

Comparison of microbial diversity in rumen and small intestine of Xinong Saanen dairy goats using 16S rRNA gene high-throughput sequencing

Cong Li^A, Yanan Geng^A, Ping Wang^A, Huaiping Shi^A and Jun Luo^{A,B}

^AKey Laboratory of Animal Genetics, Breeding and Reproduction of Shaanxi Province, College of Animal Science and Technology, Northwest A&F University, Yangling, Shaanxi 712100, China.

^BCorresponding author. Email: luojun@nwsuaf.edu.cn

SUPPLEMENTARY MATERIAL

Table S1. Sequence information of microorganisms in rumen and jejunum of Xinong Saanen dairy goat

Items	Valid sequence No.	Average length of sequences	OTU ^A No.	OTU No. for sequence abundance>1%	Coverage (%)
L (Rumen) ^B	53,379	440	1,020	18	99.58
X (Jejunum) ^C	44,709	428	649	12	99.73

^AOTU = Operational Taxonomic Unit. ^BL = Rumen. ^CX = Jejunum.

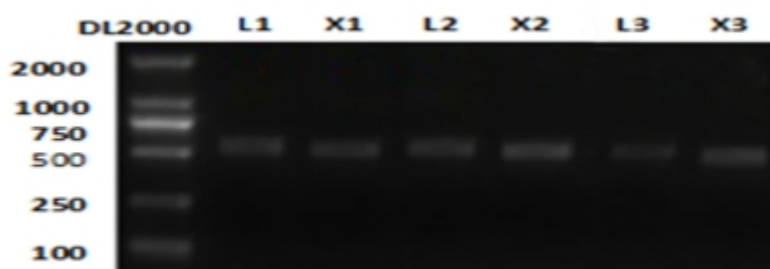


Figure S1. PCR products measured by 2% agarose gel electrophoresis

Legends: DL2000 represents the DNA Marker. The number of 1-16 represents the DNA samples.

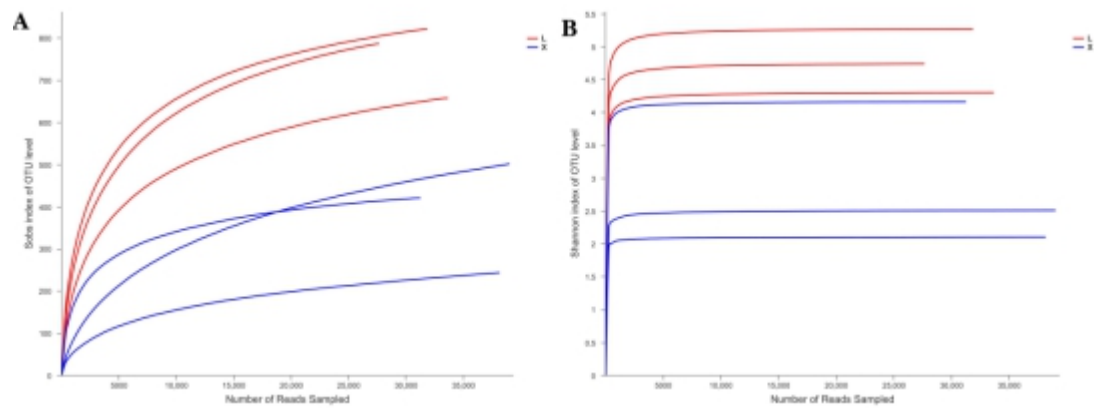


Figure S2. The Sobs curve(A) and Shannon curve(B) of rumen and jejunum microorganisms in Xinong Saanen dairy goats

Legends: L represents the Rumen group, X represents the Jejunum group.