

Figure S1 Subgroups defined by the level of FRG expression. (A) Analyzing the expression levels of FRGs and the subtype-specific clinical characteristics using a heatmap; (B) comparison of clusters B and C using the GSVA.

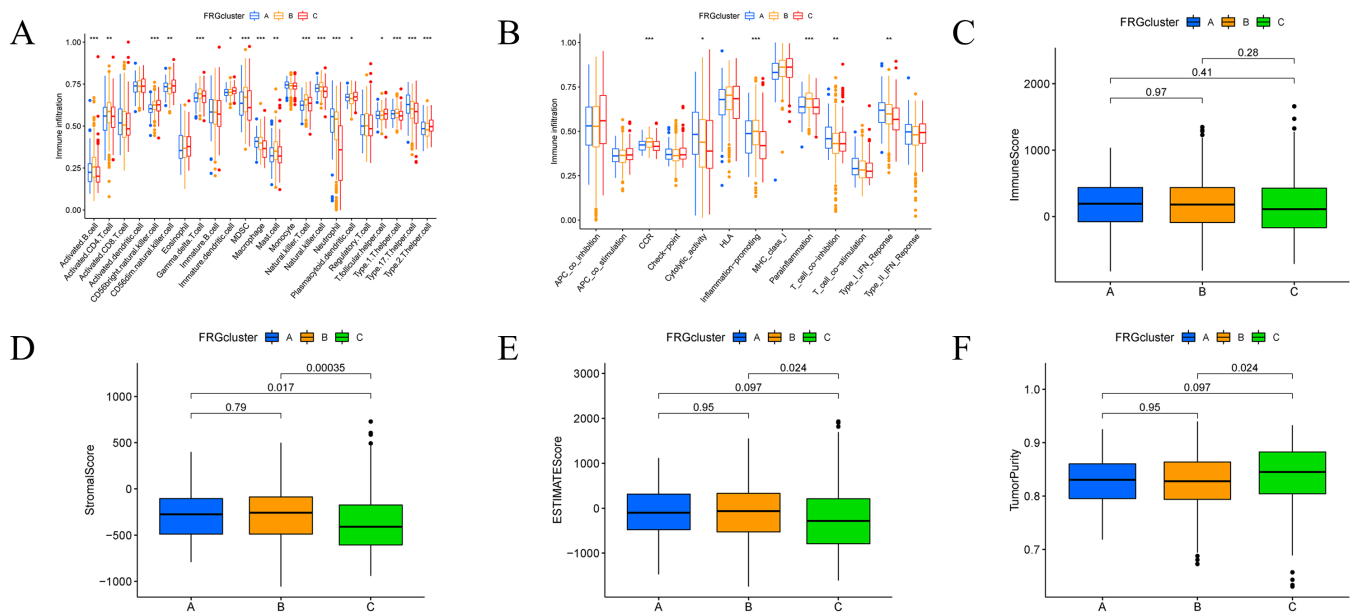


Figure S2 Subgroups defined by the level of FRG expression. (A) Infiltration of immune cells in three FRGclusters as measured by ssGSEA; (B) analysis of immune function in three FRGclusters using ssGSEA; C-F Scores for the TME derived from the ESTIMATE algorithm in three FRGclusters. *, P<0.05; **, P<0.01; ***, P<0.001.

