OMTN, Volume *27*

Supplemental information

Pyroptosis-related lncRNAs are potential biomarkers for predicting prognoses and immune responses in patients with UCEC

Jinhui Liu, Rui Geng, Senmiao Ni, Lixin Cai, Sheng Yang, Fang Shao, and Jianling Bai

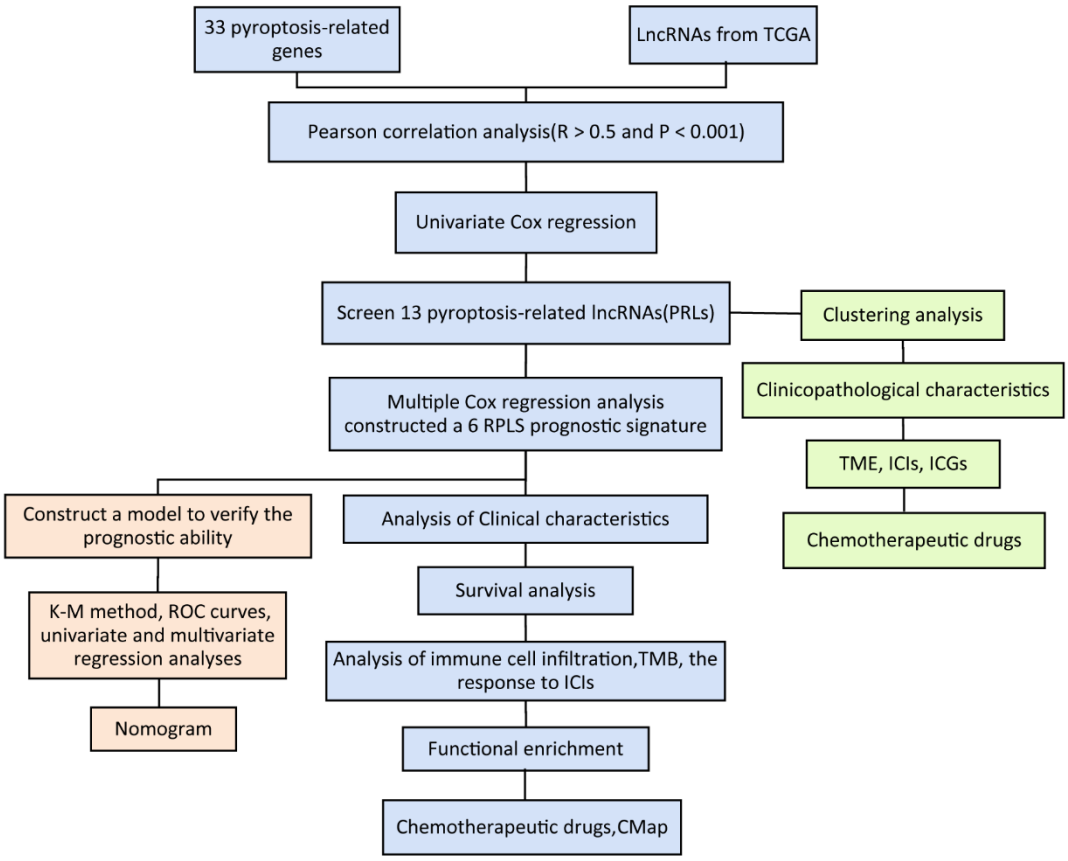

Figure S1 The flow diagram of this study.

