

Figure S1. DE miRNAs in gastric cancer. (A) Heatmap plot of top 100 DE miRNAs identified from GSE106817 dataset. Blue represents normal samples and red represents gastric cancer patients. (B) Heatmap plot of top 100 DE miRNAs identified from GSE112264 dataset. Colors as in A. (C) Heatmap plot of top 100 DE miRNAs identified from TCGA dataset. Colors as in (A). (D) Volcano plots of miRNAs identified from GSE106817 dataset. Red and blue dots indicate up and down-regulated miRNAs. (E) Volcano plots of miRNAs identified from GSE112264 dataset. (F) Volcano plots of miRNAs identified from TCGA dataset. DE miRNAs, differentially expressed miRNAs; TCGA, The Cancer Genome Atlas.

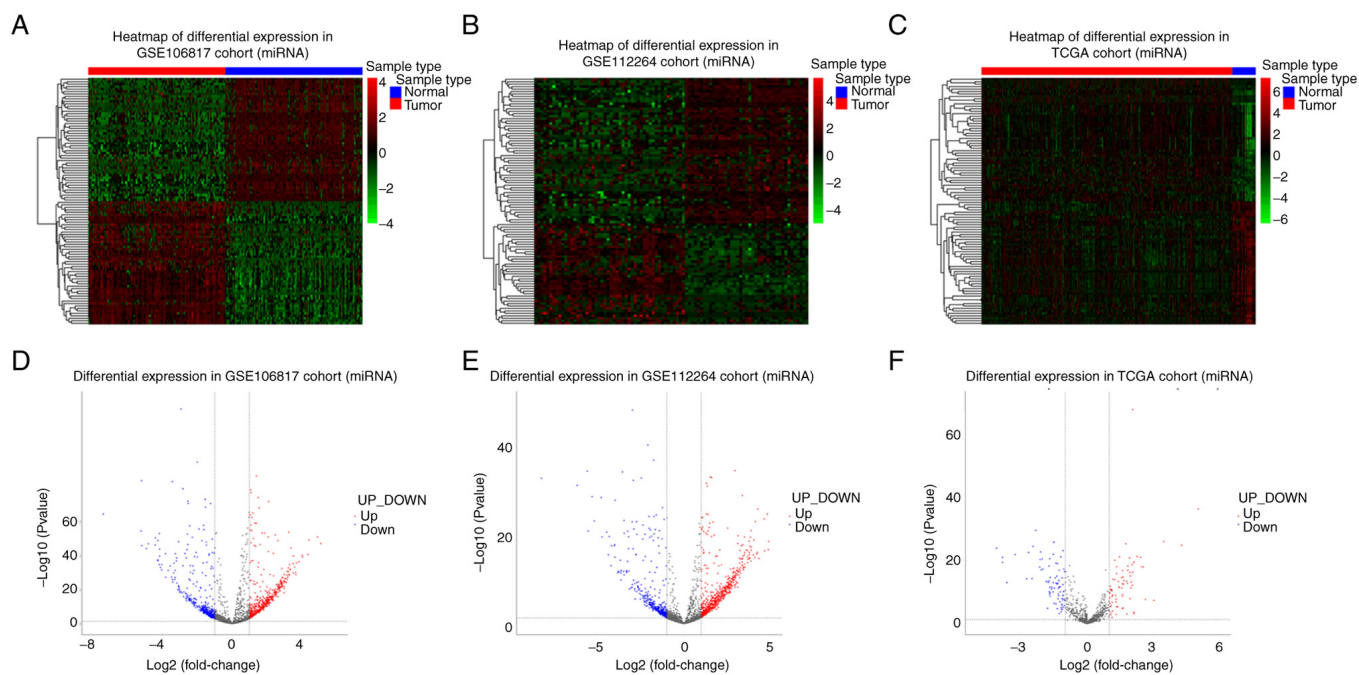


Figure S2. DEcircRNAs in gastric cancer. (A) Heatmap plot of top 100 DEcircRNAs identified from GSE83521 dataset. Blue represents normal samples and red represents gastric cancer patients. (B) Heatmap plot of top 100 DEcircRNAs identified from GSE93541 dataset. Colors as in A. (C) Volcano plots of circRNAs identified from GSE83521 dataset. Red and blue dots indicated up and downregulated circRNAs. (D) Volcano plots of circRNAs identified from GSE93541 dataset. DEcircRNAs, differentially expressed circRNAs.

