Figure S1 Volcano plot generated by the "DESeq" package for filtrating the miRNA expression data.
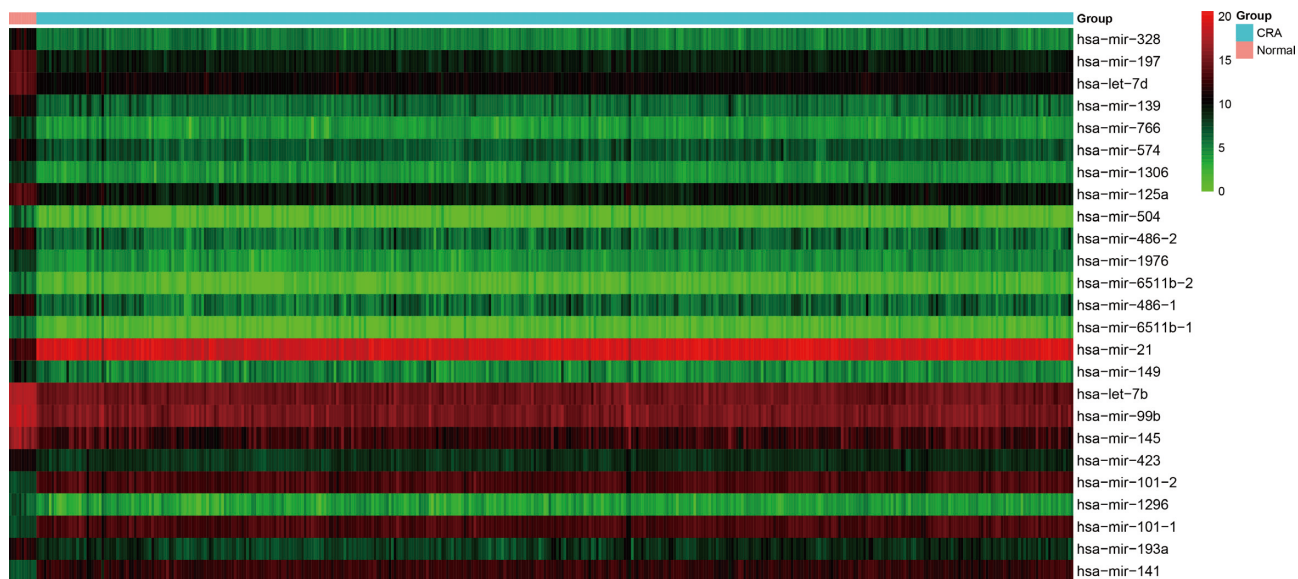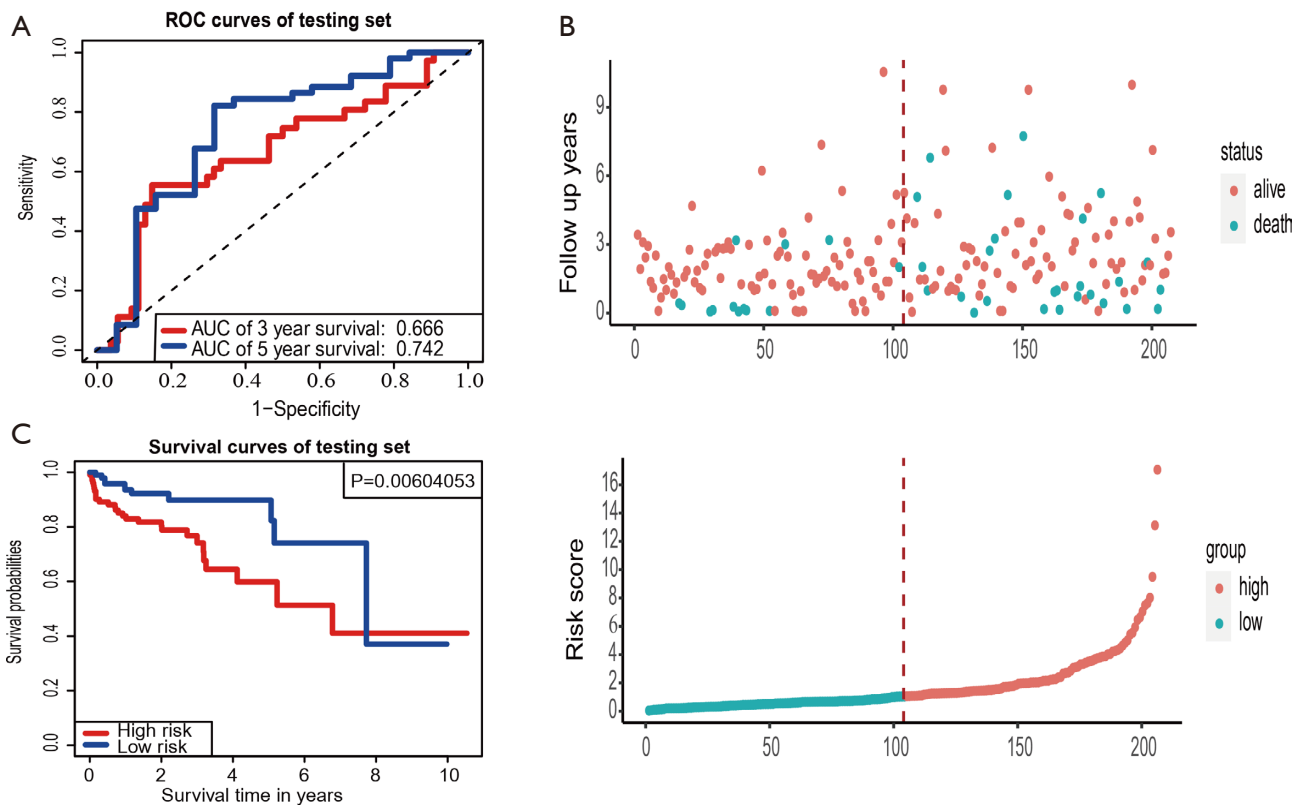

Figure S2 Heatmap generated by the top25 differentially expressed miRNAs between cancer tissues and normal tissues in CRA patients.

