Table S1. Detailed list of the primer barcode sequences used for each of the samples in this study

Age group	Sample Name	Barcode sequence
0 day old	A01	ATCACG
	A02	CGATGT
	A03	TTAGGC
	A04	TGACCA
7 days old	A05	ACAGTG
	A06	GCCAAT
	A07	CAGATC
28 days old	A08	GATCAG
	A09	TAGCTT
	A10	GGCTAC
42 days old	A11	CTTGTA
	A12	AGTCAA
	A13	AGTTCC
	A14	ATGTCA
70 days old	A15	CCGTCC
	A16	GTCCGC
	A17	GTGAAA

Table S2. Primers used for qPCR

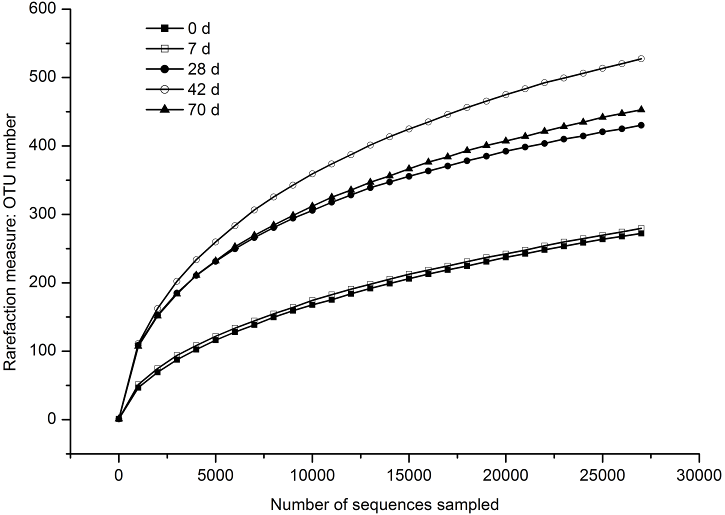
Primer's name	**Sequence (5′ to 3′)**	**Size (bp)**	**Reference**
Bacteria-F	CGGCAACGAGCGCAACCC	146	1
Bacteria-R	CCATTGTAGCACGTGTGTAGCC		
Prevotella spp.-F	GGTTCTGAGAGGAAGGTCCCC	121	2
Prevotella spp.-R	TCCTGCACGCTACTTGGCTG		
Bacteroides-F	GAGAGGAAGGTCCCCCAC	109	3
Bacteroides-R	CGCTACTTGGCTGGTTCAG		

Literature cited

1. **Denman SE, McSweeney CS.** 2006. Development of a real-time PCR assay for monitoring anaerobic fungal and cellulolytic bacterial populations within the rumen. FEMS Microbiol Ecol **58:**572-282.
2. **Stevenson DM, Weimer PJ.** 2007. Dominance of *Prevotella* and low abundance of classical ruminal bacterial species in the bovine rumen revealed by relative quantification real-time PCR. Appl Microbiol Biotechnol **75:**165-174.
3. **Layton A, McKay L, Williams D, Garrett V, Gentry R, Sayler G.** 2006. Development of *Bacteroides* 16S rRNA gene TaqMan-based real-time PCR assays for estimation of total, human, and bovine fecal pollution in water. Appl Environ Microbiol **72:**4214-4224.

Figure legends

Figure S1. Rarefaction curve (number of OTUs) of the ruminal epithelial bacteria at different ages in goats.


0 d
7 d
28 d
42 d
70 d
Rarefaction measure: OTU number
600
500
400
300
200
100
0
0
5000
10000
15000
20000
25000
30000
Number of sequences sampled