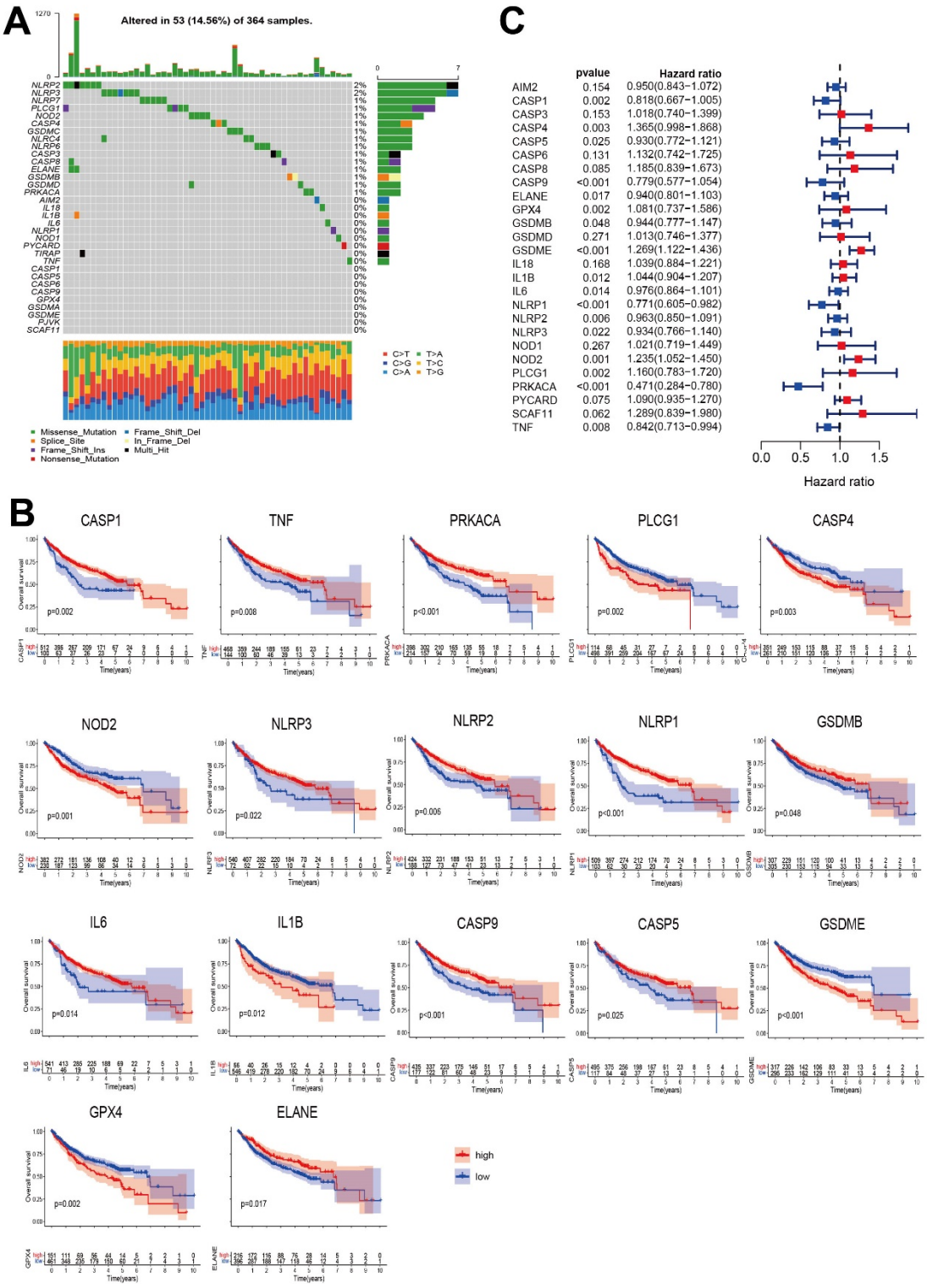
Supplemental Material:



