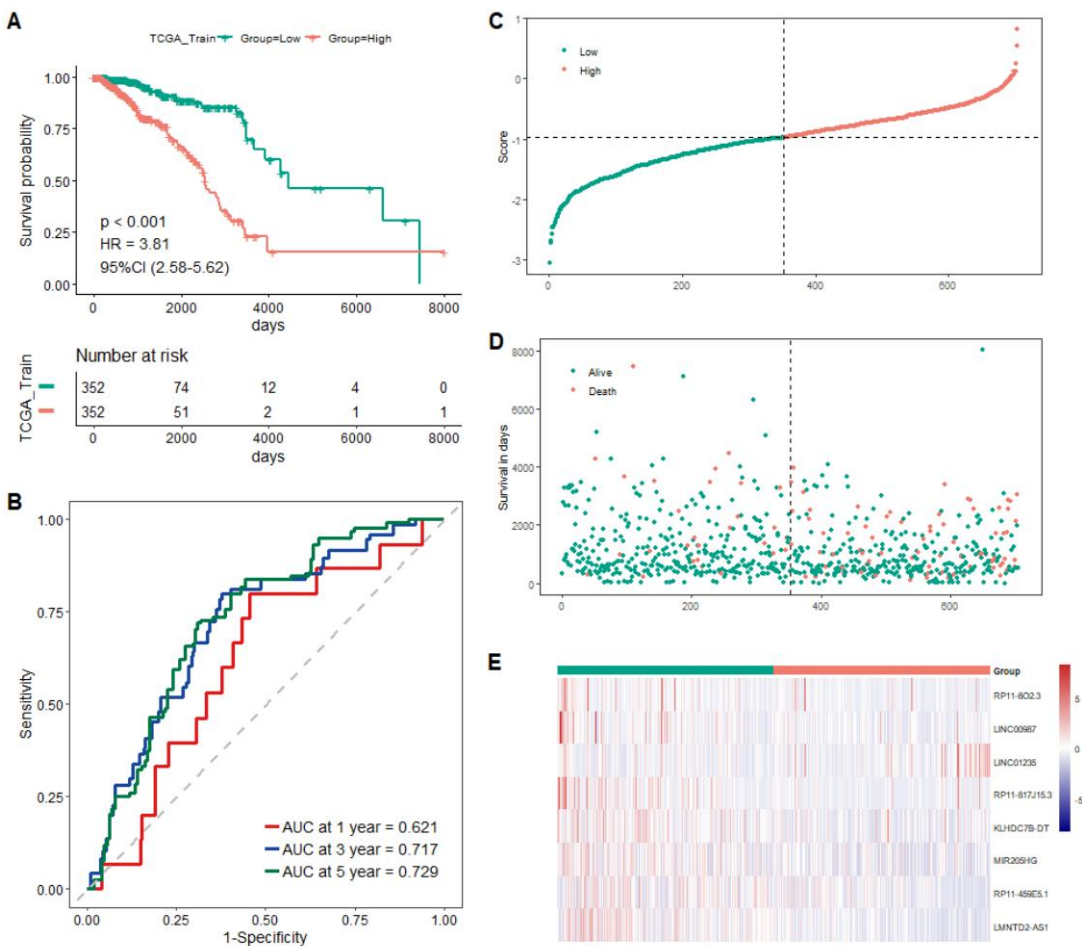


SUPPLEMENTARY MATERIAL

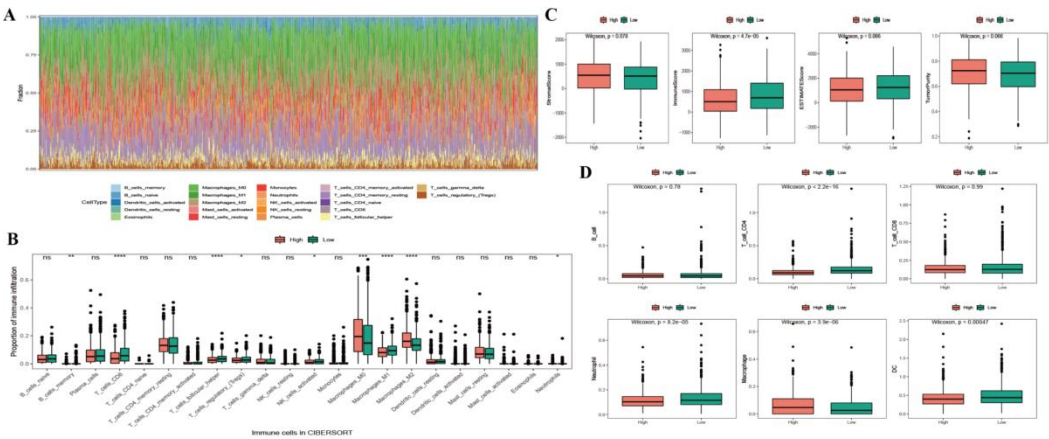
The Supplementary Material for this article can be found online at:*****.



(Supplementary Figure 1) .The TCGA training set was used to verify the prognostic efficacy of the model

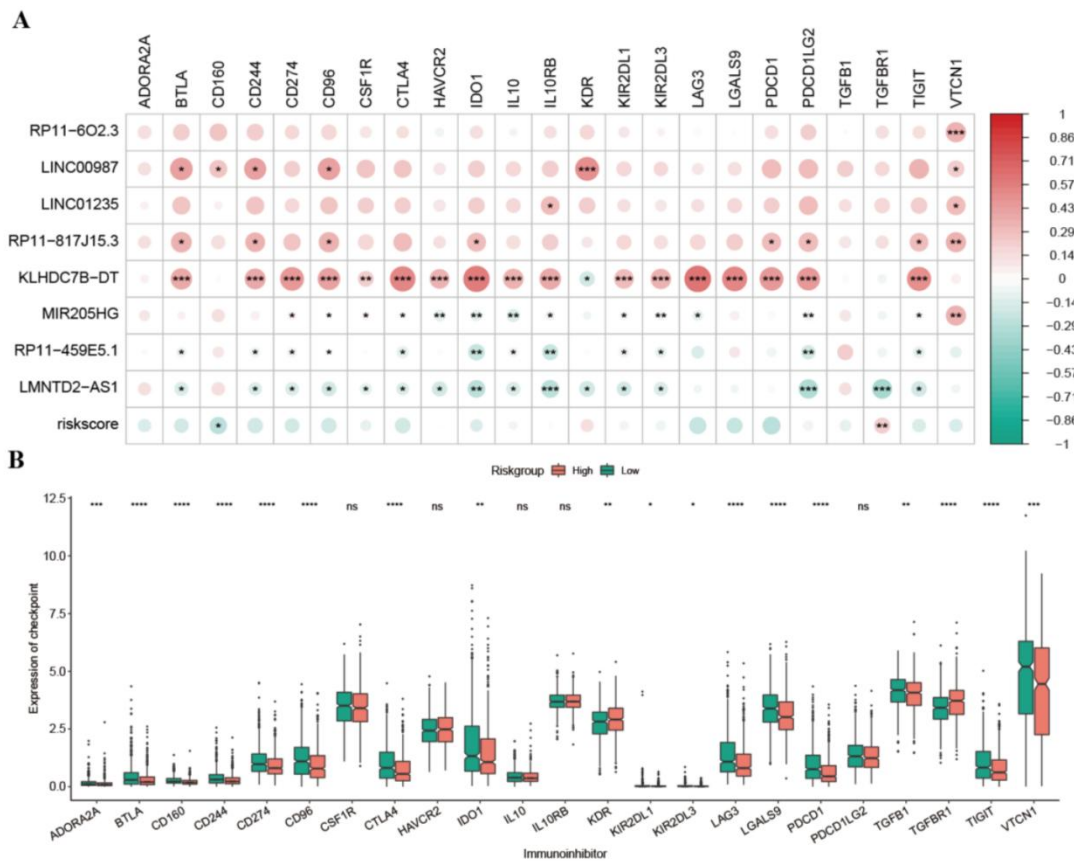
A: KM curve of TCGA training set; B: ROC curve of TCGA training set 3/5/10 years; C-E: risk triplet plot, which is the scatter plot of risk score, the scatter plot of survival time, and the heat map of the expression of model genes in the risk score grouping. Red represents the high-risk group, and green represents the low-risk group.

between HALLMARK pathway enrichment score and model gene expression and Riskscore with significant difference. The color and size of dots represent the level of correlation, and * represents the P value of significance. C: heat map of enrichment scores of KEGG pathways with significant differences screened out, * represents the significance P-value of the difference; D: Heat map of correlation between KEGG pathways with significantly differentially enriched and model gene expression and Riskscore.



