Supplementary Figure 1. GO/KEGG enrichment for CD8⁺ signature genes. (**A**) GO enrichment for CD8⁺ signature genes. (**B**) KEGG enrichment for CD8⁺ signature genes.
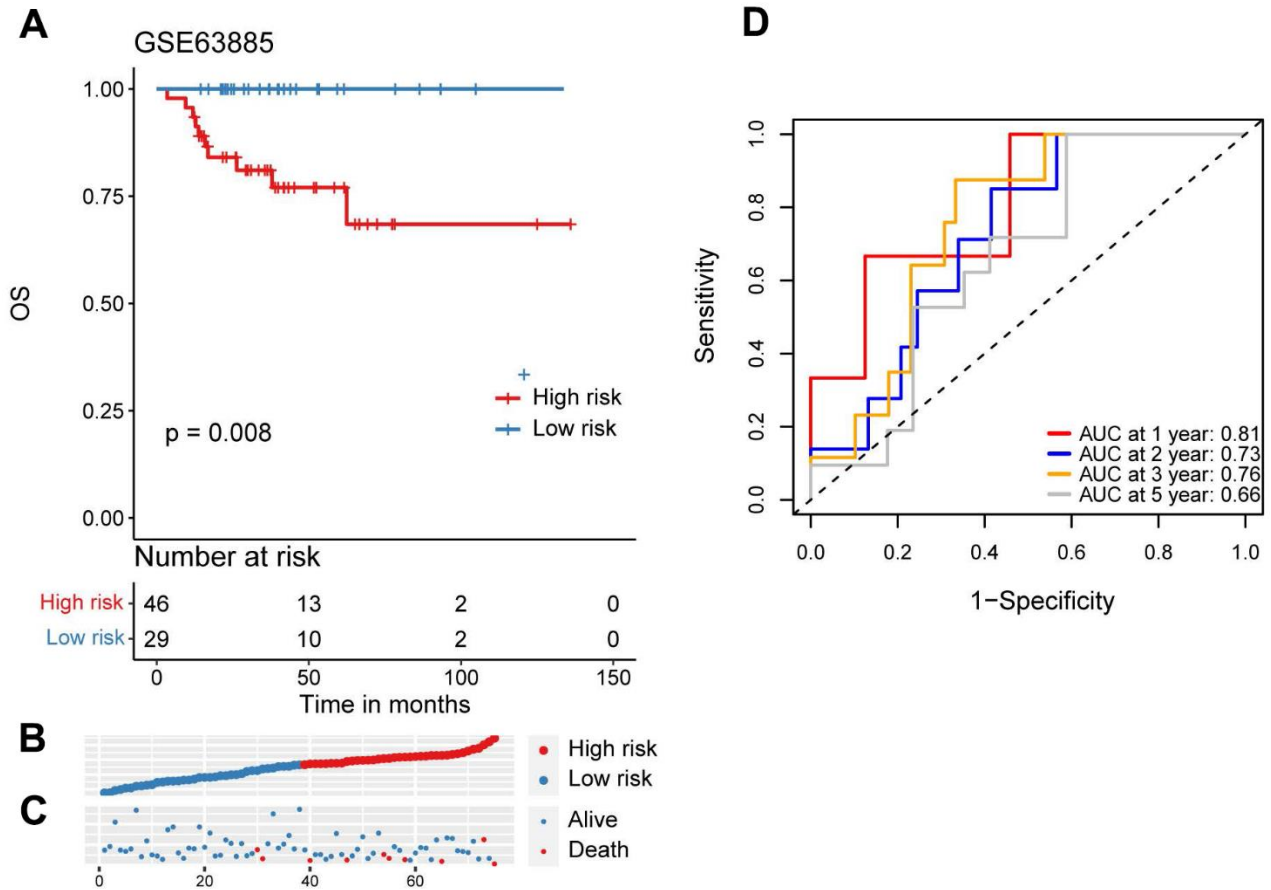
Supplementary Figure 2. Construction and validation of a prognostic model based on CD8$^+$ T cell markers in ovarian cancer.
(**A**) Kaplan-Meier survival analysis was performed on the relationship between the risk score and OS using the GSE63885 validation cohort.