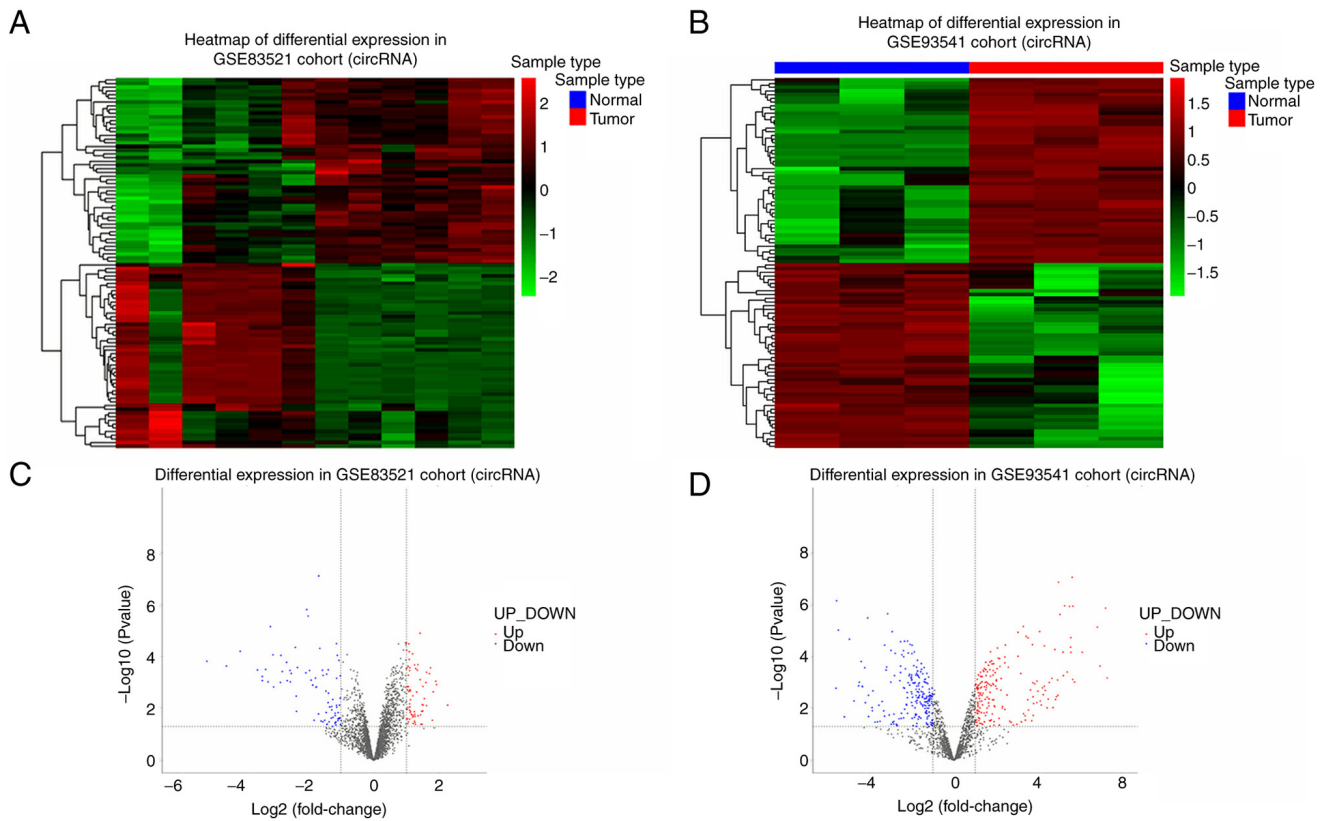


Figure S3. Identification of modules associated with gastric cancer by WGCNA from GSE106817 (miRNA) and GSE93541 (circRNA) datasets. (A) Sample clustering to detect outlier sample in GSE106817 dataset. (B) Screening the appropriate power of β in GSE106817 dataset. (C) Cluster dendrogram displaying 5 modules identified from the GSE106817 dataset. (D) Sample clustering to detect outlier samples in GSE93541 dataset. (E) Screening the appropriate power of β in the GSE93541 dataset. (F) Cluster dendrogram displaying 10 modules identified in the GSE93541 dataset.