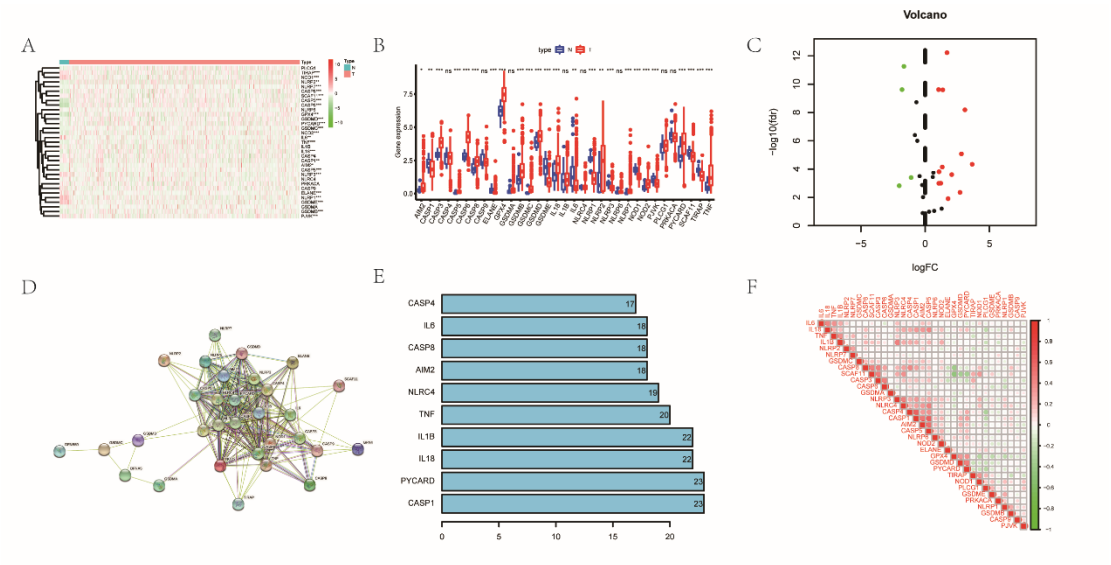

Figure S2 The expression levels of PRGs between tumor and normal samples in TCGA UCEC cohort. Heatmap(A), box plot(B) and volcano plot(C)shows the expression patterns of pyroptosis -related genes between tumor and normal tissues. (D) PPI network performed the interaction between 33 PRGs. (E) Bar graph showed genes with more nodes (F) Pearson correlation analysis of the 33 PRGs.

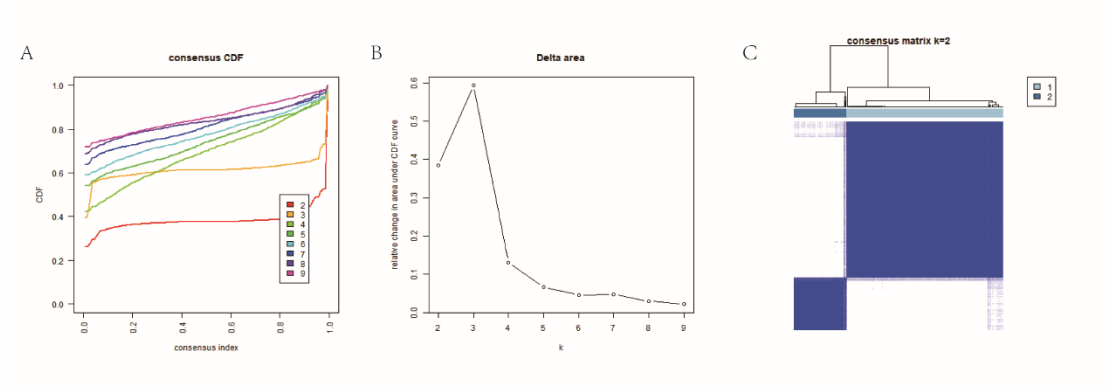

Figure S3 Consensus clustering analysis (A) Uniform clustering cumulative distribution function (CDF), k = 2-9 (k represents the number of clusters). (B) The change of area under CDF curve with k = 2-9. (C) TCGA UCEC cohort was divided into two clusters when k=2.

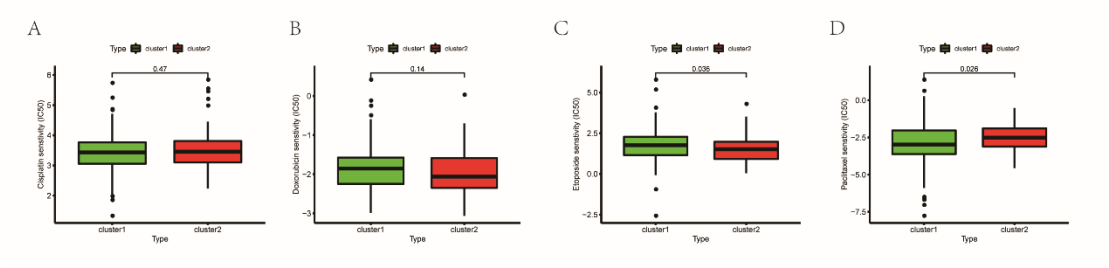

Figure S4 Drug sensitivity of the two clusters. The sensitivity of the two clusters to cisplatin (A), doxorubicin (B), etoposide (C) and paclitaxel (D) was different.

