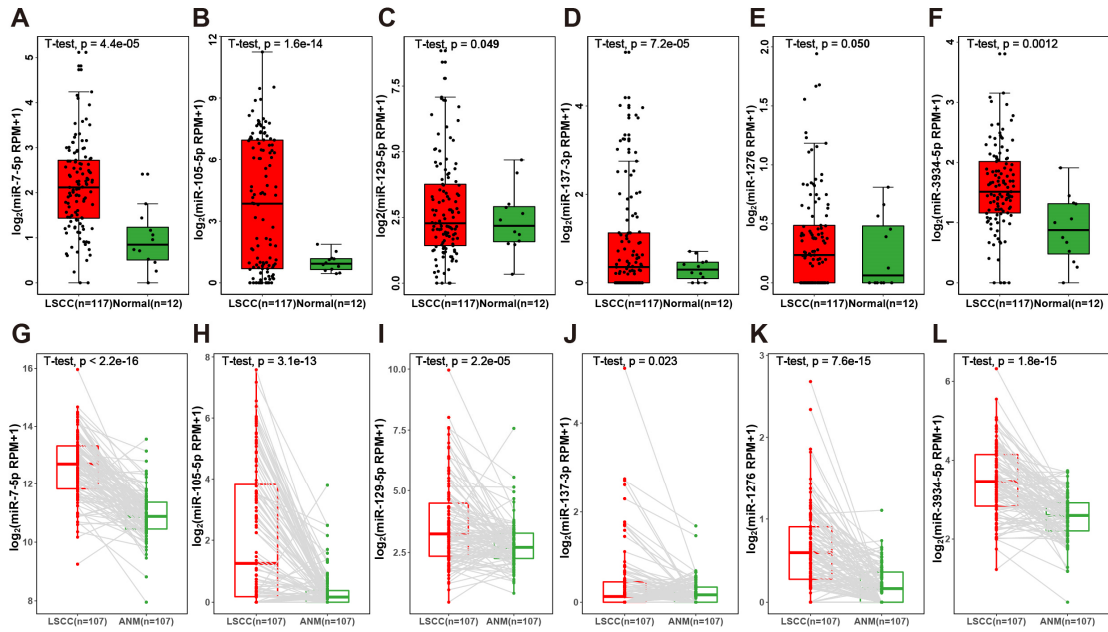
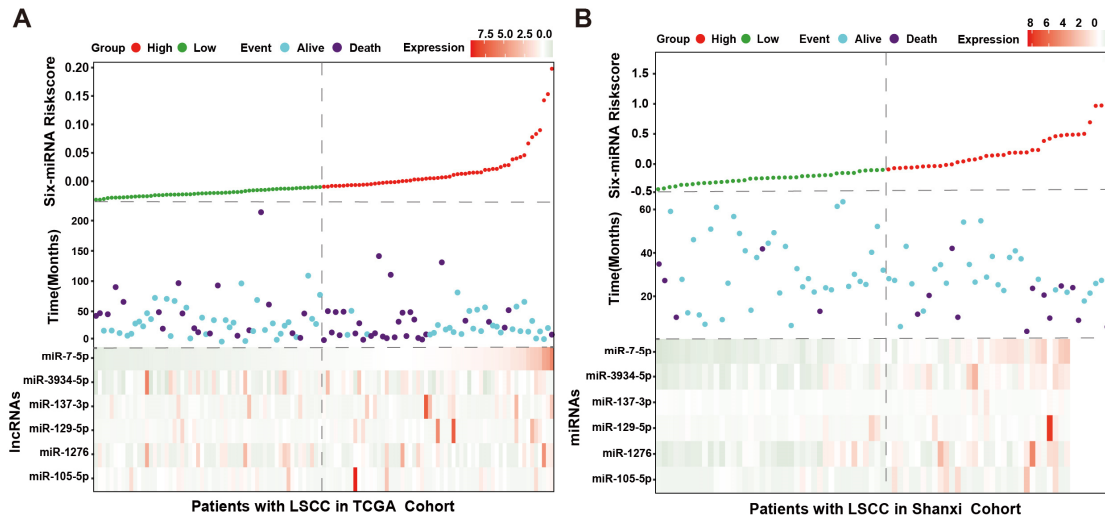