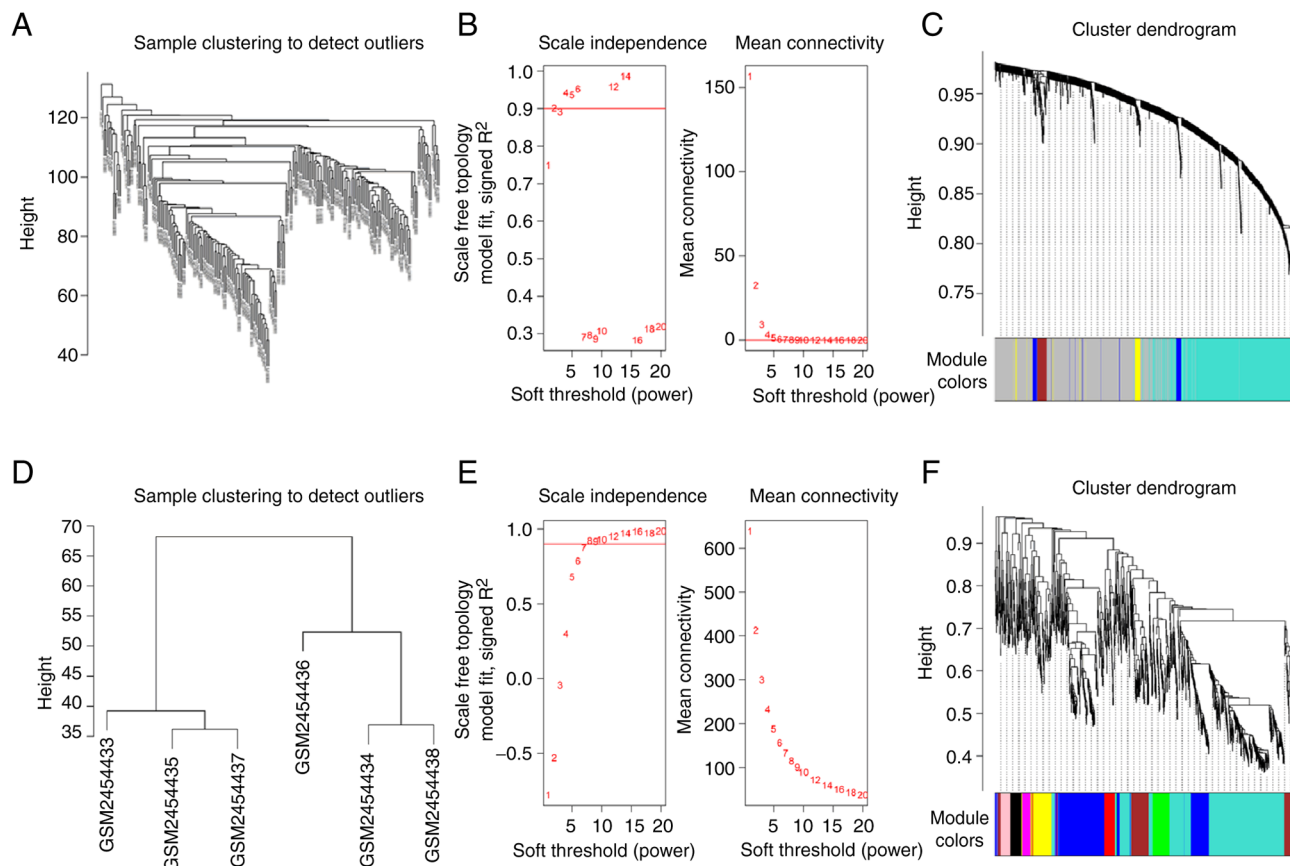


Figure S4. Diagnostic model validation. (A) ROC curve analysis for diagnostic model (mRNA) in TCGA test cohort. (B) ROC curve analysis for diagnostic model (mRNA) in TCGA-GTEx cohort. (C) ROC curve analysis for diagnostic model (mRNA) in GSE54129 cohort. (D) ROC curve analysis for diagnostic model (miRNA) in TCGA test cohort. (E) ROC curve analysis for diagnostic model (miRNA) in GSE106817 cohort. (F) ROC curve analysis for diagnostic model (miRNA) in GSE112264 cohort. ROC, receiver operating characteristic; TCGA, The Cancer Genome Atlas; AUC, area under curve.