(**B**) The rank of risk scores in the GSE63885 validation cohort. (**C**) Survival status in the GSE63885 validation cohort. (**D**) Time-dependent ROC curve analysis of the prognostic model (1, 2, 3, and 5 years) in the GSE63885 validation cohort.
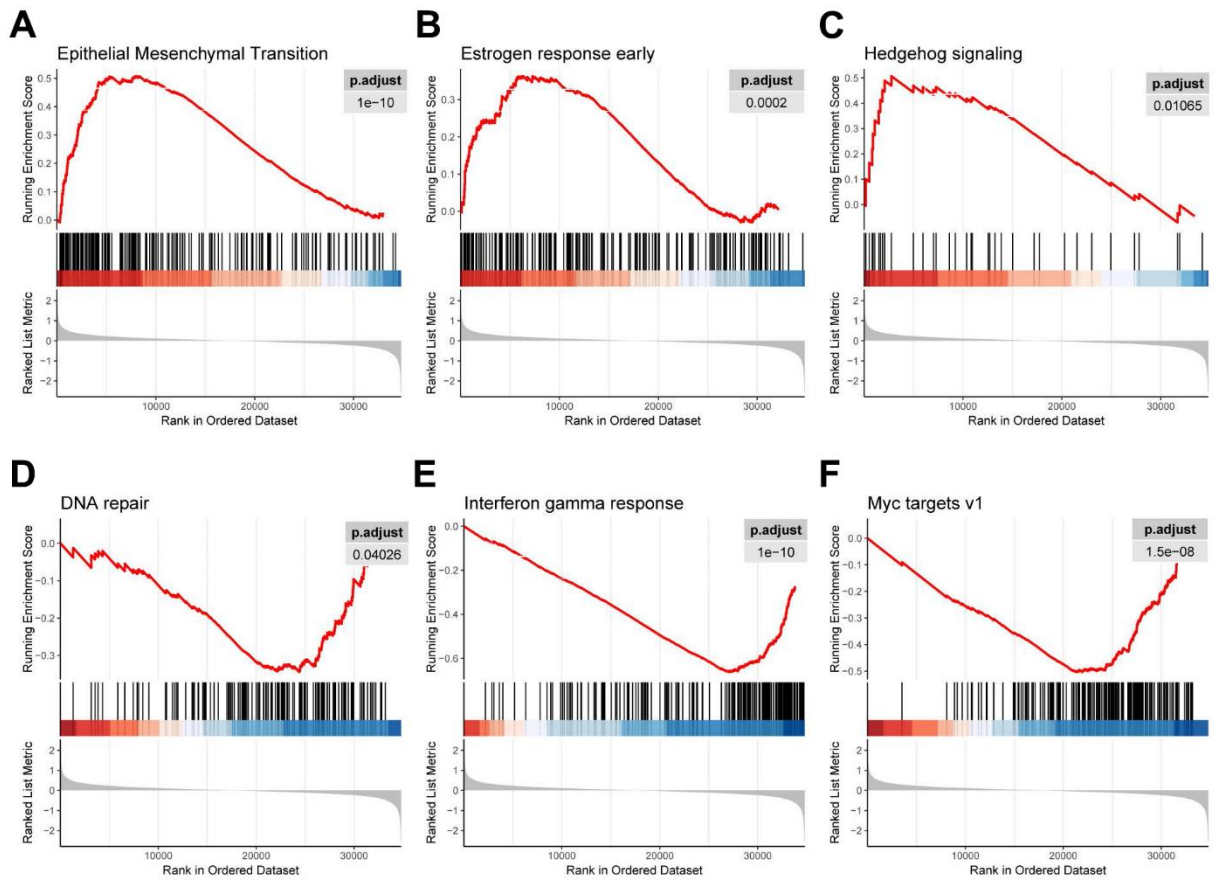
Supplementary Figure 3. Correlation between the risk score and pathway activities. (**A**–**C**) GSEA analysis showing the up-regulated pathways in the high-risk group. (**D**–**F**) GSEA analysis showing the up-regulated pathways in the low-risk group.
