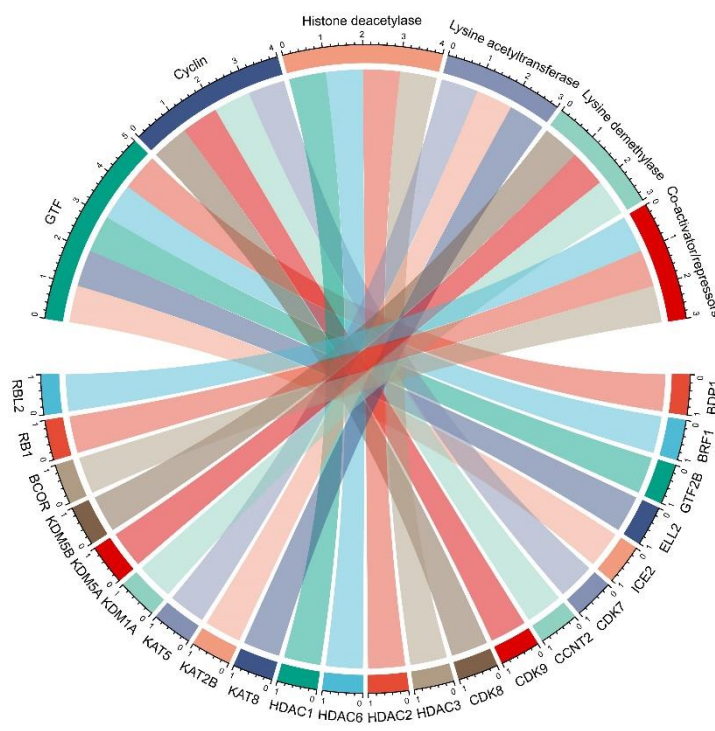
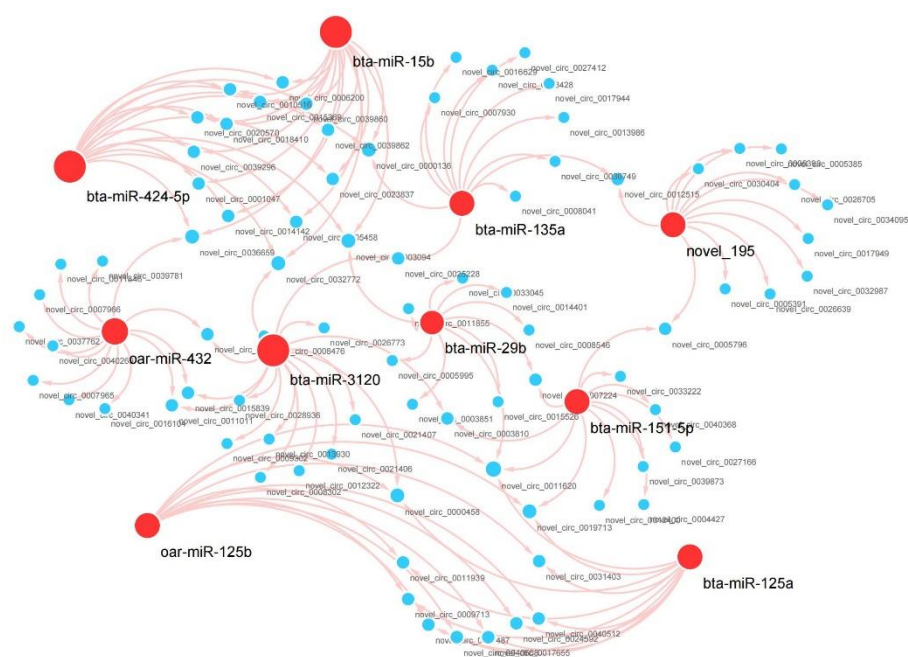


