

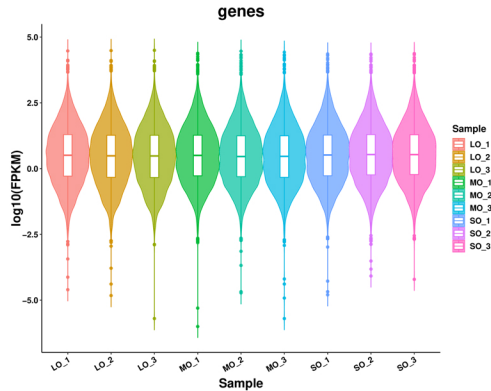
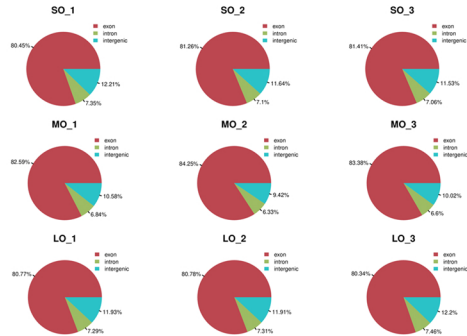
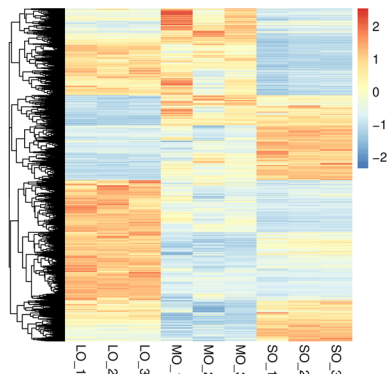
**A****B**

Figure S1. Sample Collection and Quality Control.

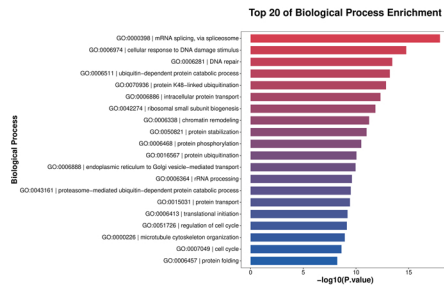
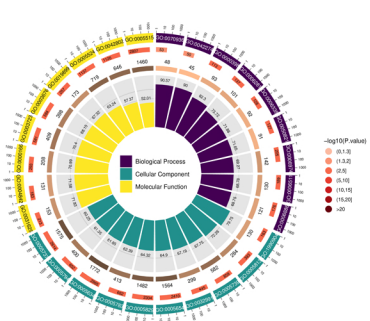
A. Violin plot for gene expression level ( $\log_{10}$ -FPKM) showing the distribution and overall range of the FPKM values in all replicates.

B. Pie chart representing gene coverage distribution

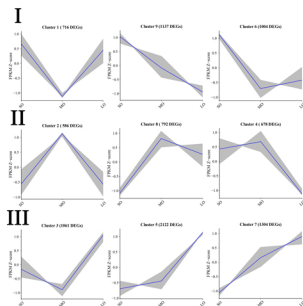
A



C



B



D

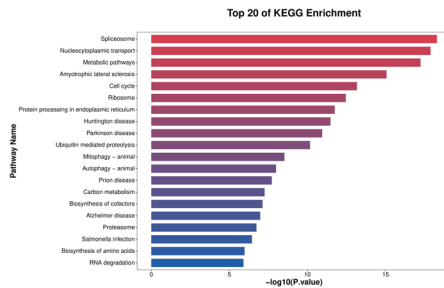
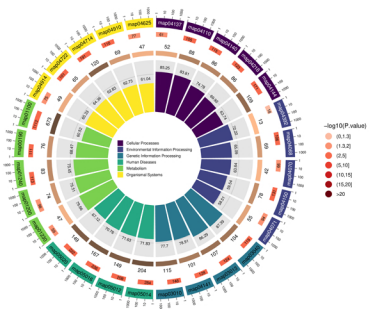


Figure S2. Gene Expression Dynamics and Transcriptional Characteristics during antral follicle development.

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

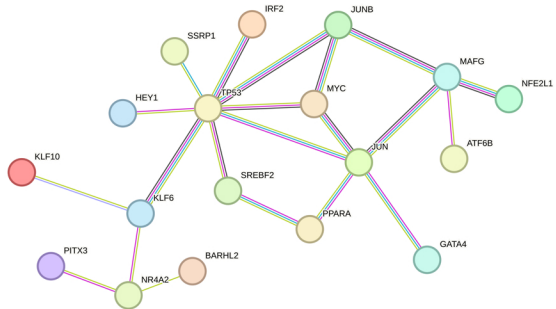
B. K-Means clustering of 9,400 putative DEGs.

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

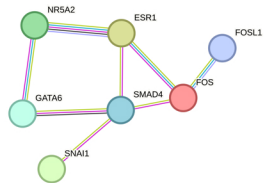


Figure S3. The PPI network of unique sheep transcription factors genes.

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