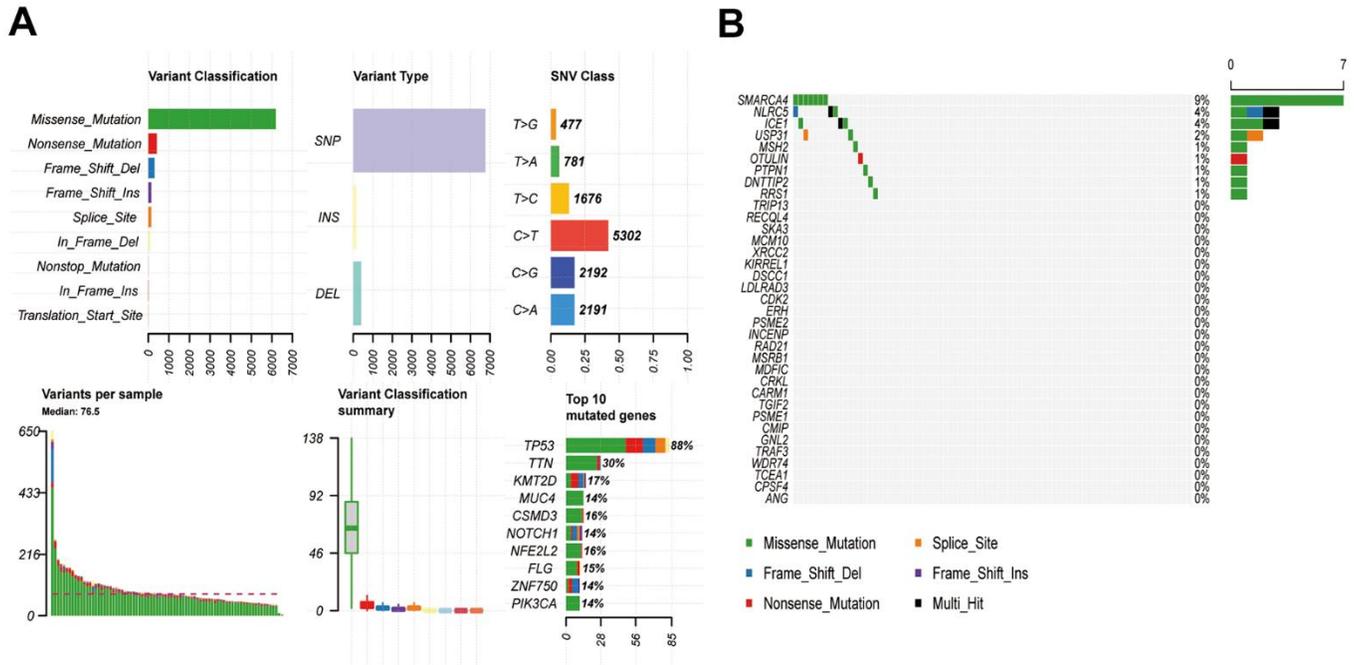
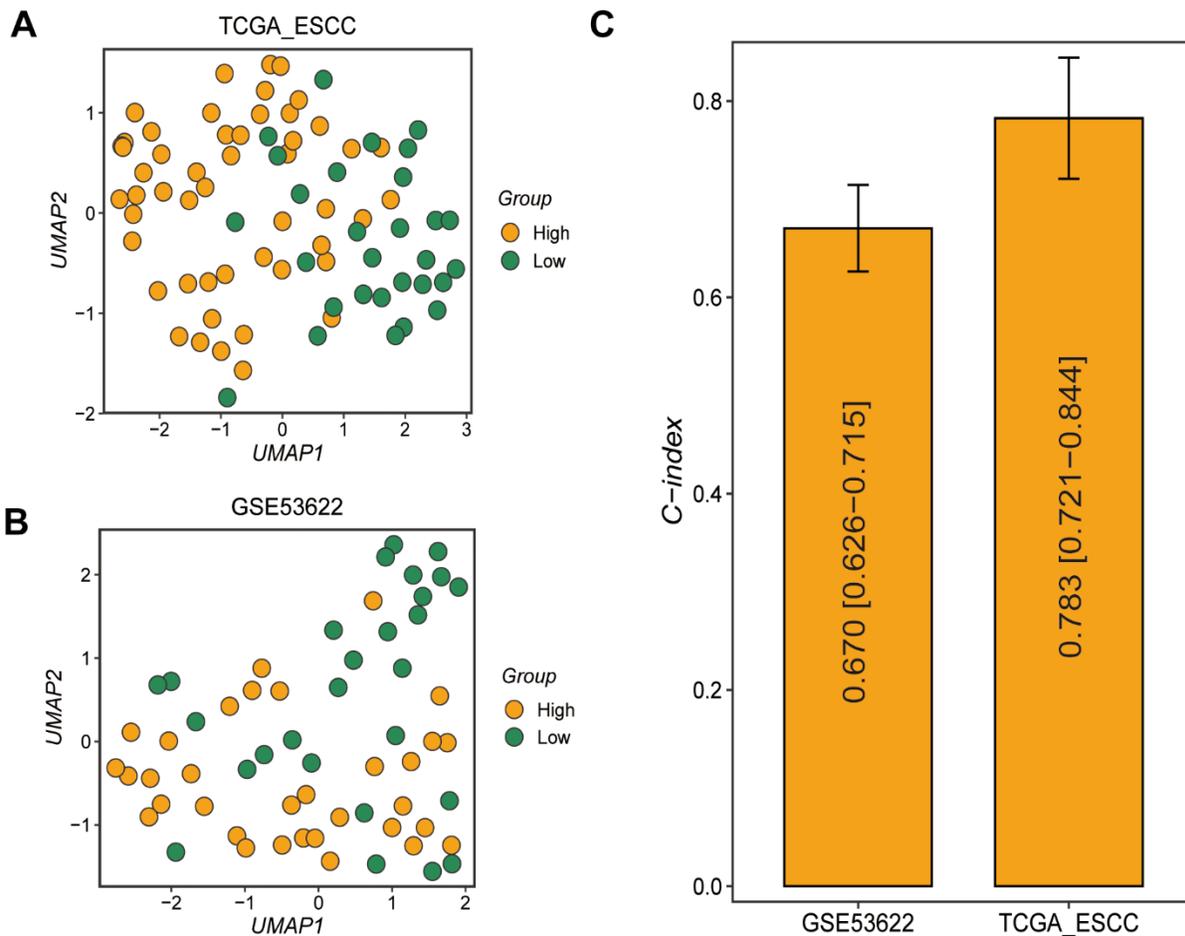


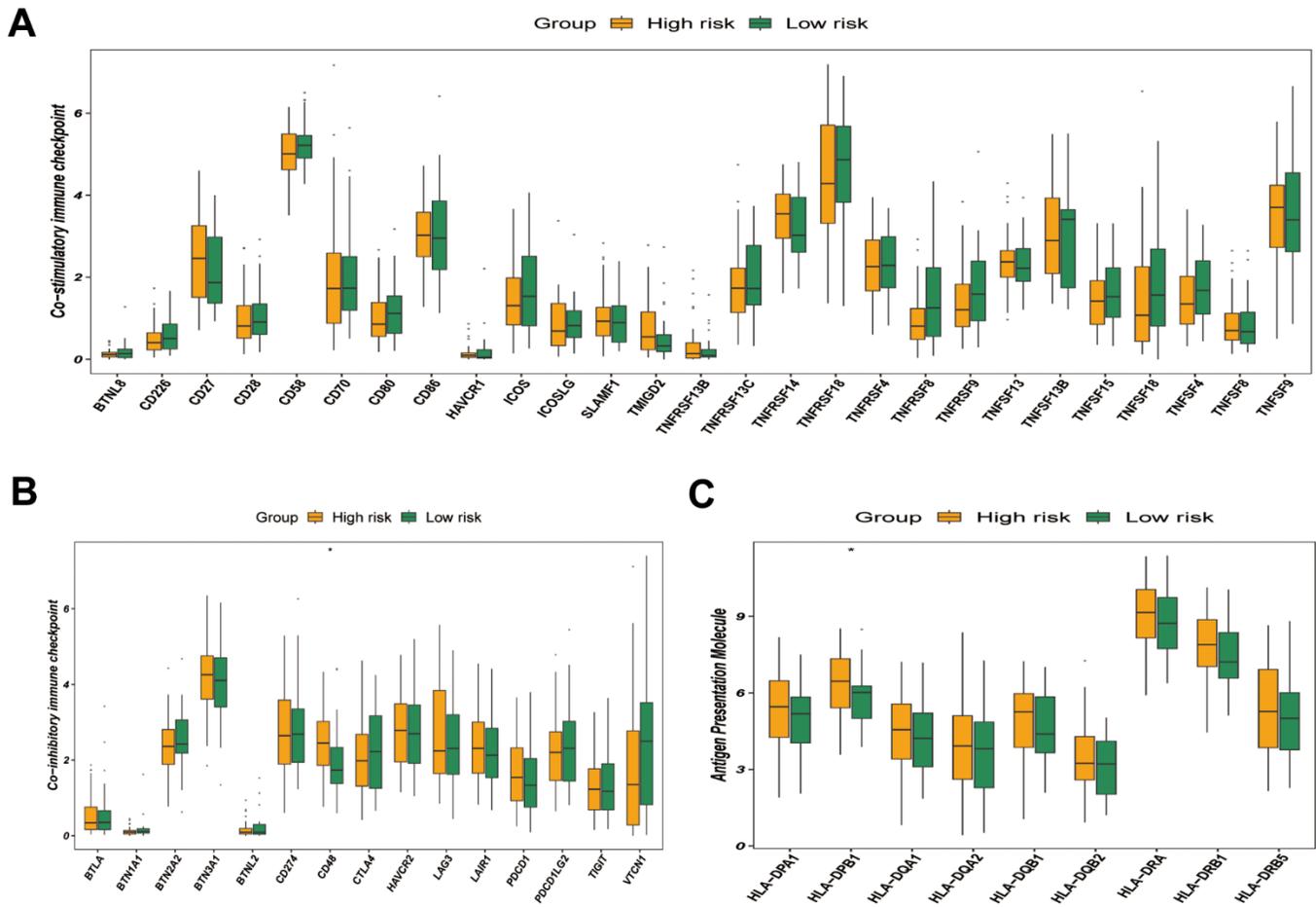
SUPPLEMENTARY FIGURES



Supplementary Figure 1. Display of mutation rates of prognostic gene related to GRTTK in the TCGA cohort. (A) Whole-genome variation in the TCGA-ESCC cohort. (B) Waterfall plots showing somatic mutation frequencies of 35 key GRTTK in the TCGA-ESCC cohort.



Supplementary Figure 2. UMAP analysis and C-index analysis in the training and validation dataset. (A) UMAP analysis reveals the distribution patterns of patients in the high and low-risk groups in TCGA-ESCC cohort. (B) UMAP analysis depicting the distribution patterns of patients in the high and low-risk groups in GSE53622 cohort. (C) The C-index was used to assess the performance of risk model.



Supplementary Figure 3. Comparative analysis of multiple immune checkpoint molecules among different risk groups in the TCGA-ESCC cohort. (A) Costimulatory molecules expression distribution in the high-risk and low-risk groups of the TCGA-ESCC cohort. (B) Distribution of coinhibitory molecules expression in the high-risk and low-risk groups of the TCGA-ESCC cohort. (C) Expression profiles of antigen presentation molecule in the high and low-risk group of the TCGA-ESCC cohort.