

Figure S1. Network analysis of the competitive endogenous RNA network. (A) Node degree distribution analysis. (B) Closeness centrality distribution. (C) Distribution of shared neighbors. (D) Shortest path distribution.

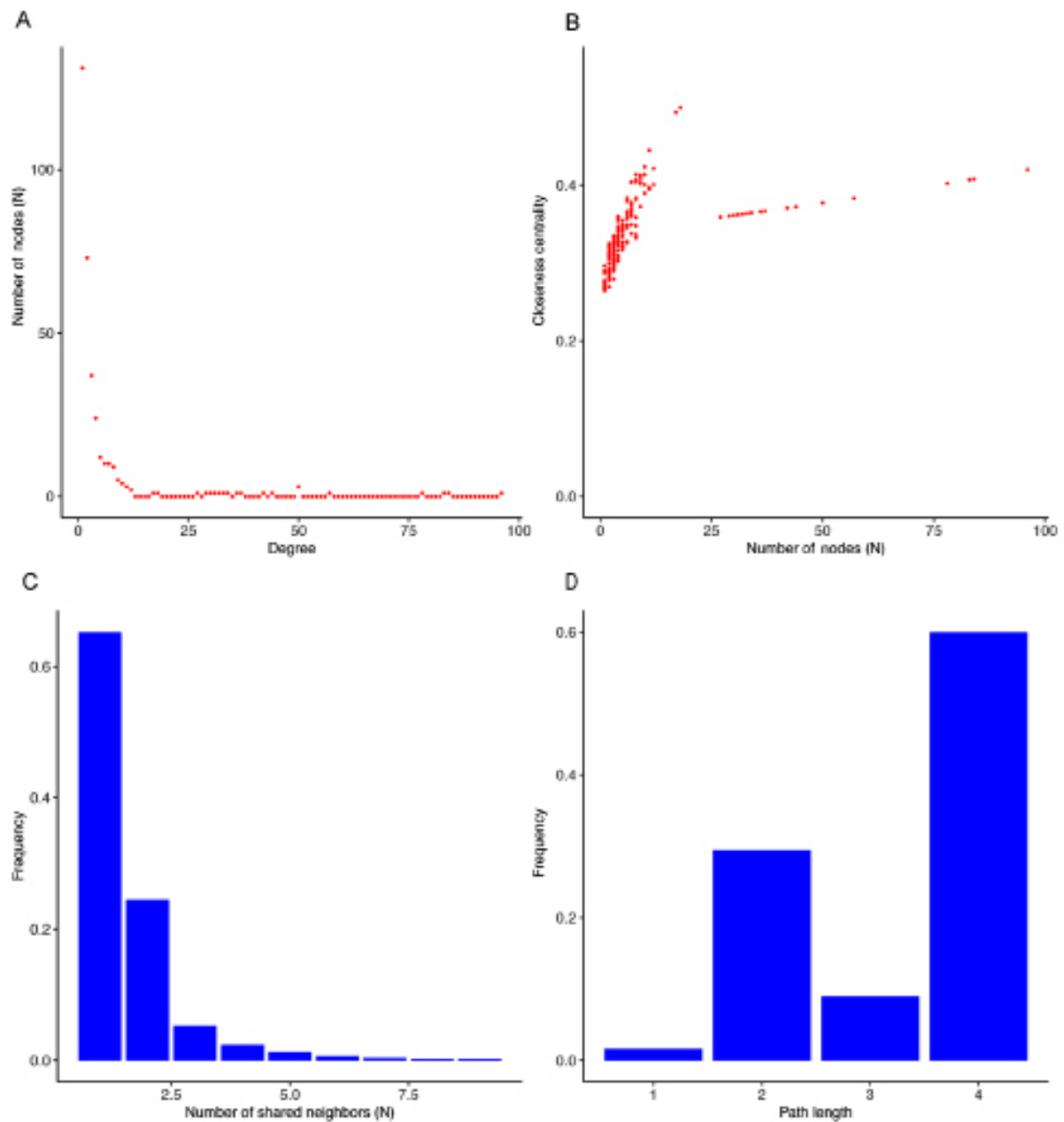


Figure S2. Expression and prognostic value of (A) MEG3, (B) RMST, (C) ZNF503-AS1, (D) HNF1A-AS1, (E) hsa-miR-506. * $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$. MEG3, maternally expressed 3; RMST, rhabdomyosarcoma 2 associated transcript; ZNF503-AS1, ZNF503 antisense RNA 1; HNF1A-AS1, HNF1A antisense RNA 1; miR, microRNA.

