

Supplementary Material

Host species affects bacterial evenness, but not diversity: comparison of fecal bacteria of cows and goats fed the same diet

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Table S1. Animals' characteristics

Sample name	Animal species	Age	Lactating	Pregnant
GN 1	Goat	4 years	Yes	No
GN 4	Goat	6 years	Yes	No
GN 6	Goat	4 years	Yes	No
GN 7	Goat	3 years	No	Yes
GN 14	Goat	3 years	No	Yes
GN 15	Goat	3 years	No	Yes
GN 16	Goat	4 years	No	Yes
GN 17	Goat	5 years	No	Yes
GN 21	Goat	3 years	No	Yes
GN 22	Goat	7 years	No	Yes
GN 23	Goat	5 years	No	Yes
GN 24	Goat	7 years	No	Yes
GN 25	Goat	2 years	No	Yes
GN 27	Goat	3 years	No	Yes
GN 28	Goat	7 years	No	Yes
GN 29	Goat	4 years	No	Yes
GN 30	Goat	6 years	No	Yes
CN 1	Cow	3 years	Yes	Yes
CN 2	Cow	3 years	Yes	Yes
CN 6	Cow	7 years	Yes	Yes
CN 9	Cow	7 years	Yes	Yes
CN 10	Cow	3 years	Yes	Yes
CN 15	Cow	4 years	No	Yes
CN 16	Cow	5 years	No	Yes
CN 17	Cow	8 years	No	Yes
CN 19	Cow	7 years	No	Yes
CN 20	Cow	7 years	No	Yes
CN 21	Cow	7 years	No	Yes
CN 22	Cow	7 years	No	Yes
CN 23	Cow	7 years	No	Yes
CN 24	Cow	8 years	No	Yes
CN 26	Cow	5 years	No	Yes
CN 28	Cow	9 years	No	Yes

Table S2. Summary of alpha diversity indices of bacterial community in cows and goats (means $\pm$ SD).

Index	Cows	Goats	p-value
Chao 1	877.19 $\pm$ 708	688.54 $\pm$ 909	0.16
Pielou Evenness	0.934 $\pm$ 0.01	0.918 $\pm$ 0.02	0.017*
Shannon	8.286 $\pm$ 1.2	7.498 $\pm$ 1.3	0.11
Faith pd	60.82 $\pm$ 20	56.16 $\pm$ 23	0.13
ASV ¹	604 $\pm$ 372	422 $\pm$ 398	0.13

ASV¹, Amplicon sequence variant.

* Significant difference (p < 0.05)

Table S3. Relative abundance (means $\pm$ SD) of bacterial taxa at phylum, class, order and family levels in the feces of goats and cows.

Taxonomic levels	Goats	Cows
Phylum		
Firmicutes	75 $\pm$ 4.3%	74.9 $\pm$ 2.5%
Bacteroidetes	17.7 $\pm$ 2.5%	19.5 $\pm$ 1.9%
Spirochaetes	1.7 $\pm$ 0.6%	0.3 $\pm$ 0.2%
Proteobacteria	2.2 $\pm$ 0.6%	2.1 $\pm$ 0.6%
Actinobacteria	1 $\pm$ 0.5%	0.5 $\pm$ 0.3%
Tenericutes	0.5 $\pm$ 0.3%	0.9 $\pm$ 0.2%
Patescibacteria	0.5 $\pm$ 0.4%	0.5 $\pm$ 0.2%
Planctomycetes	0.2 $\pm$ 0.08%	0.1 $\pm$ 0.1%
Lentisphaerae	0.5 $\pm$ 0.2%	0.7 $\pm$ 0.3%
Epsilonbacteraeota	0.4 $\pm$ 0.6%	0.07 $\pm$ 0.1%
Elusimicrobia	0.03 $\pm$ 0.02%	0.05 $\pm$ 0.03%
Kiritimatiellaeota	0.02 $\pm$ 0.01%	0.06 $\pm$ 0.04%
Cyanobacteria	0.02 $\pm$ 0.01%	0.005 $\pm$ 0.003%
Fibrobacteres	0	0.0005 $\pm$ 0.03%
Fusobacteria	0.0002 $\pm$ 0.01%	0
Class		
Clostridia	74.2 $\pm$ 4.3%	71.3 $\pm$ 2.5%
Bacteroidia	17.7 $\pm$ 2.6%	19.5 $\pm$ 2%
Spirochaetes	1.7 $\pm$ 0.6%	0.5 $\pm$ 0.2%
Bacilli	0.2 $\pm$ 0.1%	3 $\pm$ 2 %
Deltaproteobacteria	0.9 $\pm$ 0.3%	0.7 $\pm$ 0.2%
Order		
Clostridiales	74.1 $\pm$ 4.3%	71.2 $\pm$ 2.5%
Bacteroidales	17.7 $\pm$ 2.6%	19.5 $\pm$ 1.9%
Spirochaetales	1.7 $\pm$ 0.6%	0.5 $\pm$ 0.2%
Bacillales	0.06 $\pm$ 0.02%	2.9 $\pm$ 2.2%

