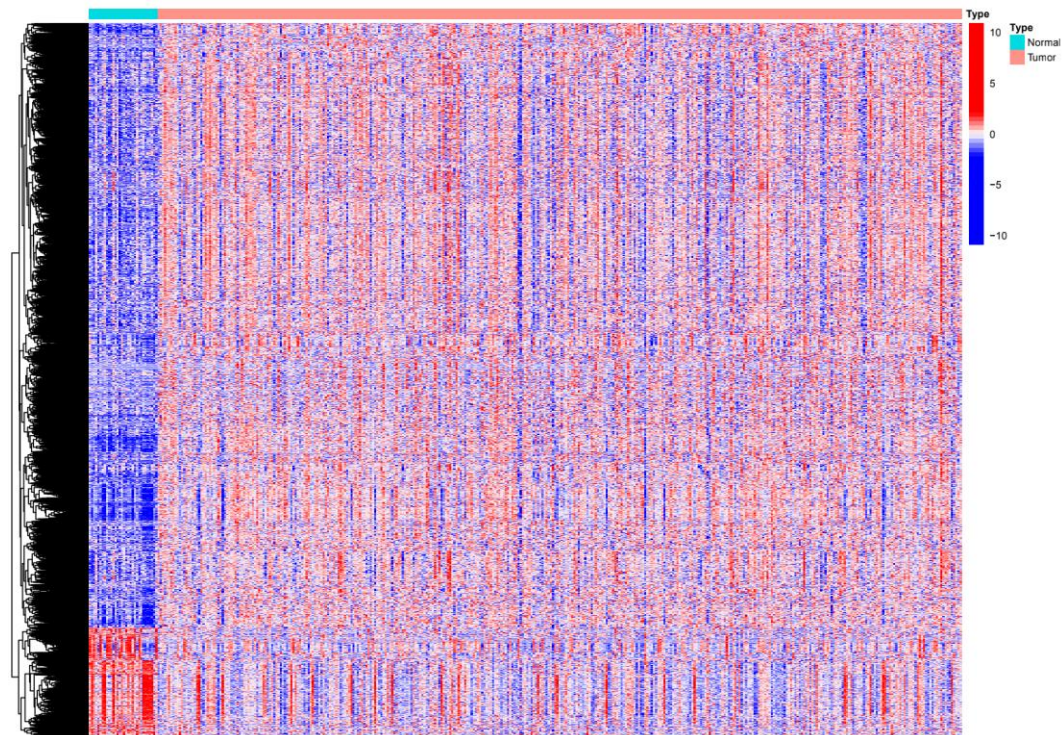


Supplementary Materials

1. “WGCNA” methods, firstly, free samples were expurgated and the rest samples were clustered based on the clinical data. Next, the similarity matrix is constructed by calculating the Pearson Coefficient between any two genes. The optimal power value (a soft threshold of $\beta=3$) was obtained by fitting index and average connectivity with power scatter plot to construct adjacency matrix. The adjacency matrix was then transformed into a topological matrix with the topological overlap measure (TOM), and genes and modules were clustered by distance (1-TOM). Finally, gene modules were determined by the dynamic cut tree method and those modules with high similarity were merged (height=0.25). Since the genes in the turquoise modules were the most significant correlation to the clinical trait ($p=4e-34$), they were used to construct the co-expression network (weight threshold>0.3). Their gene expression quantity was then extracted from the tumor samples of TCGA (n=375) and combined with the survival data, using the “limma” package of R. Thus, 36 prognostic IRGs ($p<0.05$) were obtained by univariate COX analysis, and their survival curves were made based on the best cut-off value, obtained by the surv_cutpoint function from “survminer” package of R.

