



# Characterization of microRNAs from goat (*Capra hircus*) by Solexa deep-sequencing technology

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**ABSTRACT.** MicroRNAs (miRNAs) are an important class of small noncoding RNAs that are highly conserved in plants and animals. Many miRNAs are known to mediate a myriad of cell processes, including proliferation and differentiation, via the regulation of some transcription and signaling factors, which are closely related to muscle development and disease. In this study, small RNA cDNA libraries of Boer goats were constructed. In addition, we obtained the goat muscle miRNAs by using Solexa deep-sequencing technology and analyzed these miRNA characteristics by combining it with the bioinformatics technology. Based on Solexa sequencing and bioinformatics analysis, 562 species-conserved and 5 goat genome-specific miRNAs were identified, 322 of which exceeded 100 in the expression levels. The results of real-time quantitative polymerase chain reaction from 8 randomly selected miRNAs showed that the 8 miRNAs were expressed in goat muscle,

and the expression patterns were consistent with the Solexa sequencing results. The identification and characterization of miRNAs in goat muscle provide important information on the role of miRNA regulation in muscle growth and development. These data will help to facilitate studies on the regulatory roles played by miRNAs during goat growth and development.

**Key words:** Goat; Solexa deep-sequencing technology; MicroRNA characteristics; Real-time quantitative PCR