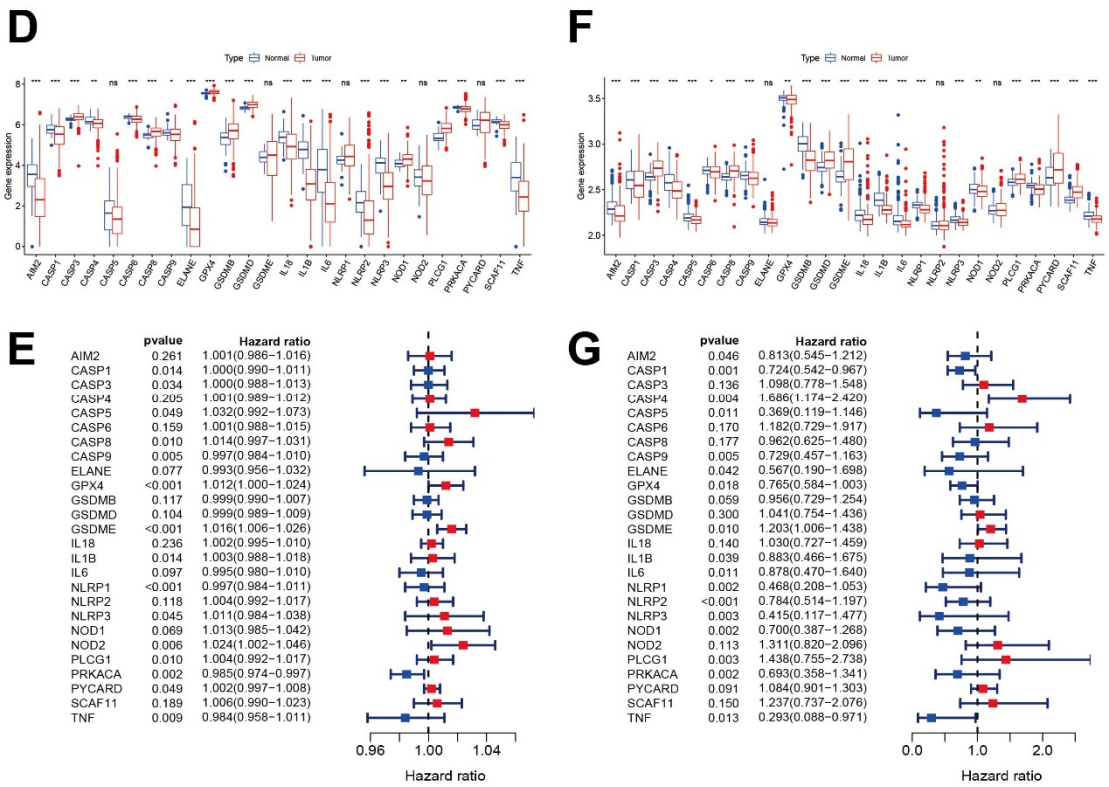
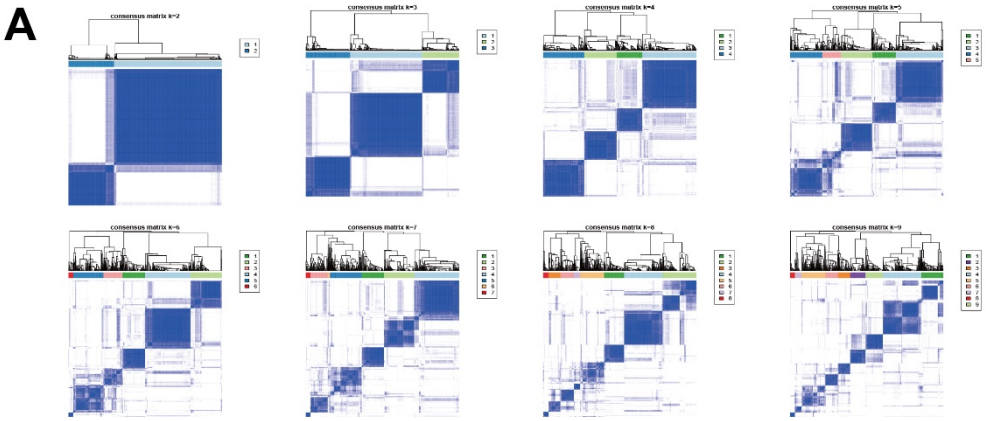
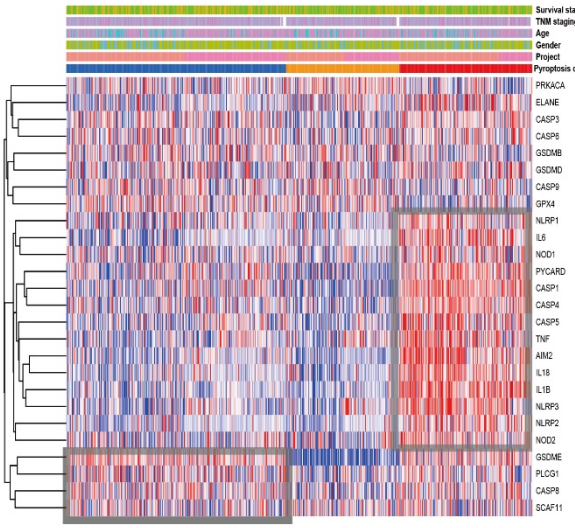
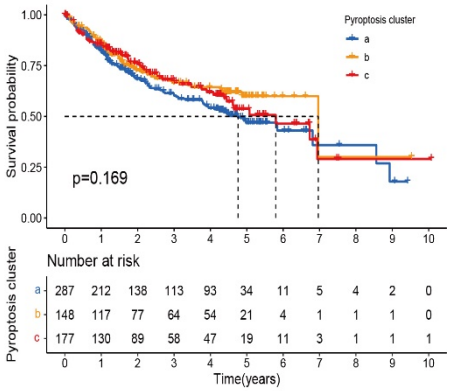


