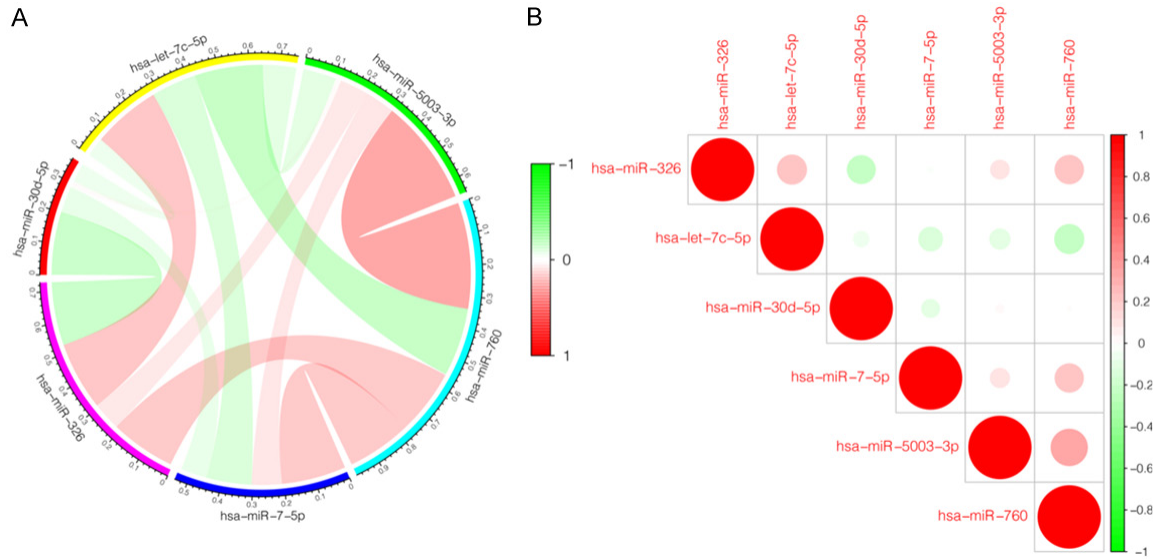
