

Figure S2. GO and KEGG enrichment analysis. (A) GO enrichment analysis. (B) KEGG enrichment analysis. GO, Gene Ontology; KEGG, Kyoto Encyclopedia of Genes and Genomes.

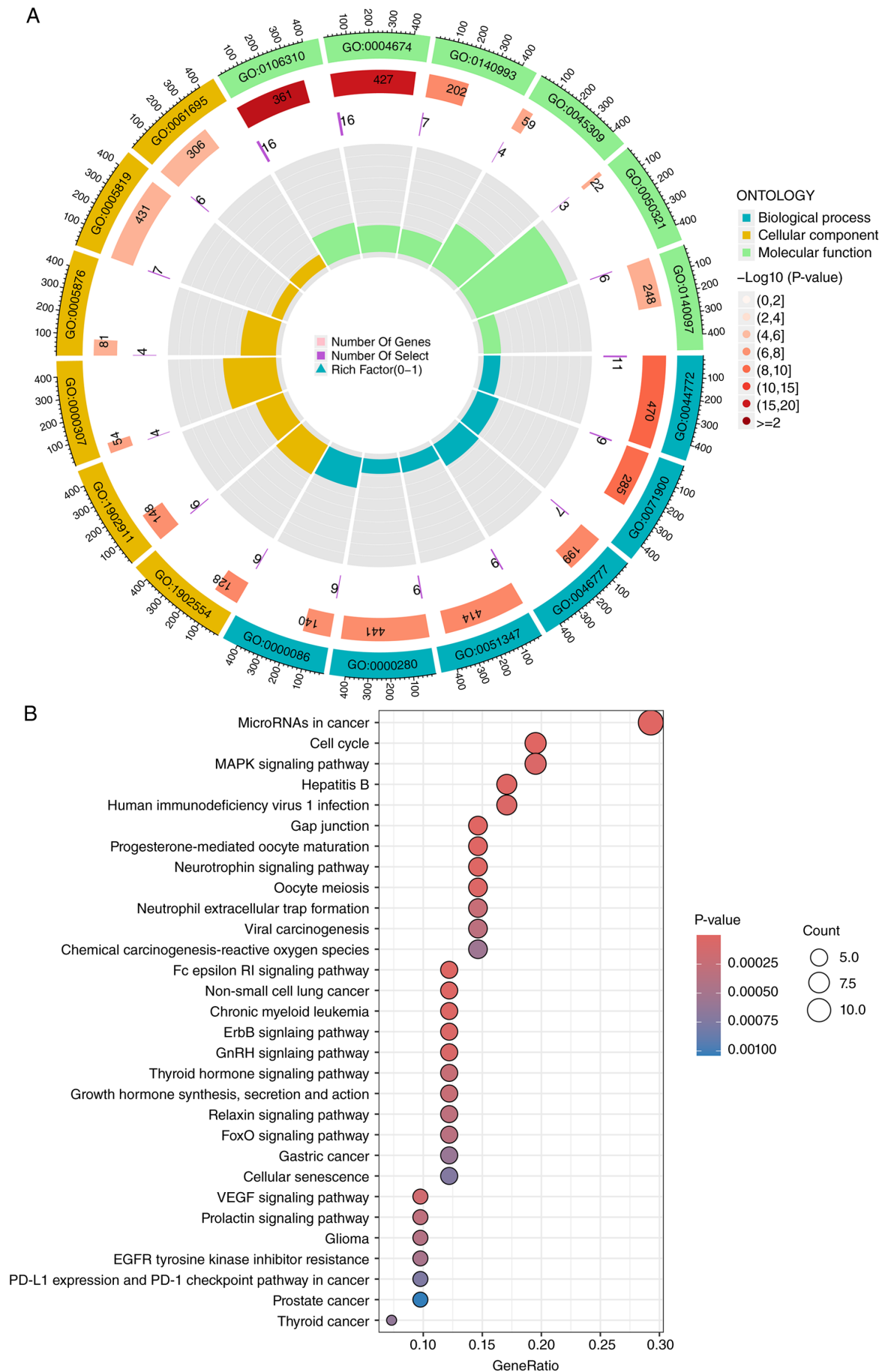


Figure S4. Univariate and multivariate Cox regression analyses in The Cancer Genome Atlas and survival curves of prognostic marker genes. (A) AURKB low expression is associated with better survival. (B) FKBP1A low expression is associated with better survival. (C) HMBS low expression is associated with better survival. (D) NQO1 low expression is associated with better survival. (E) EZH2 low expression is associated with better survival. (F) XRCC1 low expression is associated with better survival. (G) Univariate Cox regression analysis. (H) Multivariate Cox regression analysis. (I) Decision curve analysis for evaluating the clinical utility of the prognostic model.