Figure S1. General overview of pyroptosis-related genes. (**A**) Somatic mutation features of each of the pyroptosis genes in TCGA cohort. (**B**) Kaplan-Meier survival analysis of patients with high- (red) and low- (blue) expression for each pyroptosis-related gene in all patients with clinical information available. CASP1, TNF, PRKACA, PLCG1, CASP4, NOD2, NLRP3, NLRP2, NLRP1, GSDMB, IL-6, IL-1B, CASP9, CASP5, GSDME,.GPX4, ELANE (all $p < 0.05$). (**C**) Forest plots based on the results of Kaplan-Meier analysis between gene expression level and overall survival in integrated dataset; Separated analyses of pyroptosis genes, (**D**,**F**) Gene expression distributions of pyroptosis genes in normal (blue) and tumor (red) samples. (**E,G**) Forest plots based on the results of Kaplan-Meier analysis between gene expression level and overall survival in separated dataset; (**D**,**E**) TCGA-LIHC; (**F**,**G**) GSE14520.







D

Subgroup	No. of Patients	Hazard Ratio	pvalue
Age			
<=65	451	Reference	
>65	167	1.192 (0.894−1.589)	0.231
Gender			
Female	153	Reference	
Male	465	1.023 (0.881−1.188)	0.761
TNM Stage			
I	271	Reference	
II	164	1.605 (1.126−2.287)	0.009
III	137	3.425 (2.459−4.772)	<0.001
IV	5	6.929 (2.169−22.129)	0.001
unknow	41	3.318 (2.073−5.309)	<0.001

