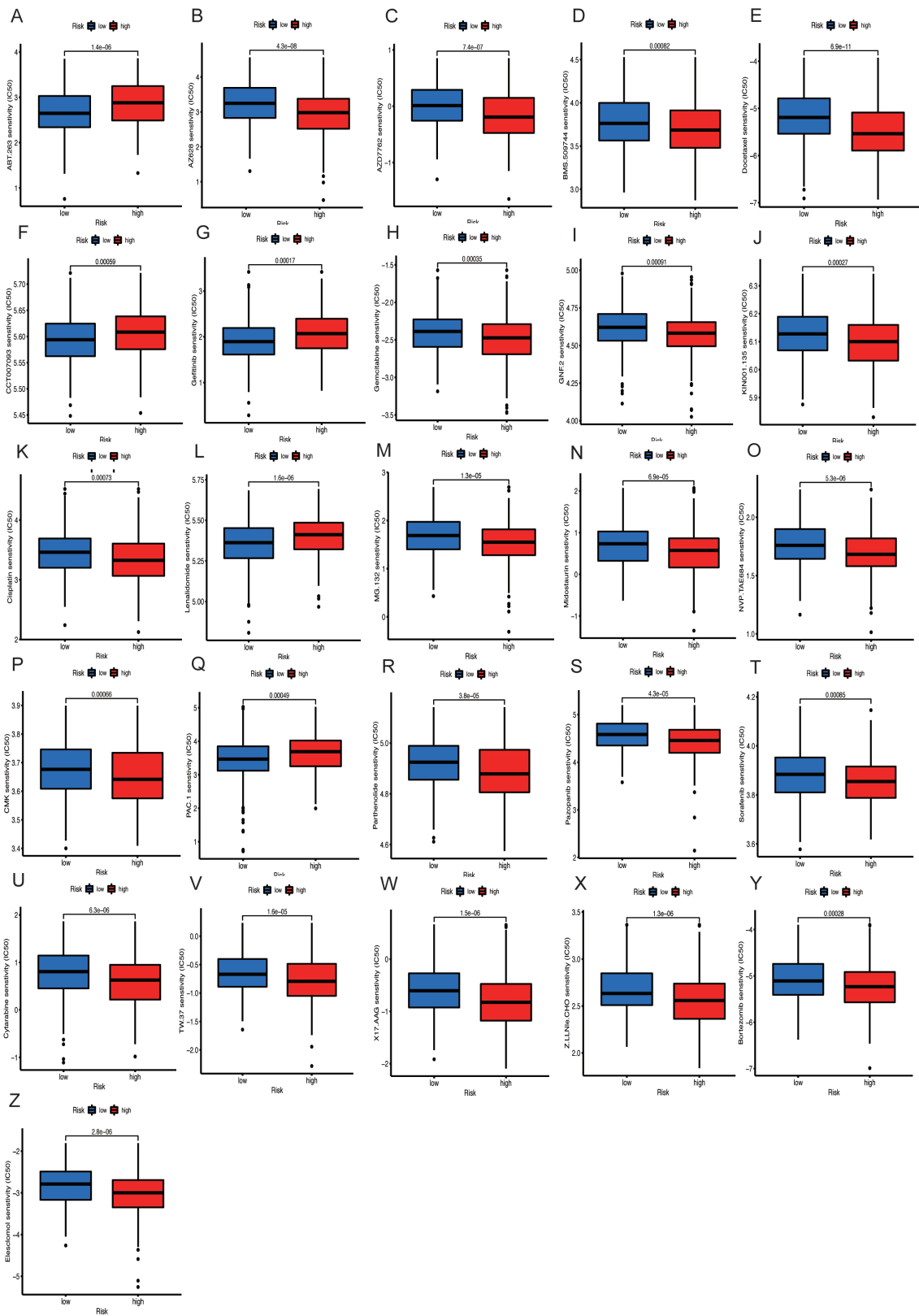


Figure S7 Analysis of differences in drug sensitivity. (A-Z) Analysis of differences in drug sensitivity between the high- and low-risk groups.