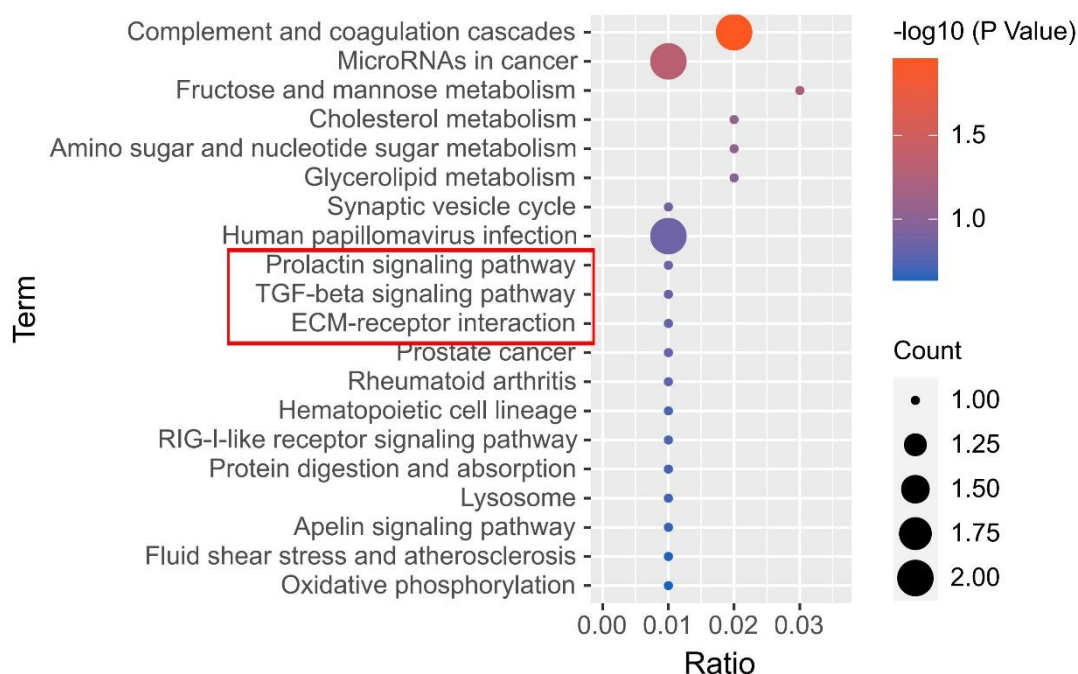
**Supplementary Figure S1.** Density distribution of circRNA on QE and HE chromosomes.



**Supplementary Figure S2.** Top 5 family statistics of TF predictions for the three genes.

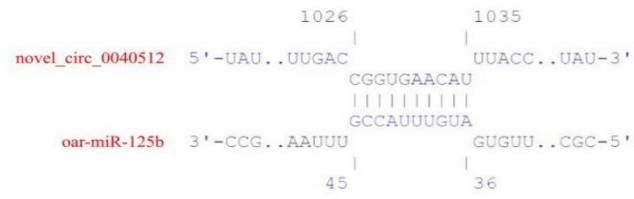


**Supplementary Figure S3.** The top 10 miRNAs with the most nodes in the circRNA-miRNA regulatory network. red circles represent miRNAs and dark blue circles represent miRNAs.

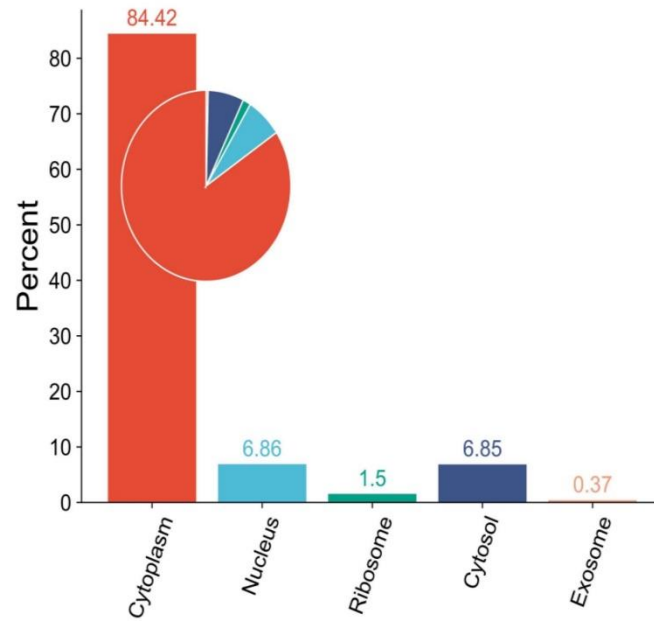


**Supplementary Figure S4.** KEGG enrichment analysis of DE miRNA target DE mRNAs.

**A**



**B**



**Supplementary Figure S5.** Novel-circ-0040512 sponge oar-miR-125b in sheep ovarian granulosa cells. (A) Predicted circRNA shear site and oar-miR-125b complementary binding site. (B) Predicted distribution of novel-circ-0040512 in cells.