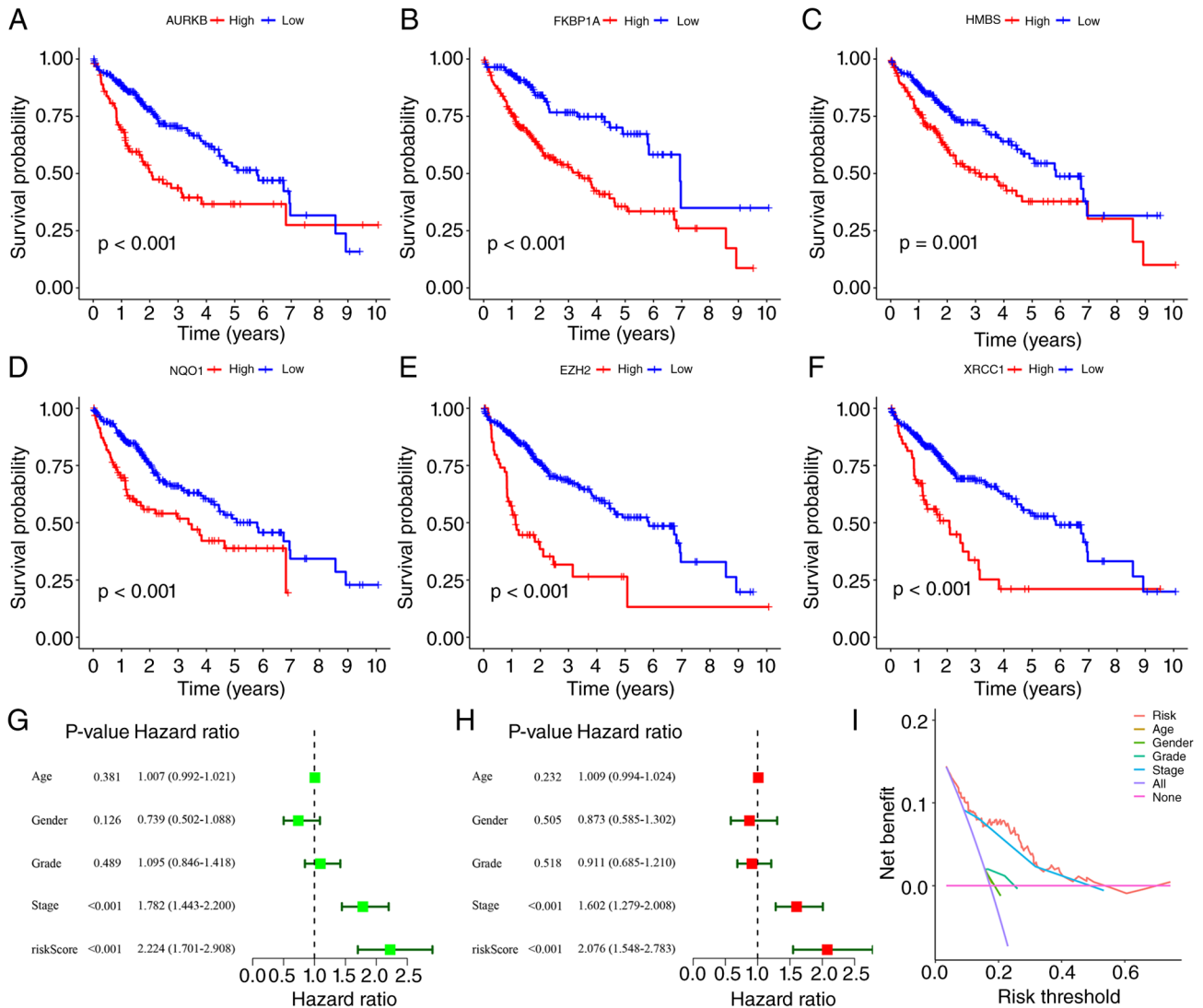


Figure S5. Validation of prognostic signature in the International Cancer Genome Consortium dataset. (A) Heatmap of signature gene expression. (B) ROC curves for predicting 1-, 2- and 4-year survival. (C) ROC curve of clinical features for predicting survival. (D) Kaplan-Meier survival curve. (E) Risk curve. (F) Univariate Cox regression analysis. (G) Multivariate Cox regression analysis. ROC, receiver operating characteristic; AUC, area under ROC curve.