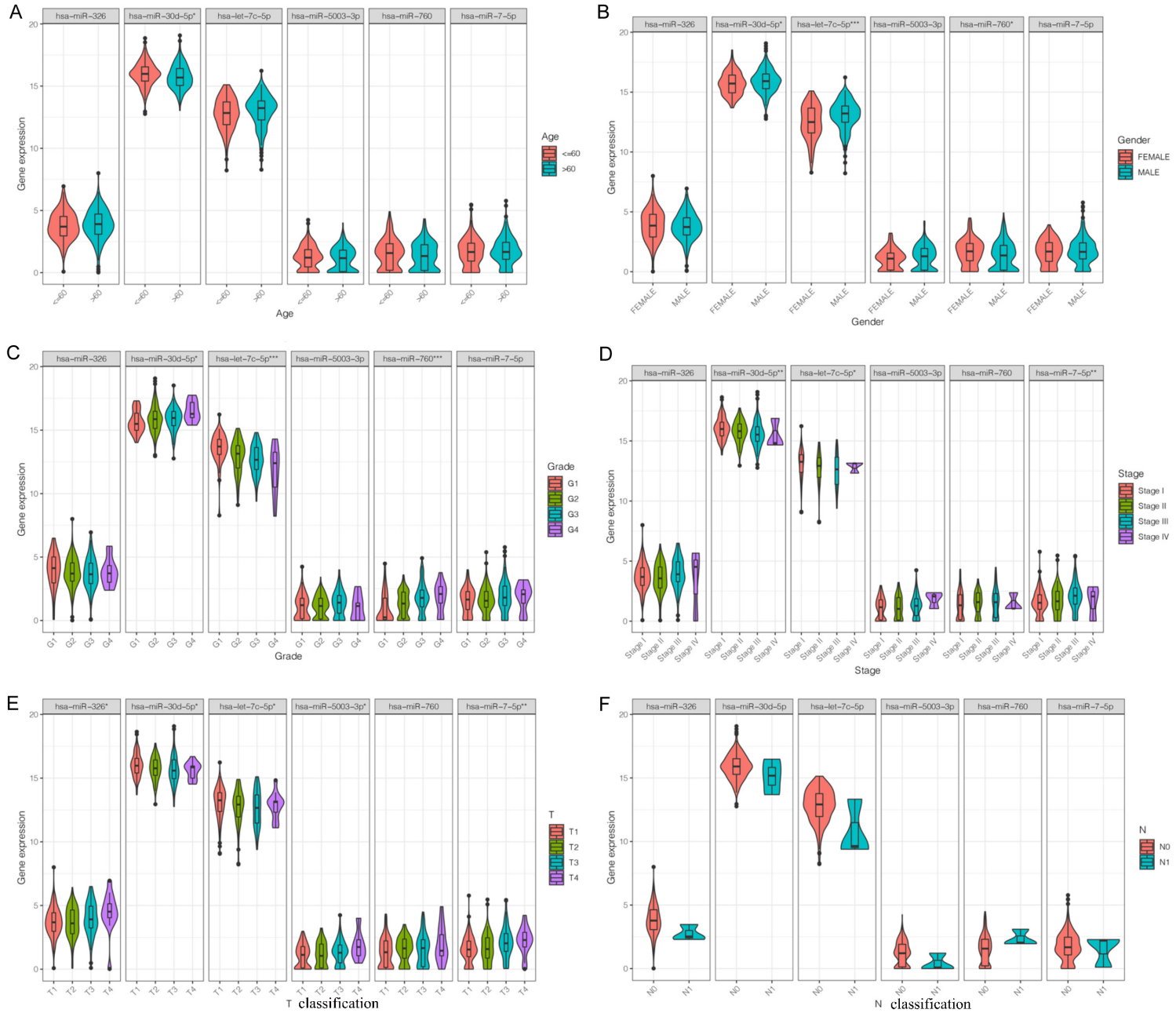