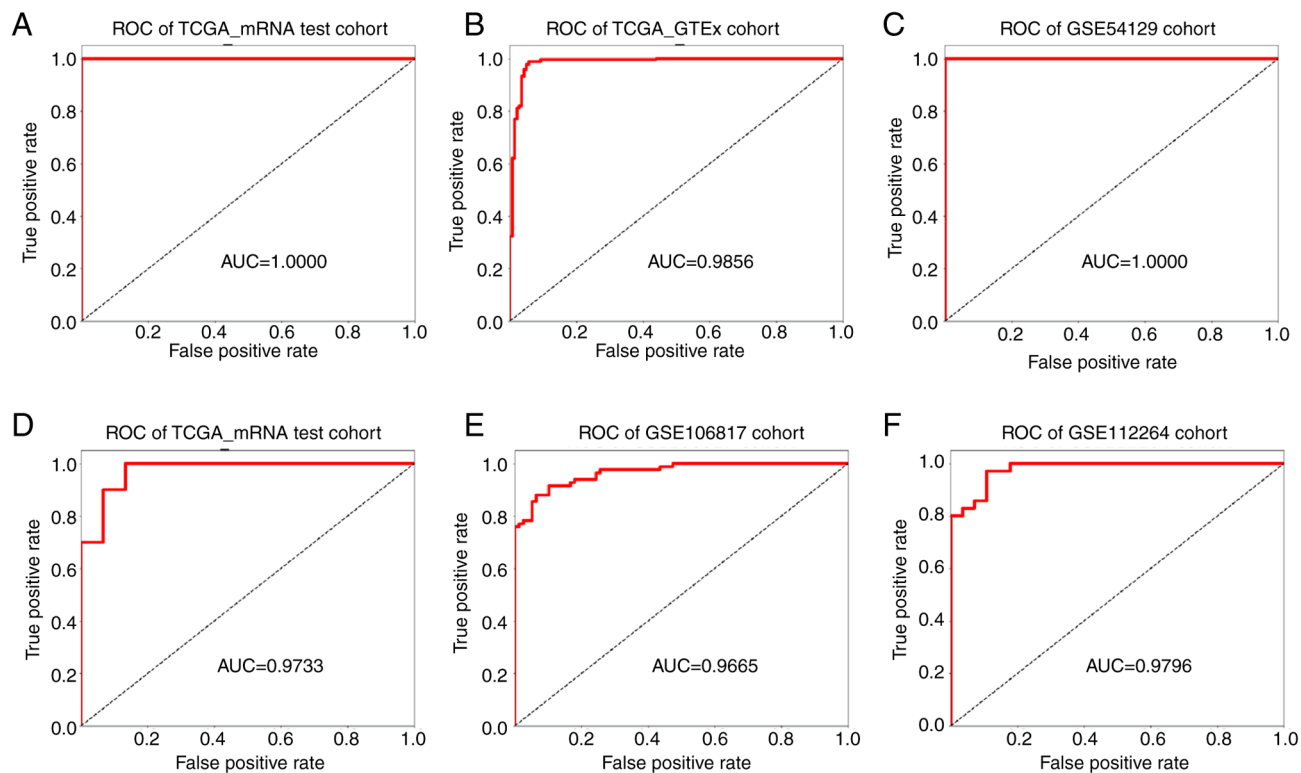


Figure S5. Prognostic model (mRNAs) validation in TCGA test cohort. (A) The overall survival status, riskscore and five-mRNAs-based prognostic signature expression levels. (B) Survival curve of low- and high-risk groups in the test cohort. (C) Time-dependent ROC curve comparison of the TCGA test cohort. AUCs at 1-5 years were calculated. TCGA, The Cancer Genome Atlas; ROC, receiver operating characteristic; AUC, area under curve; STAD, stomach adenocarcinoma.