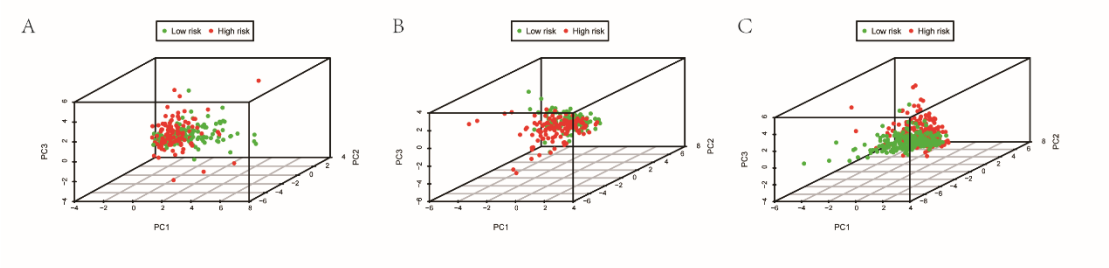

Figure S5 Principal component analysis (PCA) analysis The result of PCA in tseting set (A), training set (B) and entiring set (C).

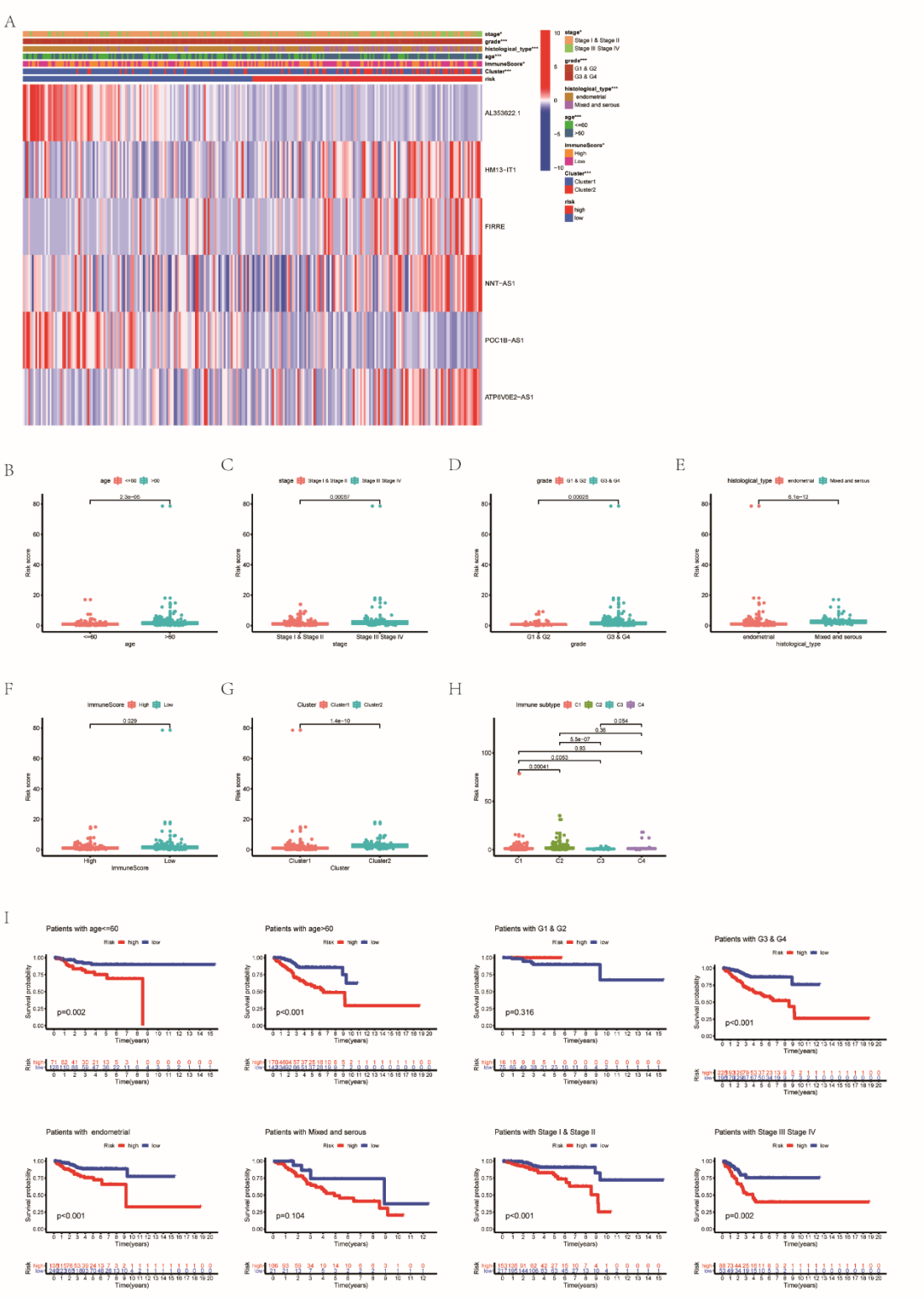

Figure S6 Effects of different clinical features and risk scores on UCEC prognosis (A)The different expression of 6 PRLs and their clinical features between the two risk groups were shown by heat map. Differences in age (B), stage (C), grade (D), histological type (E), immune score (F) and cluster (G) between the two risk groups. (H)The difference of the risk scores of the four UCEC immune subtypes. (I)

Comparison of survival probability between high and low risk groups under different clinical characteristic.

