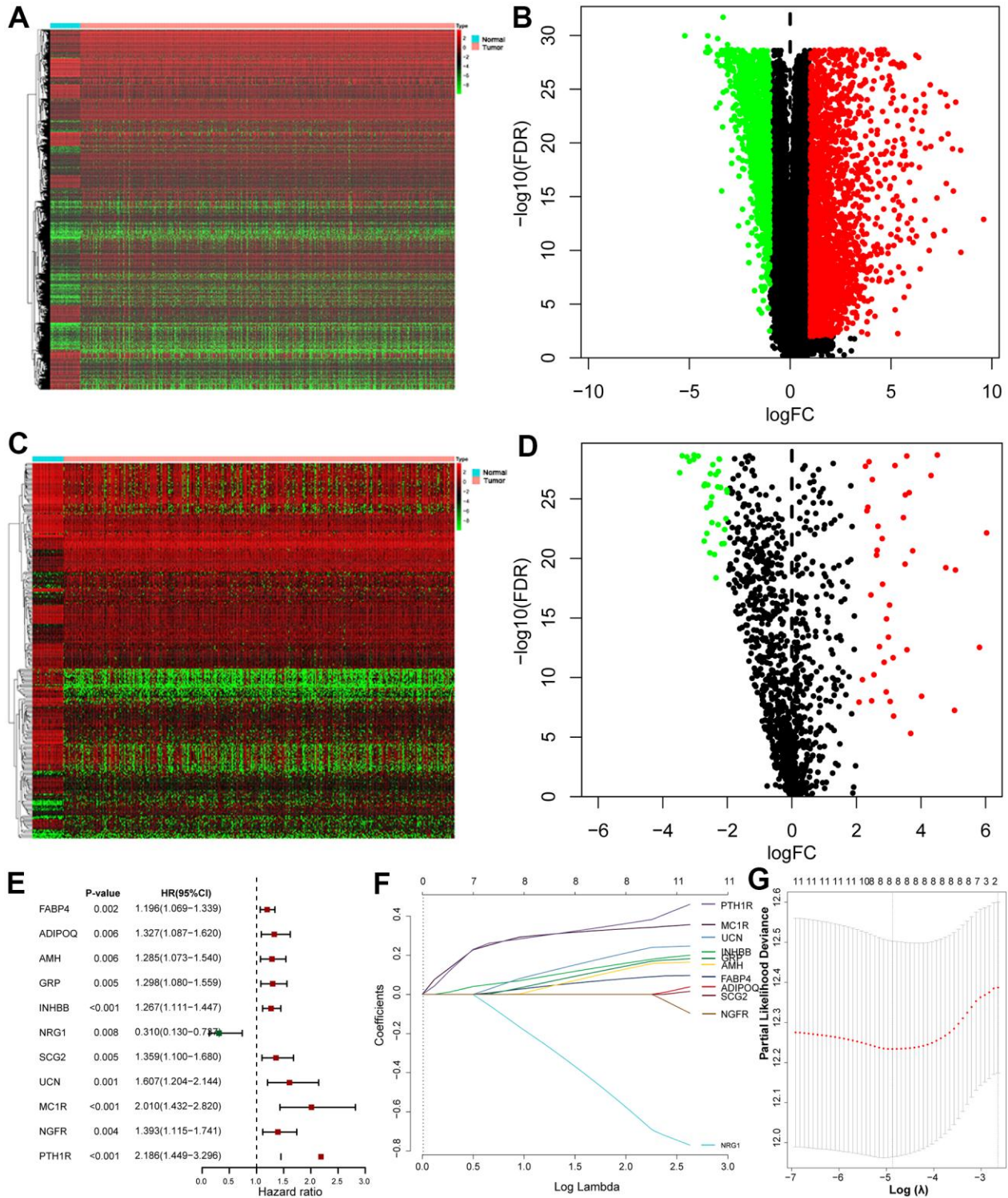
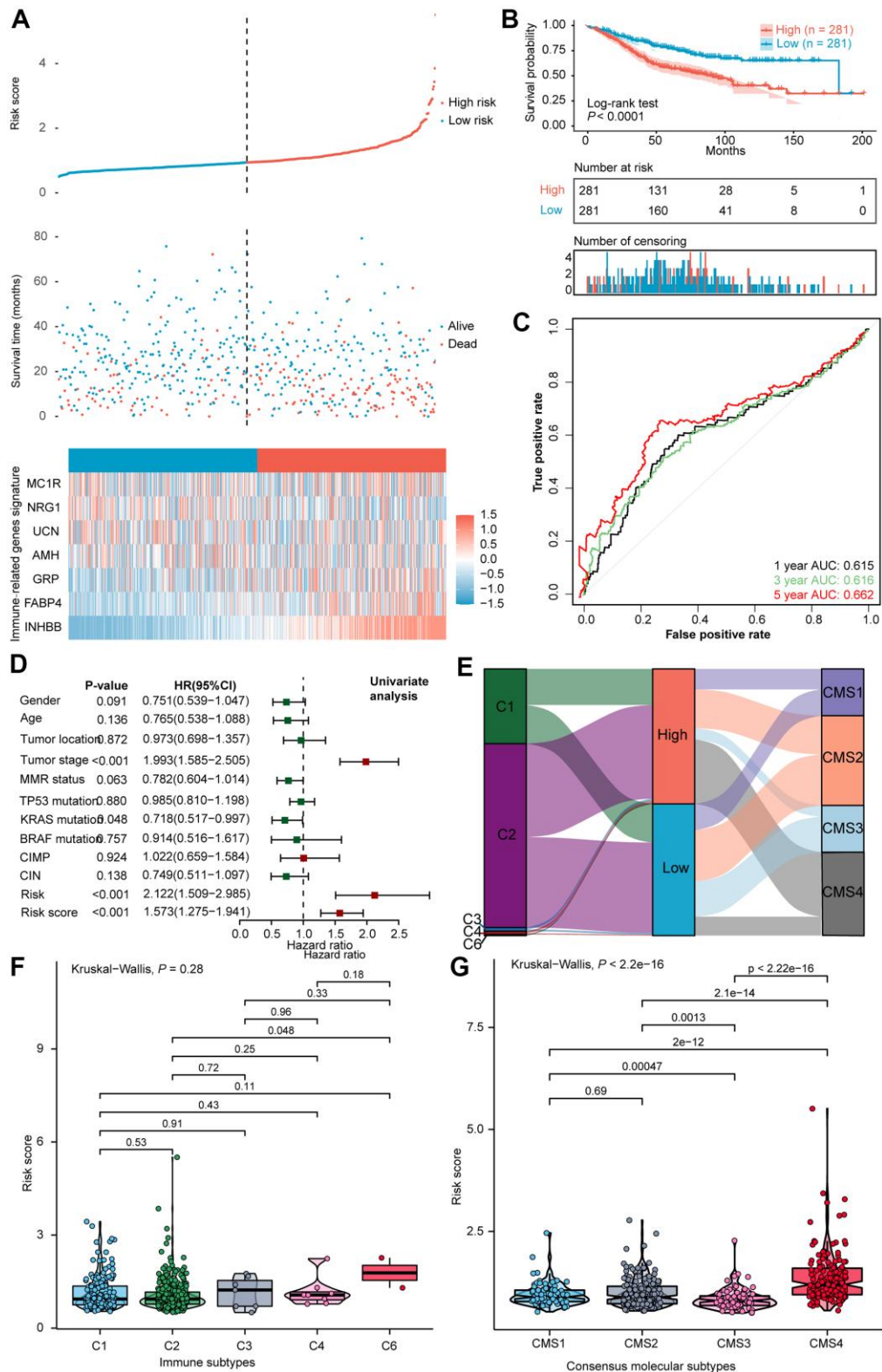


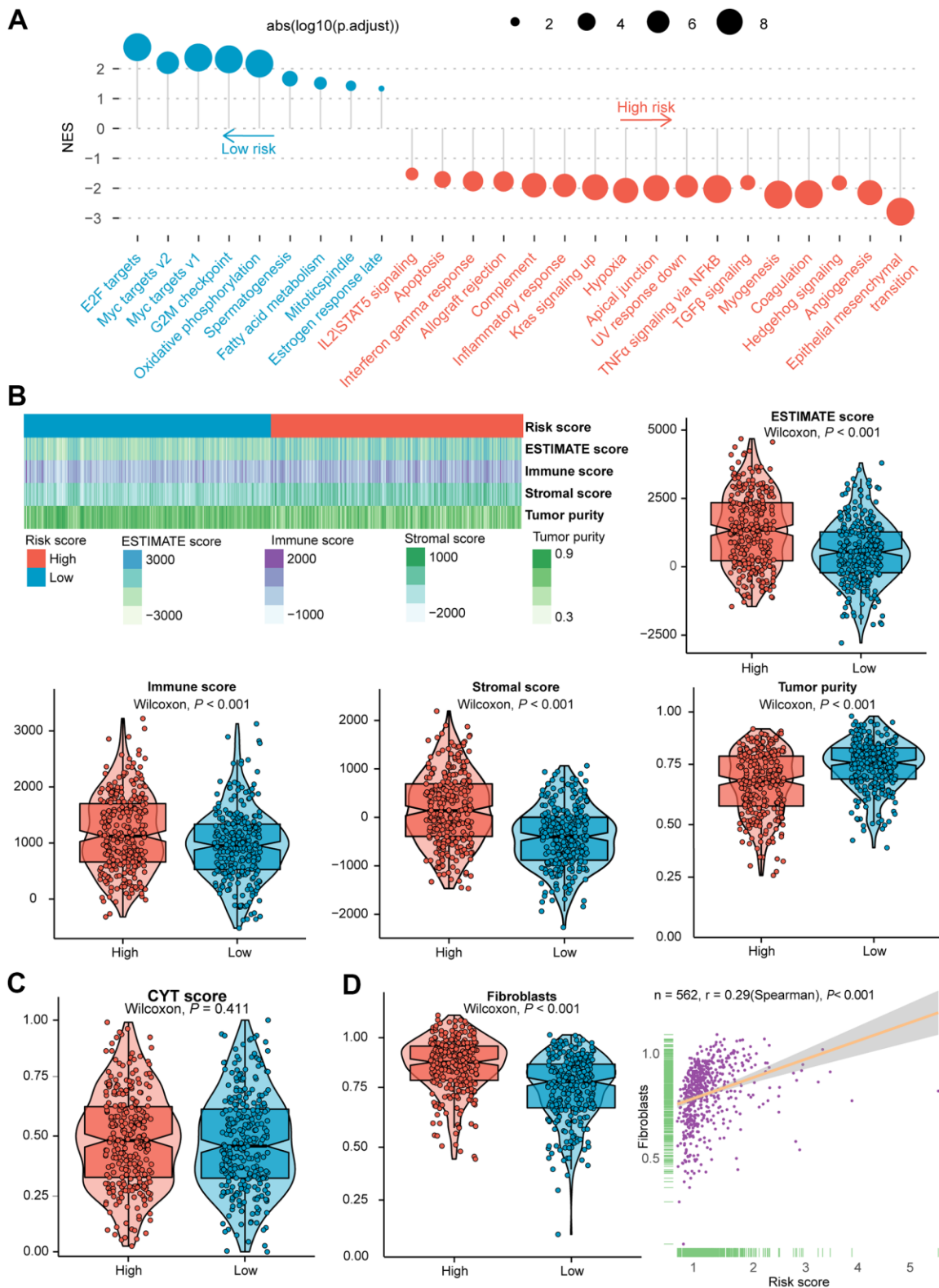
SUPPLEMENTARY FIGURES



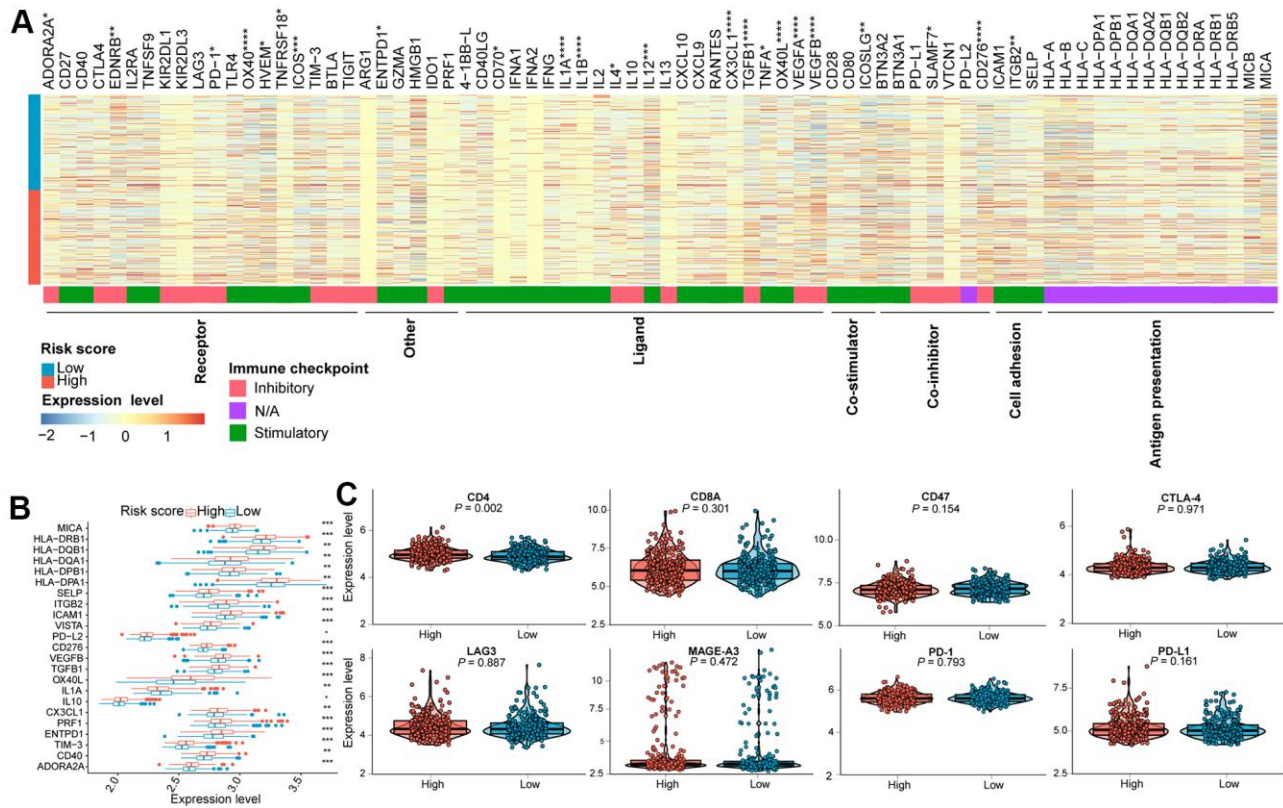
Supplementary Figure 1. Construction of the IRGs-based risk score model through TCGA training cohort. (A, B) Differentially expressed genes in CRC. **(C, D)** Differentially expressed IRGs in CRC. **(E)** Forest plot of PRIRGs via univariate Cox regression analysis. **(F)** lasso coefficient profiles of 11 PRIRGs. **(G)** Partial likelihood deviance of variables estimated by the lasso regression algorithm. CRC, colorectal cancer; IRGs, immune-related genes; PRIRGs, prognosis-related IRGs.