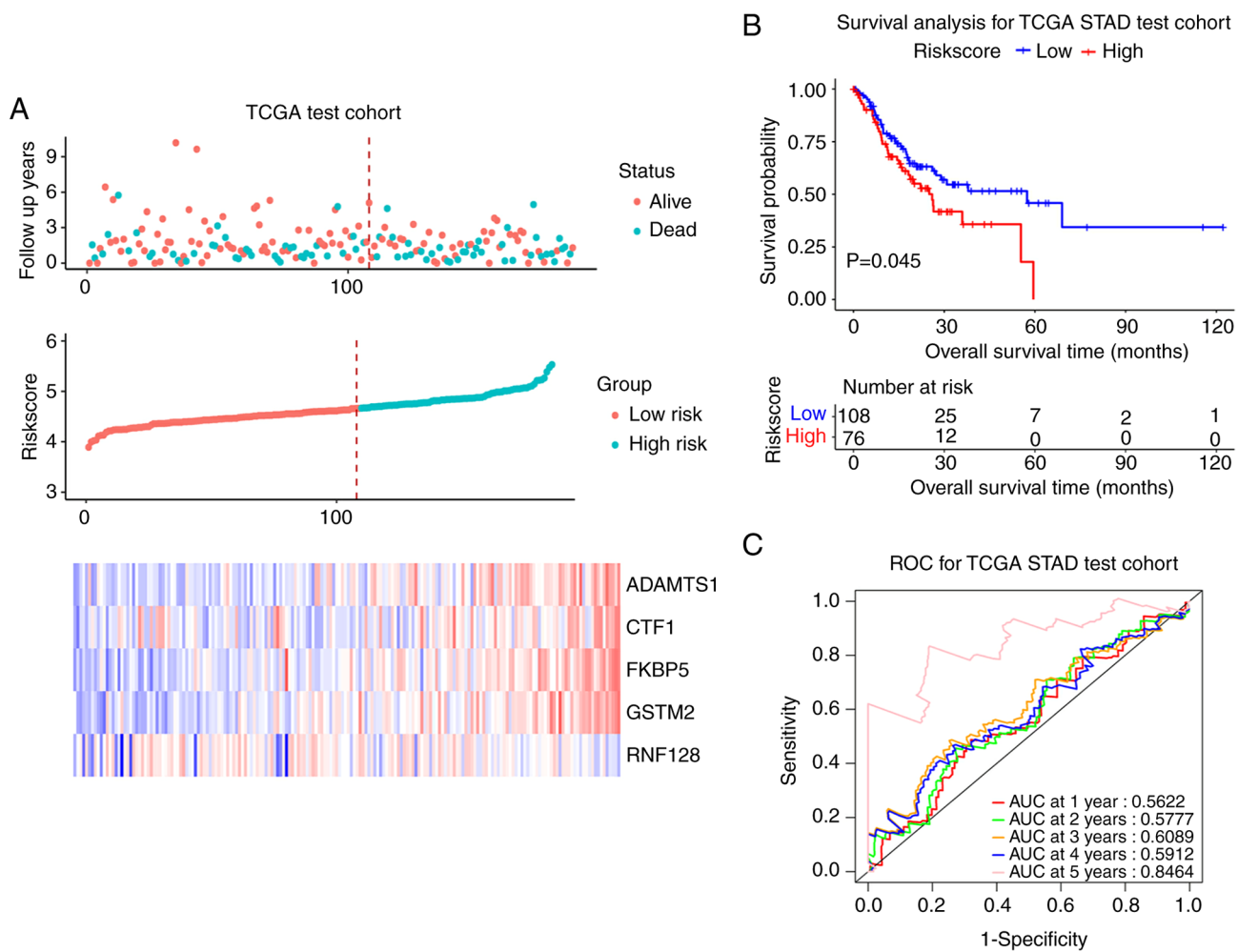


Figure S6. Prognostic model (mRNAs) validation in entire TCGA cohort. (A) The overall survival status, riskscore and five-mRNAs-based prognostic signature expression levels. (B) Survival curve of low- and high-risk groups in entire cohort. (C) Time-dependent ROC curve comparison of the TCGA entire cohort. AUCs at 1-5 years were calculated. TCGA, The Cancer Genome Atlas; ROC, receiver operating characteristic; AUC, area under curve; STAD, stomach adenocarcinoma.