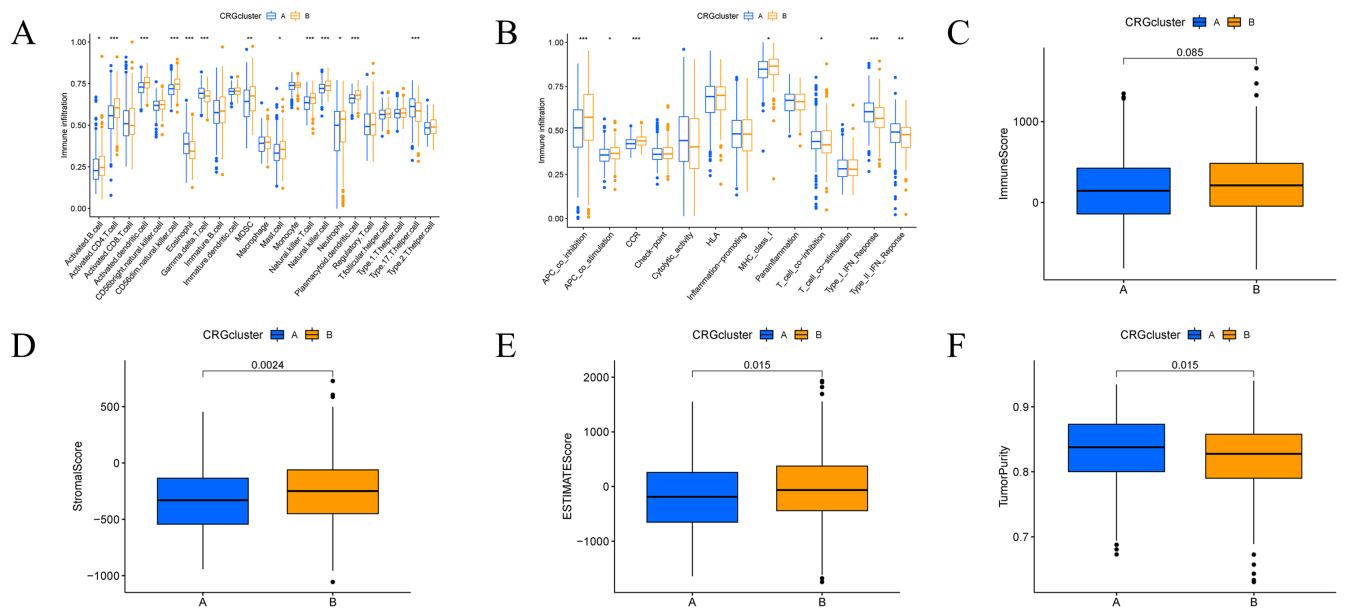


Figure S3 Subgroups defined by the level of CRG expression. (A) Infiltration of immune cells in three CRGclusters as measured by ssGSEA; (B) analysis of immune function in three CRGclusters using ssGSEA; (C-F) scores for the TME derived from the ESTIMATE algorithm in two CRGclusters. *, P<0.05; **, P<0.01; ***, P<0.001.