Desulfovibrionales	0.9 ± 0.3%	0.7 ± 0.2%
Family		
<i>Ruminococcaceae</i>	38.7 ± 2.5%	39.5 ± 2.8%
<i>Christensenellaceae</i>	13.7 ± 2.8%	7.7 ± 1%
<i>Rikenellaceae</i>	7.7 ± 1.2%	6 ± 0.7%
<i>Peptostreptococcaceae</i>	2.9 ± 2.3%	5.7 ± 1.9%
<i>Lachnospiraceae</i>	10.2 ± 2.7%	9 ± 1.1%
Family XIII	5.2 ± 1.4%	4.7 ± 0.8%
<i>Spirochaetaceae</i>	1.7 ± 0.6%	0.5 ± 0.2%
<i>Planococcaceae</i>	0.03 ± 0.01%	2.2 ± 2%
<i>p-2534-18B5 gut group</i>	0.7 ± 0.7%	1.4 ± 0.5%
<i>Prevotellaceae</i>	2.2 ± 0.5%	3.6 ± 0.9%
<i>Desulfovibrionaceae</i>	0.9 ± 0.4%	0.7 ± 0.2%
<i>p-251-o5</i>	1.1 ± 0.6%	0.4 ± 0.2%
<i>Bacteroidales RF16 group</i>	1.5 ± 0.9%	3 ± 0.5%
Unclassified family within order <i>Bacteroidales</i>	1.8 ± 1.3%	2.5 ± 0.5%
<i>Clostridiaceae 1</i>	0.5 ± 0.5%	0.5 ± 0.2%
<i>F082</i>	0.5 ± 0.5%	0.3 ± 0.08%
Unclassified family within order <i>Izimaplasmatales</i>	0.4 ± 0.2%	0.8 ± 0.2%
<i>Clostridiales vadinBB60 group</i>	1.7 ± 0.6%	3.3 ± 0.4%
<i>Paludibacteraceae</i>	0.4 ± 0.3%	1 ± 0.3%
<i>Peptococcaceae</i>	0.7 ± 0.3%	0.5 ± 0.2%
<i>Acidaminococcaceae</i>	0.6 ± 0.2%	0.3 ± 0.1%
<i>Saccharimonadaceae</i>	0.5 ± 0.4%	0.5 ± 0.2%
<i>Bacteroidaceae</i>	0.8 ± 0.3%	0.6 ± 0.2%
Genus		
<i>Christensenellaceae R-7 group</i>	13.5 ± 2.8%	7.6 ± 1%
<i>Ruminococcaceae UCG-005</i>	13 ± 4.4%	10.4 ± 3.2%
<i>Ruminococcaceae UCG-010</i>	8.7 ± 2%	14.6 ± 1.4%
<i>Alistipes</i>	3.8 ± 1.2%	4.1 ± 0.7%
<i>Romboutsia</i>	2.5 ± 1.7%	3.6 ± 1.5%
<i>Rikenellaceae RC9 gut group</i>	3.4 ± 1%	1.2 ± 0.3%
<i>Eubacterium coprostanoligenes group</i>	3 ± 1.2%	2.3 ± 0.6%
Unclassified genus within family <i>Ruminococcaceae</i>	3 ± 1.7%	2.4 ± 0.5%
Family XIII AD3011 group	2.4 ± 0.9%	2 ± 0.5%
Unclassified genus within family <i>Lachnospiraceae</i>	3.3 ± 0.9%	2.6 ± 0.3%
Unclassified genus within family <i>Lachnospiraceae</i>	2.1 ± 1.5%	2 ± 1%
Unclassified genus within family <i>Ruminococcaceae</i>	2.1 ± 1%	2 ± 0.7%
<i>Ruminococcaceae UCG-013</i>	1.5 ± 0.7%	1.3 ± 0.6%
Unclassified genus within family <i>Bacteroidales RF16 group</i>	1.3 ± 0.8%	2.7 ± 0.5%
Unclassified genus within family <i>Clostridiales vadinBB60 group</i>	1.4 ± 0.5%	3 ± 0.4%