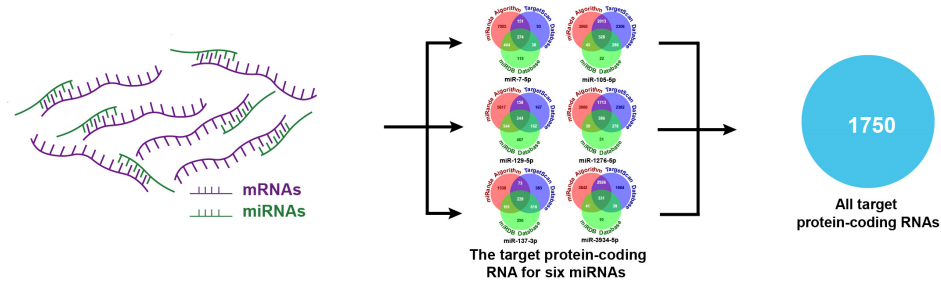
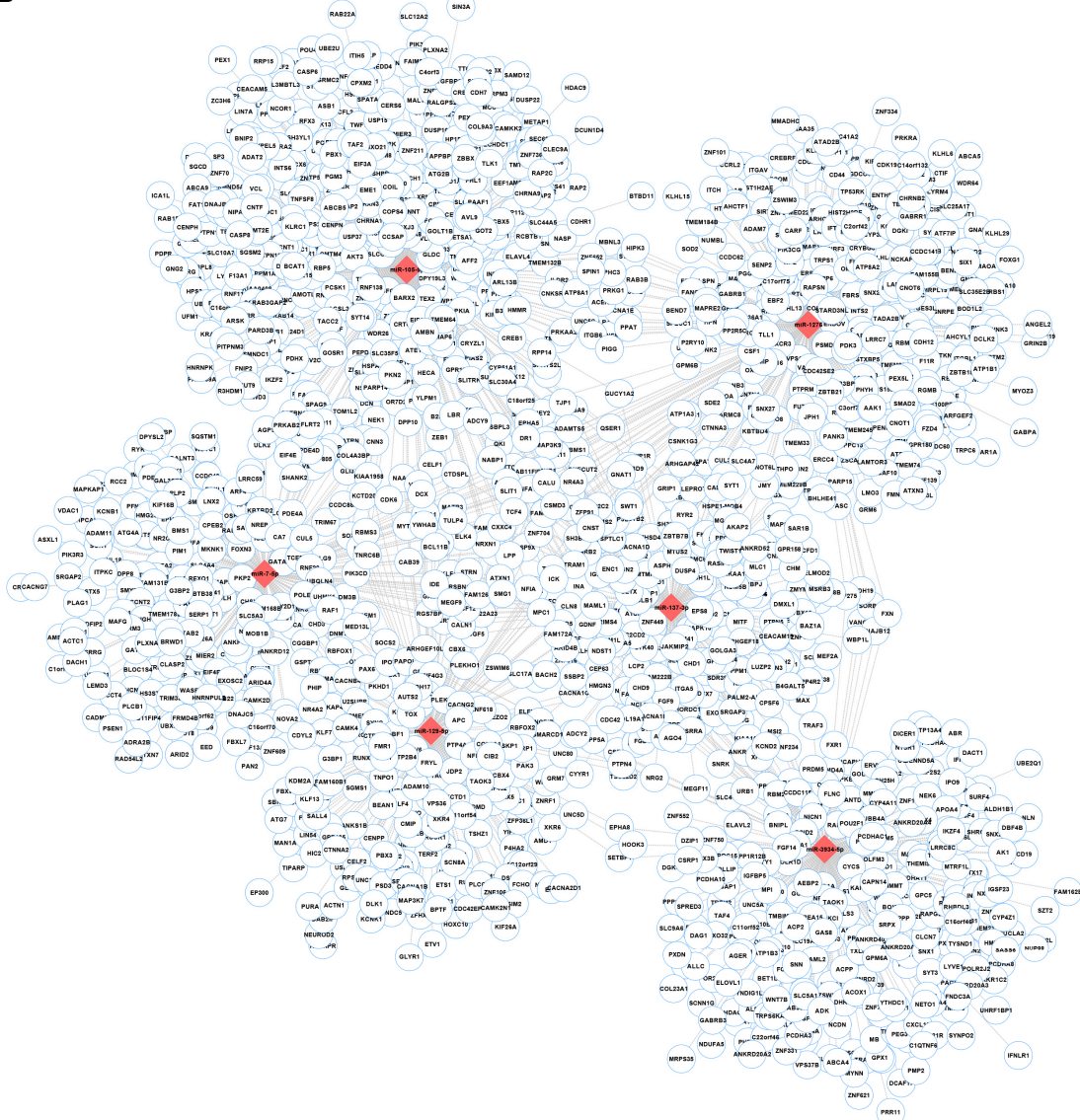
Supplementary Figure S1. Kaplan-Meier survival curve of significantly dysregulated miRNAs from univariate Cox regression analysis in TCGA cohort patients. (A-I) The Kaplan-Meier survival curve for the overall survival of upregulated miRNAs: miR-137-3p (A), miR-3934-5p (B), miR-767-5p (C), miR-1276 (D), miR-129-5p (E), miR-7-5p (F), miR-1305 (G), miR-196a-5p (H), miR-105-5p (I). **(J-M)** The Kaplan-Meier survival curve for the overall survival of downregulated miRNAs: miR-101-5p (J), miR-125b-5p (K), miR-497-5p (L) and miR-133a-3p (M).