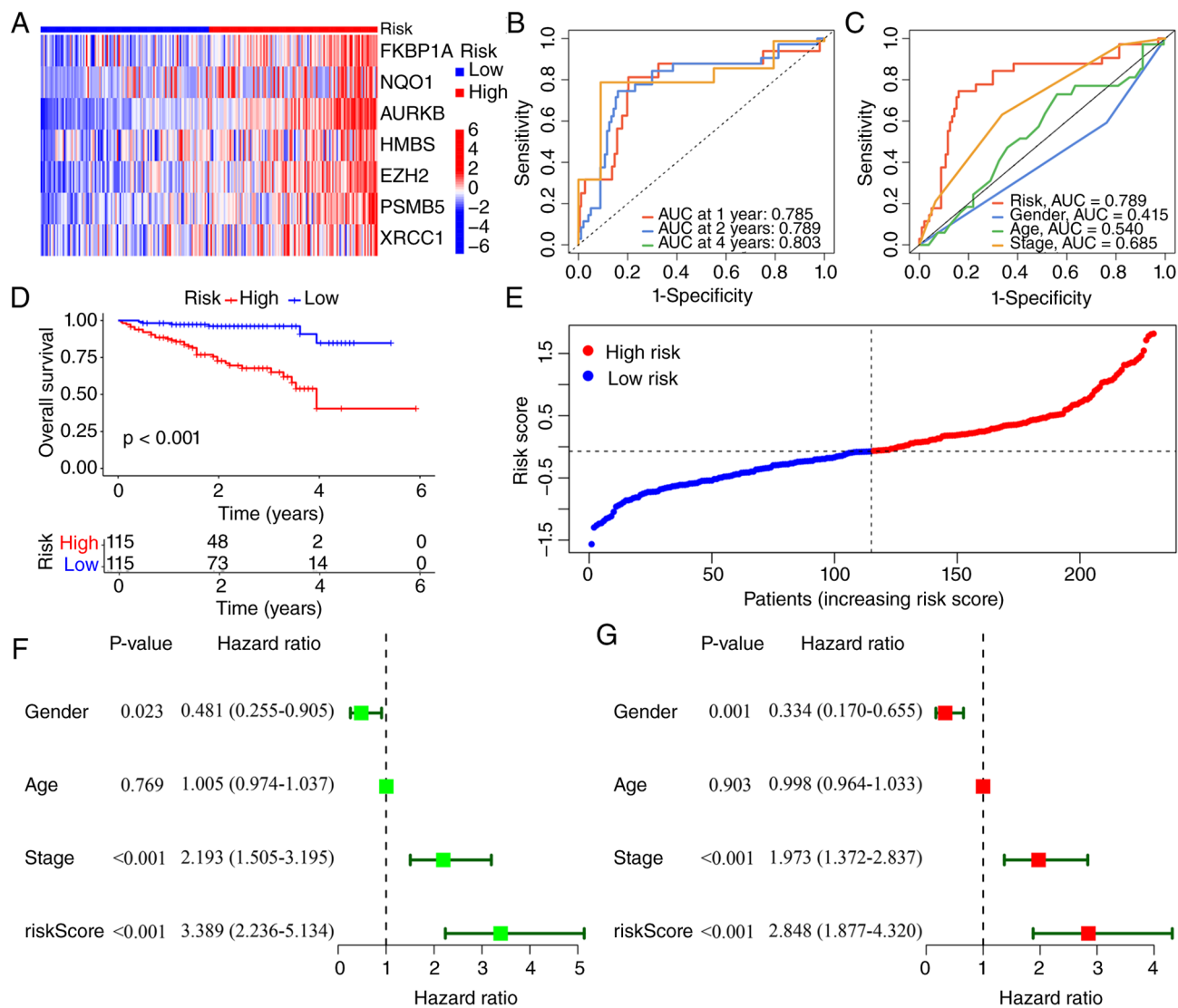


Figure S6. Validation of prognostic signature in GSE14520 gene set. (A) Heatmap of signature gene expression. (B) ROC curves for predicting 1-, 2- and 4-year survival. (C) ROC curve of clinical features for predicting survival. (D) Kaplan-Meier survival curve. (E) Risk curve. (F) Univariate Cox regression analysis. (G) Multivariate Cox regression analysis. ROC, receiver operating characteristic; AUC, area under ROC curve.