0.25 4.0

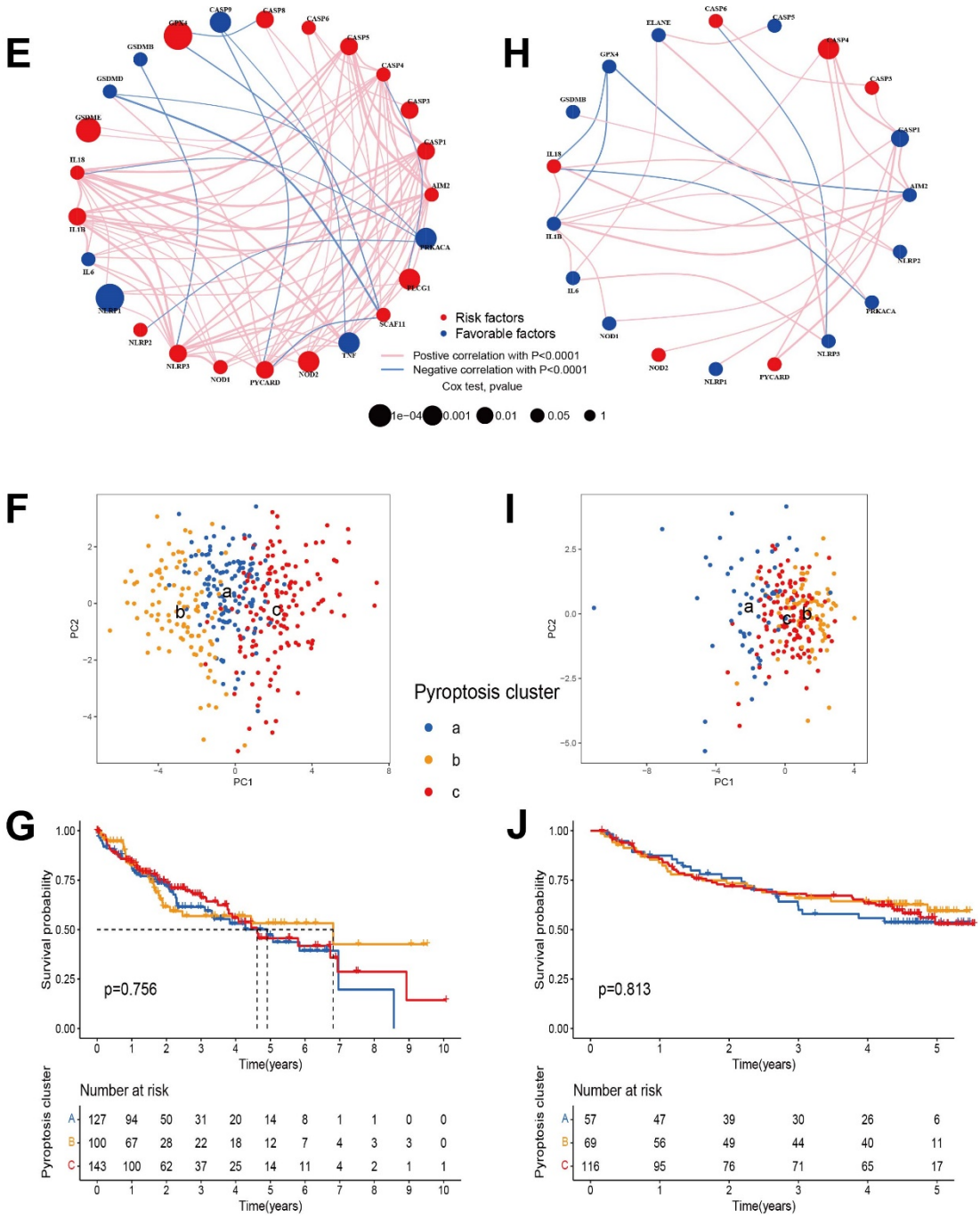


Figure S2. Characteristics of pyroptosis patterns. (**A**) the consensus distributions for k (2 to 9) based on pyroptosis genes. (**B**) Unsupervised clustering of pyroptosis genes. The clusters of clinical characteristics and pyroptosis patterns were used as sample annotations (red represents high expression level; blue, low level). (**C**) Overall survival analysis of pyroptosis clusters a (blue), b (yellow) and c (red). (**D**) Subgroup analysis estimating clinical prognostic value of patients' age, gender, and cancer stage by univariate Cox regression. The length of the horizontal line represents the 95% confidence interval for each group. The vertical dotted line represents the hazard ratio (HR) of all patients. Analyses of individual dataset (**E–G**) TCGA-LIHC, (H-J) GSE14520; (**E,H**) The correlation network of the pyroptosis-related genes (red line: positive correlation; blue line: negative correlation. The size (*p* value from 0.001 to 1) of the dot reflects the strength of the relationship between each gene and prognosis). The colors of dots represent protective (blue) and risk roles (red); Identification of potential immune subtypes of HCC based on pyroptosis genes. (**F,I**) PCA plots of clusters a (blue), b (yellow) and c (red); (**G,J**) Overall survival analysis of pyroptosis clusters a (blue), b (yellow) and c (red).