# A miRNAs prognostic signature for hepatocellular carcinoma

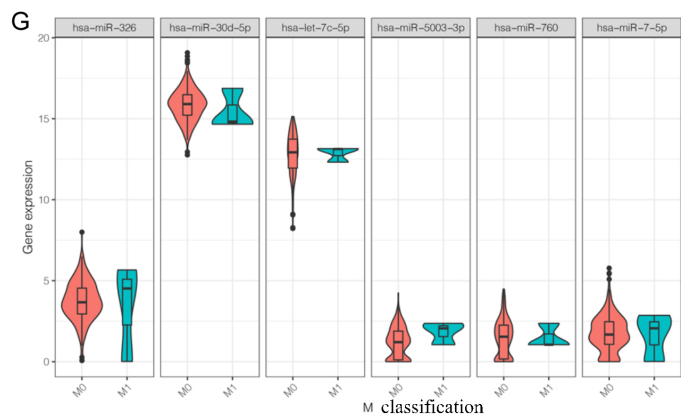


**Figure S1.** Correlation analysis among six miRNAs. A, B. Pearson correlation analysis of the six miRNAs in HCC.

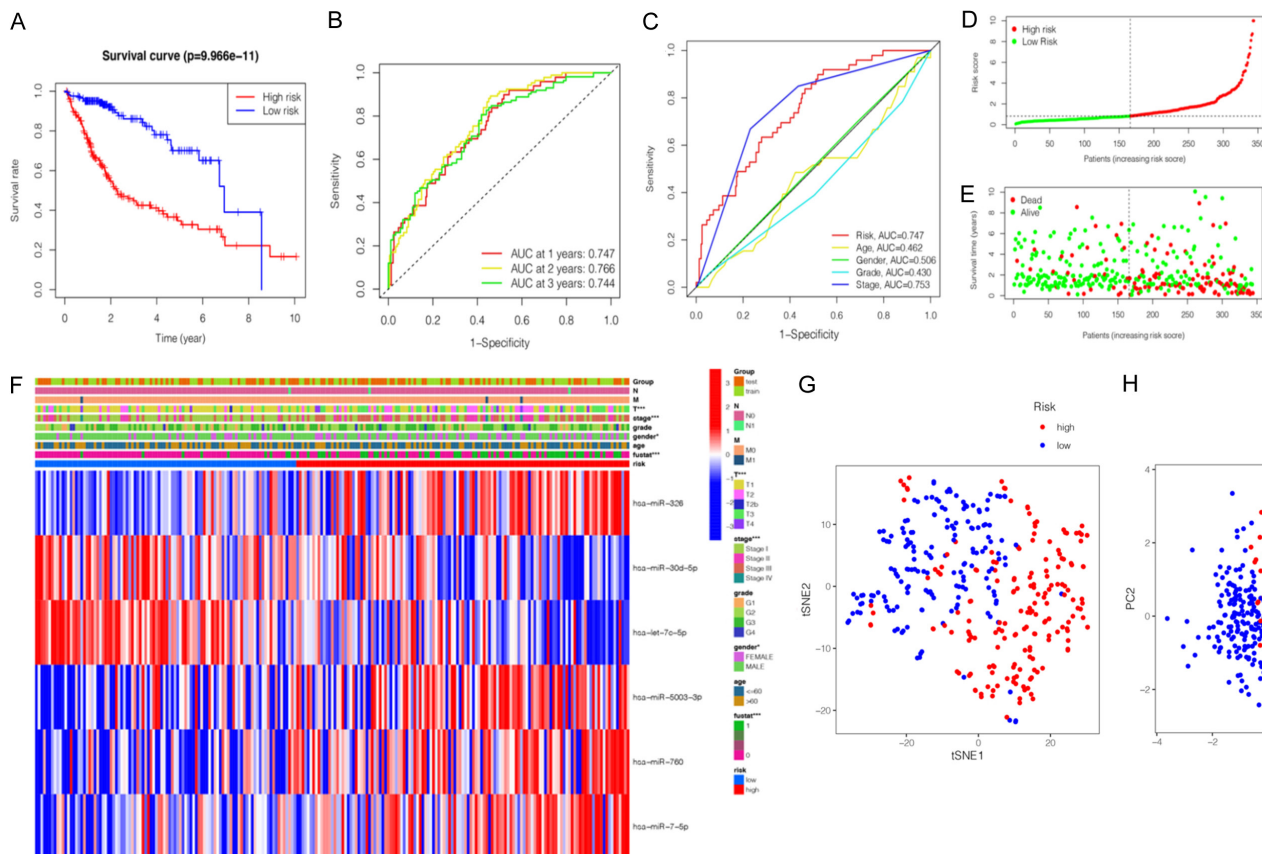
# A miRNAs prognostic signature for hepatocellular carcinoma



