

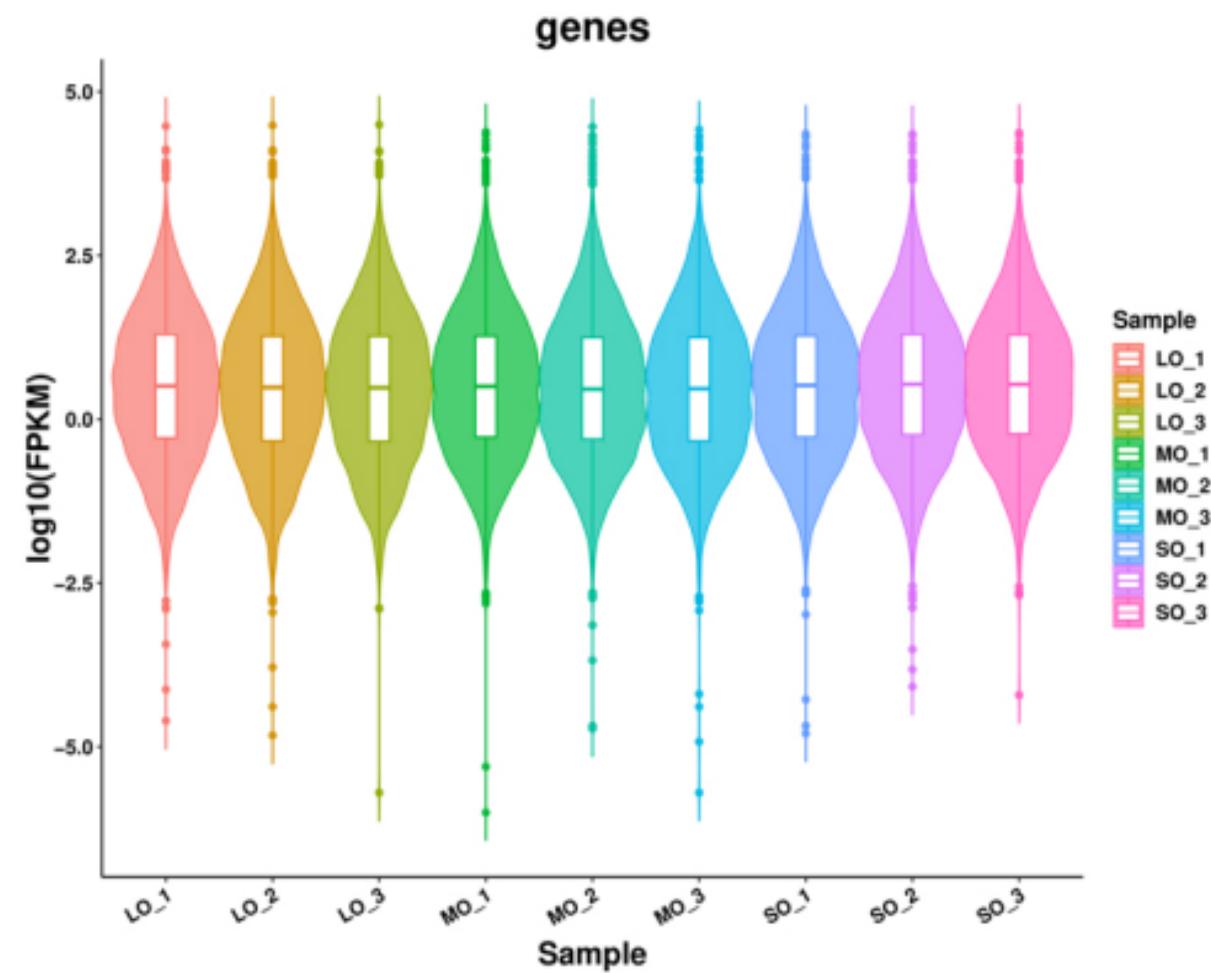
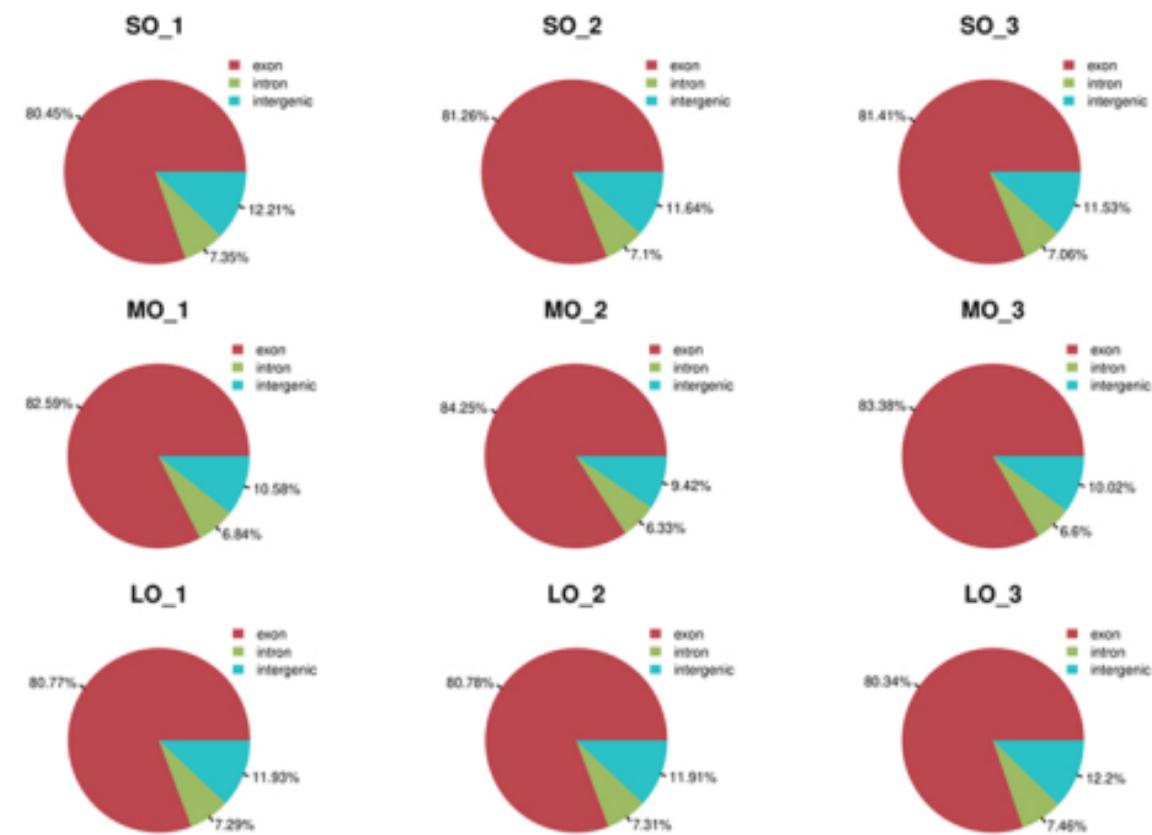
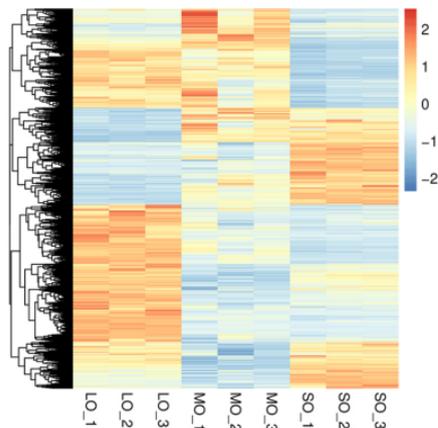
A**B**