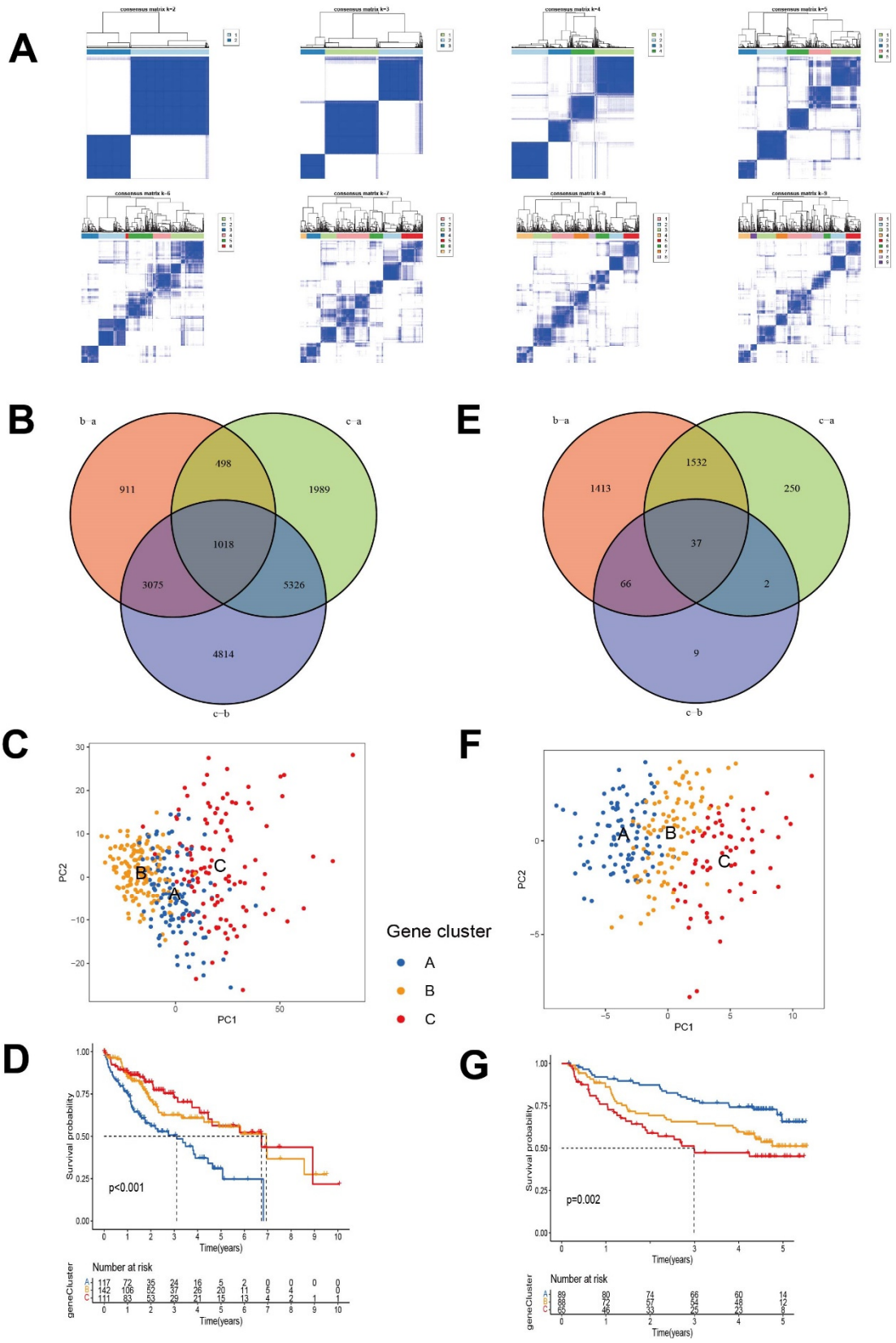


Figure S3. Identification of DEG-related subtypes. (**A**) The consensus distributions for k (2 to 9) based on screened DEGs. Separated analyses of (**B–D**) TCGA-LIHC and (**E–G**) GSE14520; (B)(E) Overlapping analyses of significant genes using a Venn diagram. (**C,F**) PCA plots of gene clusters A (blue), B (yellow) and C (red); (**D,G**) Overall survival analysis of gene clusters A (blue), B (yellow) and C (red).

