

Table S1 AF-related miRNAs from HMDD

hsa-miR-1	hsa-miR-15b	hsa-miR-21	hsa-miR-355p
hsa-miR-106a	hsa-miR-17	hsa-miR-215	hsa-miR-3613
hsa-miR-106b	hsa-miR-18	hsa-miR-223	hsa-miR-363
hsa-miR-10a	hsa-miR-183-5p	hsa-miR-23a	hsa-miR-377-5p
hsa-miR-10b	hsa-miR-19	hsa-miR-24	hsa-miR-4279
hsa-miR-122	hsa-miR-192	hsa-miR-25	hsa-miR-451
hsa-miR-124-3p	hsa-miR-193a-5p	hsa-miR-26a	hsa-miR-466
hsa-miR-126	hsa-miR-193b	hsa-miR-26b	hsa-miR-4666a
hsa-miR-1266	hsa-miR-196a-2	hsa-miR-27b	hsa-miR-483
hsa-miR-133a	hsa-miR-199a-3p	hsa-miR-29	hsa-miR-486
hsa-miR-133a-1	hsa-miR-199a-5p	hsa-miR-29a-3p	hsa-miR-499
hsa-miR-133a-2	hsa-miR-199b-3p	hsa-miR-30a-5p	hsa-miR-519b
hsa-miR-133b	hsa-miR-19a-3p	hsa-miR-30b-5p	hsa-miR-574
hsa-miR-142	hsa-miR-19b-1	hsa-miR-30c-1	hsa-miR-590-5p
hsa-miR-144	hsa-miR-19b-2	hsa-miR-30c-2	hsa-miR-892a
hsa-miR-146a	hsa-miR-19b-3p	hsa-miR-30d	hsa-miR-92-1
hsa-miR-146b-5p	hsa-miR-208a	hsa-miR-3149	hsa-miR-93
hsa-miR-150	hsa-miR-208b	hsa-miR-3171	
hsa-miR-155	hsa-miR-20a	hsa-miR-328	

HMDD, Human microRNA Disease Database.

Table S2 Gene count in the coexpression module network

Module color	Gene count
Black	377
Blue	1,457
Brown	649
Green	476
Green-yellow	149
Grey	1,591
Magenta	229
Pink	375
Purple	191
Red	455
Tan	134
Turquoise	1,984
Yellow	529

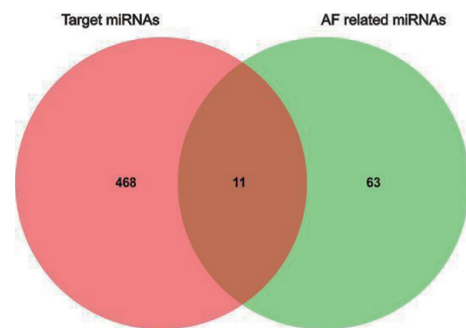


Figure S1 Venn diagram analysis of the predicted target miRNAs based on DECs and AF-related miRNAs from HMDD. miRNA, microRNA; DECs, differentially expressed circRNAs; HMDD, Human microRNA Disease Database.

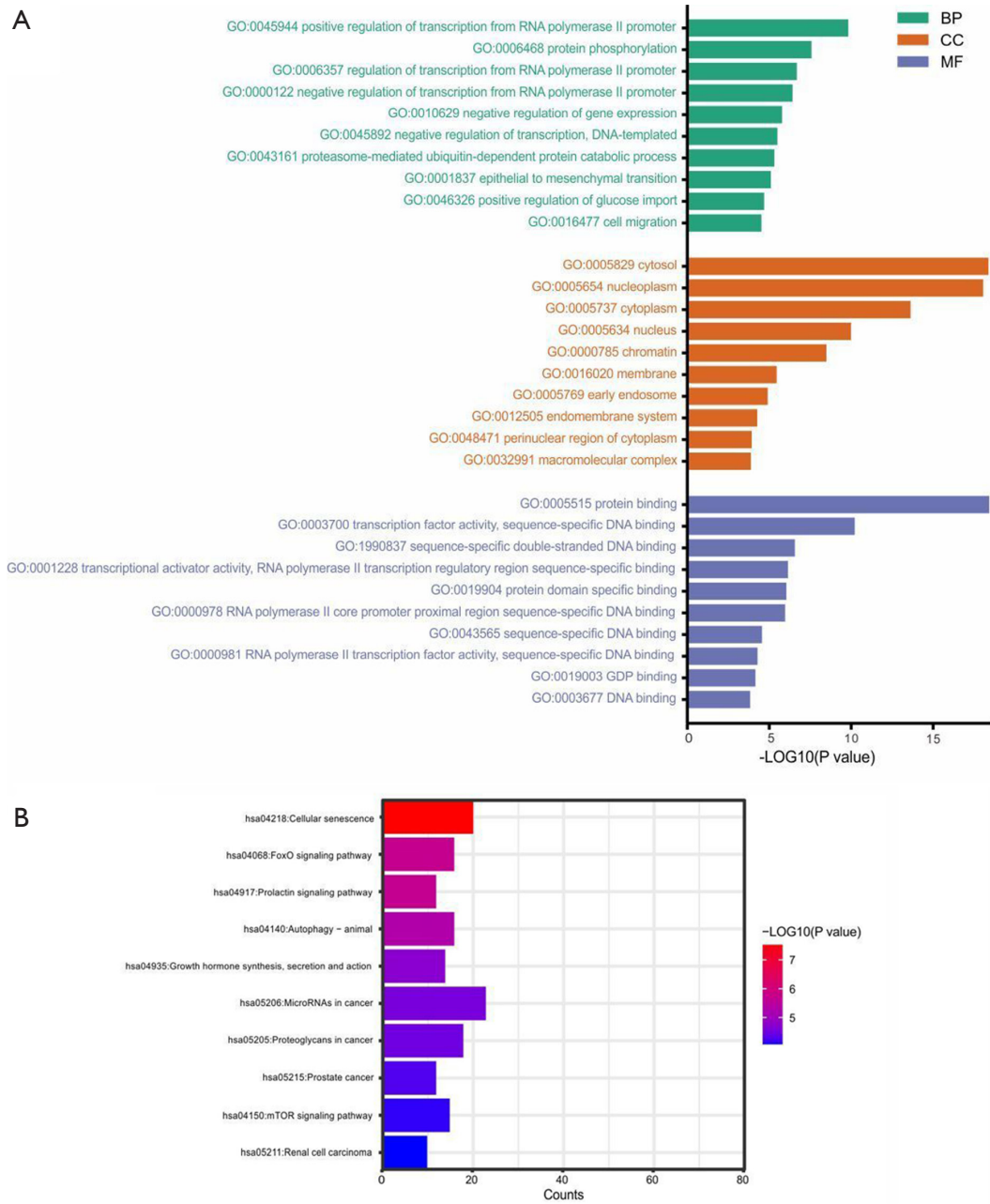


Figure S2 Functional enrichment analysis of predicted mRNAs. (A) Top 10 GO terms of the predicted mRNAs classified by BP, CC, and MF. (B) Top 10 KEGG pathways of the predicted mRNAs. BP, biological process; CC, cellular component; MF, molecular function; GO, Gene Ontology; KEGG, Kyoto Encyclopedia of Genes and Genomes; GDP, guanosine diphosphate; FoxO, Forkhead box O; mTOR, mammalian target of rapamycin; mRNA, messenger RNA.