A



B

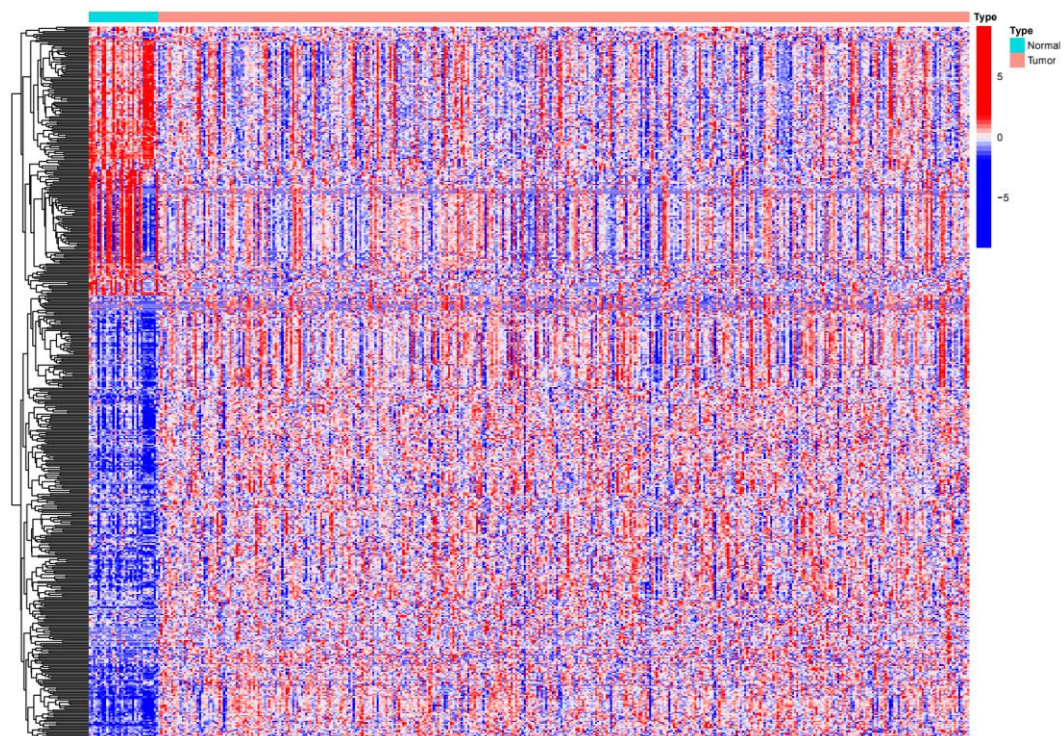
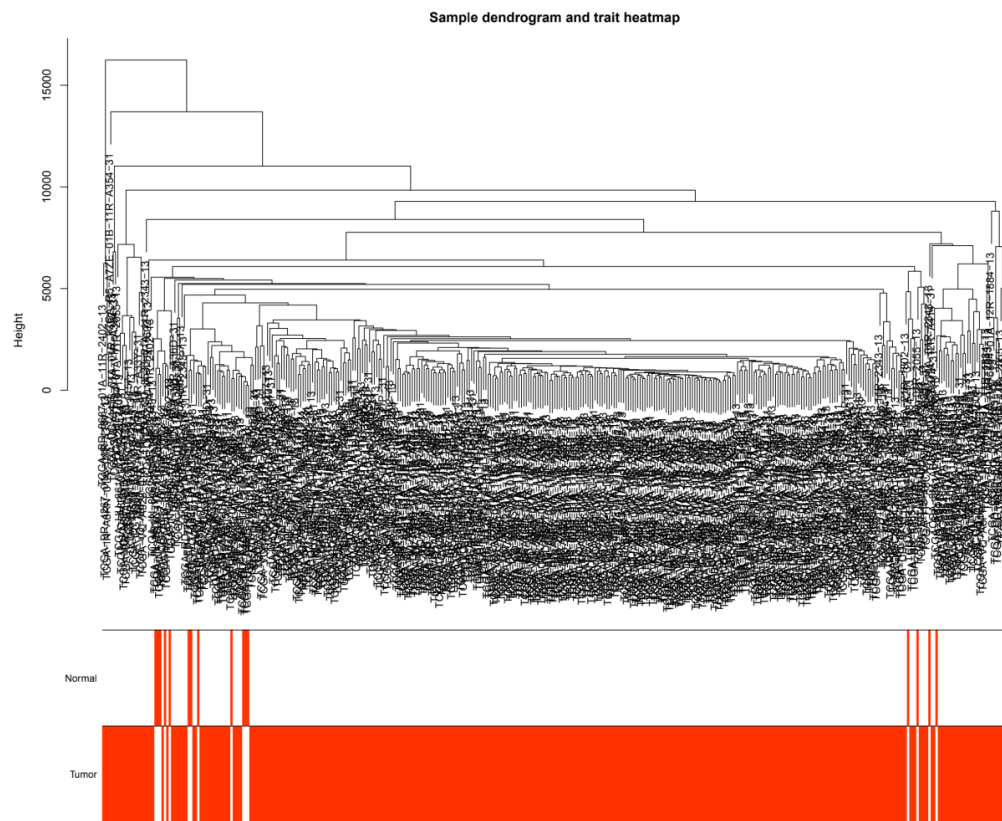
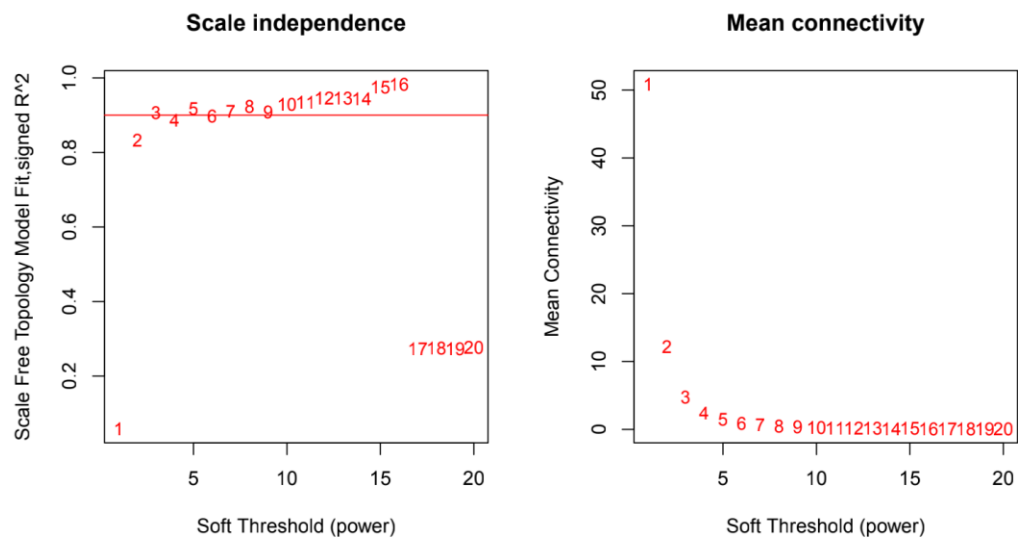


Figure S1. Differentially expressed genes in GC. (A) Heatmap displaying all differentially expressed genes between 375 HNSCC samples (red) and 32 para-cancer samples (blue), 8833 genes in total ($p < 0.05$, $|\log_2FC| > 1$). (B) Heatmap displaying 493 immune-related differentially expressed genes, filtering from the results of Fig.S1A.