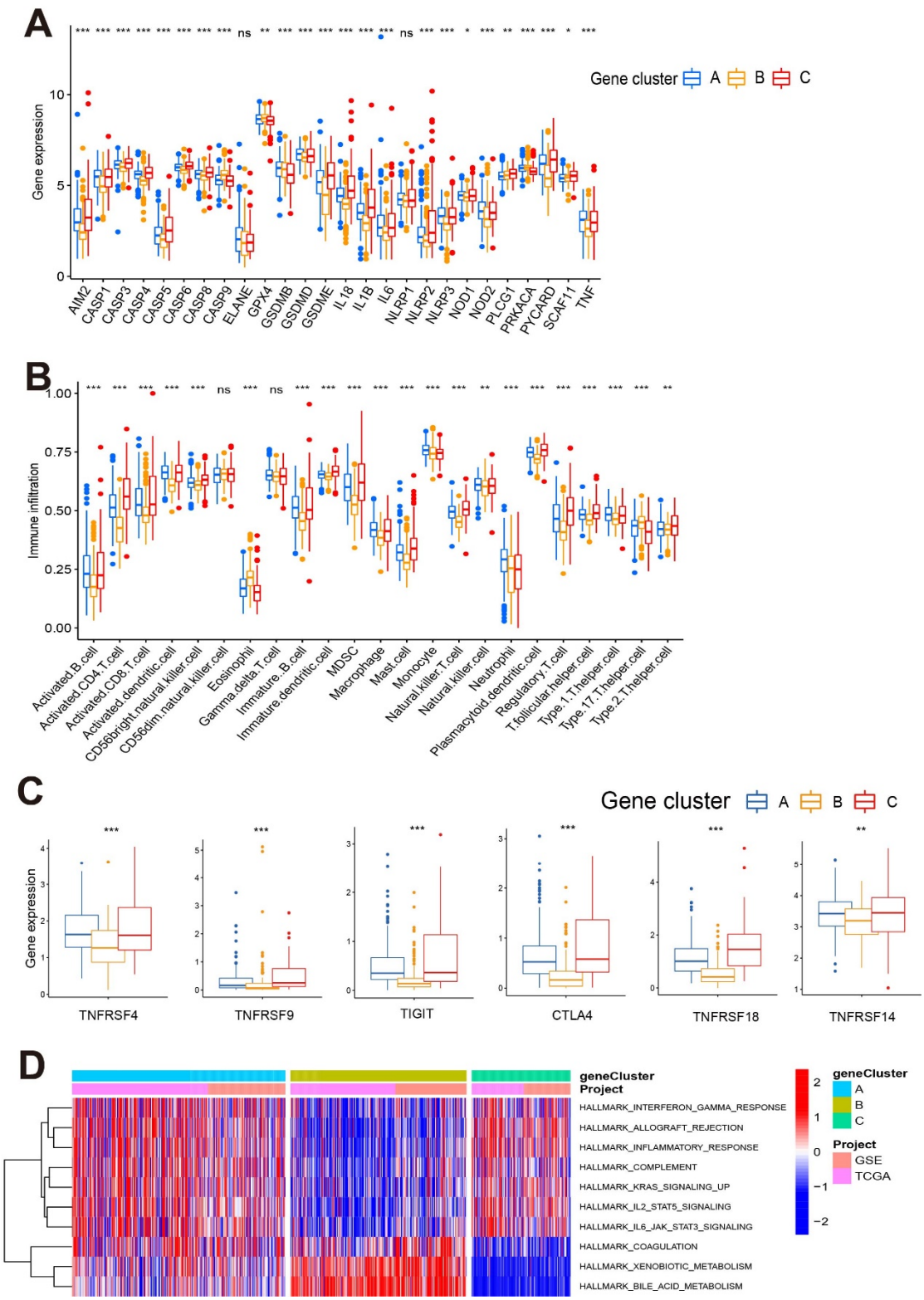


Figure S4. The expression distribution and GSVA enrichment features of gene clusters A–C. (**A**) the distribution of pyroptosis genes and (**B**) difference in the abundance of infiltrating immune cells among the three clusters. (**C**) Statistical analysis of selected immune modulators. (**D**) Heatmap distribution of the hallmark gene sets among the three clusters (red: activated pathways, blue: inhibited pathways, adjusted p value < 0.05). * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$.