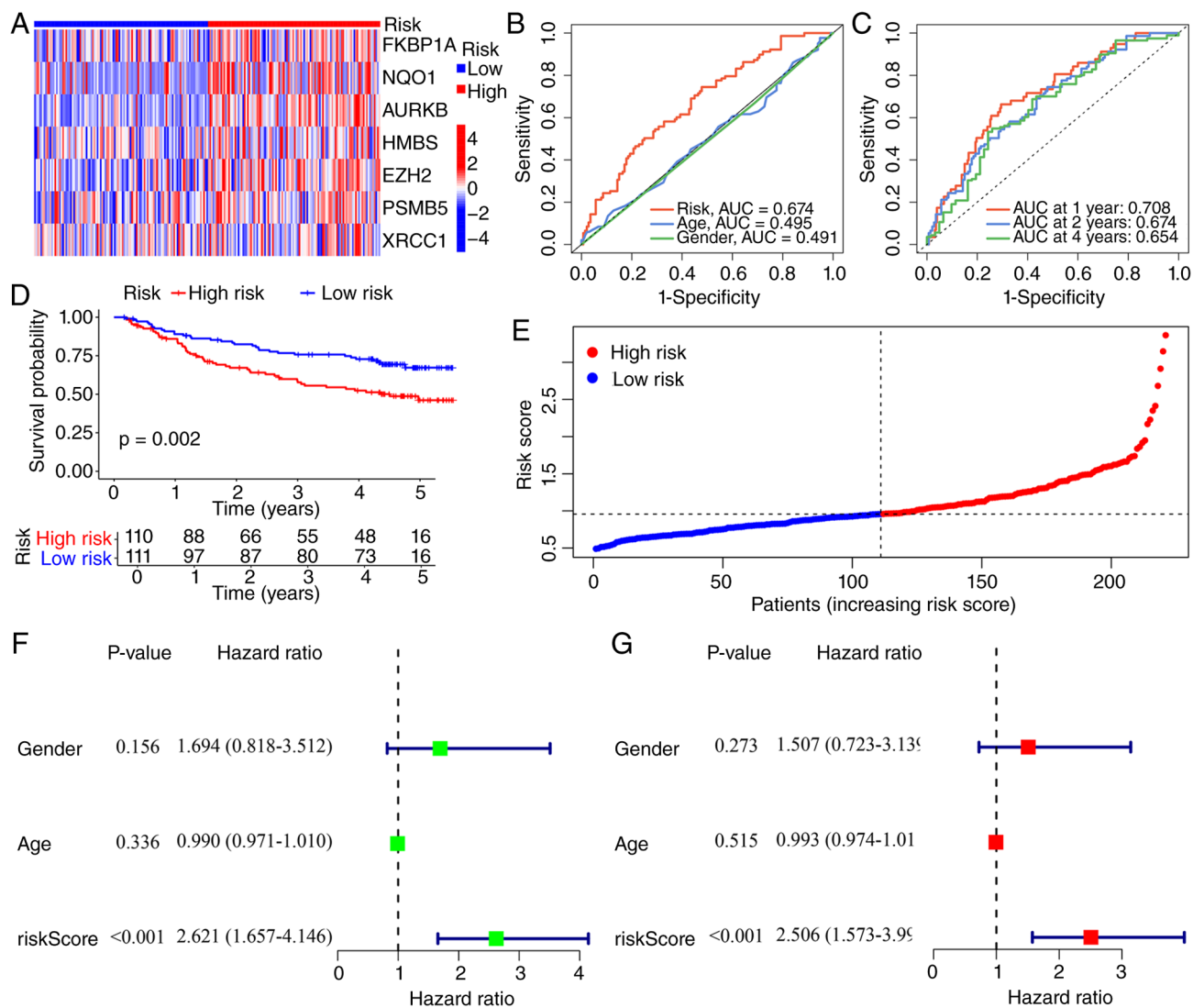


Figure S7. Construction of nomograms. (A) C-index of the diagnostic nomogram. (B) C-index of the prognostic nomogram. (C) The diagnostic nomogram. (D) The prognostic nomogram. (E) DCA analysis of the diagnostic nomogram. (F) DCA analysis of the prognostic nomogram. (G) DCA analysis of the prognostic nomogram and risk score. OS, overall survival. * $P < 0.05$; ** $P < 0.01$; *** $P < 0.001$. DCA, decision curve analysis.