<i>Unclassified genus within family Paludibacteraceae</i>	0.4 ± 0.3%	1 ± 0.3%
<i>Ruminococcaceae UCG-014</i>	1.4 ± 0.8%	1.3 ± 0.4%
<i>Ruminococcaceae UCG-009</i>	1 ± 0.6%	1.2 ± 0.6%
<i>Mailhella</i>	0.9 ± 0.3%	0.7 ± 0.2%
<i>Treponema 2</i>	1.7 ± 0.6%	0.5 ± 0.2%
<i>Solibacillus</i>	0.008 ± 0.003%	1.5 ± 1.7%
<i>Prevotellaceae UCG-003</i>	1 ± 0.4%	1.5 ± 0.5%
<i>Ruminococcaceae UCG-002</i>	1 ± 0.9%	0.5 ± 0.2%
<i>Paeniclostridium</i>	0.09 ± 0.3%	1.3 ± 0.4%
<i>Unclassified genus within family p-2534-18B5</i>	0.7 ± 0.7%	1.5 ± 0.5%
<i>Prevotellaceae UCG-004</i>	0.7 ± 0.5%	1.2 ± 0.2%
<i>Unclassified genus within order Bacteroidales</i>	0.4 ± 0.3%	0.7 ± 0.5%
<i>Ruminococcaceae NK4A214 group</i>	1.2 ± 0.7%	0.7 ± 0.3%
<i>Mogibacterium</i>	1 ± 1.1%	0.7 ± 0.3%
<i>Unclassified genus within order Bacteroidales</i>	1 ± 0.5%	0.2 ± 0.1%
<i>Ruminiclostridium 9</i>	0.4 ± 0.4%	0.7 ± 0.7%
<i>Unclassified genus within family Peptostreptococcaceae</i>	0.3 ± 0.6%	0.8 ± 0.5%
<i>Eubacterium brachy group</i>	0.4 ± 0.3%	0.5 ± 0.3%
<i>Clostridium sensu stricto 1</i>	0.5 ± 0.5%	0.5 ± 0.1%
<i>Escherichia-Shigella</i>	0.5 ± 0.2%	0.05 ± 0.05%
<i>Lysinibacillus</i>	0.01 ± 0.005%	0.7 ± 0.5%
<i>Unclassified genus within order Izimaplasmatales</i>	0.4 ± 0.2%	0.8 ± 0.2%
<i>Ruminococcus 1</i>	0.6 ± 1.3%	0.4 ± 0.2%
<i>Unclassified genus within family Peptococcaceae</i>	0.6 ± 0.3%	0.4 ± 0.2%
<i>Unclassified genus within family Family XIII</i>	0.5 ± 0.6%	0.5 ± 0.4%
<i>Unclassified genus within order Bacteroidales</i>	1.3 ± 1.4%	1.2 ± 0.2%
<i>Eubacterium nodatum group</i>	0.5 ± 0.6%	0.7 ± 0.3%
<i>Lachnospiraceae NK3A20 group</i>	0.8 ± 1.3%	0.6 ± 0.3%
<i>Lachnospiraceae AC2044 group</i>	0.5 ± 0.7%	0.2 ± 0.1%
<i>Unclassified genus within order Bacteroidales</i>	0.009 ± 0.06%	0.5 ± 0.2%
<i>Dorea</i>	0.6 ± 0.6%	0.5 ± 0.3%
<i>Phascolarctobacterium</i>	0.6 ± 0.2%	0.3 ± 0.1%
<i>dgA-11 gut group</i>	0.5 ± 0.6%	0.6 ± 0.1%
<i>Bacillus</i>	0.02 ± 0.01%	0.5 ± 0.3%
<i>Candidatus Saccharimonas</i>	0.5 ± 0.4%	0.5 ± 0.2%
<i>Bacteroides</i>	0.8 ± 0.3%	0.6 ± 0.2%
<i>Lachnospiraceae NK4A136 group</i>	0.7 ± 0.5%	0.6 ± 0.3%
<i>Alloprevotella</i>	0.09 ± 0.06%	0.6 ± 0.4%
<i>Roseburia</i>	0.5 ± 0.2%	0.5 ± 0.3%