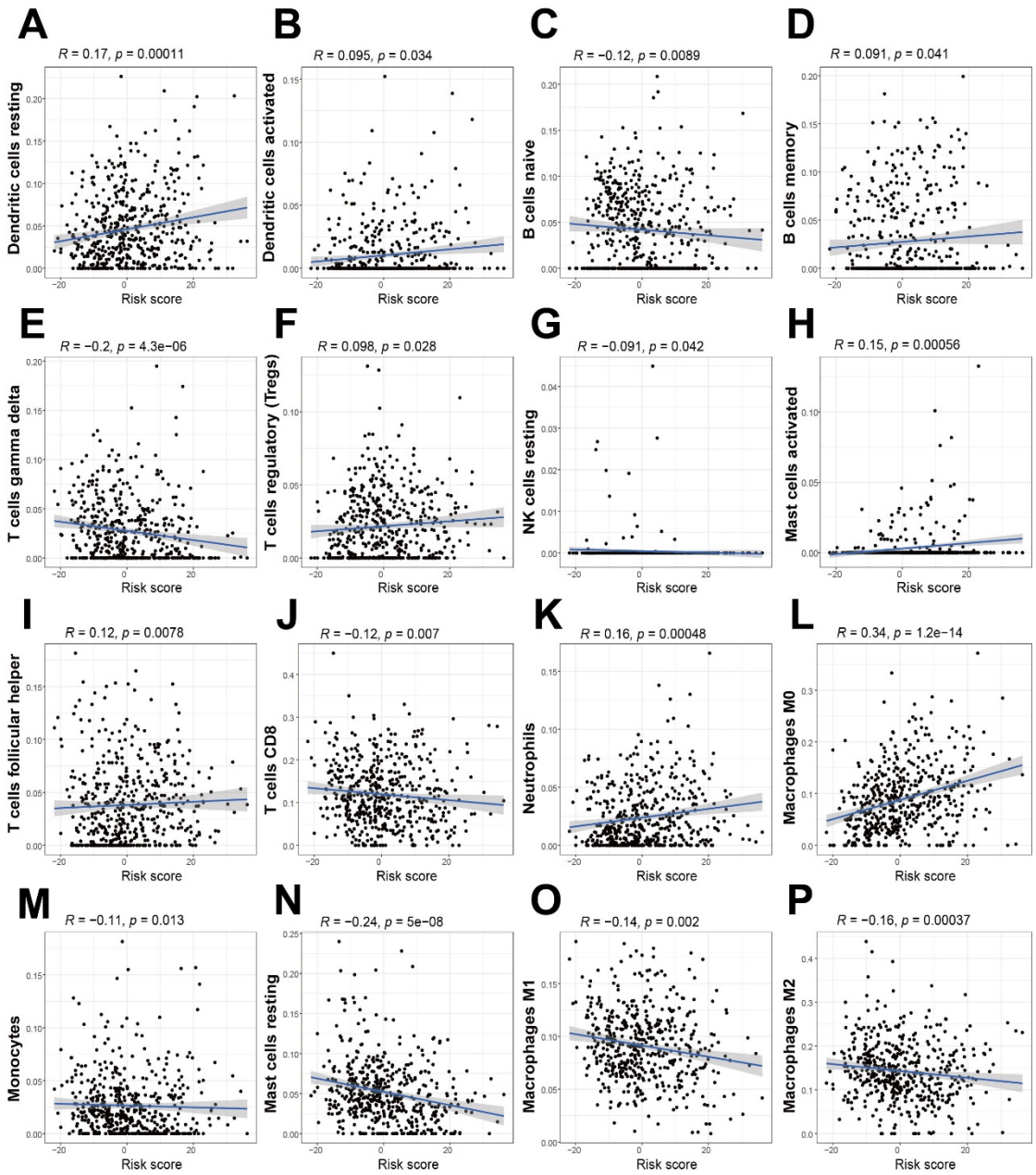


Figure S5. The association between pyroptosis risk scores and different immune subtypes (**A**) resting dendritic cell, (**B**) activated dendritic cell, (**C**) naïve B cell, (**D**) memory B cell, (**E**) gamma delta T cell, (**F**) Treg, (**G**) resting NK cell, (**H**) activated mast cell, (**I**) follicular helper T cell, (**J**) CD8+ T cell, (**K**) neutrophil, (**L**) M0 macrophage, (**M**) monocyte, (**N**) resting mast cell, (**O**) M1 macrophage, (**P**) M2 macrophage.