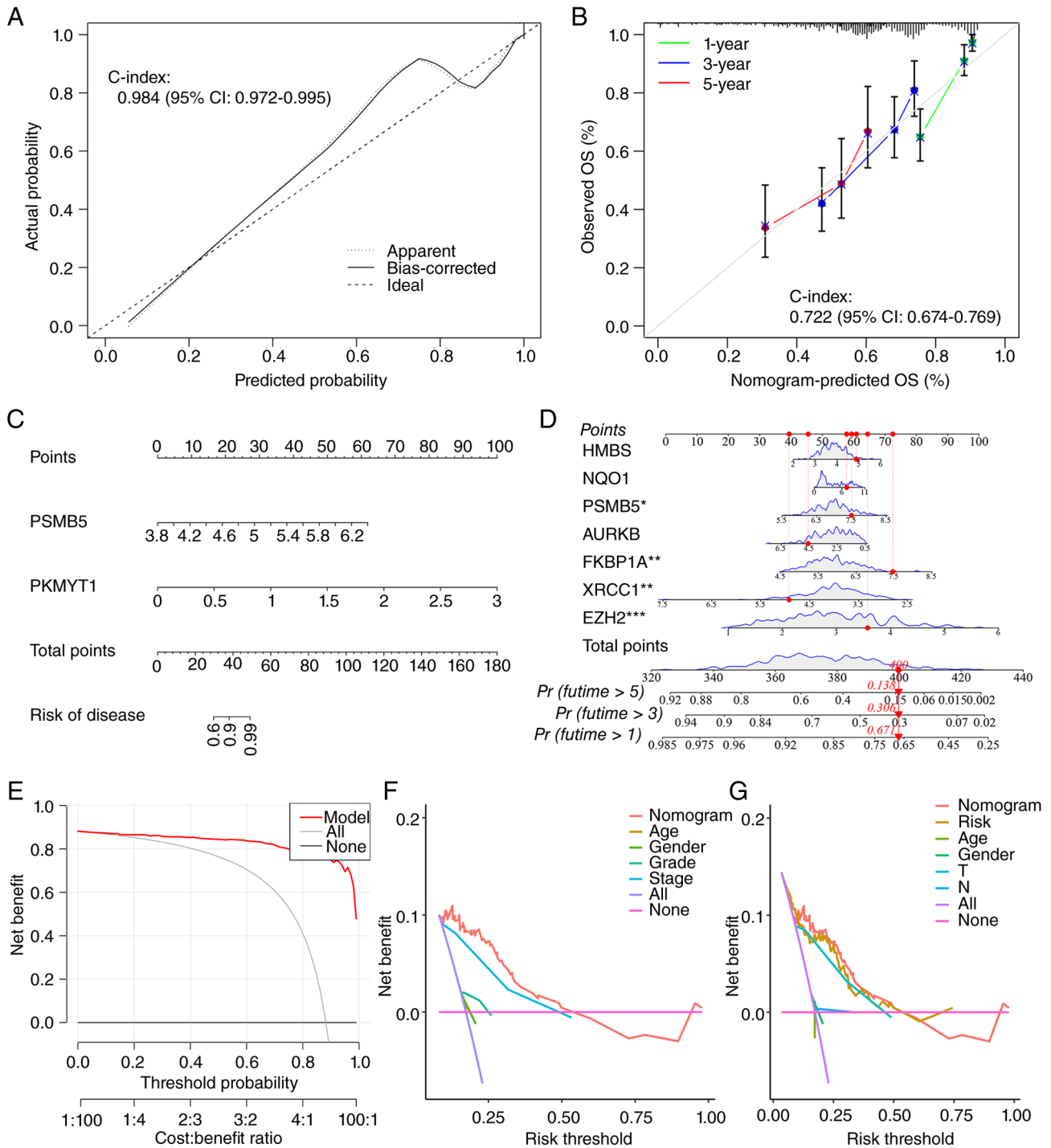


Figure S8. Analysis of the hub gene. (A) Venn diagram of the hub gene. (B) Overall survival analyses for PSMB5 expression in hepatocellular carcinoma. (C) Protein-protein interaction network and functions of PSMB5. RF, random forest; LASSO, least absolute shrinkage and selection operator; SVM-RFE, support vector machine-recursive feature elimination; StepCox[both], stepwise Cox regression with both-direction selection; SuperPC, supervised principal components; LIHC, liver hepatocellular carcinoma; PSMB5, proteasome 20S subunit beta 5; MHC, major histocompatibility complex; Fc, fragment crystallizable.

