**Supplement 1**

The determination procedure of microbrome in rumen and cecum of fatting lambs. There are three sequential steps for the methods: DNA extracting, PCR products detecting, and data analysis.

**DNA extracting:** DNA samples were extracted from rumen and cecum digesta using QIAamp DNA Stool Mini Kits (Qiagen Inc., Hilden, Germany) according to the manufacturer’s instructions. The concentration and purity of the DNA samples were checked with gel electrophoresis. The microbial 16S rRNA sequences were amplified with universal primers 515 F (5`-GTG CCA GCM GCC GCG GTA A-3’) and 806 R (5`-GGA CTA CHV GGG TWT CTA AT-3`) targeting the V3-V4 region according to the PCR methods described before[1].

**PCR products detecting:** The PCR products were detected by 2% gel electrophoresis and purified with QIAquick Gel Extraction Kit (Qiagen Inc., Hilden, Germany). A library was constructed using Ion Plus Fragment Library Kit 48 rxns (Thermo Scientific Inc., Waltham, USA) and quantified by Qubit 2.0 Fluorometer (Thermo Fisher Scientific, Waltham, USA) to pool at equal concentrations. Pyrosequencing for 16S rDNA was carried out on the Illumina HiSeq2500 PE250 platform (Illumina, San Diego, USA). All of the procedures were conducted by Novogene Bioinformatics Technology Co. Ltd. (Beijing, China).

**Data analysis:** The clean reads were obtained after the quality filtering by Cutadapt (Martin M. , 2011) (V1.9.1, <http://cutadapt.readthedocs.io/en/stable/>) and Chimera removal by UCHIME algorithm (UCHIME Algorithm, <http://www.drive5.com/usearch/manual/uchime_algo.html>). Then the clean reads were clustered into operational taxonomic units (OTUs) using Uparse in QIIME software (Uparse v7.0.1001, http://drive5.com/uparse/) with a similarity threshold of 97%. The OTUs were obtained from Mothur, and were sorted from most to least abundant. 16S rRNA gene sequences were aligned using the multiple sequence alignment method MUSCLE(Version 3.8.31，**[http://www.drive5.com/muscle/](http://www.drive5.com/muscle/" \t "_blank" \o "muscle)**). And the OTUs were further subjected to the taxonomy-based analysis by the RDP algorithm using the Greengenes database (<http://greengenes.lbl.gov>). Alpha diversity (Shannon) and beta diversity (weighted UniFrac, principal coordinate analysis (PCOA)) were analyzed using QIIME (Version 1.9.1).