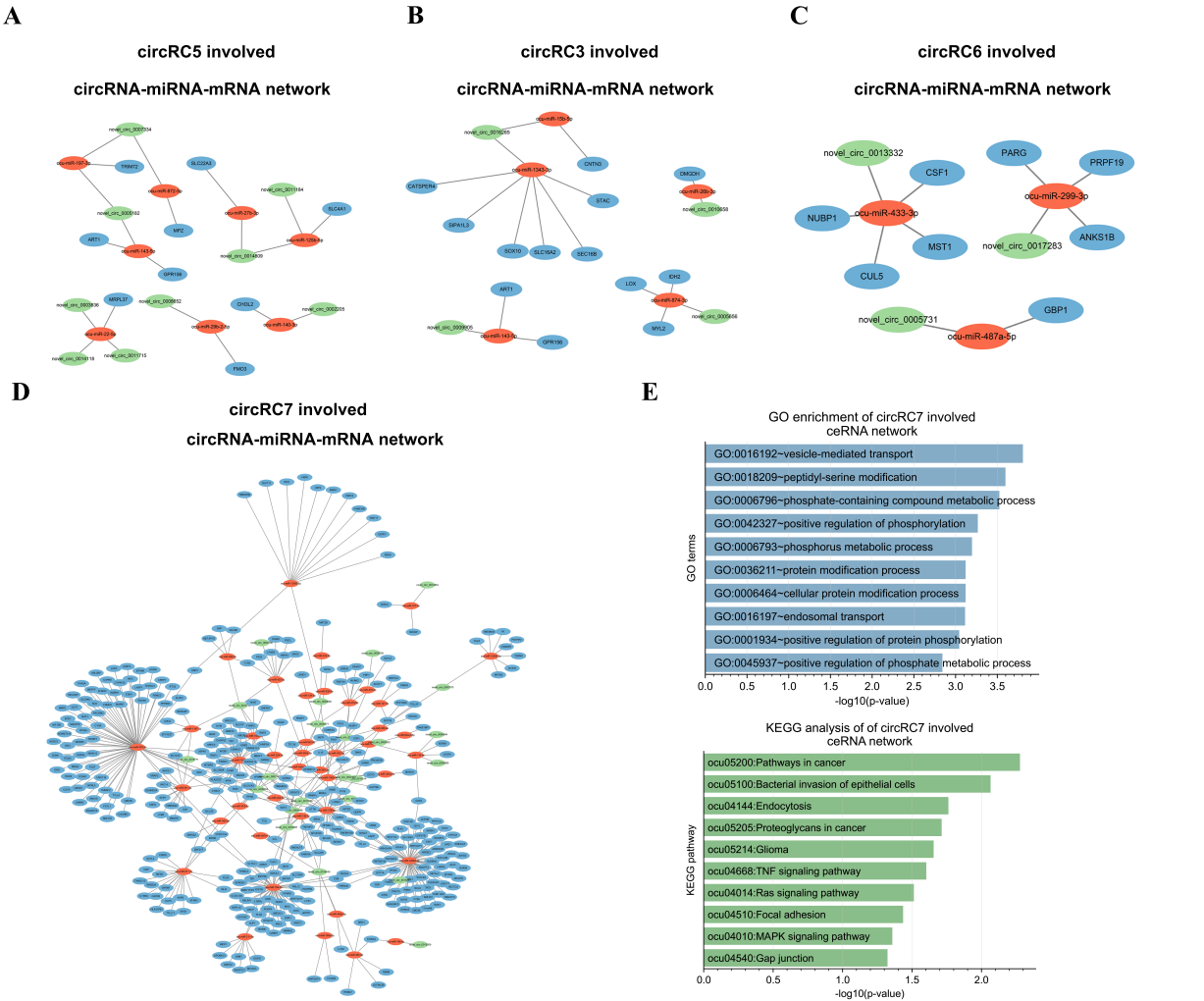

Figure S7. Prediction of ceRNA networks using stage-selective circRNAs and functional annotation. (A - D) Prediction of ceRNA networks using circRNAs in circRC5, circRC3, circRC6, and circRC7. The red, blue, and green nodes show the miRNAs, mRNAs, and circRNAs, respectively. (E) GO-BP enrichment and KEGG pathway analysis of circRC7 involved ceRNA network.