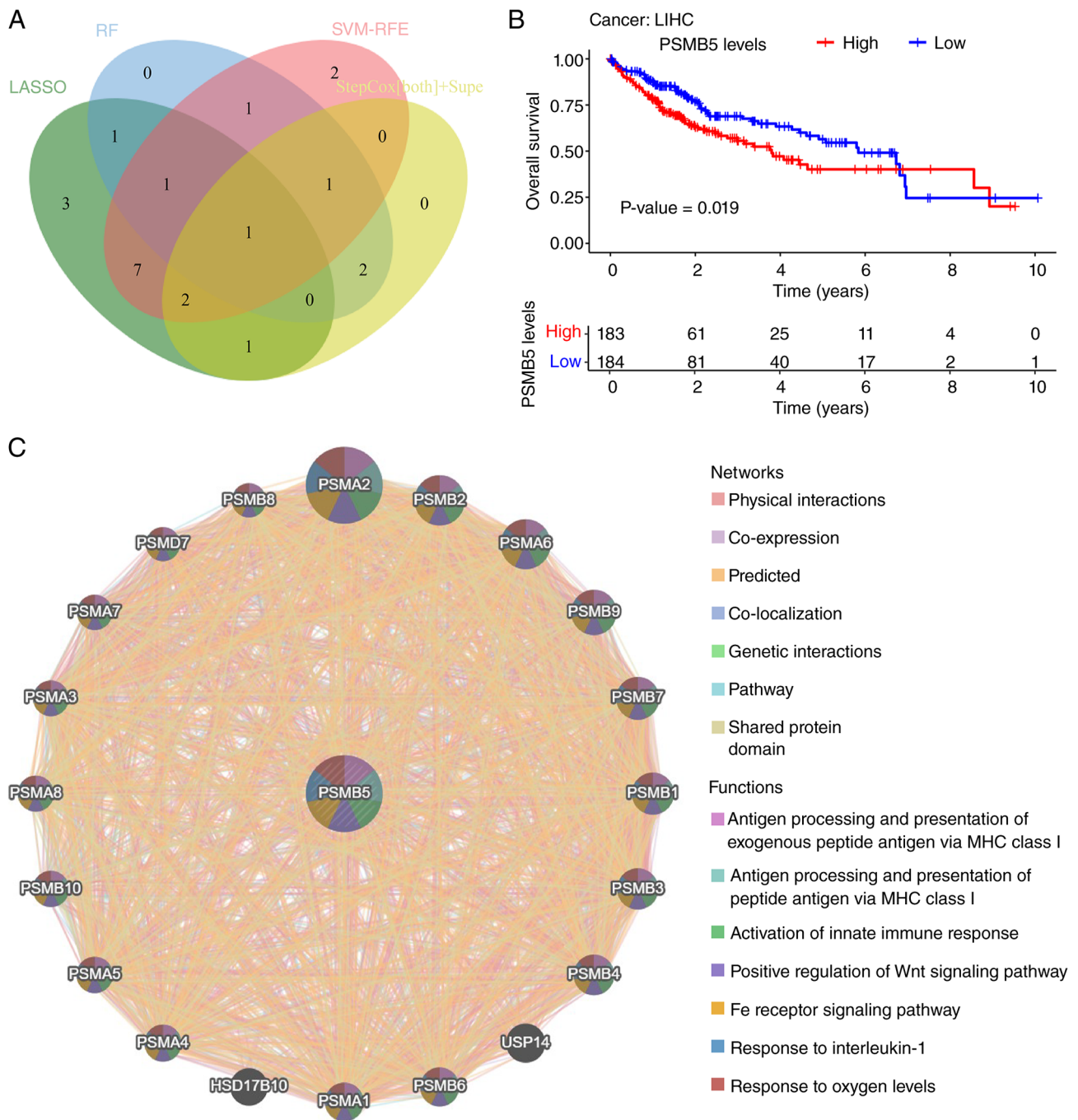


Figure S9. Single-cell RNA analyses. (A) 6 clusters determined at 0.2 resolution. (B) Sample clusters. (C) Harmony ElbowPlot. (D) MIF, CD74 and CXCR4 expression in cells. (E) PSMB5 expression in cells. UMAP, uniform manifold approximation and projection; MIF, macrophage migration inhibitory factor; CD74, cluster of differentiation 74; CXCR4, C-X-C motif chemokine receptor 4; PSMB5, proteasome 20S subunit beta 5; Treg, regulatory T cell.