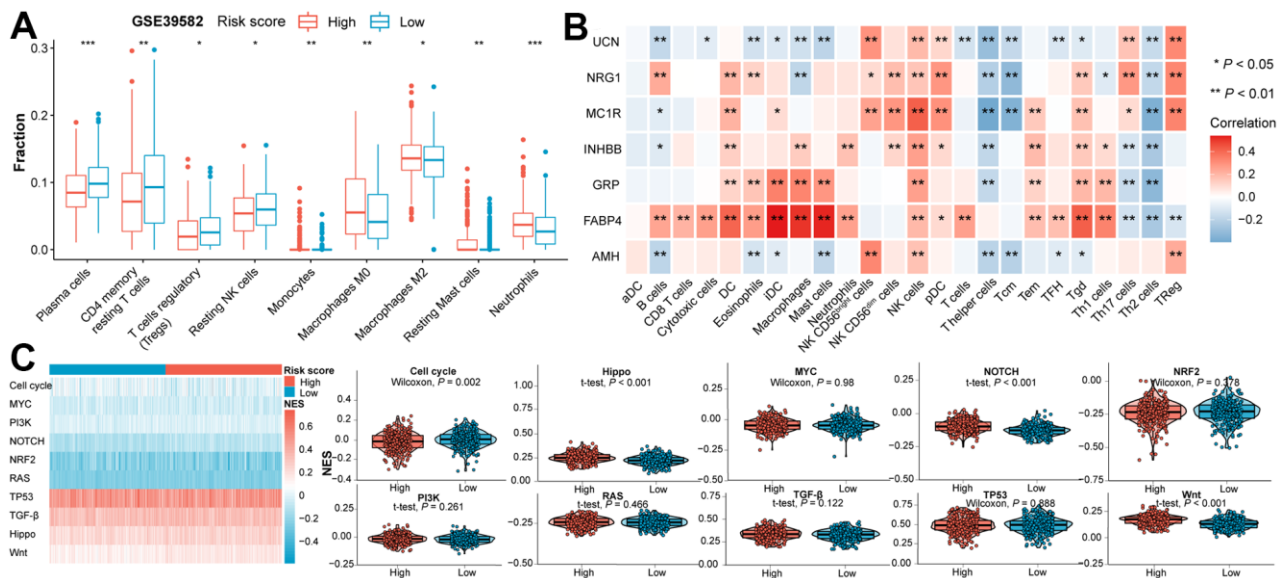
Supplementary Figure 2. Exploration of the predictive power and clinical characteristics of seven IRGs signature in the validation cohort. (A) Distribution of risk score, survival status, and the expression of seven IRGs of CRCs. (B) Kaplan-Meier survival curve of the high- and low- risk subgroups. (C) ROC curve analysis of IRGs in the validation cohort. (D) Univariate Cox analysis of prognostic factors and OS of CRCs. (E) Alluvial diagram for the two subtypes versus different immune subtypes and CMS. (F) Violin plot illustrated the correlation between risk score and immune subtypes, and (G) CMS. AUC, area under the curve; OS, overall survival; CRC, colorectal cancer; IRGs, immune-related genes; ROC, receiver operating characteristic; CMS, consensus molecular subtypes.



Supplementary Figure 3. Evaluation of the role of the risk score in the validation cohort. (A) Results of GSEA of the high-risk group (red) compared with the low-risk group (blue). Color toward gray represents no statistical significance. (B) Heatmap and violin plots of the ESTIMATE score, immune score, stromal score, tumor purity between high- and low- risk subtypes. (C) Violin plot of the CYT score between high- and low- risk subtypes. (D) Violin plot of fibroblasts between two subtypes, and the association between risk score and the NES of fibroblasts. Statistical significance at the level of ns ≥ 0.05 , * < 0.05 , ** < 0.01 and *** < 0.001 . GSEA, gene set enrichment analysis; CYT, cytolytic activity; NES, normalized enrichment score.



Supplementary Figure 4. (A) The differential expression levels of immune checkpoint molecules within distinctive subgroups in the TCGA CRCs. (B) The differential expression level of immune checkpoint molecules between two subclasses with statistical significance in the validation cohort. (C) Violin plots of the CD4, CD8A, CD47, CTLA4, LAG3, MAGE-A3, PD-1 and PD-L1 expression levels for two subtypes in the validation cohort.



Supplementary Figure 5. (A) Immune infiltration between high- and low- risk subtypes with statistical significance in the validation cohort. (B) Correlation analysis between the expression of seven IRGs and the infiltration of immune cells in the validation cohort. (C) Heatmap and violin plots of the NES of 10 oncogenic pathways between two subtypes in the validation cohort. Statistical significance at the level of $n_s \geq 0.05$, * < 0.05 , ** < 0.01 and *** < 0.001 .