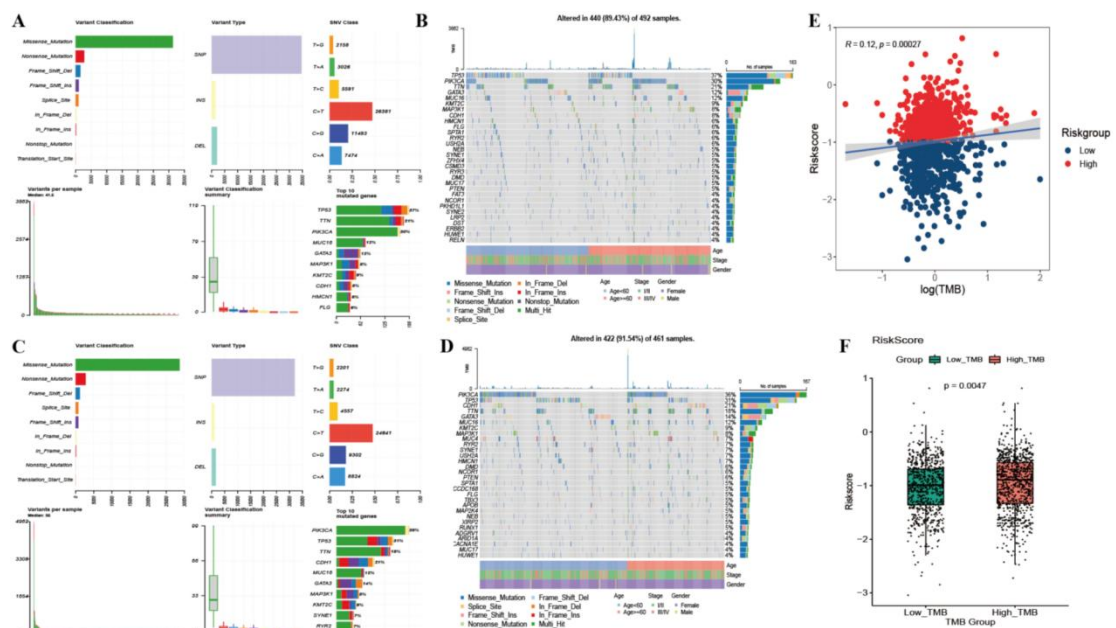
Supplementary Figure 4. Differences in the proportion of immune infiltrating cells between model groups

A: bar chart of the immune infiltration proportion results of CIBERSORT algorithm; B: CIBERSORT algorithm boxplot of the difference in the proportion of 22 immune cells infiltration, red is the high-risk group, green is the low-risk group. C: boxplots of stromal score, immune score, ESTIMATE score and tumor purity of the low and high risk groups, respectively. Red represents the high risk group and green represents the low risk group. D: Boxplot of the proportion of immune infiltrating cells in the low and high risk groups in the TIMER algorithm, with red for the high risk group and green for the low risk group.



Supplementary Figure 5. Correlation between model gene expression and proportion of immune cell infiltration

A: Heat map of correlation between model gene expression and immune checkpoint expression, red represents positive correlation, green represents negative correlation, and * represents significance; B: Boxplots of differential expression of 23 immune checkpoint inhibitors between low and high risk groups, with red representing the high-risk group and green representing the low-risk group.



Supplementary Figure 6. Genomic mutational differences between model groups

Summary information map of mutation in high and low risk group A/C; B/D: SNV waterfall plot of TOP30 (mutation frequency) gene in the high and low risk groups; E: Scatter plot of RiskScore correlation with TMB, red for high-risk group, blue for low-risk group; F: Boxplot of RiskScore distribution differences between high and low TMB groups, red for high TMB group and green for low TMB group.