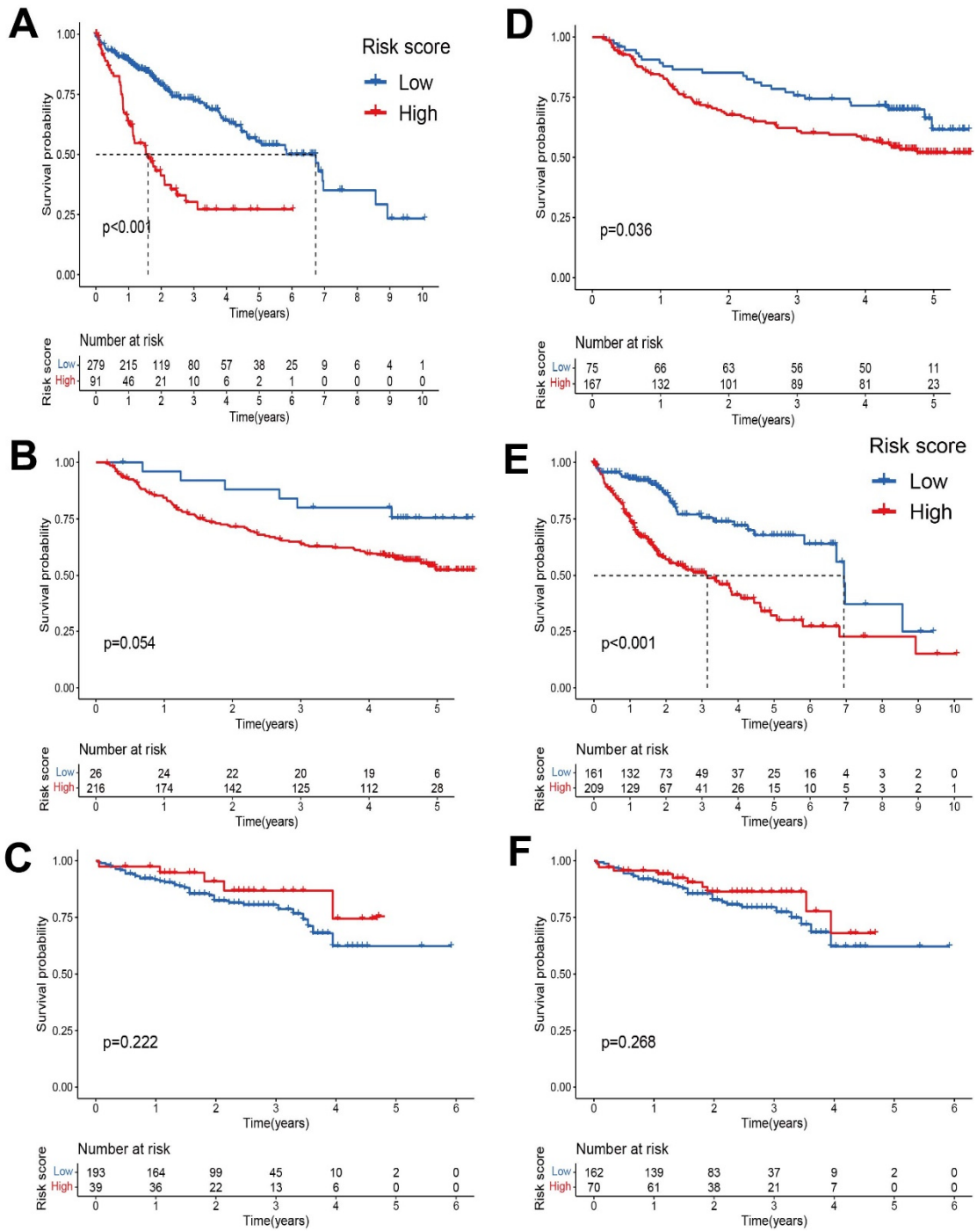


Figure S6. Cross verification of high (red)- and low (blue)- pyroptosis risk scoring system in overall survival analyses among separated databases. (**A**) Independent risk scoring classification within TCGA-LIHC, (**D**) independent risk scoring classification within GSE14520; (**B**) the efficiency of risk scoring system generated from TCGA-LIHC in classifying GSE14520 patients; (**E**) the efficiency of risk scoring system generated from GSE14520 in classifying TCGA-LIHC patients; And the further verification of the risk classification generated from TCGA-LIHC (**C**) and GSE14520 (**F**) in external ICGC data sets.

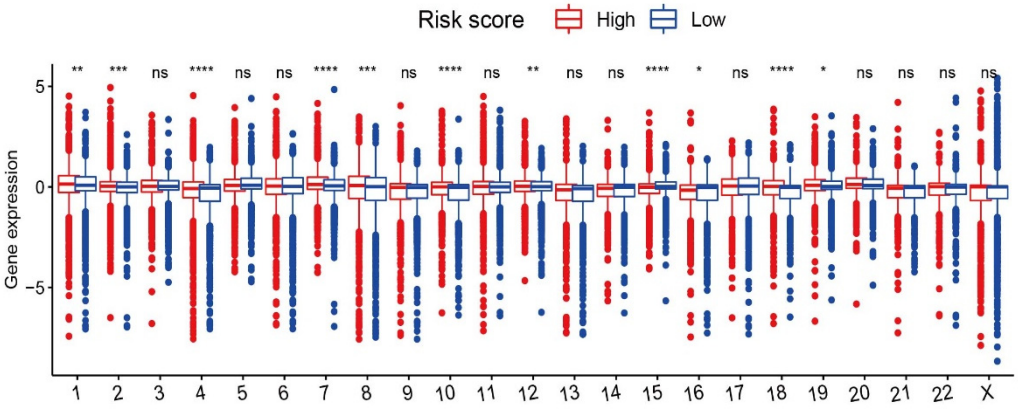


Figure S7. Statistical analysis of CNVs in whole chromosomes. * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$.