Figure S3 Performance verification in the test set. (A) ROC curve analysis of the seven-miRNA signature. (B) Kaplan-Meier overall survival analysis of the CRA patients using the seven-miRNA signature. (C) Distributions of the risk scores and survival statuses of the seven miRNAs in the CRA patients.
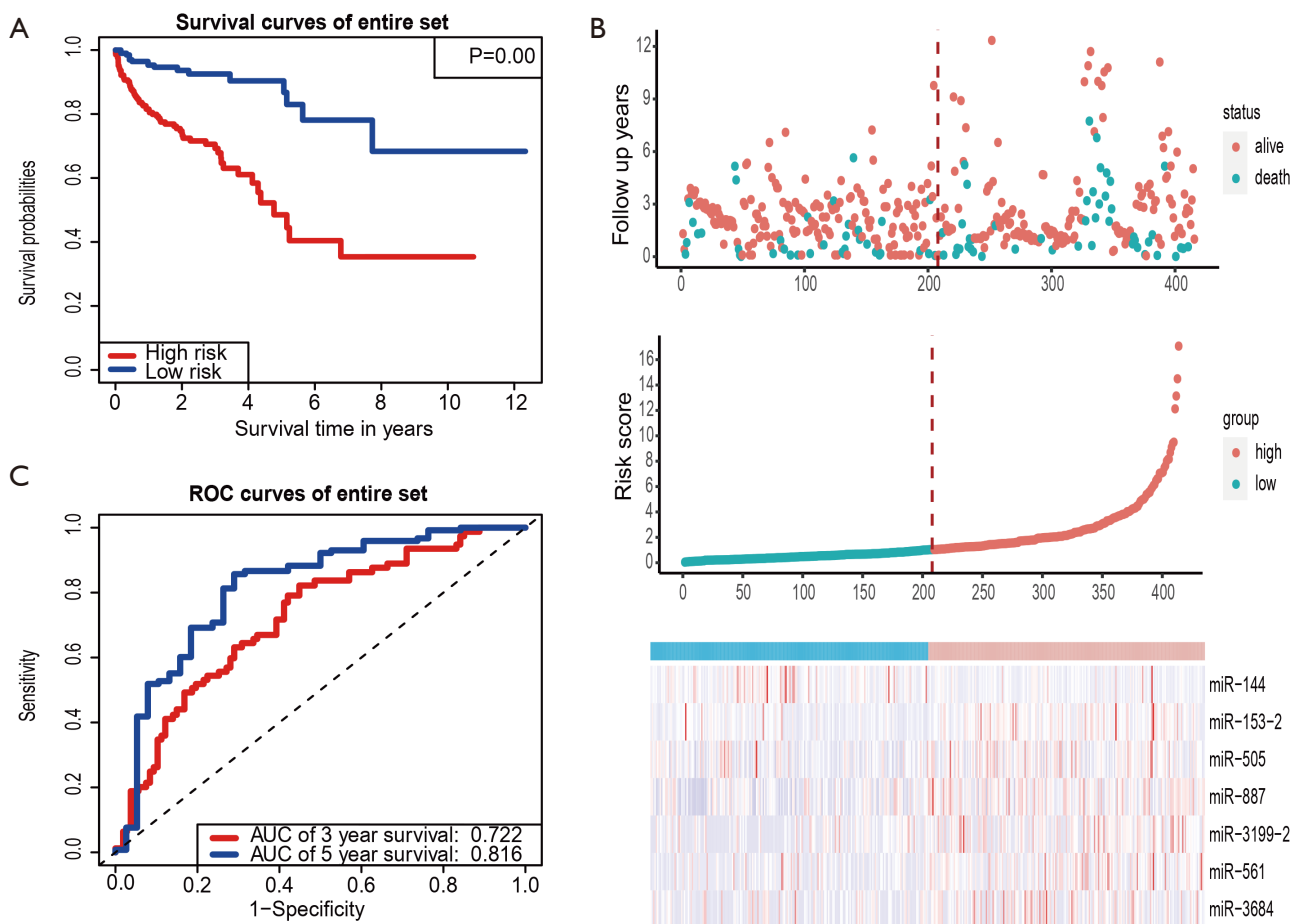
Figure S4 Performance verification in the entire set. (A) Kaplan-Meier overall survival analysis of CRA patients using the seven-miRNA signature. (B) ROC curve analysis of the seven-miRNA signature. (C) Distributions of the risk scores, survival statuses and expression profiles of the seven miRNAs in the CRA patients.