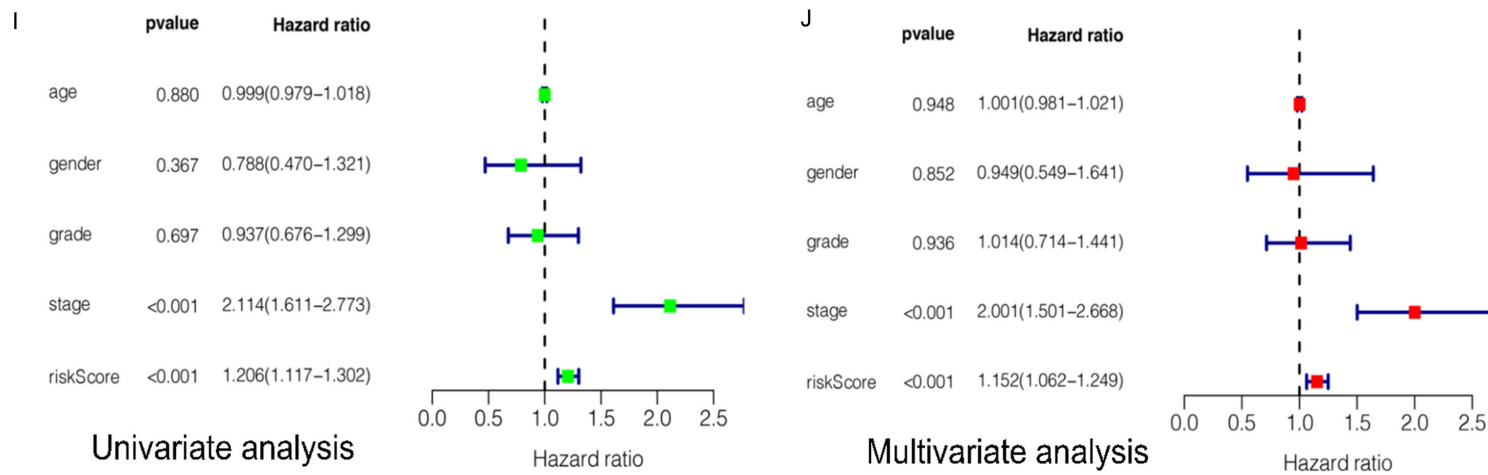
# A miRNAs prognostic signature for hepatocellular carcinoma



**Figure S2.** The relationships between six miRNAs and clinicopathological parameters. (A) age (B) gender (C) clinical grade (D) clinical stage (E) T classification (F) N classification (G) M classification.