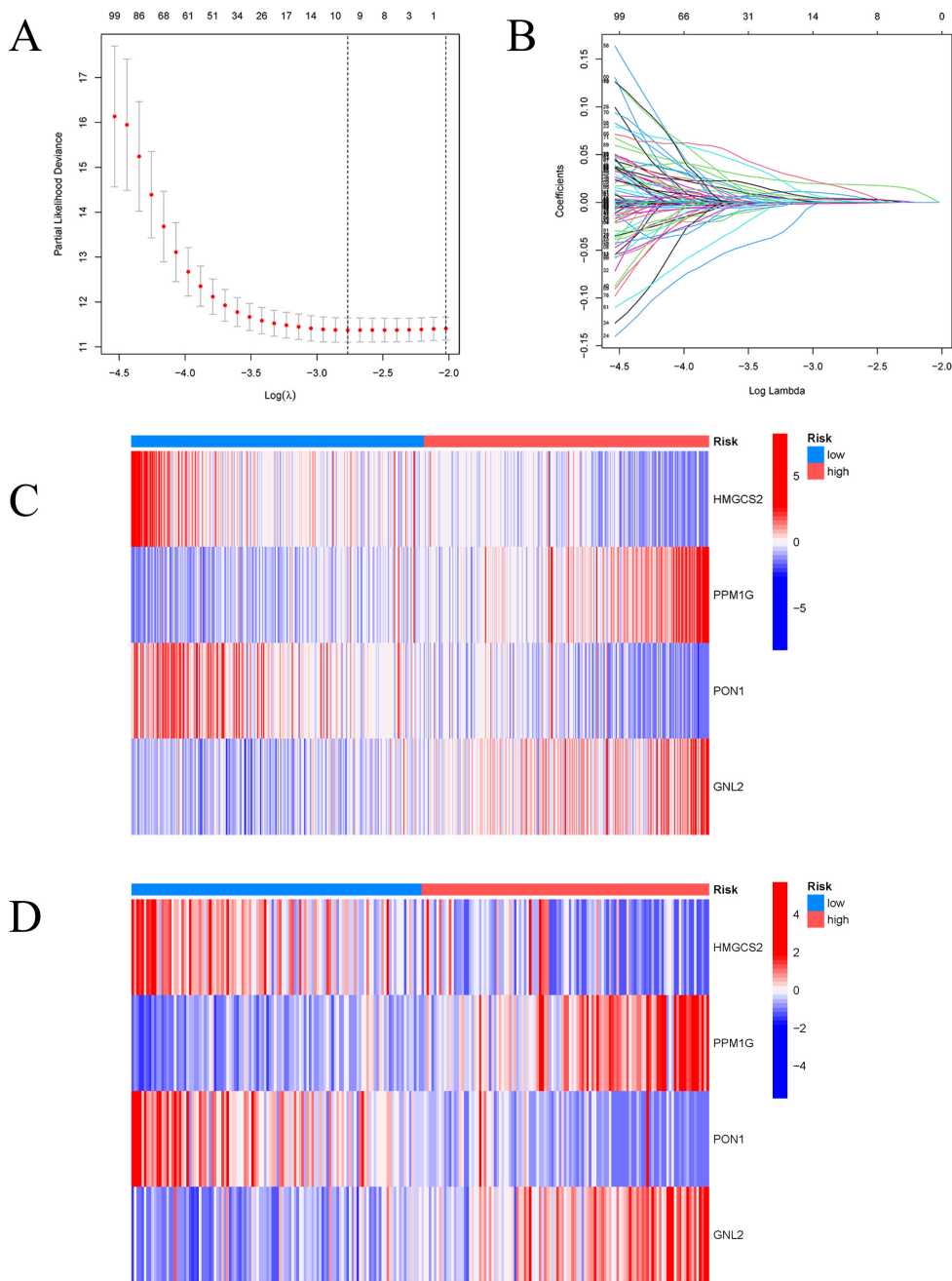


Figure S4 Construction of a prognostic signature of HCC. (A) The LASSO coefficient distribution of genes related with cuproptosis and ferroptosis. (B) The 10-fold cross validation of variable selection in LASSO algorithm. (C) Comparison of the two groups' expression of the model genes in TCGA-GEO cohort. (D) Comparison of the two groups' expression of the model genes in ICGC cohort.