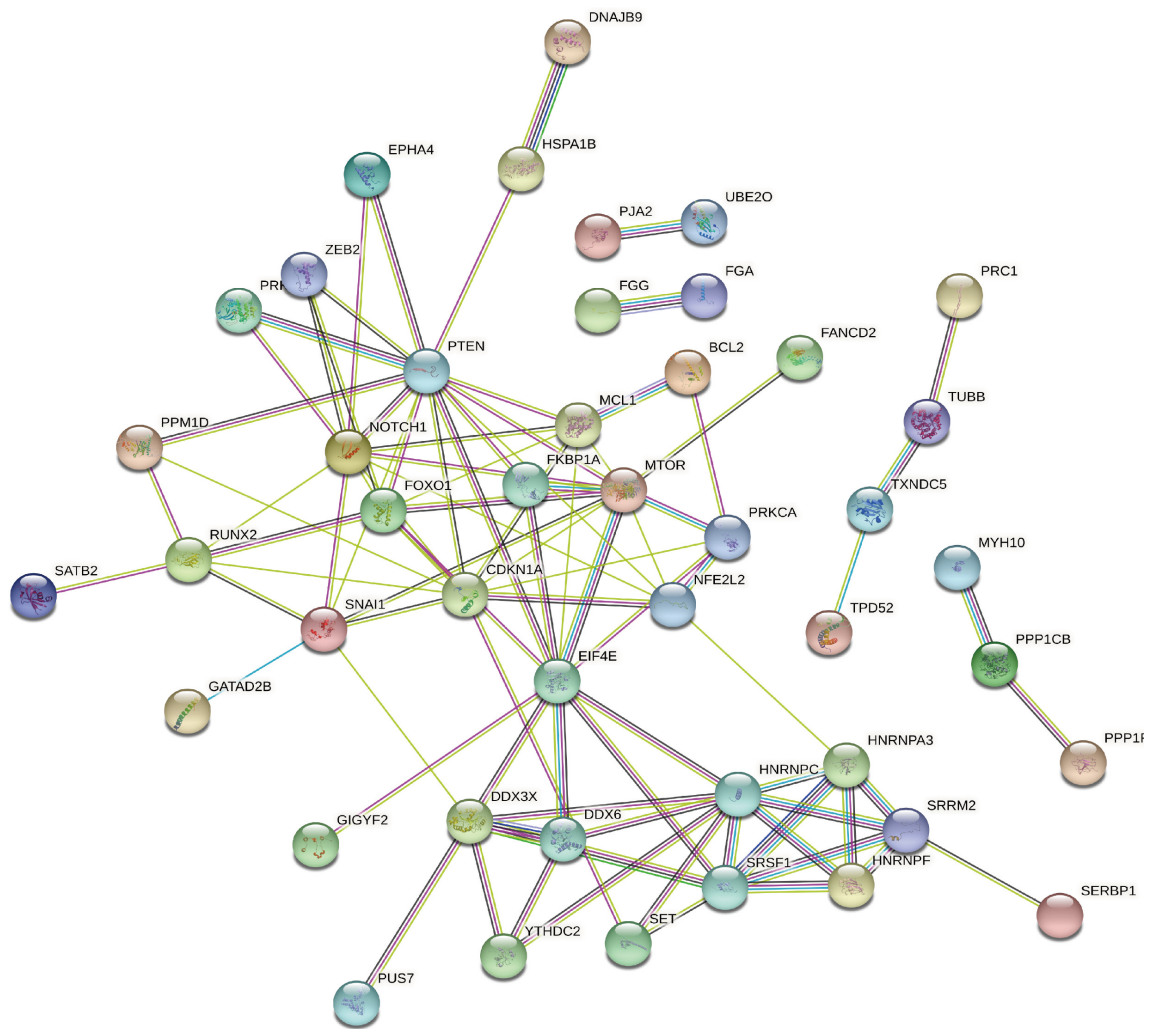
Figure S5 Interaction network of the target genes from the STRING dataset.