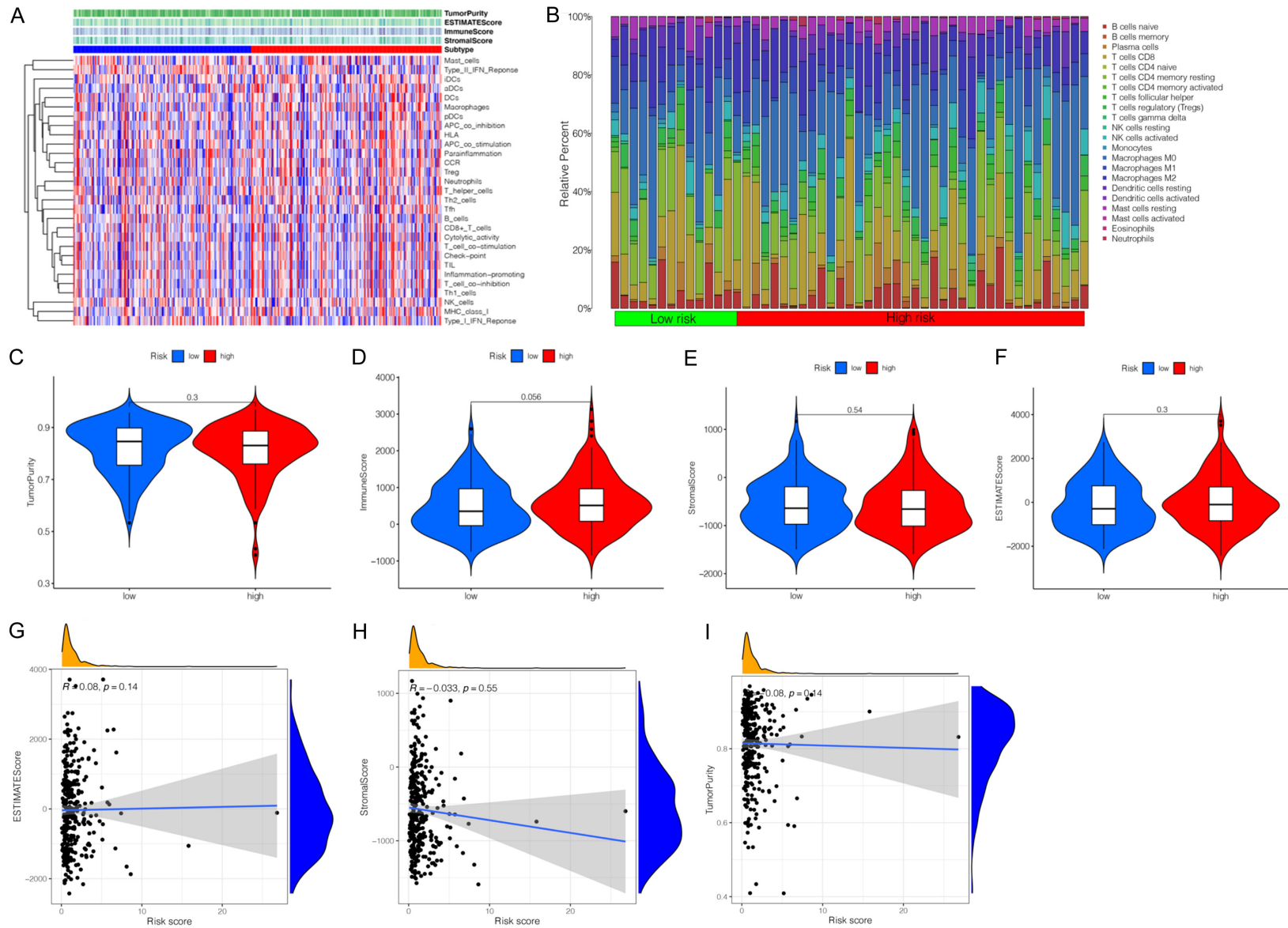


## A miRNAs prognostic signature for hepatocellular carcinoma



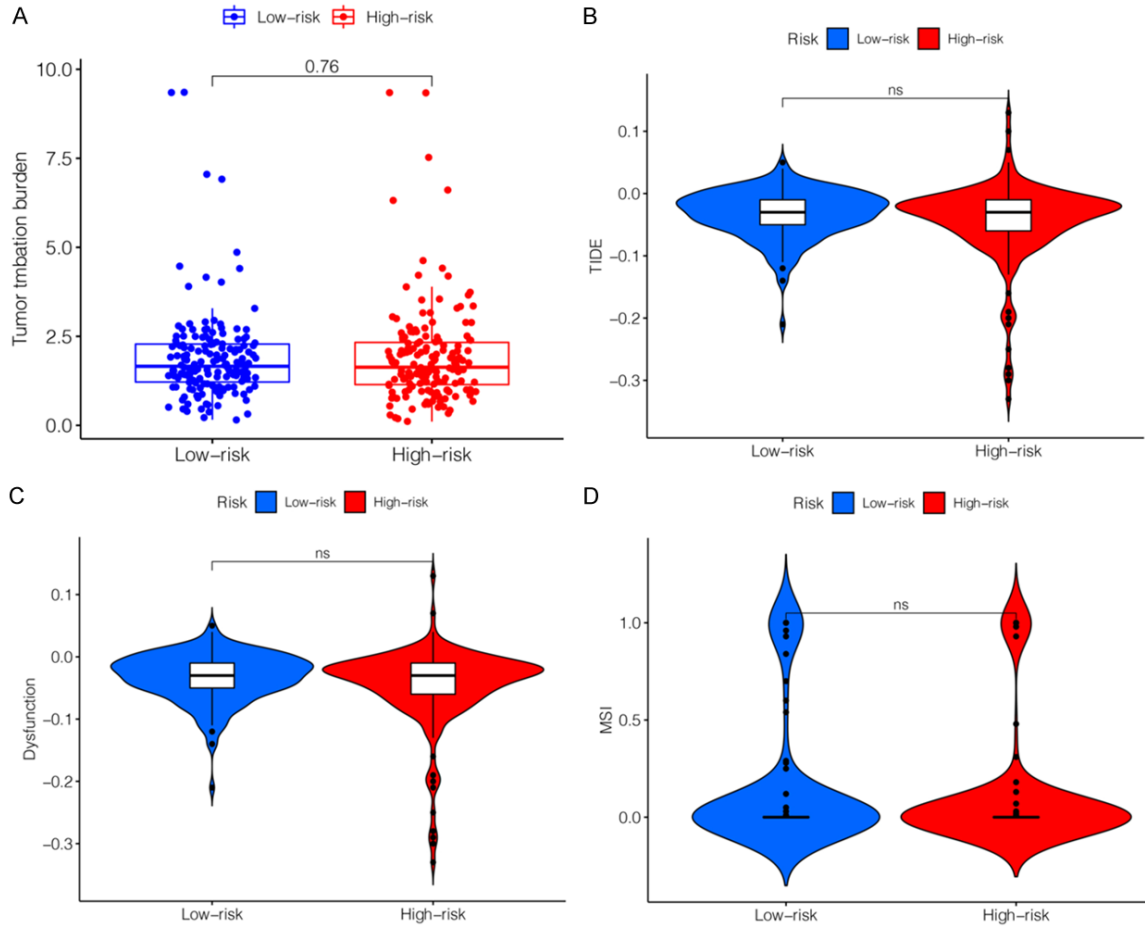
**Figure S3.** Validation and evaluation prognostic miRNA-related signature for hepatocellular carcinoma (HCC) in entire cohort. (A) Kaplan-Meier survival curves for the high- and low-risk subgroups. (B) Time dependent receiver operating characteristic (ROC) curves of prognostic signature predicting the overall survival (OS) at 1-, 2-, and 3-years. (C) ROC curves for prognostic signature and other clinicopathological characteristics in predicting the OS of HCC patients. (D) Distribution of miRNA-related risk score between the high- and low-risk subgroups. (E) Distribution of survival status of HCC patients in high- and low-risk subgroups. (F) Heatmap showed the relationship between the expression levels of six miRNAs and other clinicopathological factors. (G, H) Principal component analysis (PCA) and t-distributed stochastic neighbor embedding (t-SNE) of prognostic signature between the high-risk and low-risk subgroups. (I) Univariate Cox regression analyses of prognostic signature and other clinicopathological characteristics. (J) Multivariate Cox regression analyses prognostic signature and other clinicopathological characteristics.