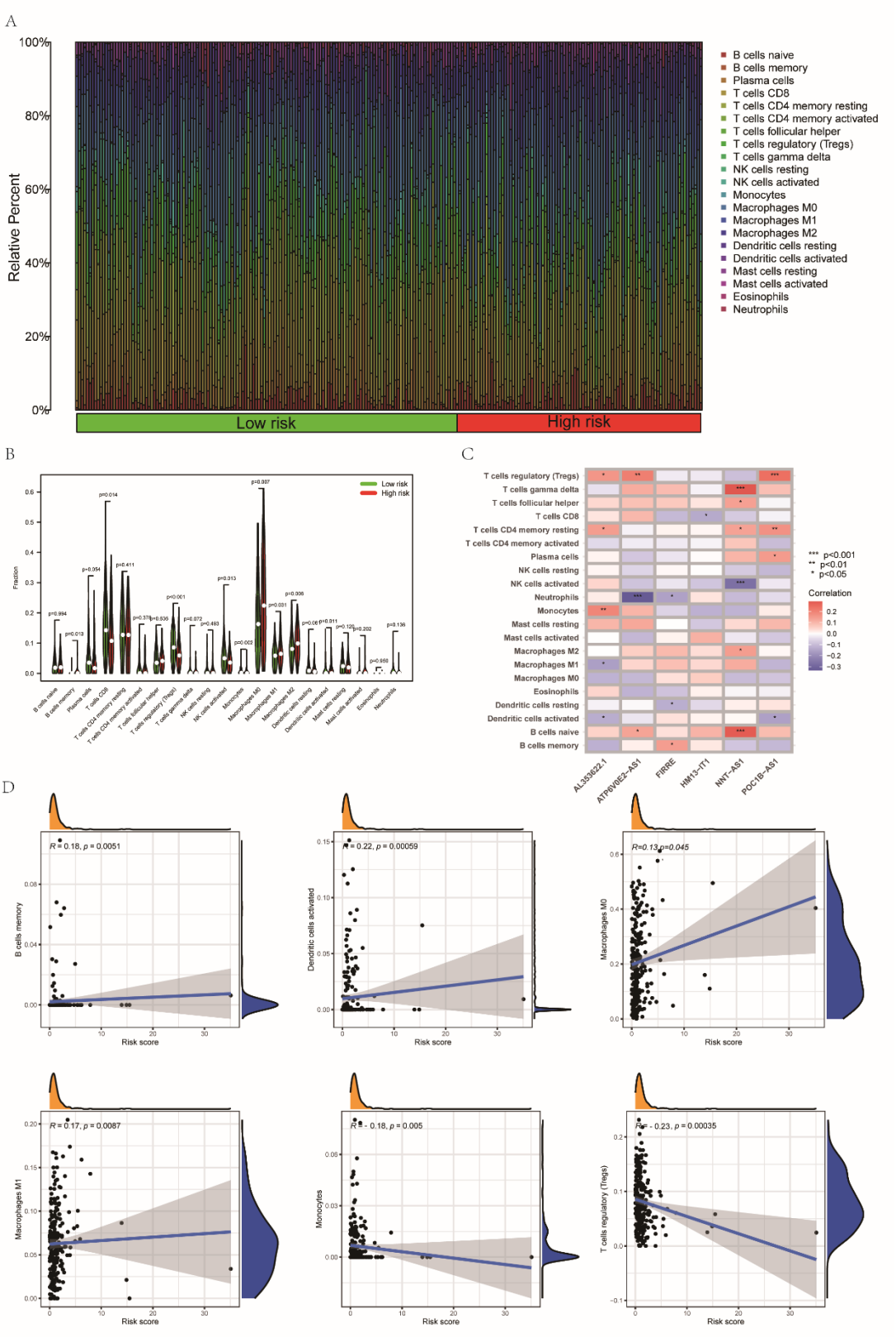

Figure S7 The correlation between tumor infiltrating immune cells and the model. (A)Bar plot showed the relative percent of 21 tumor infiltrating immune cells in the high- and low-risk groups. (B)Violin plot showed the difference of the fraction of each immune cells between the two risk groups. (C)The correlations between 21 tumor

