

### Supplementary Materials Tables Title

**Table S1.** Primer sequences and amplification efficiency for real-time quantitative reverse-transcription PCR (RTqPCR).

**Table S2.** Source information and basic statistics of goat mammary glands samples for transcriptome analysis.

**Table S3.** Transcript expression levels of all mammary gland samples.

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**Table S6.** Gene ontology functional annotation and Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway enrichment analysis of genes in each module

**Table S7.** Information on differentially expressed transcripts in mammary tissue at different developmental stages.

**Table S8.** Clustering results and Gene ontology and Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway enrichment analysis of differentially expressed transcripts.

**Table S9.** Gene ontology and Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway enrichment analysis of metabolism-related genes.

**Table S10.** Gene ontology and Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway enrichment analysis of immune-related genes.

**Table S11.** Gene ontology and Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway enrichment analysis of mammary gland development-related genes.

**Table S12.** Cluster analysis of genes in the PI3K-Akt signaling pathway.

**Table S13.** Gene ontology and Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway enrichment analysis of genes related to apoptosis and autophagy.