## A miRNAs prognostic signature for hepatocellular carcinoma



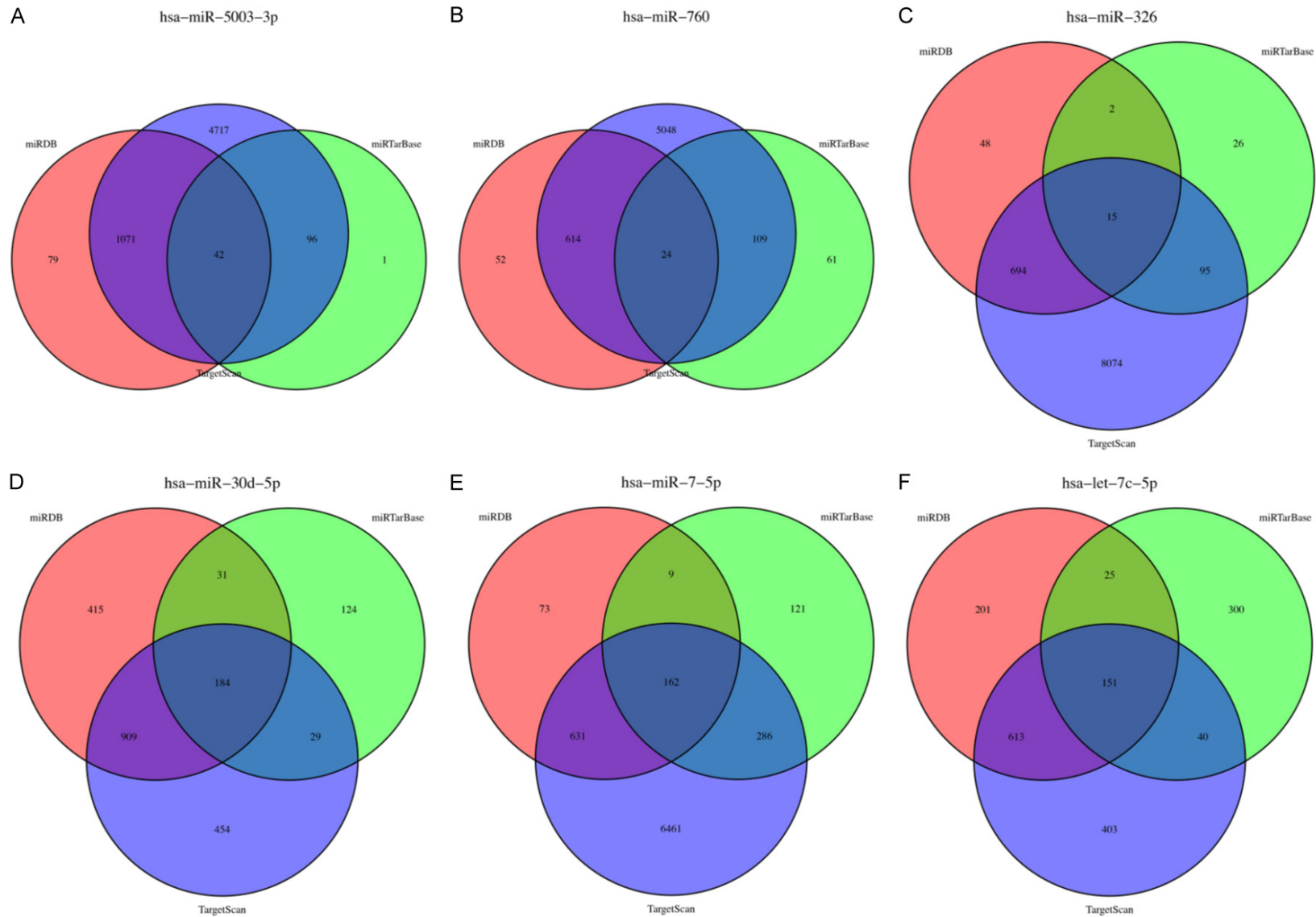
**Figure S4.** The relationships between miRNA signature and tumor immune microenvironment (TIME). A. Heatmap for the immune cells infiltrating status between low- and high-risk subgroups. B. The composition of tumor-related immune cells in two risk subgroups. C-F. The comparison of TumorPurity, ImmuneScore, StromaScore, ESTIMATEScore in high- and low-risk subgroups. G-I. Correlation between the risk score and ESTIMATEScore, StromaScore, TumorPurity.

