

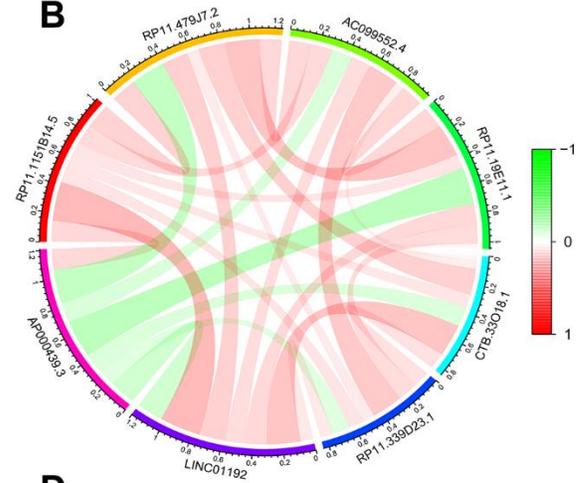
SUPPLEMENTARY FIGURES

A

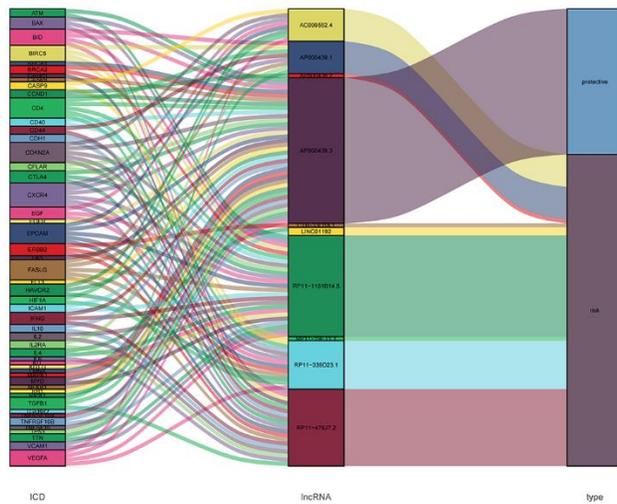
LncRNA	HR	lower 95%CI	upper 95%CI		pvalue
AP000439.3	0.844	0.792	0.899		0.000
RP11.1151B14.5	1.311	1.140	1.508		0.000
RP11.479J7.2	1.432	1.257	1.632		0.000
AC099552.4	1.979	1.504	2.603		0.000
RP11.19E11.1	1.291	1.167	1.428		0.000
CTB.33O18.1	1.277	1.125	1.449		0.000
RP11.339D23.1	1.550	1.320	1.821		0.000
LINC01192	1.390	1.187	1.628		0.000