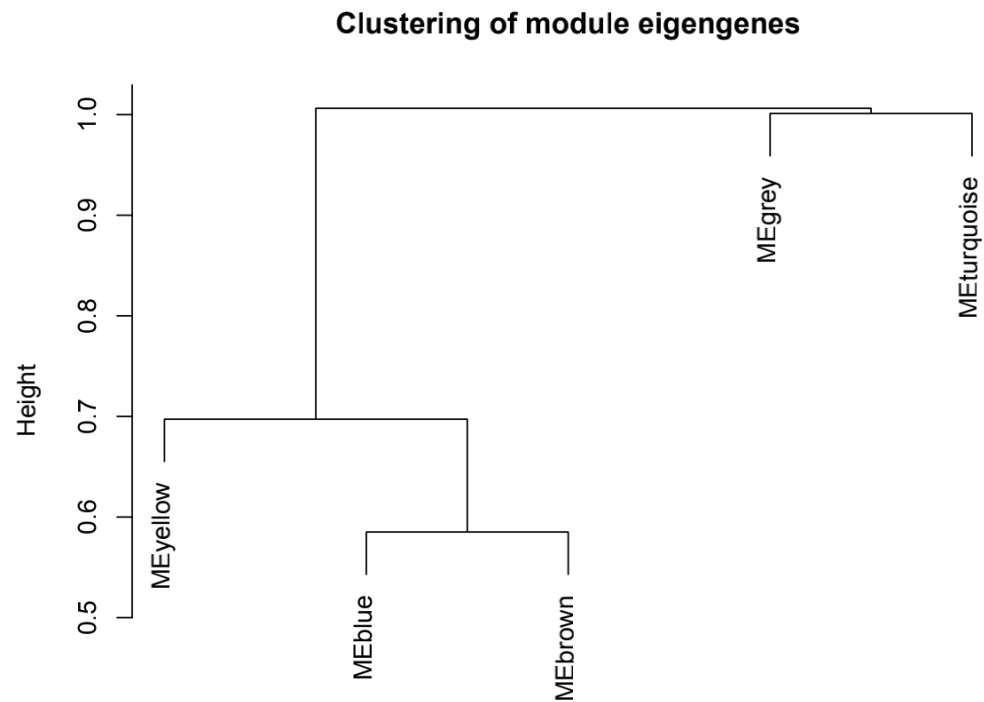
A



B



C



D

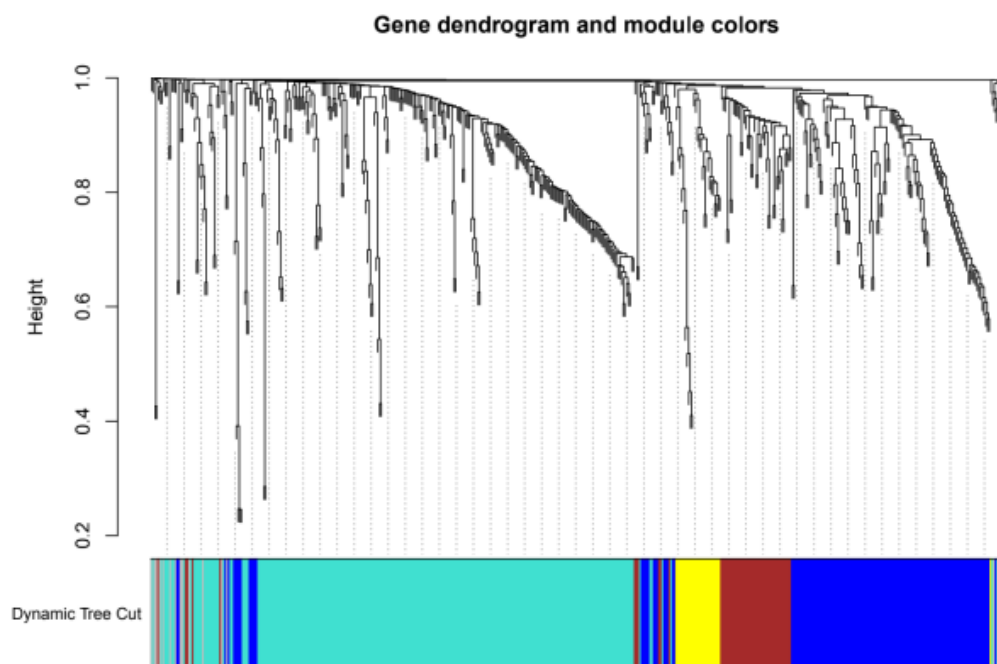


Figure S2. Results of the Weighted gene coexpression network analysis (WGCNA). (A)The sample dendrogram and heatmap shows the clustering and phenotypic information. (B)In the left graph, the horizontal line indicates that the threshold value is 0.90. As seen from the graph, the optimal soft threshold for WGCNA was 3. (C)5 eventual network modules are obtained after merging.(Height = 0.25). (D)The merged graphical result shows the final clustering of samples under different network modules.

