



# Discovery of differentially expressed genes in cashmere goat (*Capra hircus*) hair follicles by RNA sequencing

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**ABSTRACT.** The mammalian hair follicle (HF) is a unique, highly regenerative organ with a distinct developmental cycle. Cashmere goat

(*Capra hircus*) HFs can be divided into two categories based on structure and development time: primary and secondary follicles. To identify differentially expressed genes (DEGs) in the primary and secondary HFs of cashmere goats, the RNA sequencing of six individuals from Arbas, Inner Mongolia, was performed. A total of 617 DEGs were identified; 297 were upregulated while 320 were downregulated. Gene ontology analysis revealed that the main functions of the upregulated genes were electron transport, respiratory electron transport, mitochondrial electron transport, and gene expression. The downregulated genes were mainly involved in cell autophagy, protein complexes, neutrophil aggregation, and bacterial fungal defense reactions. According to the Kyoto Encyclopedia of Genes and Genomes database, these genes are mainly involved in the metabolism of cysteine and methionine, RNA polymerization, and the MAPK signaling pathway, and were enriched in primary follicles. A microRNA-target network revealed that secondary follicles are involved in several important biological processes, such as the synthesis of keratin-associated proteins and enzymes involved in amino acid biosynthesis. In summary, these findings will increase our understanding of the complex molecular mechanisms of HF development and cycling, and provide a basis for the further study of the genes and functions of HF development.

**Key words:** Cashmere goat; Differentially expressed gene; Hair follicle; RNA-Seq; Whole transcriptome sequencing