0.5 1 1.5
Hazard ratios

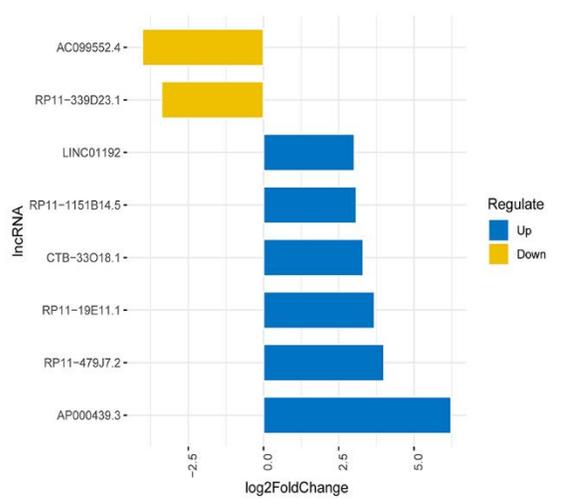
B



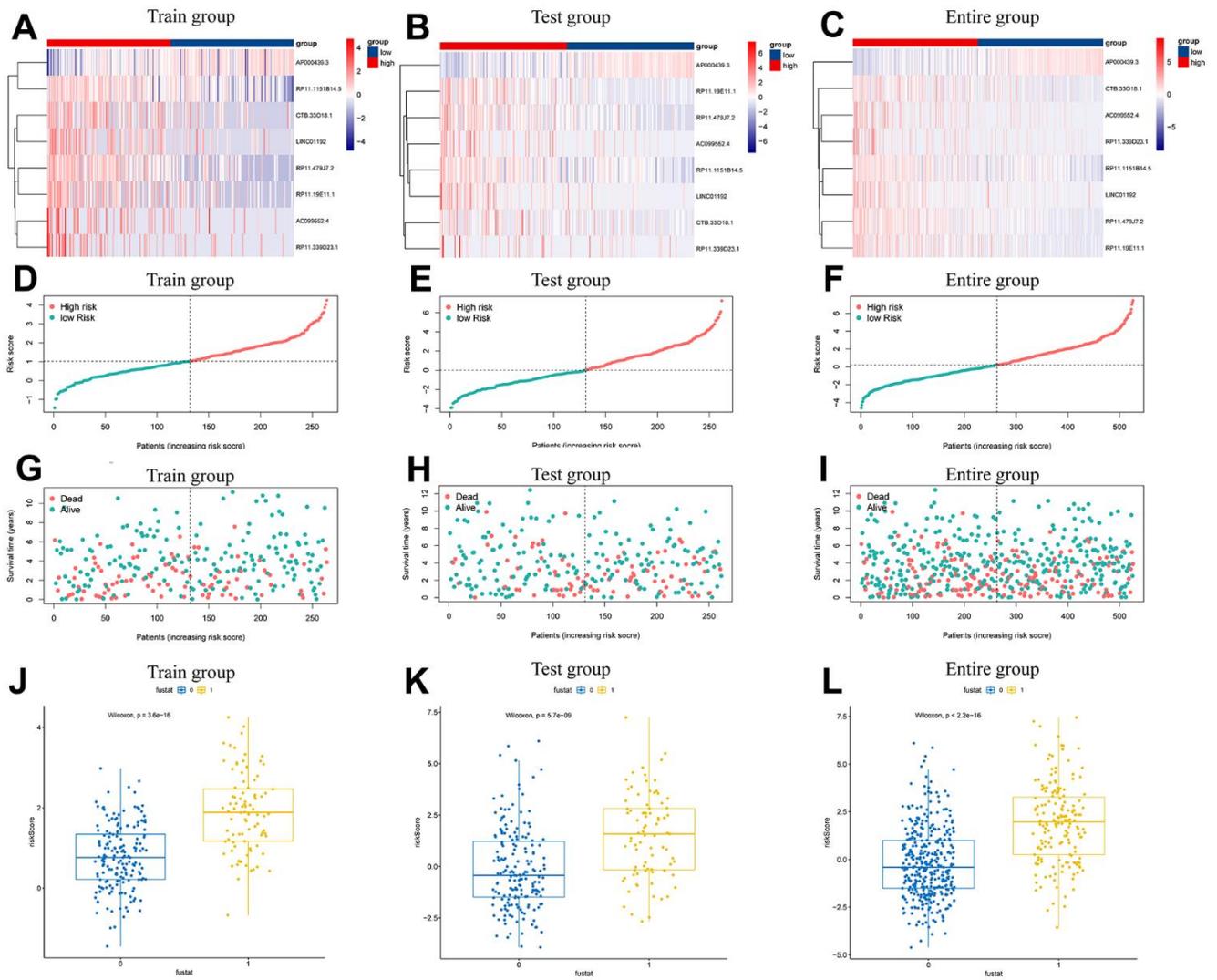
C



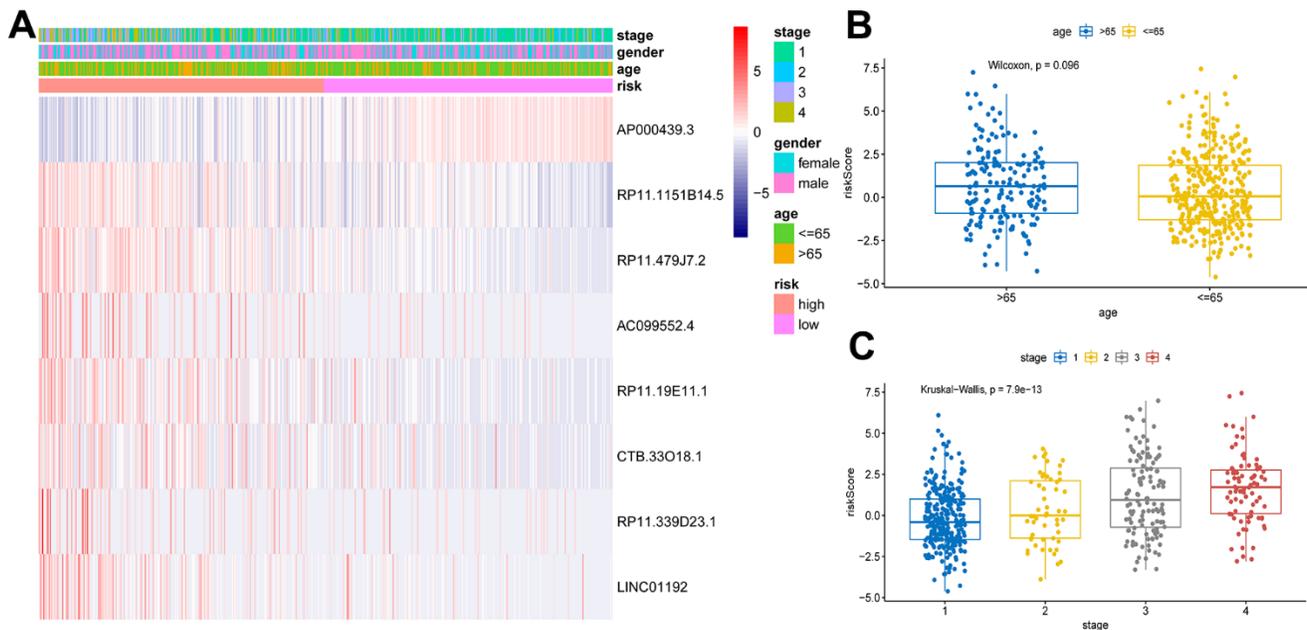
D



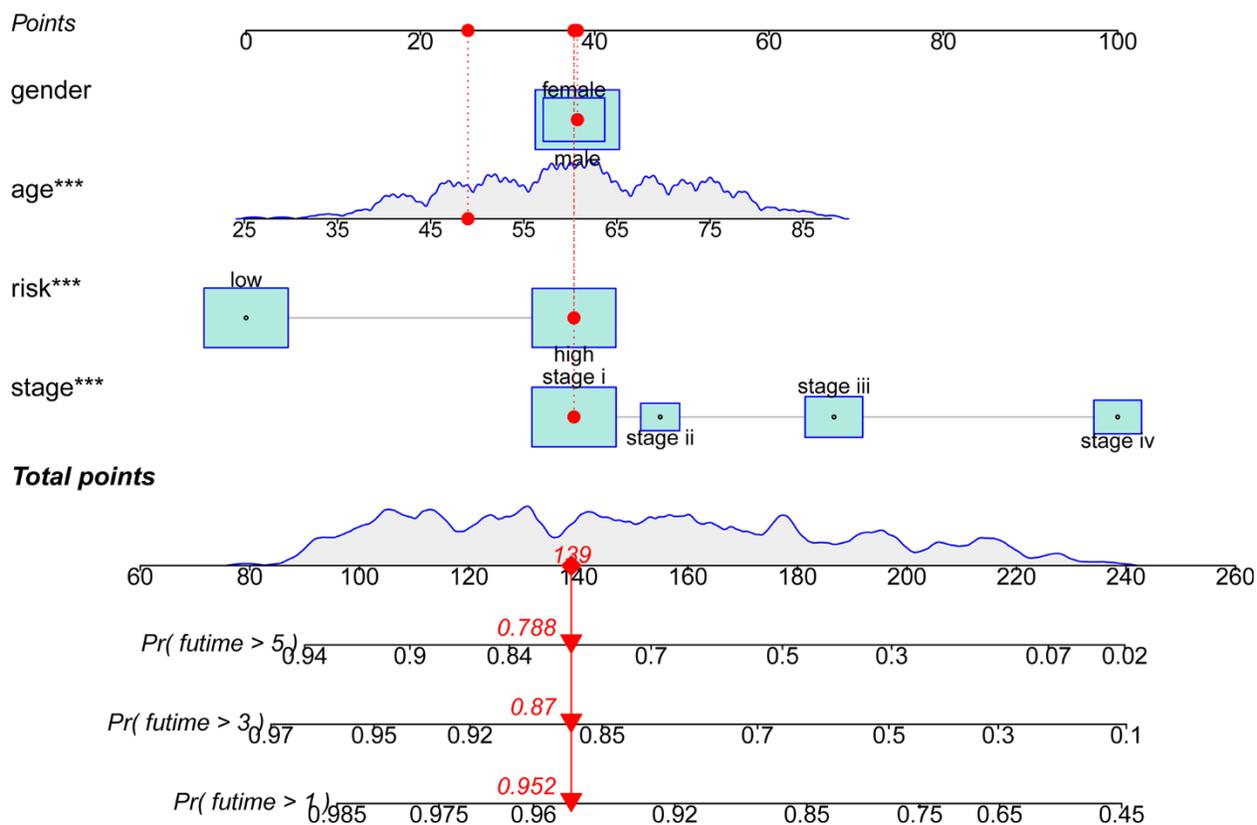
Supplementary Figure 1. Construct a prognostic model. Forest plots associated with multifactor regression (A); Correlation circle plot of 8 ICD-related lncRNAs (B); Mulberry plots of 8 ICD-related lncRNAs with ICD-related genes (C); Deviation plots indicating up- and down-regulation changes of 8 ICD-related lncRNAs (D).