Figure S1. Sample Collection and Quality Control.

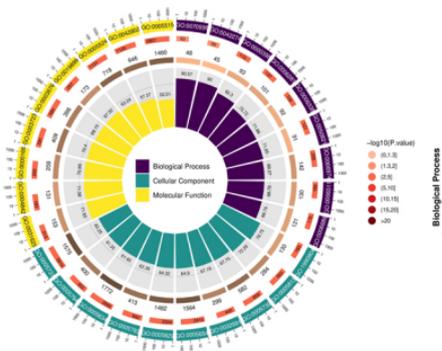
A. Violin plot for gene expression level (\log_{10} -FPKM) showing the distribution and overall range of the FPKM values in all replicates.

B. Pie chart representing gene coverage distribution

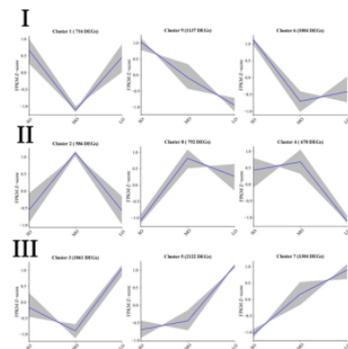
A



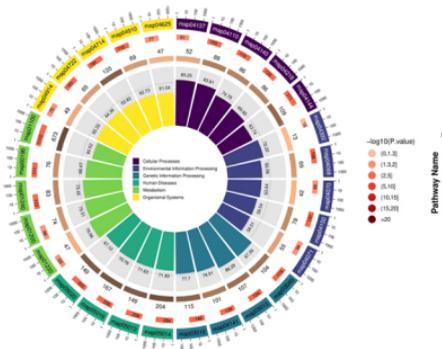
C



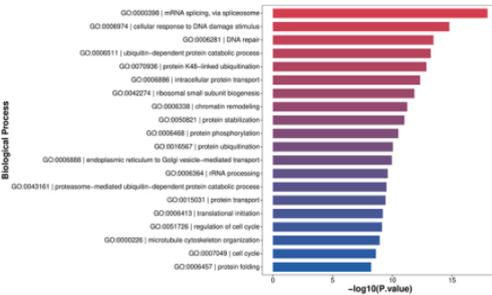
B



D



Top 20 of Biological Process Enrichment



Top 20 of KEGG Enrichment

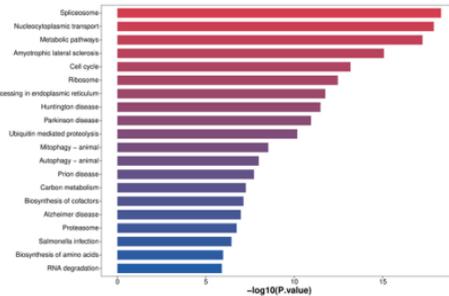


Figure S2. Gene Expression Dynamics and Transcriptional Characteristics during antral follicle development.

