

Figure S1 Bioinformatic analysis of downregulated miRNAs. (A) GO analysis of downregulated miRNAs. (B) KEGG analysis of downregulated miRNAs. miRNAs, microRNAs; GO, Gene Ontology; KEGG, Kyoto Encyclopedia of Genes and Genomes.

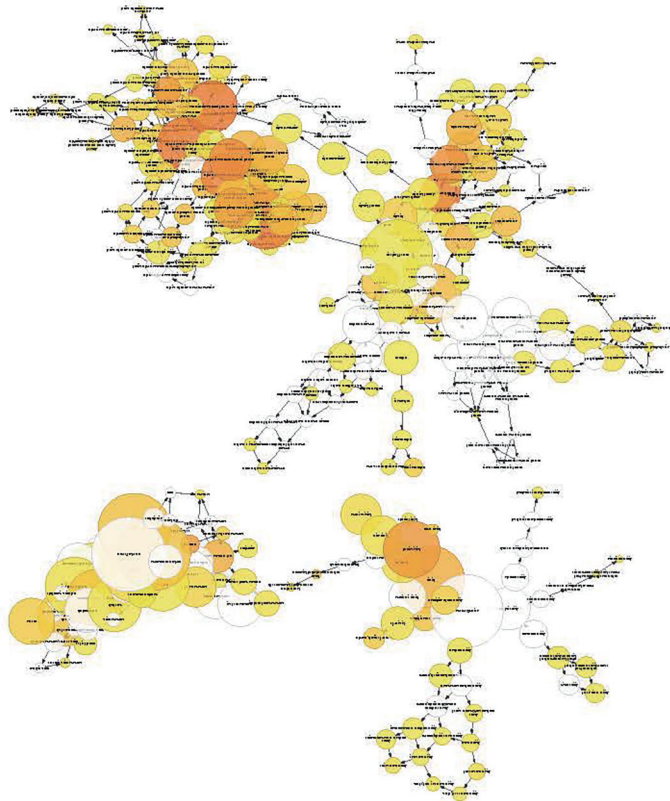


Figure S2 Bingo network of miR-432-5p target genes. The whole image of Figure 3D.

	Predicted consequential pairing of target region (top) and miRNA (bottom)	Site type	Context++ score	Context++ score percentile	Weighted context++ score	Conserved branch length	P _{CT}	Predicted relative K _D
Position 161-168 of SCNN1A 3' UTR hsa-miR-432-5p	5' ...GGCCUCAGGAAGUUCUCCAAGA... 3' GGUGGGUUAACUGGAUGAGGUUCU 	8mer	-0.21	92	-0.21	0.013	N/A	-2.228
Position 800-806 of SCNN1G 3' UTR hsa-miR-432-3p	5' ...GACUUC AUGAUUUUG-CAUCCA AU... 3' UCUGUACCUCCUCCGUAGGUC 	7mer-A1	-0.14	75	-0.14	0	N/A	N/A

Figure S3 The predictive results of *SCNN1A* and *SCNN1G* showing their binding capacities to miR-432. miRNA, microRNA; 3'UTR, 3'untranslated region.