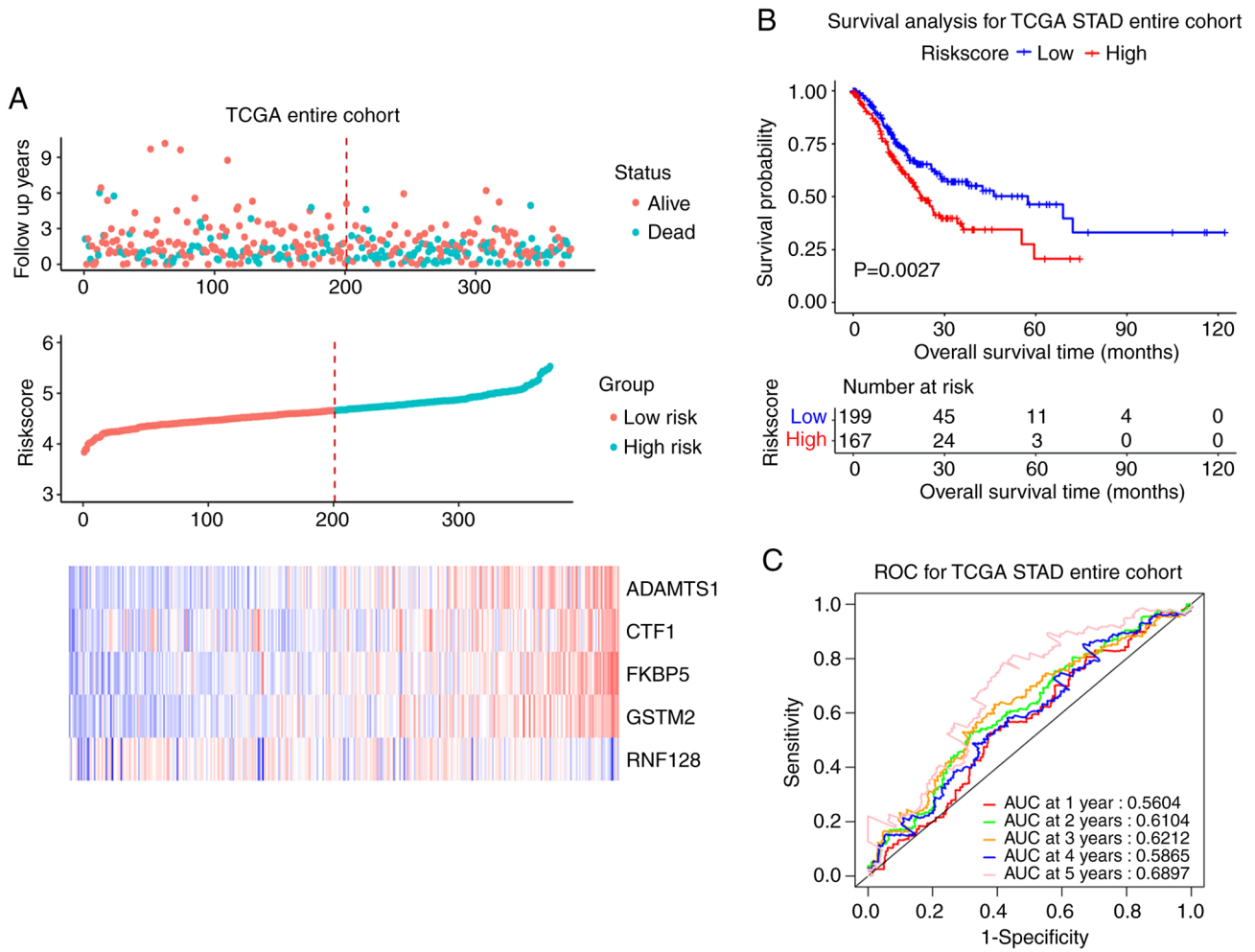


Figure S7. Prognostic model (miRNAs) validation in TCGA test cohort. (A) The overall survival status, riskscore and five-mRNAs-based prognostic signature expression levels. (B) Survival curve of low- and high-risk groups in test cohort. (C) Time-dependent ROC curve comparison of the TCGA test cohort. AUCs at 1-5 years were calculated. TCGA, The Cancer Genome Atlas; ROC, receiver operating characteristic; AUC, area under curve; STAD, stomach adenocarcinoma.