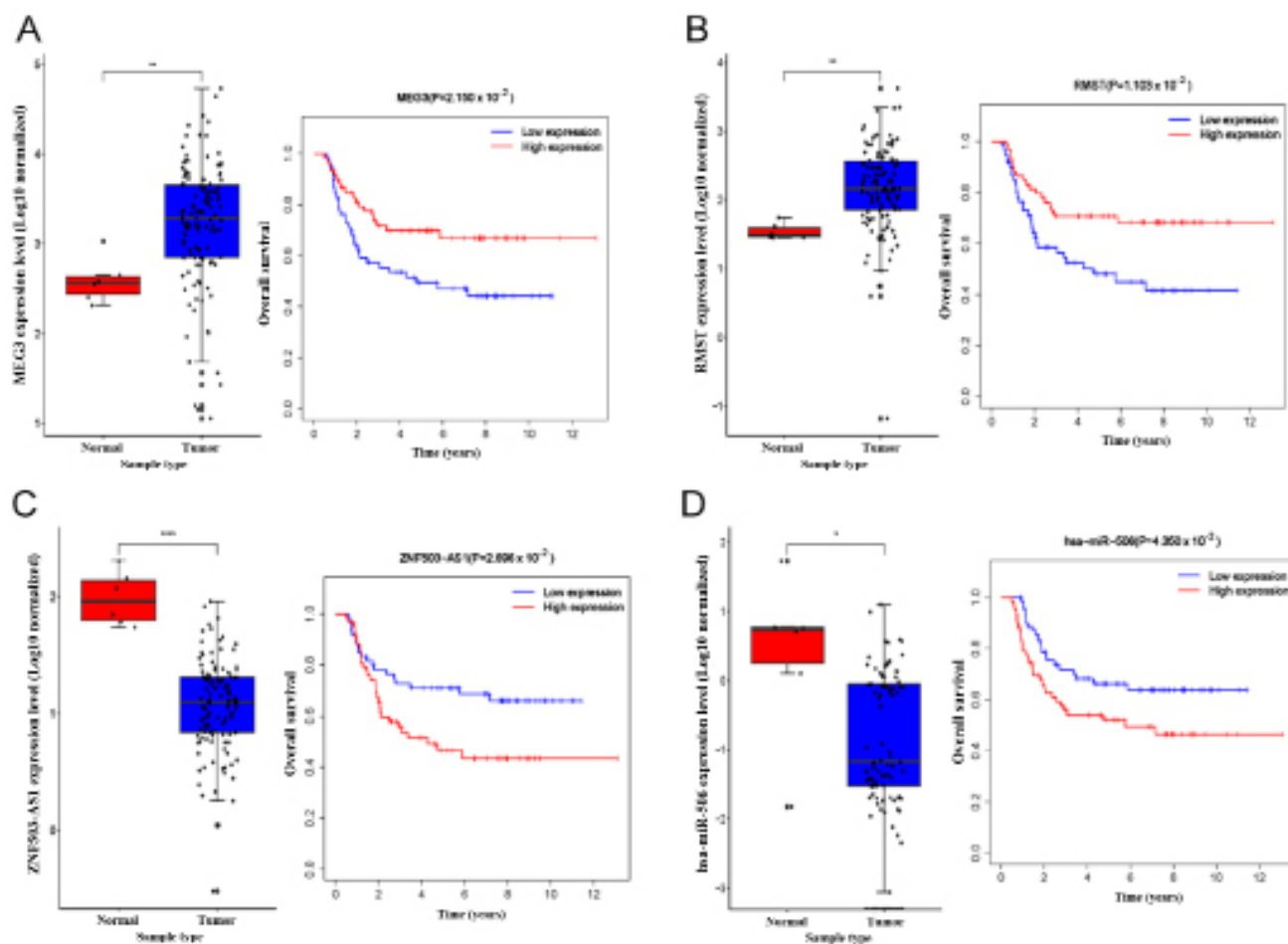


Figure S3. Validation of the differentially expressed miRNAs associated with patient survival time. (A) Box plots of hsa-miR-132 (B) hsa-miR-429 miRNA expression levels in the GSE50505 validation dataset. (C) Box plots of hsa-miR-132 miRNA expression levels in the GSE57370 validation dataset. miRNA/miR, microRNA; ns, not significant.

