**Identification and expression analysis of long noncoding RNAs in fat-tail of sheep breeds**

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**Supplementary Information I1**

**Figure I1** A hierarchical clustering analysis of all the biological samples. LB and ZL denotes Lori-Bakhtiari and Zel sheep breeds.

Distance

**Figure I2** Comparisons of GC content (a), transcript length (b) and exon number (c) among novel and annotated transcripts. In all figures, a, b, c and d denote the results of statistical analysis and the boxes sharing a common letter are not significantly different (p<0.05).

**Figure I3** Gene expression patterns of different genes in different samples. In all figures, a, b, c and d denote the results of statistical analysis and the boxes sharing a common letter are not significantly different (p<0.05).