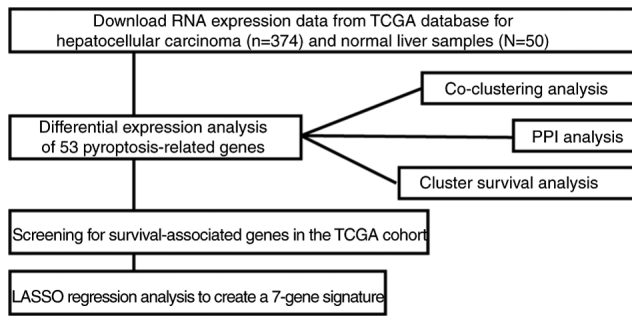Figure S1. Working steps for database analysis.

Figure S2. Expression levels and tumor clustering of genes associated with pyroptosis. (A) A heat map of differentially expressed genes associated with pyroptosis between normal and tumor tissues. (B) Protein-protein interaction network. (C) Association network (red: positive relationship; the thicker the line reflects stronger link). (D) Consensus clustering analysis (k=2). (E) Heatmap and pathologic characters of the two clusters. (F) Kaplan-Meier overall survival curves in both groups of patients. *P<0.05, **P<0.01 and ***P<0.001.
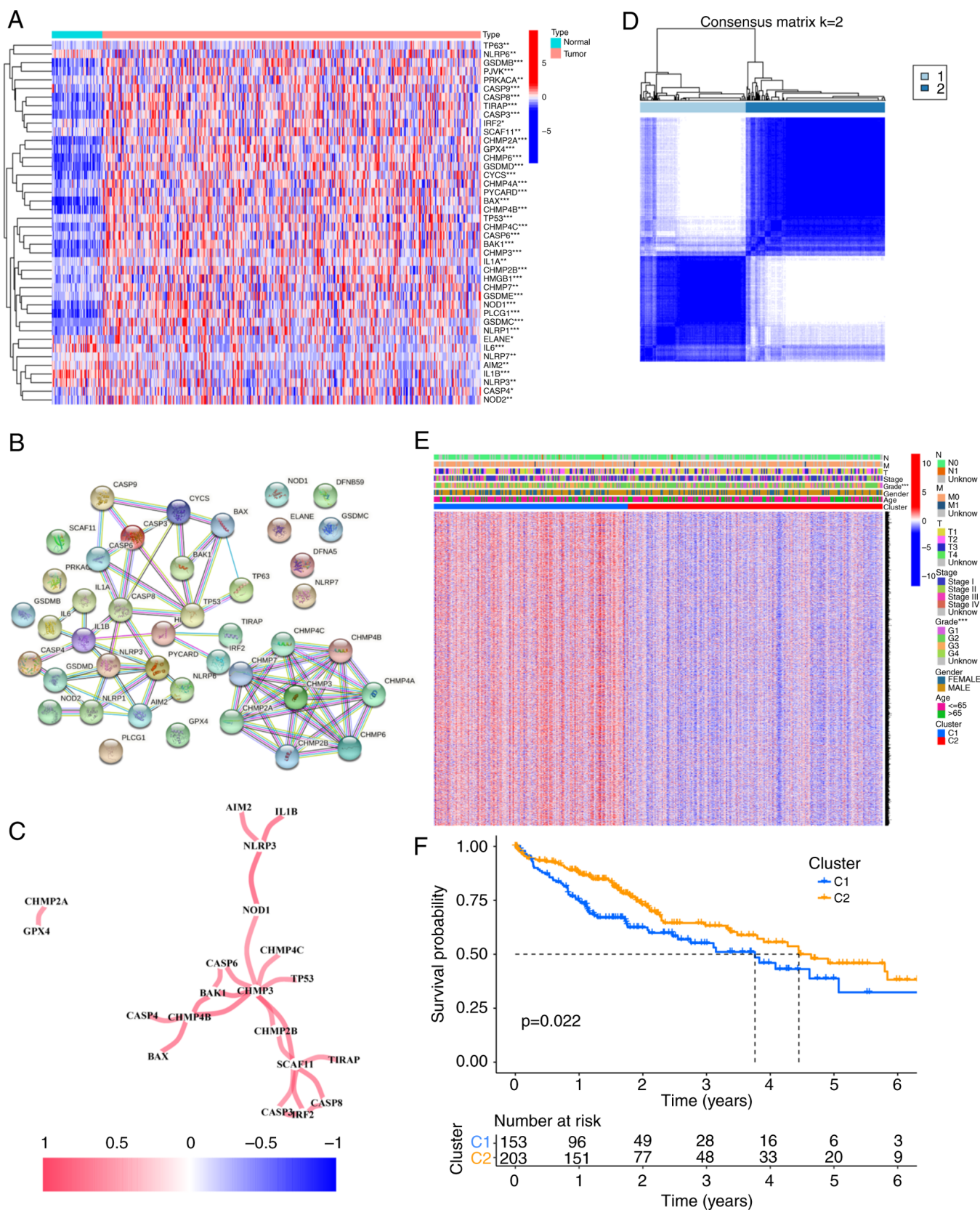
Figure S3. Construction of risk signature in The Cancer Genome Atlas cohort. (A) Univariate cox regression analysis of HCC for each pyroptosis-related gene, and 8 genes with P<0.05. (B and C) Least absolute shrinkage and selection operator regression analysis of the 7 overall survival-related genes. (D) Risk score-based patient clustering. (E) Principal Component Analysis plot for HCC based on the risk score. (F) The survival status of patients in both groups. (G) Kaplan-Meier curves for different subgroups of patients. (H) Receiver operating characteristic curves. HCC, hepatocellular carcinoma.