# A miRNAs prognostic signature for hepatocellular carcinoma



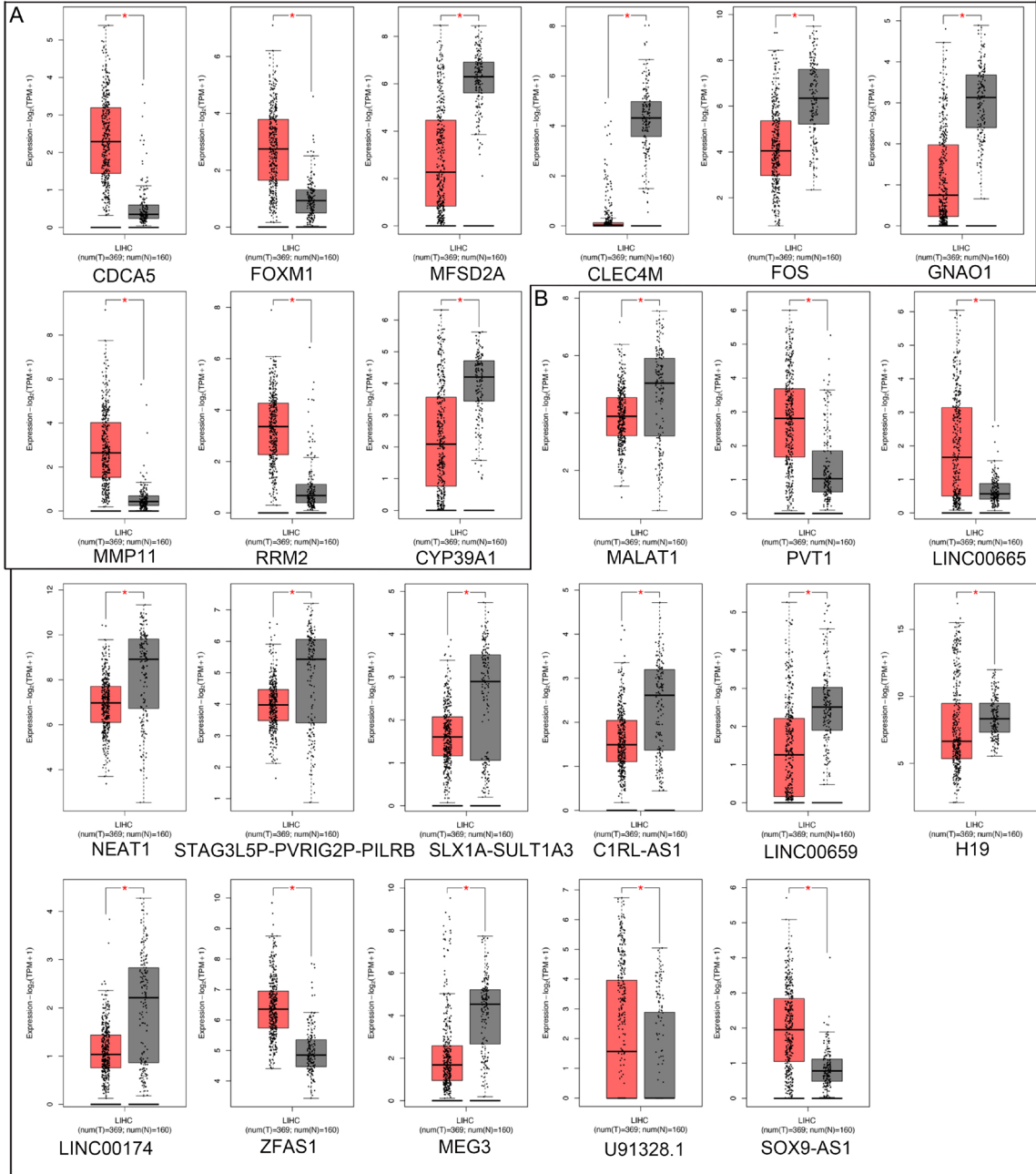
**Figure S5.** The comparison of TIDE (A), Dysfunction (B), MSI (C), tumor tmbation burden (D) in high- and low-risk subgroups.

A miRNAs prognostic signature for hepatocellular carcinoma



**Figure S6.** Venn diagram depicting overlap to display co-expression target genes of six miRNAs among three online databases. (A) hsa-miR-5003-3p, (B) hsa-miR-760, (C) hsa-miR-326, (D) hsa-miR-30d-5p, (E) hsa-miR-7-5p, (F) hsa-let-7c-5p.

# A miRNAs prognostic signature for hepatocellular carcinoma



**Figure S7.** The differential expression levels of miRNA related genes and lncRNAs. A. miRNA related gene. B. lncRNAs.