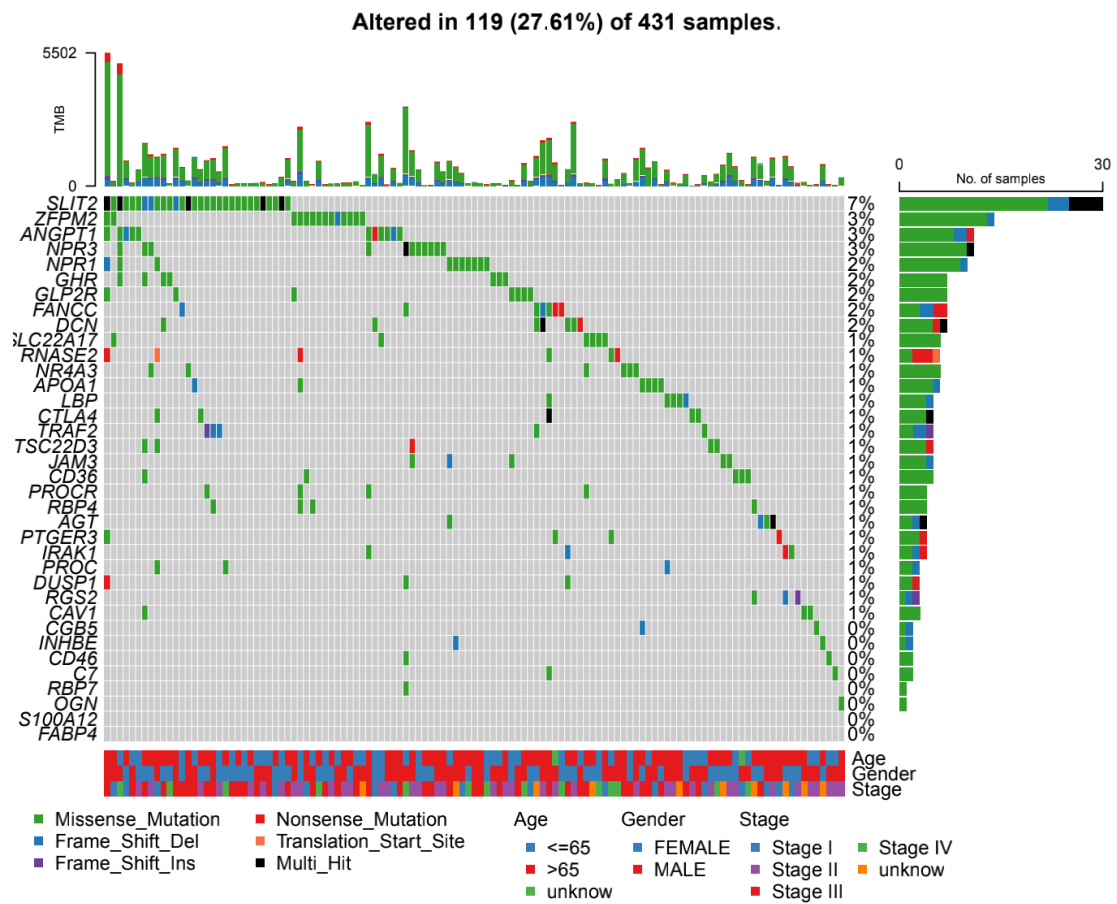
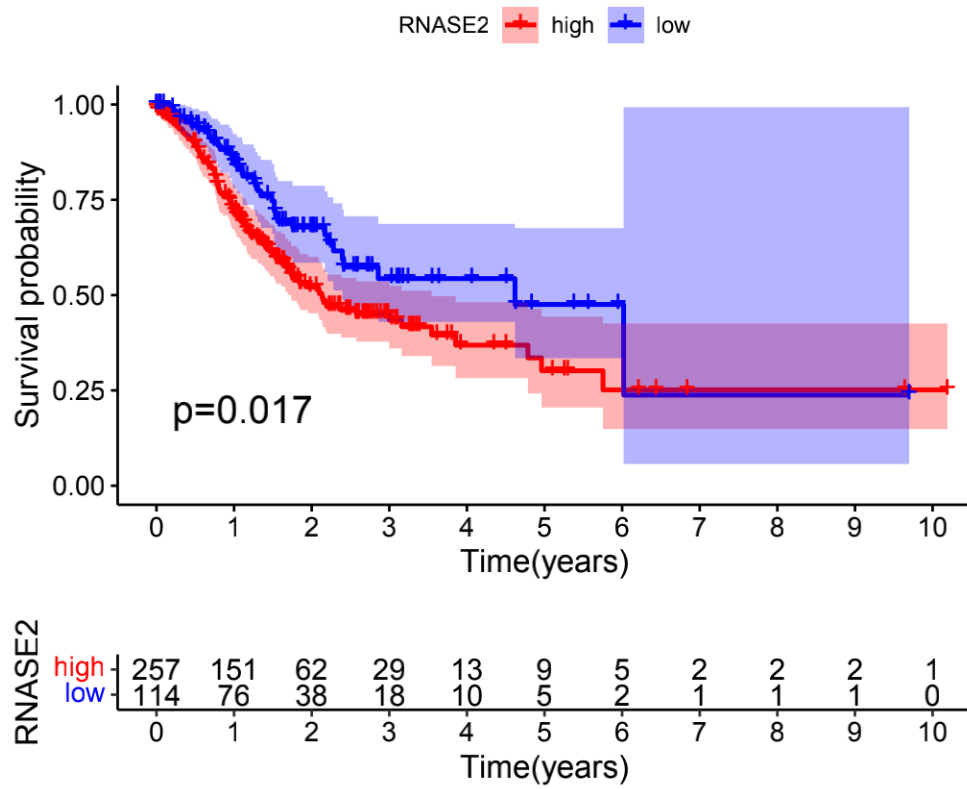