infiltrating cells and 6 PRLs. (D)The correlation between risk score and 6 tumor infiltrating immune cells.

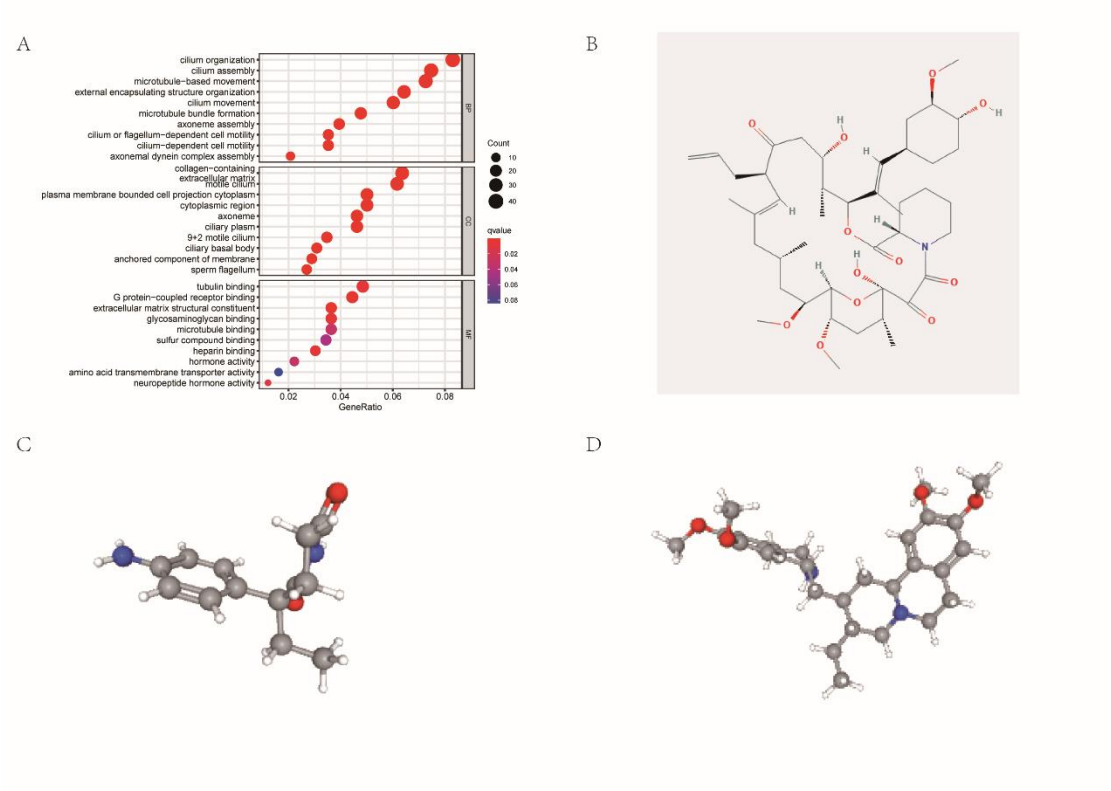

Figure S8 GO analysis and CMAP GO (A) enrichment analysis of different expressed genes between two risk groups. (B) Two-dimensional structure of tacrolimus. Three-dimensional structure of aminoglutethimide (C) and emetine (D).