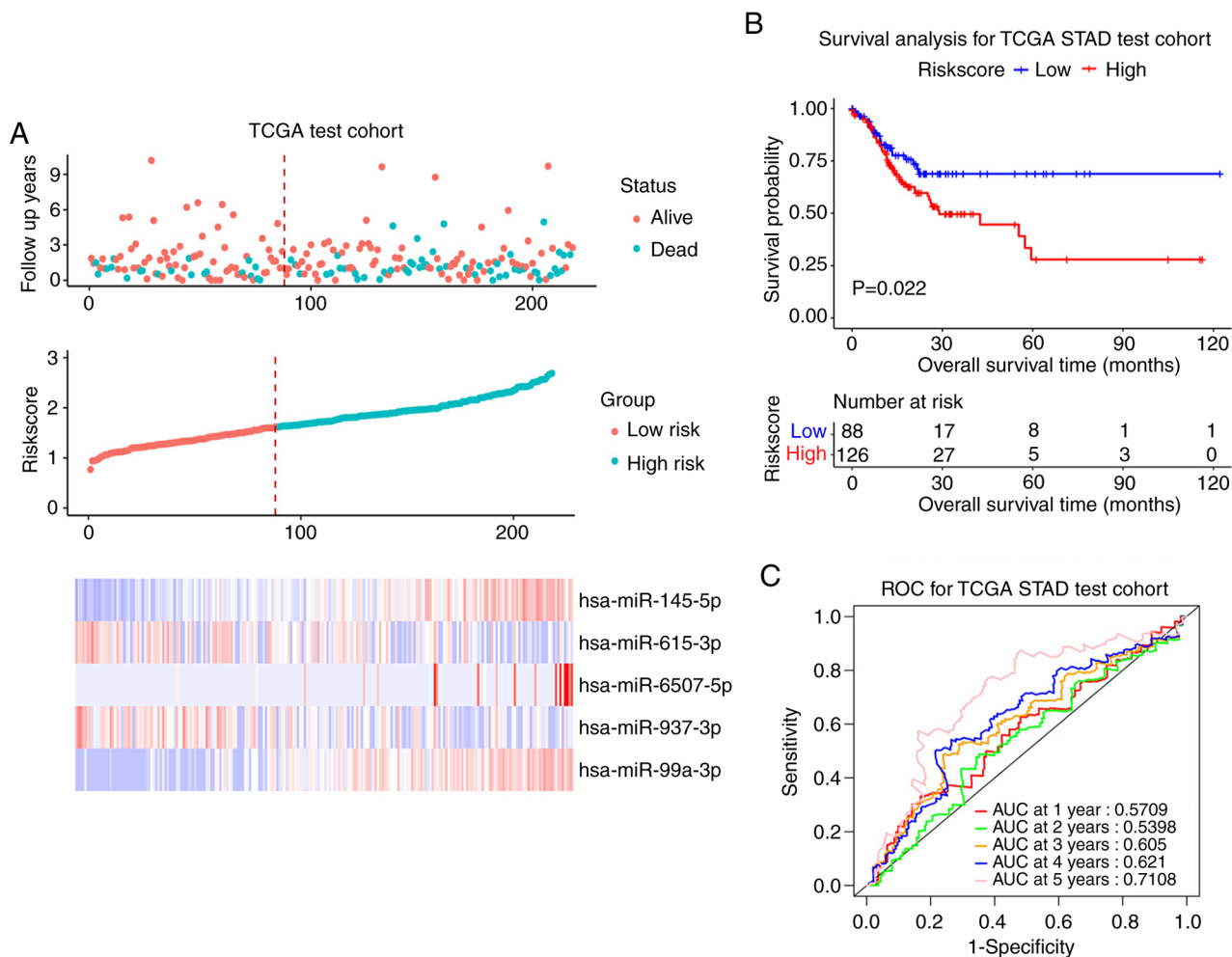


Figure S8. Prognostic model (miRNAs) validation in TCGA entire cohort. (A) The overall survival status, riskscore and five-mRNAs-based prognostic signature expression levels. (B) Survival curve of low- and high-risk groups in entire cohort. (C) Time-dependent ROC curve comparison of the TCGA test cohort. AUCs at 1-5 years were calculated. TCGA, The Cancer Genome Atlas; ROC, receiver operating characteristic; AUC, area under curve; STAD, stomach adenocarcinoma.