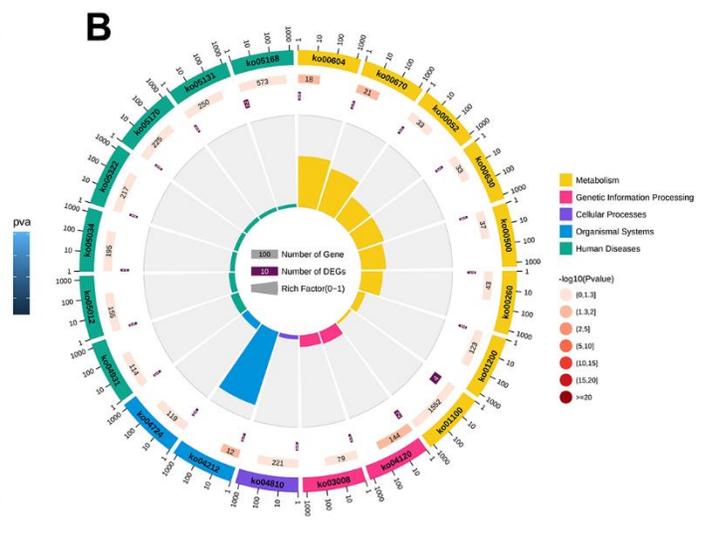
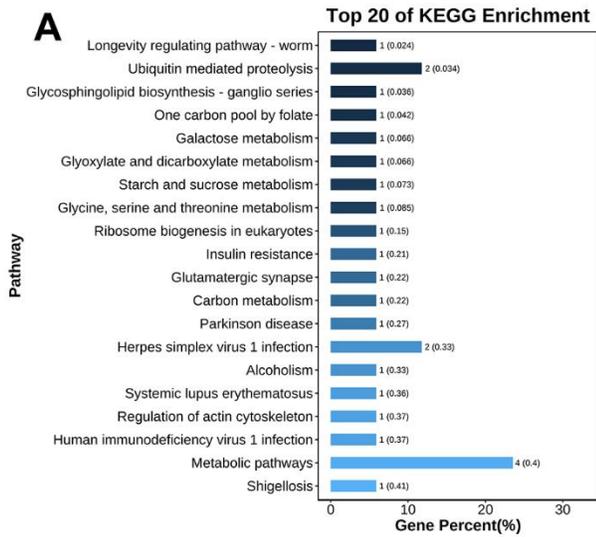
Supplementary Figure 2. The model prediction effect is validated by the training group, test group, and the entire group. Heat map of 8 ICD-related lncRNA expressions (A–C). Risk curve for risk scores (D–F) and Scatterplot (G–I) for the survival status of each patient; Scatterplot of risk scores of patients with different survival statuses (J–L).