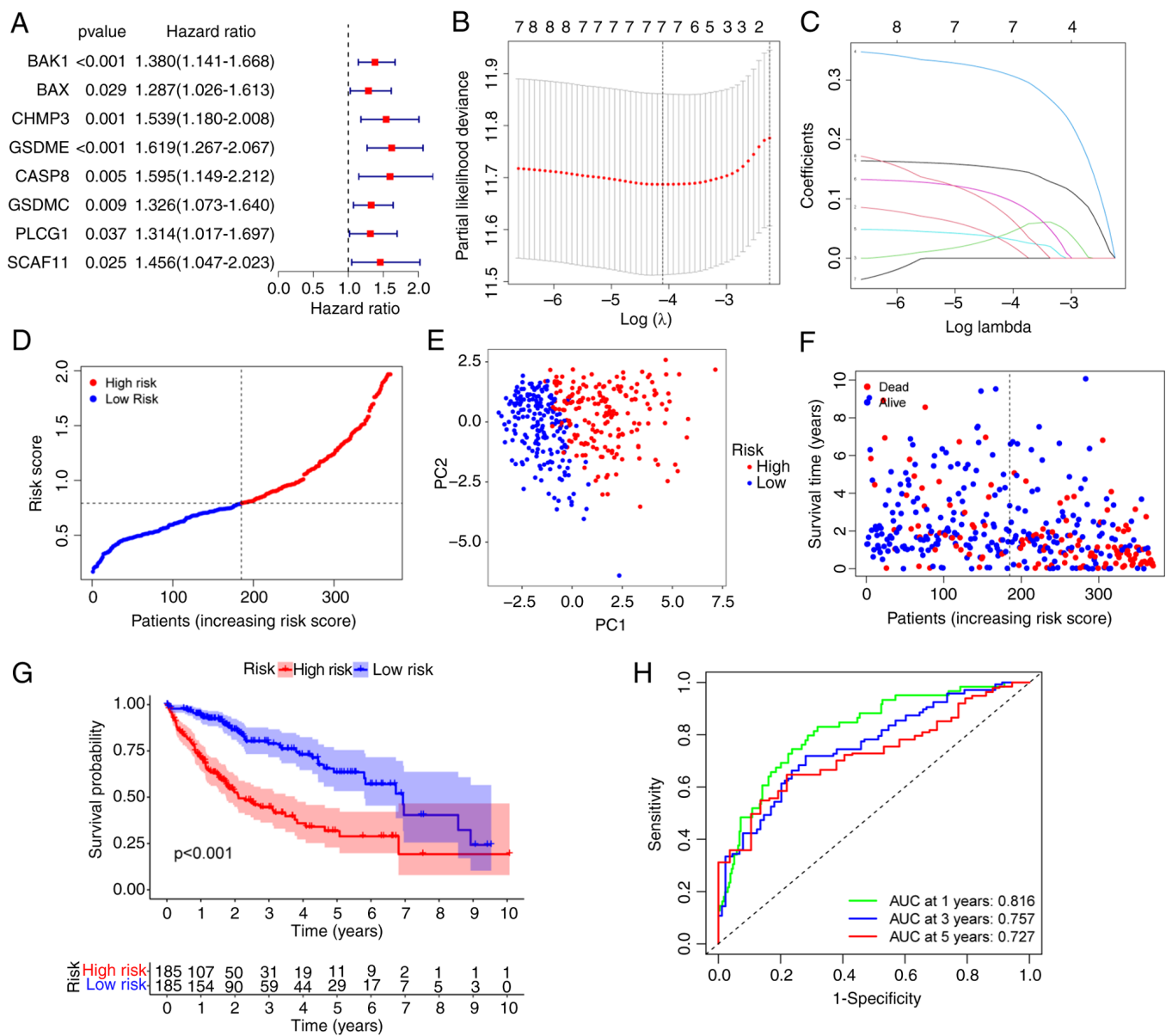
Figure S4. Univariate and multivariate Cox regression analyses for the risk score. (A) Univariate analysis. (B) Multivariate analysis. (C) A Heatmap for the connections between clinicopathologic features and the risk groups. *P<0.05, **P<0.01 and ***P<0.001.