Table S4. Bacterial genera with low relative abundance (<0.5%).

Bacterial Genera	Goats	Cows
<i>Campylobacter</i>	0.205487039	0.068372032
<i>Unclassified genus within family Bacteroidales RF16 group</i>	0.034904713	0.146632321
<i>Candidatus Soleaferrea</i>	0.090622646	0.118998084
<i>Aeriscardovia</i>	0.19412372	0.009989841
<i>Oscillibacter</i>	0.112159937	0.26544436
<i>Unclassified genus within family F082</i>	0.072324842	0.290483833
<i>Unclassified genus within order Bacteroidales</i>	0.437372695	0.040015672
<i>Acinetobacter</i>	0.094868718	0.007357635
<i>Turicibacter</i>	0.068361282	0.001323213
<i>Olsenella</i>	0.092104969	0.004248563
<i>Unclassified genus within family Clostridiales vadinBB60 group</i>	0.287309216	0.001223652
<i>Unclassified genus within order Clostridiales</i>	0.008928542	0.00289023
<i>Ruminiclostridium</i>	0.044308574	0.002383758
<i>Acetitomaculum</i>	0.111697452	0.371959423
<i>Ruminococcus 2</i>	0.38557856	0.000280199
<i>Unclassified genus within family F082</i>	0.039164039	0
<i>Unclassified genus within order Rhodospirillales</i>	0.393251765	0.392198582
<i>Ruminiclostridium 1</i>	0.196015514	0.009298194
<i>Anaerovorax</i>	0.194184408	0.005645208
<i>Lachnospiraceae UCG-001</i>	0.02399202	0.130025831
<i>Unclassified genus within order Bacillales</i>	0.008109183	0.182411911
<i>Hydrogenoanaerobacterium</i>	0.05441	0.038661984
<i>Ruminiclostridium 5</i>	0.118847485	0.192531491
<i>Unclassified genus within family p-251-o5</i>	0.147796395	0.218738607
<i>Parasutterella</i>	0.083633751	0.249746037
<i>Streptococcus</i>	0.034878205	0.100936321
<i>p-1088-a5 gut group</i>	0.128003013	0.121434956
<i>Tyzzereella 4</i>	0.110738302	0.295803099
<i>Prevotella 1</i>	0.215896091	0.097044175
<i>Negativibacillus</i>	0.026507436	0.216014105
<i>Eubacterium hallii group</i>	0.026333045	0.134797991
<i>Lachnospiraceae FCS020 group</i>	0.299603784	0.062404075
<i>Unclassified genus within family vadinBE97</i>	0.053538045	0.132981656
<i>Unclassified genus within order DTU014</i>	0.038714808	0.063831195
<i>Saccharofermentans</i>	0.054322805	0.077583444
<i>Defluviitaleaceae UCG-011</i>	0.004299088	0.018969931
<i>Unclassified genus within family Mitochondria</i>	0.00252867	0.017283334
<i>Ruminiclostridium 6</i>	0.049003878	0.070188367
<i>Unclassified genus within family Victivallaceae</i>	0.151371411	0.044556509