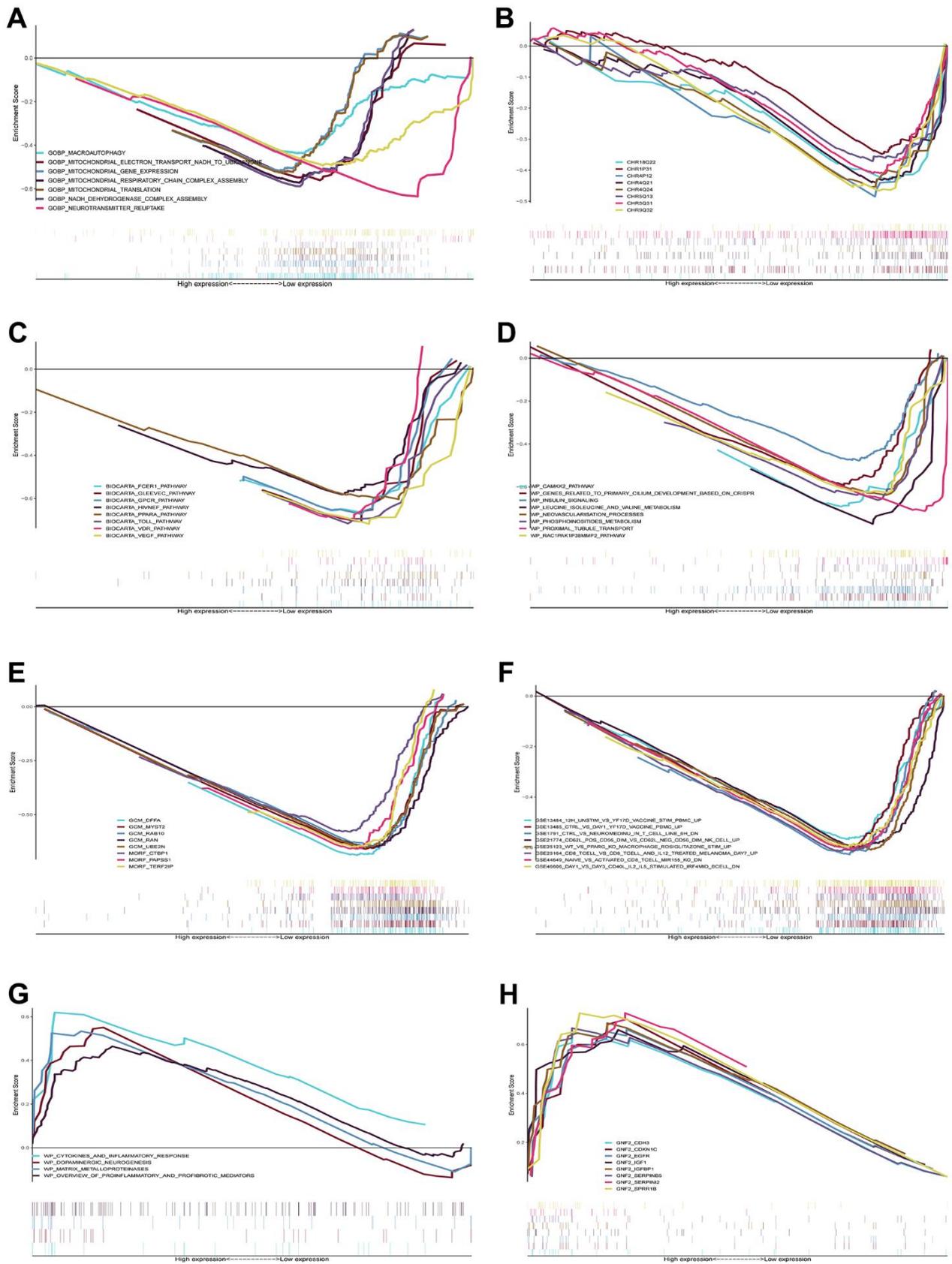
Supplementary Figure 3. Further validation of model effects. IncRNA signature expression heat map with clinical information (A); Correlation analysis of risk signature with age (B) and stage (C).