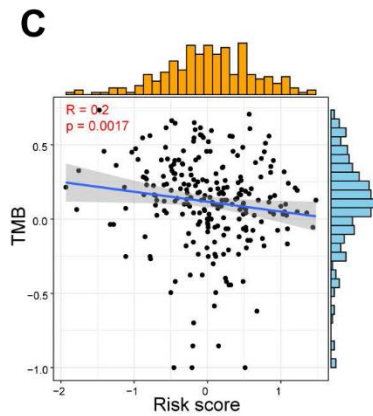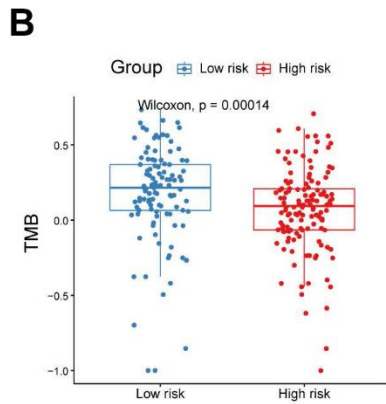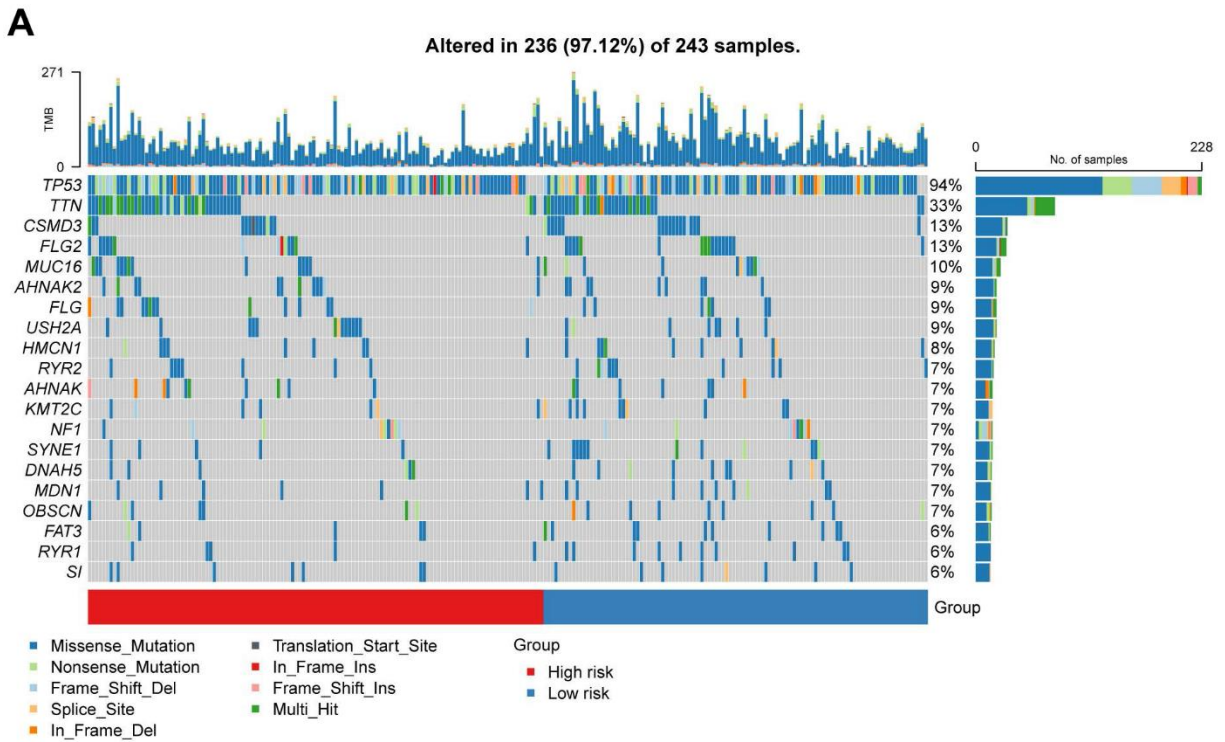
Supplementary Figure 4. Mutation analysis of high/low-risk groups (**A**). Comparison of the mutation landscape between groups with high/low risk. (**B**) TMB score in high/low-risk groups. (**C**) Spearman correlation between TMB score and risk score.