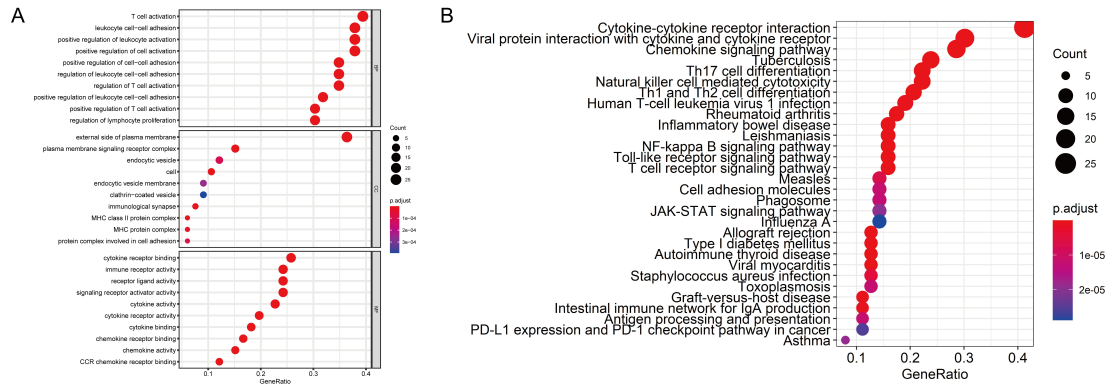
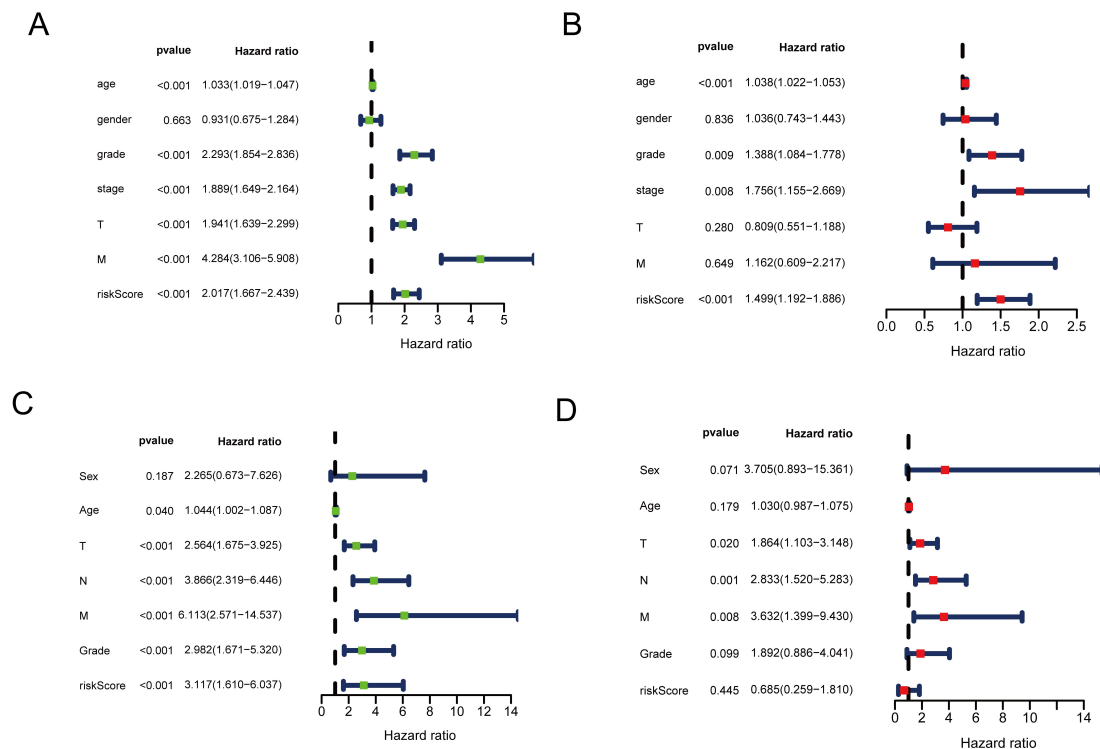


Supplementary Material



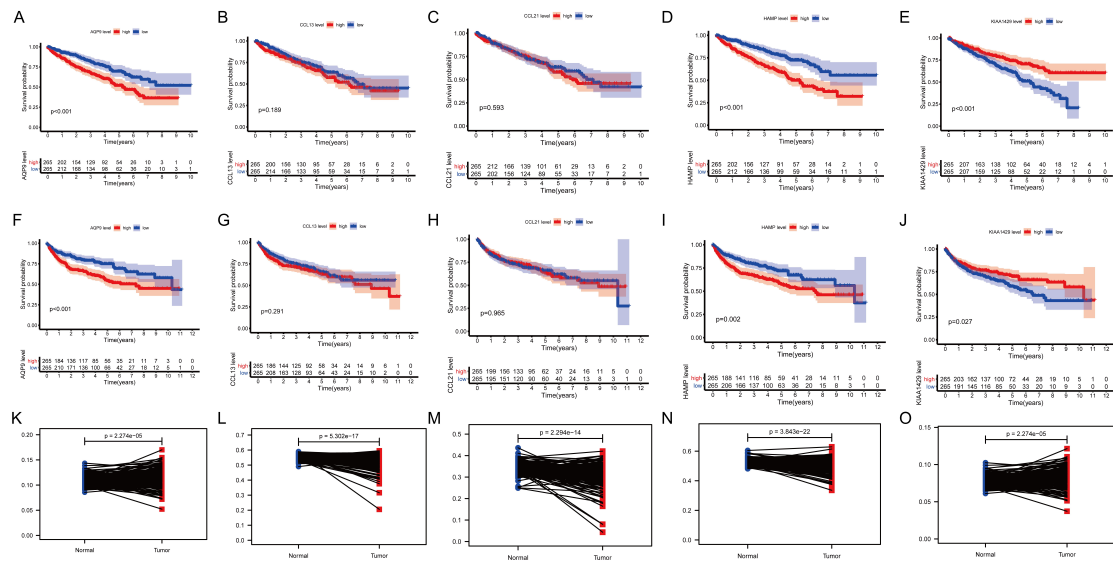
Supplementary Figure 1. Functional enrichment analysis of 67 immune genes.

(A) Gene Ontology (GO) term in molecular function (MF), biological process (BP) and cellular component (CC); (B) Kyoto Encyclopedia of Genes and Genomes (KEGG) for 67 immune genes.



Supplementary Figure 2. Independent prognostic analysis of risk score and clinical characteristics. (A) Univariate and (B) multivariate Cox regression analysis of risk score and clinical characteristics in TCGA cohort, (C) Univariate and (D) multivariate Cox regression analysis of risk score and

clinical characteristics in E-MTAB-1980 cohort. T, tumor; M, metastasis; N, lymph nodes.



Supplementary Figure 3. Kaplan-Meier survival validation of five genes in the risk model. (A-E) Overall survival for *AQP9*, *CCL13*, *CCL21*, *HAMP* and *KIAA1429* in ccRCC of TCGA; (F-J) progression-free survival for *AQP9*, *CCL13*, *CCL21*, *HAMP* and *KIAA1429* in ccRCC of TCGA; (K-O) methylation differences between tumor and normal tissues of ccRCC for *AQP9*, *CCL13*, *CCL21*, *HAMP* and *KIAA1429* in TCGA.