<i>Victivallis</i>	0.022060465	0.064739362
<i>Prevotellaceae</i> UCG-001	0.054497196	0.002233703
<i>Gordonibacter</i>	0.064175898	0.007135601
<i>Unclassified genus within family Barnesiellaceae</i>	0.119819889	0.254935566
<i>Eubacterium oxidoreducens</i> group	0.008631379	0.051116851
<i>Ruminococcaceae</i> UCG-004	0.002160914	0.150107099
<i>Ruminobacter</i>	0.054845978	0.017644395
<i>Lachnoclostridium</i>	0.088939424	0.047354443
<i>Unclassified genus within order Mollicutes</i> RF39	0.084666843	0.012353282
<i>Desulfovibrio</i>	0.047259968	0
<i>Unclassified genus within family vadin</i> BE97	0.19706186	0.010547716
<i>Odoribacter</i>	0.02371718	0.061755384
<i>Lachnospiraceae</i> UCG-006	0.049701443	0.063312242
<i>Lachnoclostridium</i> 10	0.066007004	0.064350148
<i>Porphyromonas</i>	0.068535673	0
<i>Unclassified genus within family Christensenellaceae</i>	0.11640601	0.06564753
<i>Prevotellaceae</i> Ga6A1 group	0.036883702	0.016087537
<i>Garciella</i>	0	0.063960933
<i>Eubacterium ventriosum</i> group	0.048655096	0.067593603
CHKCI002	0.024240353	0.016476752
<i>Unclassified genus within order Victivallales</i> ;__;__	0.017090321	0.008951936
<i>CPla-4</i> termite group	0.037145289	0
<i>Unclassified genus within order Rhodospirillales</i>	0.036186138	0.029710048
<i>Unclassified genus within family Victivallaceae</i>	0.040458718	0.097822604
<i>Unclassified genus within order Izimaplasmatales</i>	0.035837356	0.001556858
DNF00809	0.098356539	0.081086376
<i>Unclassified genus within family Muribaculaceae</i>	0.043772148	0.031266907
<i>Selenomonas</i> 1	0.023368398	0.030488477
uncultured <i>Parabacteroides</i> sp.	0.020229359	0.084719045
unidentified bacterium RFN82	0.009242724	0.026466593
<i>Unclassified genus within family Eggerthellaceae</i>	0.02894891	0.034380623
<i>Unclassified genus within family Victivallaceae</i>	0.035052596	0.002724502
<i>Unclassified genus within family Eggerthellaceae</i>	0.020926923	0.014660417
<i>Lachnospiraceae</i> UCG-008	0.069233238	0.076415801
<i>Elusimicrobium</i>	0.031651971	0.048651825
<i>Aerococcus</i>	0.009233238	0.006227434
<i>Blautia</i>	0.056241106	0.078751088
<i>Collinsella</i>	0	0.02088785
<i>Unclassified genus within family Corynebacteriaceae</i>	0	0.040867533
<i>Unclassified genus within family Rikenellaceae</i>	0.049788638	0.022574447
<i>Lachnospiraceae</i> UCG-004	0.002092692	0.024131305
<i>Marvinbryantia</i>	0.036186138	0.080437685
<i>Microbacterium</i>	0.006365272	0.033731932