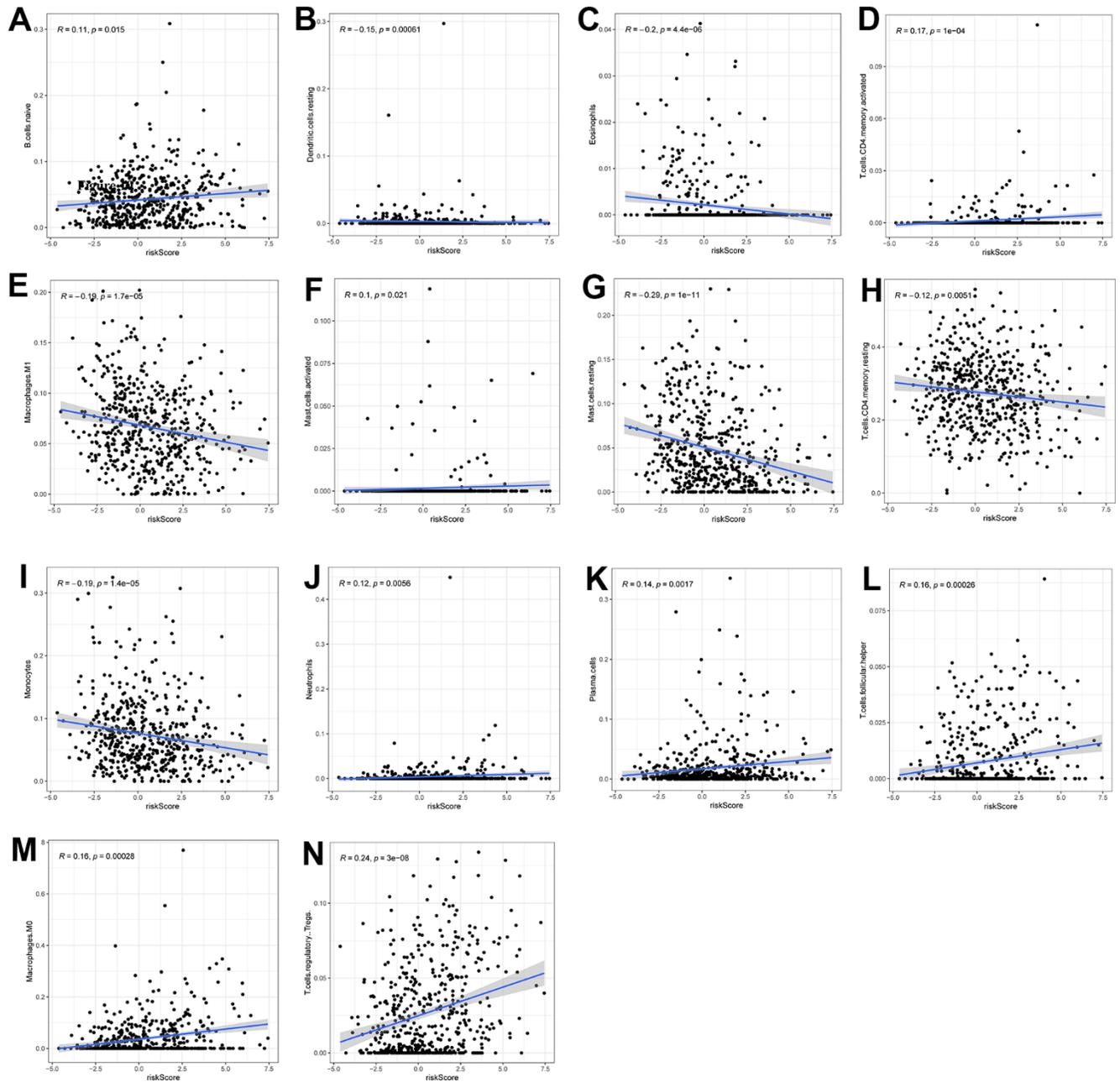
Supplementary Figure 4. Nomogram with patient verification.



