

Supplementary Table 3. A summary of the RNA-seq reads alignment to the goat reference genome.

Sample	JG	BG
Total Reads	3711416(100%)	3648953(100%)
Total BasePairs	181859384(100%)	178798697(100%)
Total Mapped Reads	2863343(77%)	2823329(77%)
perfect match	2049528(55%)	1978574(54%)
<=3bp mismatch	813815(22%)	844755(23%)
unique match	2361451(64%)	2321499(64%)
multi-position match	501892(14%)	501830(14%)
Total Unmapped Reads	848073(23%)	825624(23%)