<i>Parabacteroides</i>	0.008196378	0.014660417
<i>Unclassified genus within family Lachnospiraceae</i>	0.002615865	0.030358739
<i>Ruminococcaceae</i> UCG-008	0.009591506	0.02737476
<i>Murdochiella</i>	0.015259215	0
<i>Stenotrophomonas</i>	0.004708558	0.029191095
<i>Anaerococcus</i>	0.035139792	0
<i>Caproiciproducens</i>	0.032175144	0.007524816
<i>Syntrophorhabdus</i>	0.01185859	0
<i>Bilophila</i>	0.015782388	0.007135601
<i>Unclassified genus within order Gastranaerophilales</i>	0.024501939	0.00505979
<i>Lachnospiraceae</i> XPB1014 group	0.014474455	0.005189528
<i>Coproccoccus</i> 2	0.023455593	0.018163348
<i>Eubacterium eligens</i> group	0.01107383	0.004800313
<i>Atopobium</i>	0.035488574	0.007654554
<i>Ruminococcus gauvreauii</i> group	0.030780016	0.031656121
<i>Lachnospiraceae</i> NC2004 group	0.016043974	0
<i>Unclassified genus within family Muribaculaceae</i>	0.009765897	0.019849945
<i>Pseudobutyrvibrio</i>	0.02371718	0.005578743
<i>Corynebacterium</i> 1	0.01787508	0.00363267
<i>Unclassified genus within family Clostridiaceae</i> 1	0	0.024131305
<i>Ruminococcaceae</i> UCG-001	0.026594632	0
uncultured <i>Kiritimatiella</i> bacterium	0.010899439	0.005169211
<i>Unclassified genus within order WCHB1-41</i>	0.012294567	0.003742091
<i>Cellulosilyticum</i>	0.006278077	0.003581877
<i>Ruminococcus gnavus</i> group	0.006539663	0.000239159
<i>Unclassified genus within family Planococcaceae</i>	0.006714055	0.019330992
<i>Ruminococcus torques</i> group	0.011335417	0.016476752
<i>Lachnospiraceae</i> UCG-002	0.03400625	0.015698322
<i>Lachnospiraceae</i> NK4B4 group	0.012904936	0
<i>Cutibacterium</i>	0.009678702	0
<i>Unclassified genus within family Clostridiales</i> vadinBB60 group	0.007411619	0.014790155
<i>Howardella</i>	0.014561651	0.00363267
<i>Unclassified genus within family Bacteroidales</i> BS11 gut group	0.008109183	0
<i>Lachnospira</i>	0	0.01946073
<i>Eubacterium xylanophilum</i> group	0.016305561	0.002983979
uncultured <i>Porphyromonadaceae</i> bacterium	0	0.013103558
GCA-900066575	0.016828734	0.021147327
<i>Unclassified genus within family Lachnospiraceae</i>	0.007760401	0
<i>Coproccoccus</i> 3	0.02040375	0.010768271
<i>Unclassified genus within family Clostridiales</i> vadinBB60 group	0.007237228	0.004021884
<i>Butyrvibrio</i>	0.009765897	0.014141464

<i>Agathobacter</i>	0.007498814	0.00363267
<i>S5-A14a</i>	0.009765897	0
<i>Family XIII UCG-001</i>	0.019095817	0.000648691
<i>Unclassified genus within family gir-aah93h0</i>	0.000174391	0.013492773
<i>Unclassified genus within order Mollicutes RF39</i>	0.007237228	0.004670575
<i>FD2005</i>	0.007760401	0
<i>Unclassified genus within order Micrococcales</i>	0.006190881	0
<i>Anaerosporebacter</i>	0.004185385	0.001556858
<i>Finegoldia</i>	0.004474455	0
<i>Eubacterium ruminantium group</i>	0.000962276	0.031266907
<i>Unclassified genus within order Rhodospirillales</i>	0.011771394	0.002335288
<i>Papillibacter</i>	0.003836603	0
<i>Barnesiella</i>	0.003749407	0
<i>Enterococcus</i>	0.000539663	0.00142712
<i>Acetobacter</i>	0	0.013233297
<i>Fastidiosipila</i>	0.0044446971	0
<i>Peptococcus</i>	0.011248221	0.009211412
<i>Enterorhabdus</i>	0.003400625	0
<i>Negativicoccus</i>	0.00505734	0
<i>Faecalibacterium</i>	0.006975641	0.010898009
<i>Anaerotruncus</i>	0.002877452	0.012195391
<i>Syntrophococcus</i>	0.013340914	0.013752249
<i>Unclassified genus within family Dysgonomonadaceae</i>	0.005231731	0
<i>Unclassified genus within family Actinomycetaceae</i>	0	0.008043768
<i>Unclassified genus within family Ruminococcaceae</i>	0.002964647	0.005578743
<i>Butyrivibrio 2</i>	0	0.009211412
<i>Unclassified genus within family Veillonellaceae</i>	0.001918301	0.015568584
<i>Unclassified genus within order OPB41</i>	0	0.004151622
<i>Peptoniphilus</i>	0.003923798	0
<i>Pseudomonas</i>	0.000610369	0.006357172
<i>Saccharomonospora</i>	0	0.00648691
<i>Devosia</i>	0	0.005967957
<i>Gallicola</i>	0.003836603	0
<i>Sarcina</i>	0	0.007265339
<i>Tyzzerella</i>	0.004098189	0.003892146
<i>Prevotella 7</i>	0.00331343	0
<i>Ruminococcaceae UCG-011</i>	0.002179888	0.000648691
<i>Methylobacterium</i>	0	0.004411099
<i>Curtobacterium</i>	0	0.006746386
<i>Delftia</i>	0	0.004800313
<i>horsej-a03</i>	0	0.004800313
<i>Unclassified genus within order WCHB1-41</i>	0	0.007784292
<i>Lachnospiraceae FE2018 group</i>	0.002615865	0