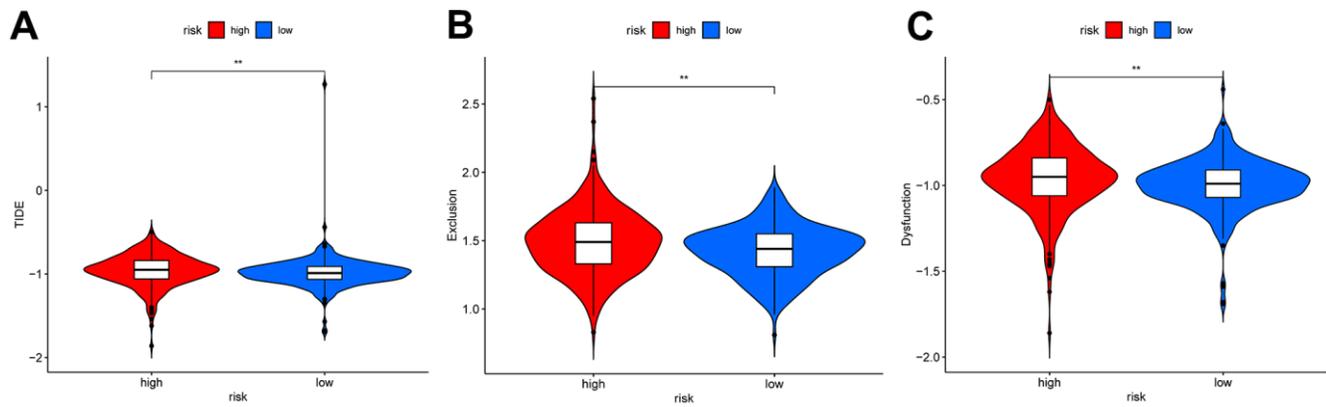
Supplementary Figure 5. KEGG enrichment analysis. Bar chart (A); Circle chart (B).