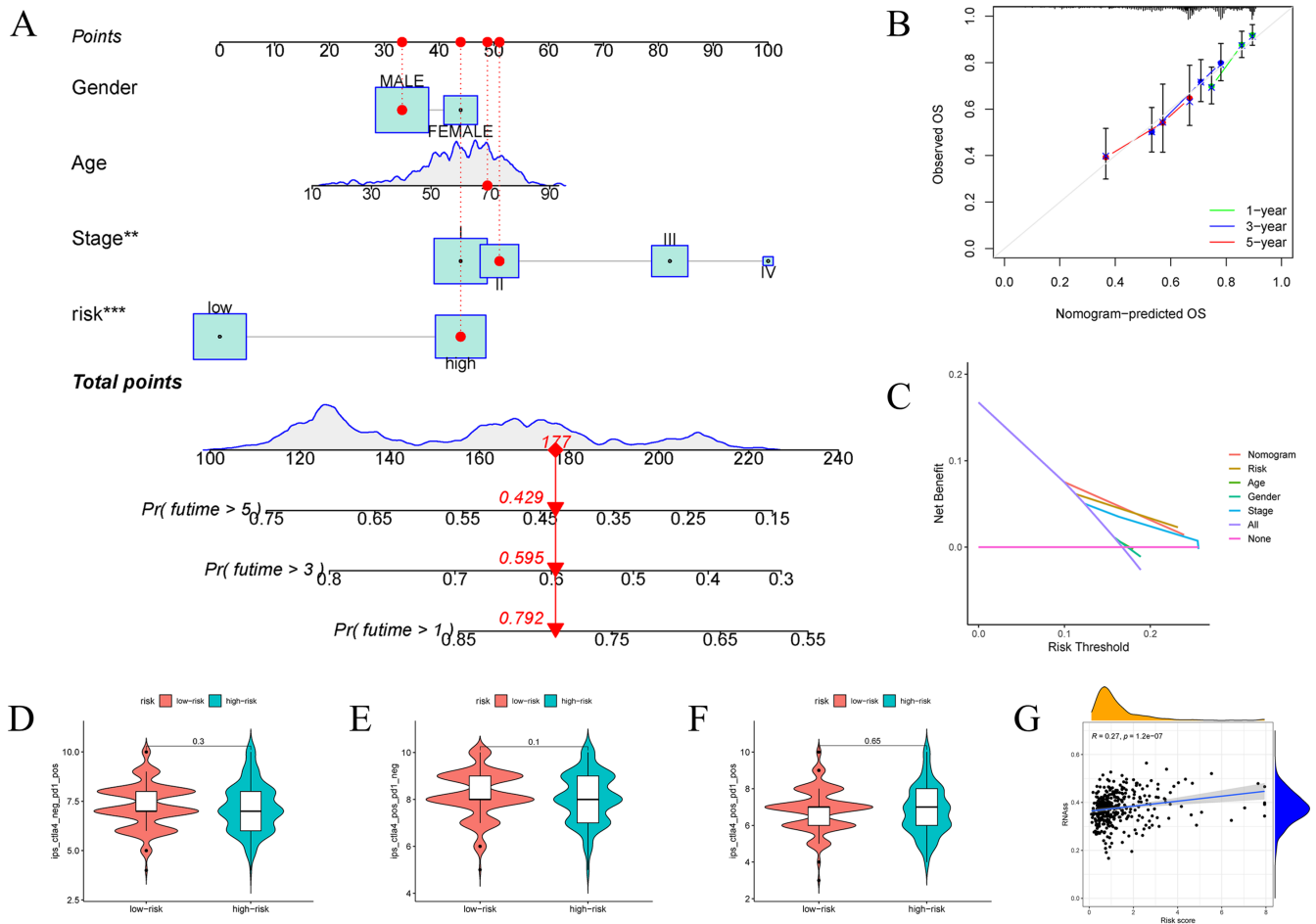


Figure S5 Establishment of a nomogram. (A) 1-, 3-, or 5-Year Prediction of OS Using a Nomogram; (B) the calibration curves; (C) DCA curve; (D-F) comparative analysis of the IPS of ips_ctla4_neg_pd1_pos; ips_ctla4_pos_pd1_neg; ips_ctla4_pos_pd1_pos; (G) the connection between risk score and cancer stem cell index. **, $P < 0.01$; ***, $P < 0.001$.

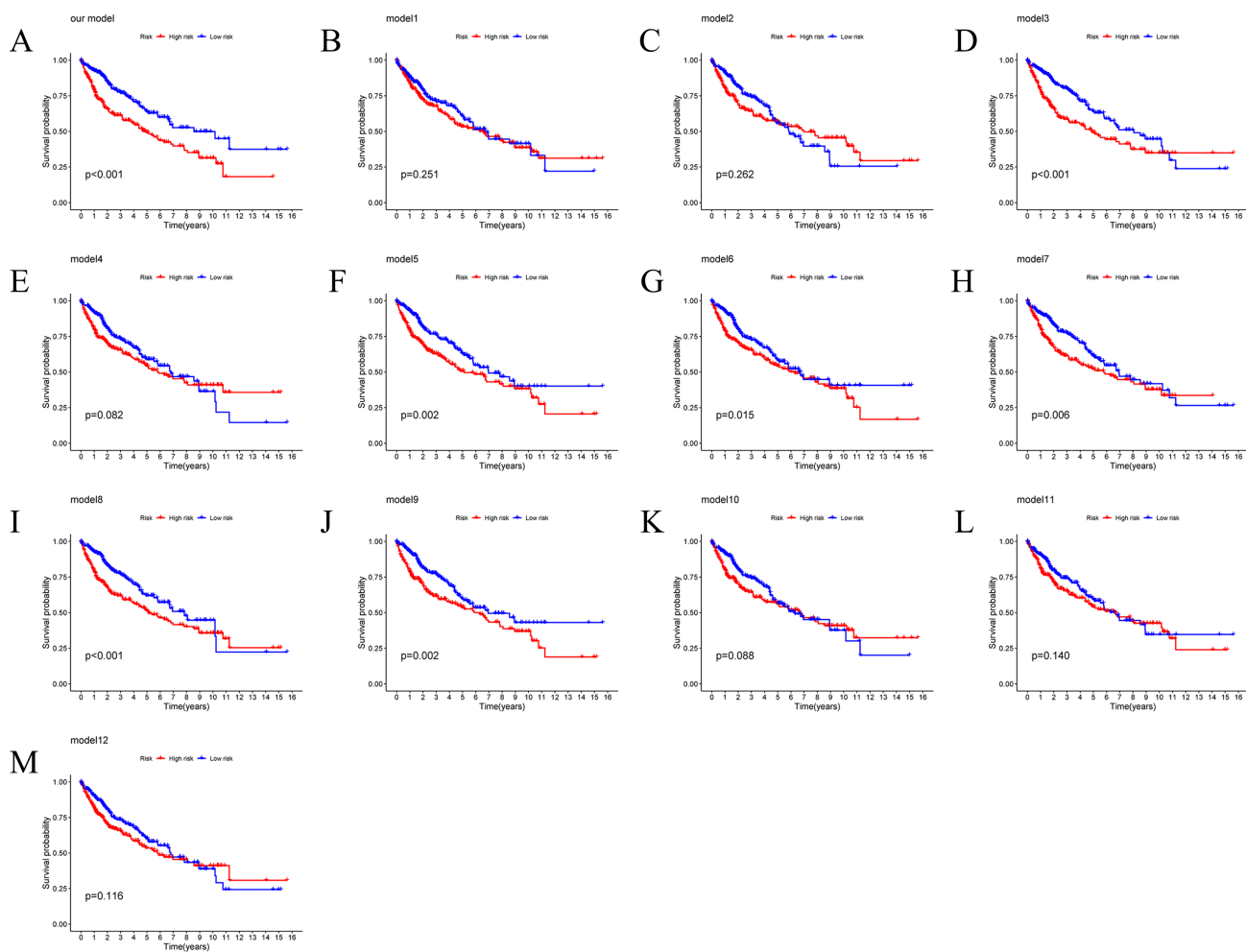


Figure S6 Comparison with other models. (A-M) Kaplan-Meier survival analysis of 13 models.