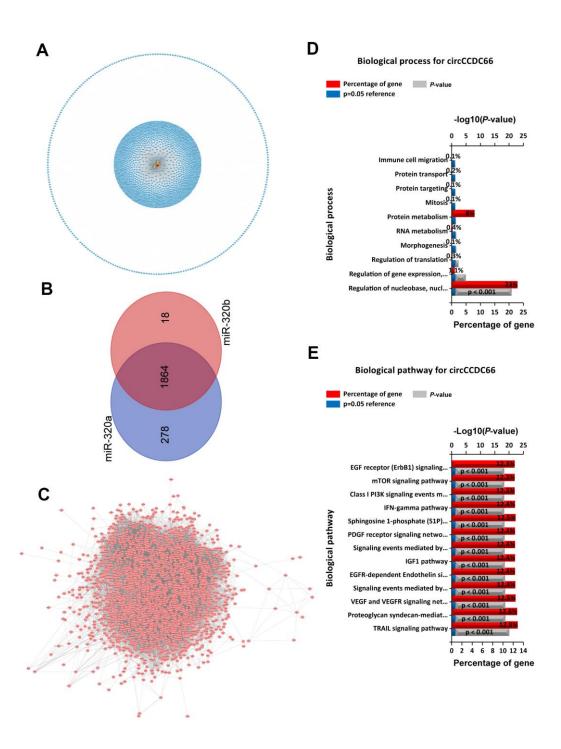
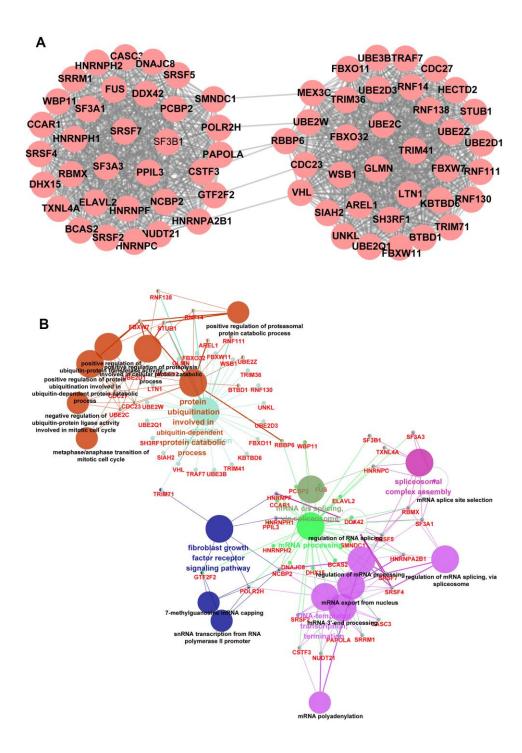
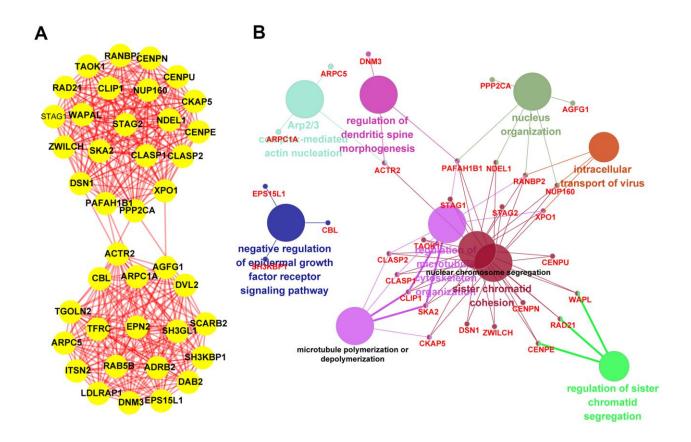
## **SUPPLEMENTARY FIGURES**



**Supplementary Figure 1. Bioinformatics analysis of circCCDC66-miR-320a/b axis.** (A) circCCDC66-miR-320a/b-mRNAs networks in gliomas using Starbase datasets. (B) miRNA-320a and miRNA-320b have1864 common targets. (C) The interaction between the proteins. (D) GO analysis and KEGG pathway analysis of circCCDC66. (E) Biological pathway for circCCDC66.



Supplementary Figure 2. Part I of identification of key targets of circCCDC66-miR-320a/b axis. (A) There are 68 nodes in network 1. (B) Bioinformatics analysis of network 1.



Supplementary Figure 3. Part II of identification of key targets of circCCDC66-miR-320a/b axis. (A) The network 2 included 40 nodes. (B) Bioinformatics analysis of network 2.