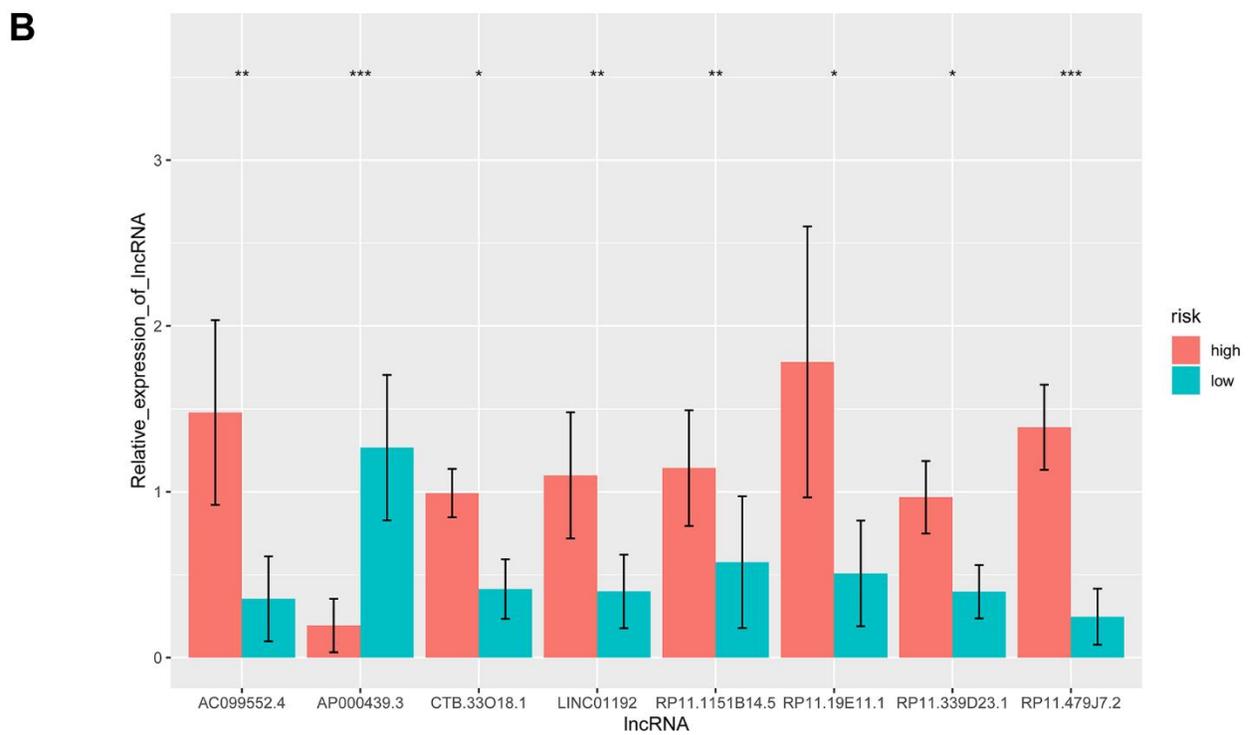
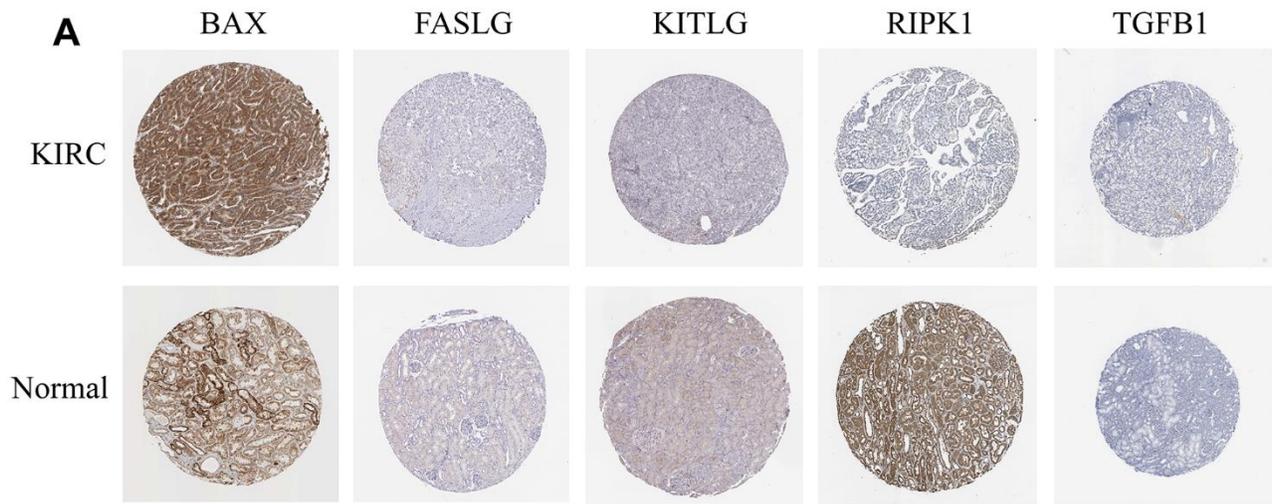
Supplementary Figure 6. GSEA enrichment analysis. Enrichment pathways in low-risk group in different gene sets (A–F); Enrichment pathways in high-risk group in different gene sets (G, H).



Supplementary Figure 7. Correlation plot of risk scores with immune cells. Scatter plot of the correlation between risk scores and naïve B cells (A), resting dendritic cells (B), eosinophils (C), activated CD4 memory T cells (D), macrophages M1 (E), activated mast cells (F), resting mast cells (G), resting CD4 memory T cells (H), monocytes (I), neutrophils (J), plasma cells (K), T follicular helper cells (L), macrophages M0 (M), regulatory T cells (Treg) (N).



Supplementary Figure 8. The ICD-relevant lncRNA risk pattern in tumor therapy. Differences in TIDE (A) and immune exclusion (B) and dysfunction (C) in high and low-risk groups. * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$.



Supplementary Figure 9. *In vitro* experimental validation of the risk model. Immunohistochemical staining images of partial ICD-associated gene proteins in KIRC tissue and normal tissue (A); Relative expression of 8 ICD-related lncRNAs in different risk subgroups (B). * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$, **** $p < 0.0001$.