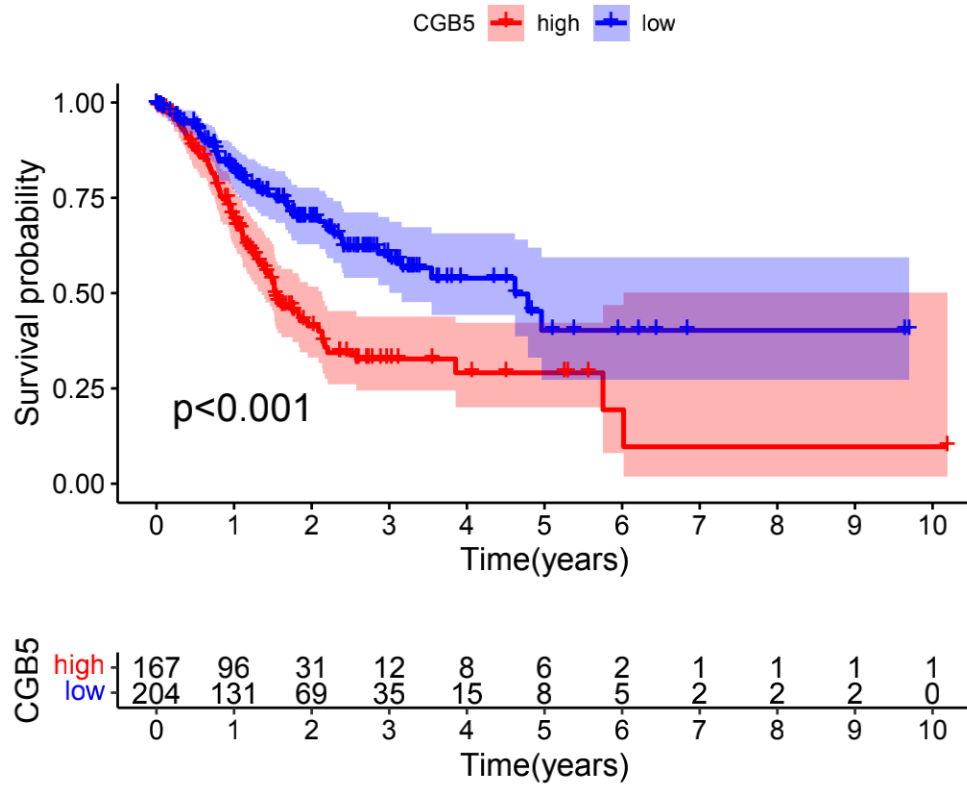