Supplementary Figure S2. Different expression of six-miRNAs signature between LSCC and normal tissues. (A-F) Different expression of miR-7-5p (A), miR-105-5p (B), miR-129-5p (C), miR-137-3p (D), miR-1276 (E), and miR-3934-5p (F) in TCGA cohort. (G-L) Different expression of miR-7-5p (G), miR-105-5p (H), miR-129-5p (I), miR-137-3p (J), miR-1276 (K), and miR-3934-5p (L) in LSCC in Shanxi cohort.



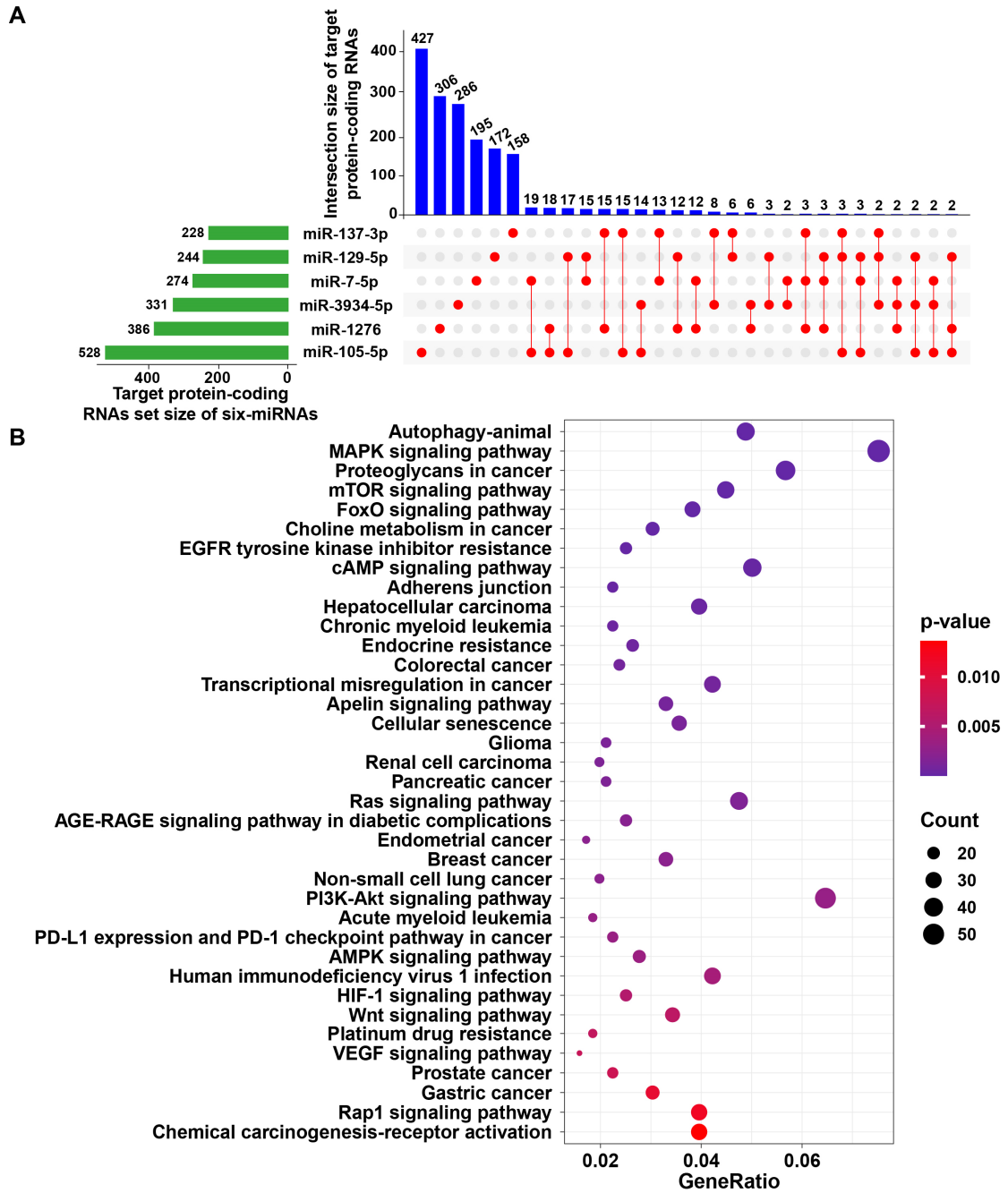
Supplementary Figure S3. Outcome of patients and miRNAs expression distribution between six-miRNAs risk score high and low risk group. (A) Outcome of patients and miRNAs expression distribution between six-miRNAs risk score high and low group in TCGA cohort. **(B)** Outcome of patients and miRNAs expression distribution between six-miRNAs risk score high and low group in Shanxi cohort.

A**B**

Supplementary Figure S4. Target protein-coding RNA prediction of six-miRNAs.

(A) Schematic representation for target protein-coding RNA prediction of six-miRNAs.

(B) An interaction network of six-miRNAs and its targeted genes.



Supplementary Figure S5. Enrichment analysis for target protein-coding RNA of six-miRNAs. (A) Upset plot of targeted protein-coding RNAs of six-miRNAs. (B) KEGG pathway enrichment plot of targeted protein-coding RNA of six-miRNAs.