A. Hierarchical clustering of 9,400 putative DEGs expression in oocytes during antral follicle development.

B. K-Means clustering of 9,400 putative DEGs.

C. Gene ontology LoopCircos of 9,400 putative DEGs; Top 20 GO terms (biological processes) of 9,400 putative DEGs in the oocytes at three stages of antral follicle development.

D. KEGG enrichment LoopCircos of 9,400 putative DEGs; Top 20 KEGG of 9,400 putative DEGs in the oocytes at three stages of antral follicle development.

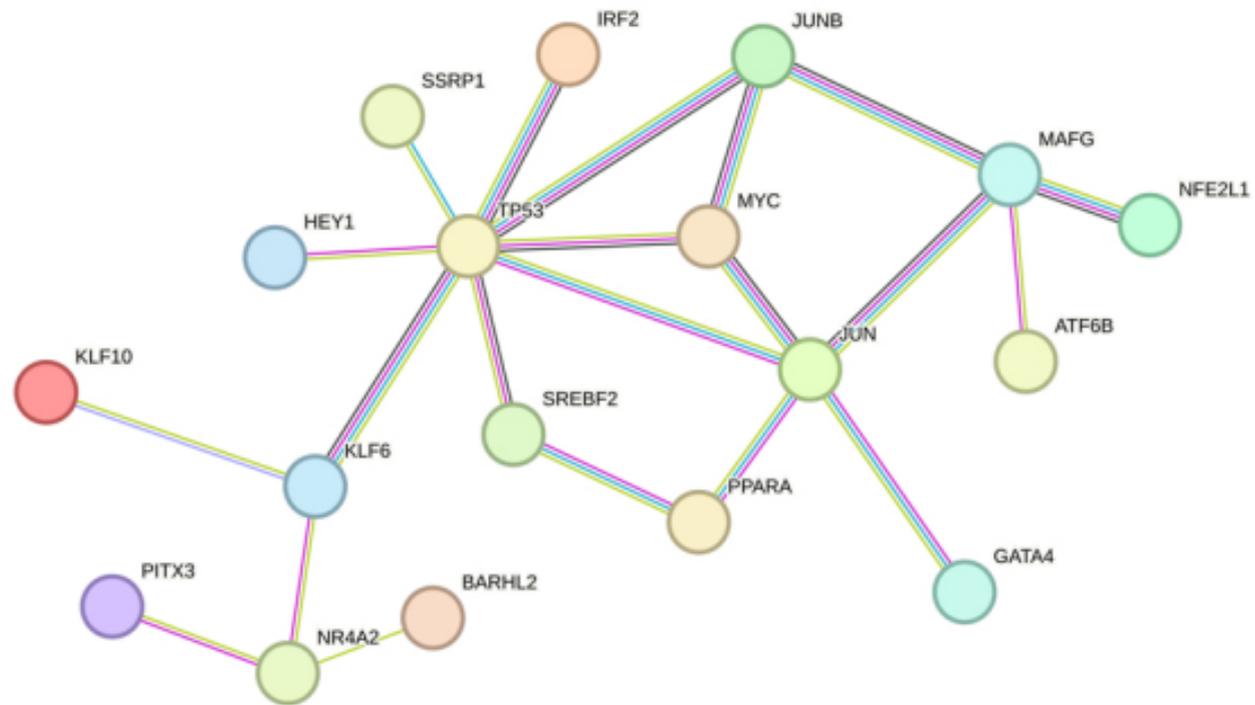
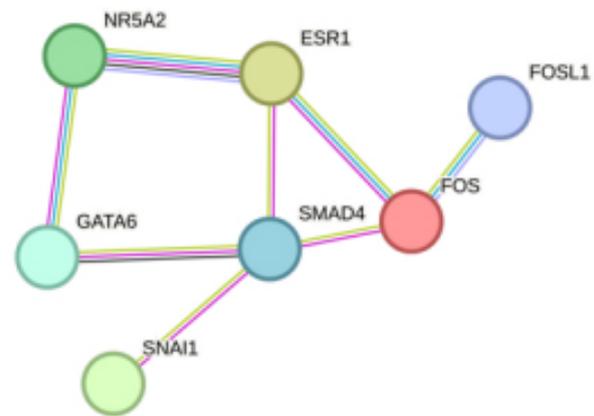
A**B**

Figure S3. The PPI network of unique sheep transcription factors genes.

A. The PPI network of transcription factors in oocytes of large follicle stage.

B. The PPI network of co-expressed in oocytes of medium and large antral follicle stag