Figure S3. Mutation research of 36 immune-related prognostic genes. The mutation rate of 36 immune-related prognostic gene in TCGA cohort (n = 431).

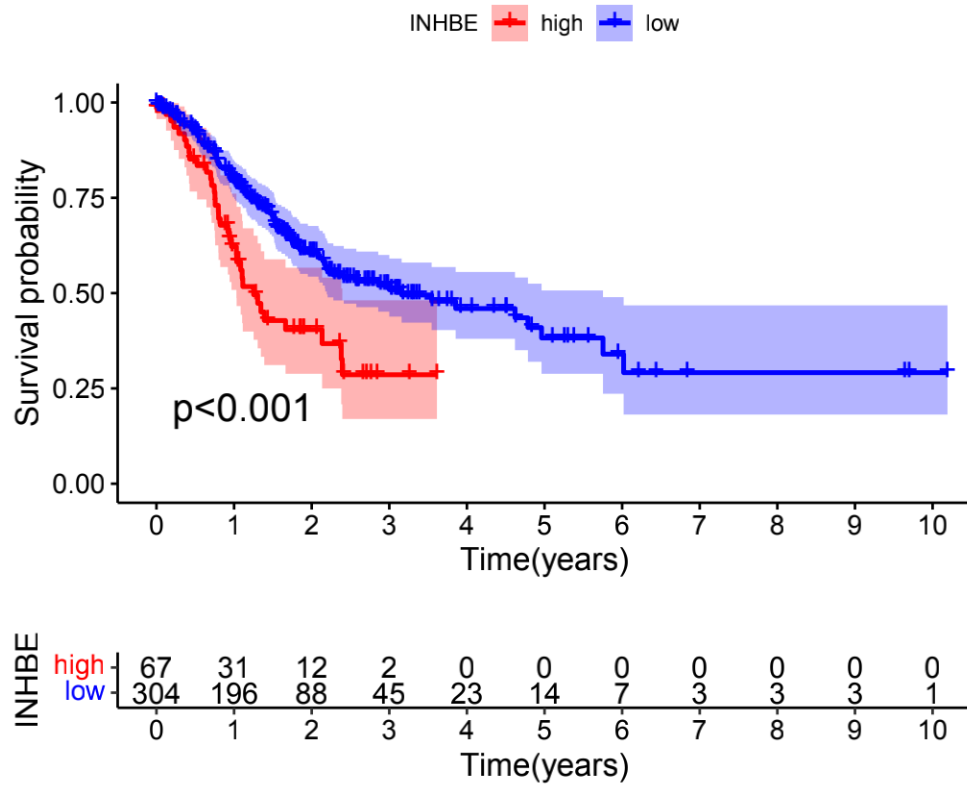
A



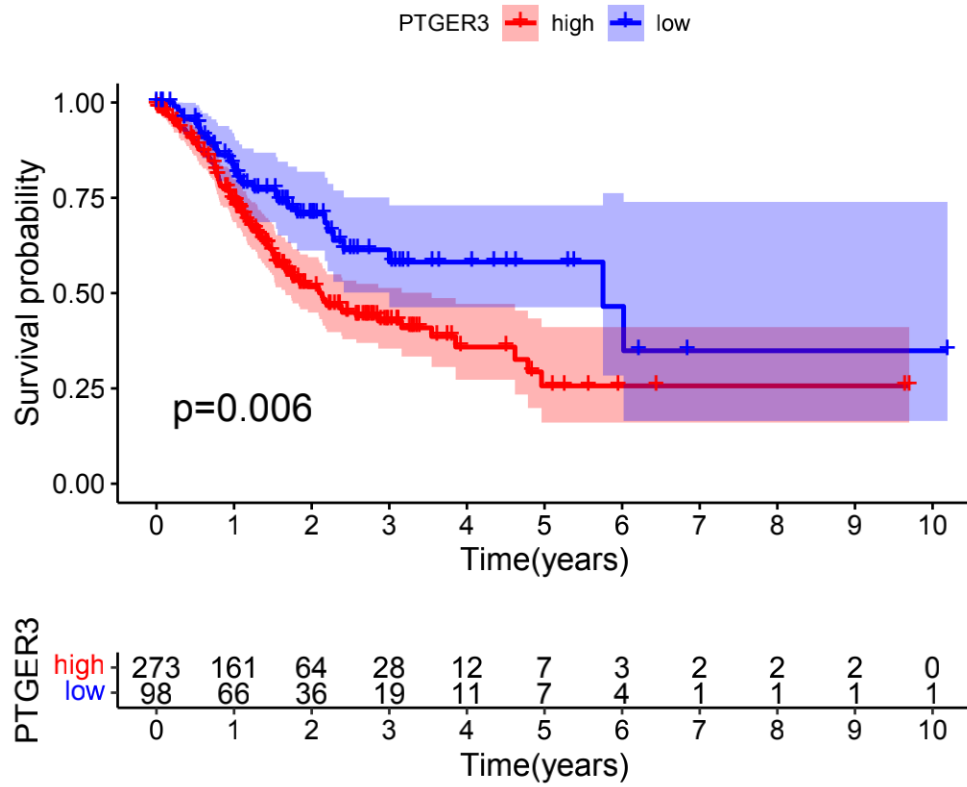
B



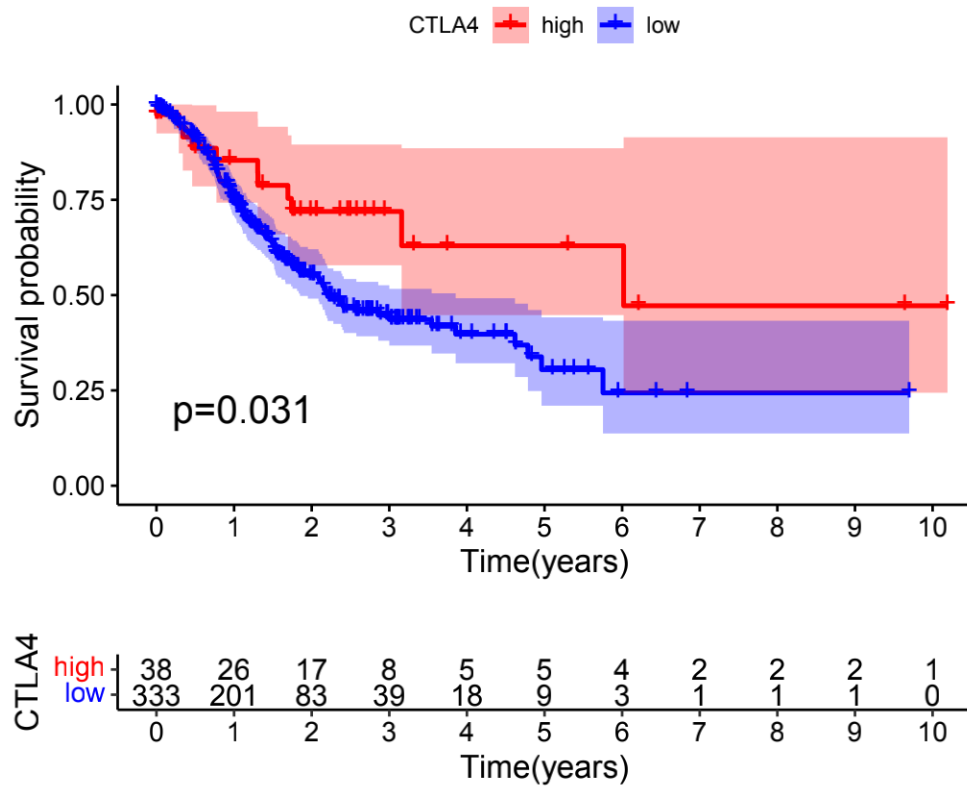
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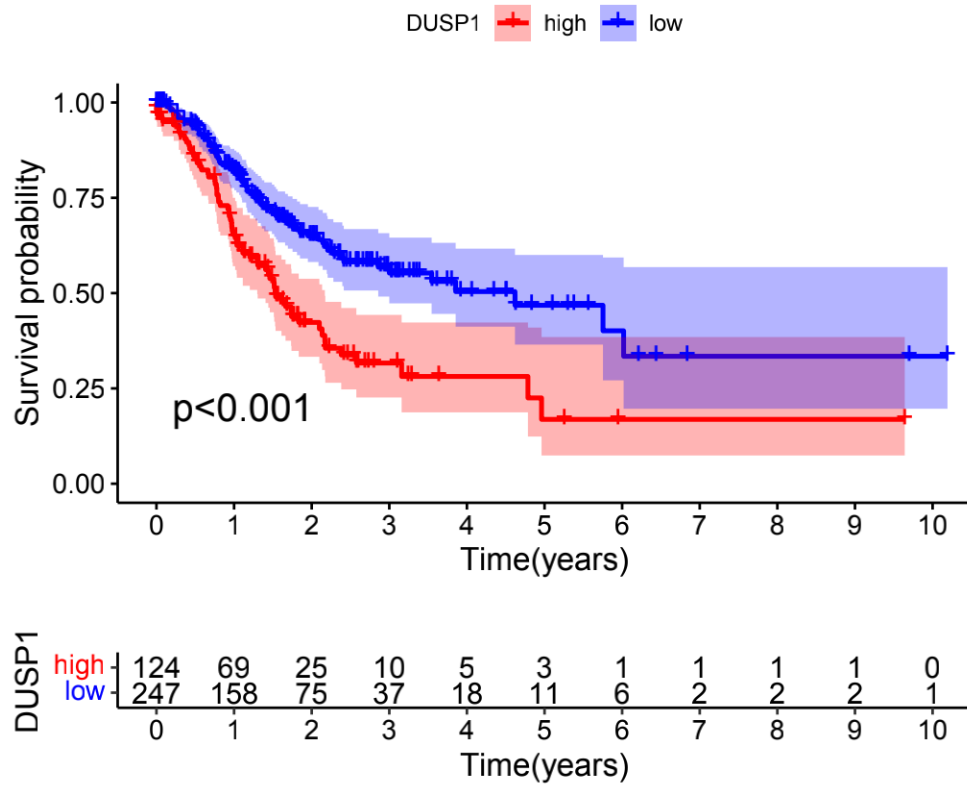
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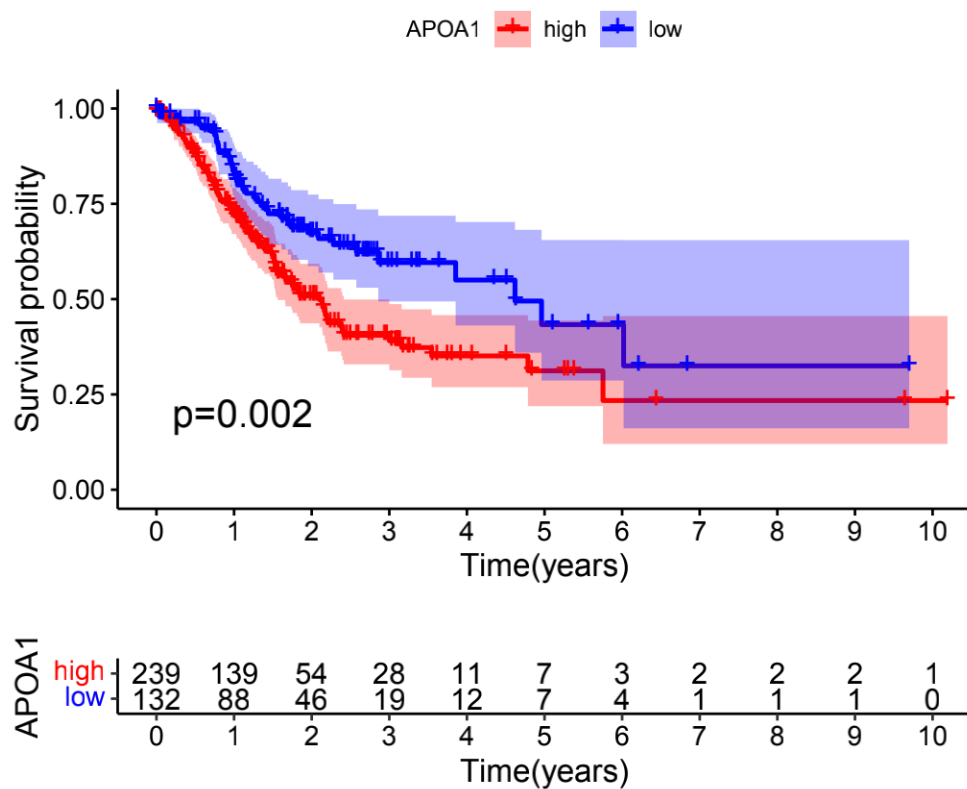
E



F



G



H

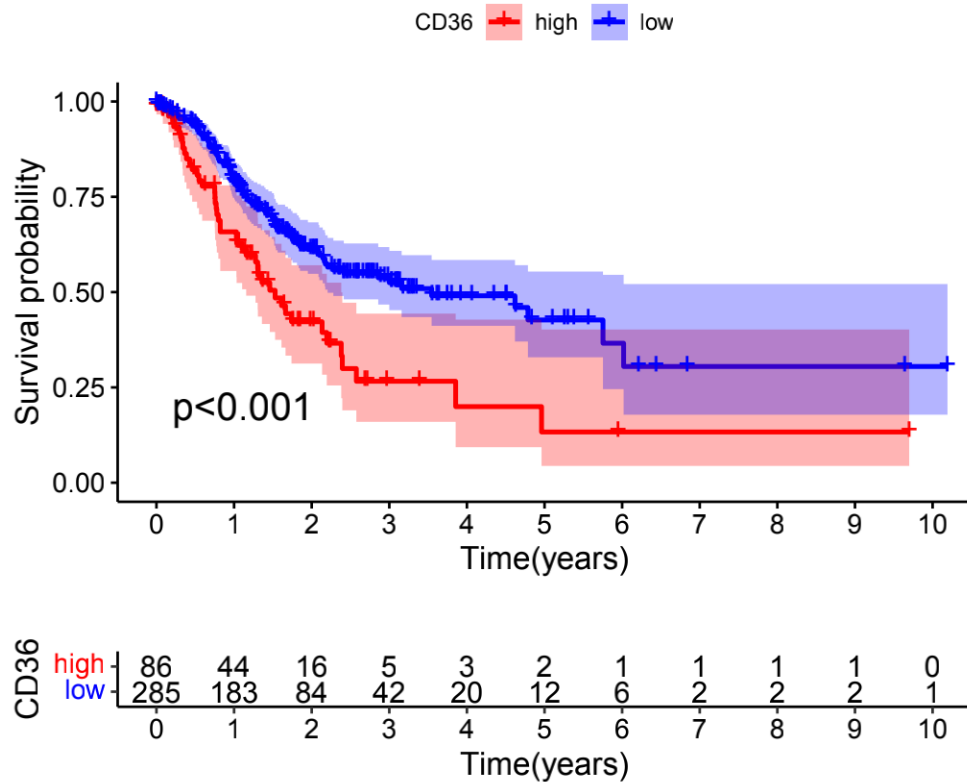


Figure S4. Kaplan-Meier curves of 8 modeling genes. K-M survival analysis of the 8 modeling genes in TCGA cohort. (A) RNASE2 ($p = 0.017$). (B) CGB5 ($p < 0.001$). (C) INHBE ($p < 0.05$). (D) PTGER3 ($p = 0.006$). (E) CTLA4 ($p = 0.031$). (F) DUSP1 ($p < 0.001$). (G) APOA1 ($p = 0.002$). (H) CD36 ($p < 0.001$).

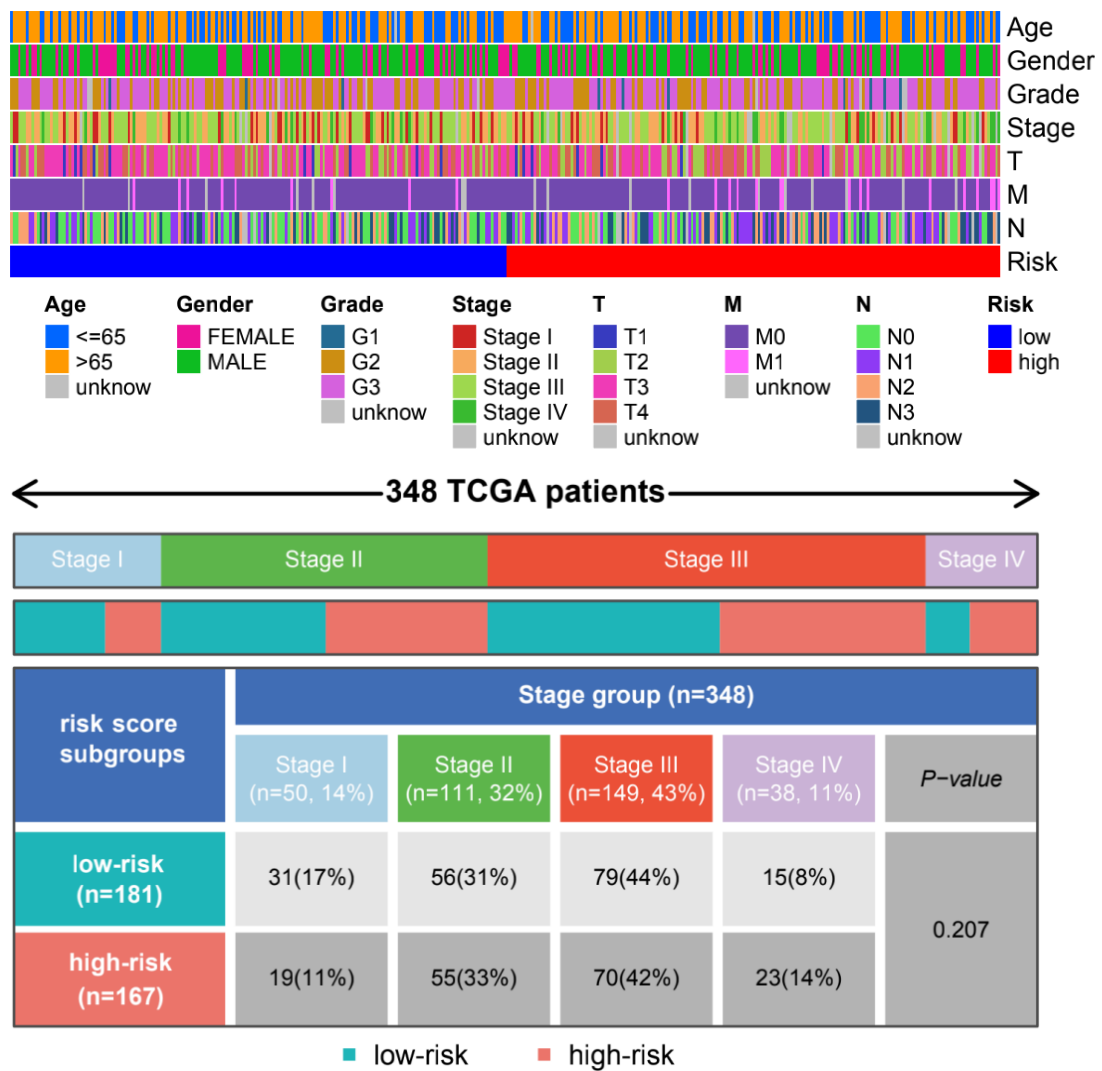


Figure S5. Clinical characteristics of different risk subgroups.