<i>Allorhizobium-Neorhizobium-Pararhizobium-Rhizobium</i>	0.000348782	0.006357172
<i>Lachnospiraceae UCG-010</i>	0	0.006876125
<i>Mycobacterium</i>	0.000174391	0.00505979
<i>Lactobacillus</i>	0	0.008692459
<i>Unclassified genus within order WCHB1-41</i>	0	0.002724502
<i>Unclassified genus within order Mollicutes RF39</i>	0.003139038	0.006616648
<i>Parvibacter</i>	0.001656715	0
<i>Succiniclasticum</i>	0.002354279	0
<i>Thermobifida</i>	0	0.002983979
<i>Tyzzereella 3</i>	0.000871955	0.001686597
<i>Unclassified genus within family Nocardiaceae</i>	0	0.002205549
<i>Paenibacillus</i>	0.002703061	0
<i>Incertae Sedis</i>	0	0.002075811
<i>Micromonospora</i>	0	0.002075811
<i>Shuttleworthia</i>	0.002615865	0
<i>Libanicoccus</i>	0	0.001686597
<i>Unclassified genus within family Planococcaceae</i>	0	0.001686597
<i>Unclassified genus within family Propionibacteriaceae</i>	0.001046346	0
<i>Oceanobacillus</i>	0	0.001556858
<i>Enhydrobacter</i>	0	0.001556858
<i>Anaerovibrio</i>	0	0.001556858
<i>Sphingobacterium</i>	0	0.002724502
<i>Unclassified genus within family Microbacteriaceae</i>	0	0.002594764
<i>Dolosigranulum</i>	0	0.001297382
<i>Mycoplasma</i>	0	0.002983979
<i>Pediococcus</i>	0	0.002335288
<i>Unclassified genus within order Coriobacteriales</i>	0.000871955	0
<i>SP3-e08</i>	0.00078476	0
<i>Unclassified genus within family Thermoactinomycetaceae</i>	0	0.001167644
<i>Aureimonas</i>	0	0.001167644
<i>UBA1819</i>	0	0.001167644
<i>Eisenbergiella</i>	0.00078476	0
<i>Nocardioides</i>	0	0.001037906
<i>Prevotellaceae YAB2003 group</i>	0.000959151	0.001037906
<i>Unclassified genus within family Dermatophilaceae</i>	0	0.000908167
<i>Schwartzia</i>	0	0.000908167
<i>Succinivibrio</i>	0	0.000778429
<i>Unclassified genus within family vadinBE97</i>	0	0.000778429
<i>Thermoactinomyces</i>	0	0.000778429
<i>Pirellula</i>	0	0.000778429
<i>Sutterella</i>	0.00078476	0
<i>Unclassified genus within family Paracaedibacteraceae</i>	0.000435978	0
<i>Saccharopolyspora</i>	0	0.000648691

<i>Weissella</i>	0	0.000648691
<i>Lawsonella</i>	0.00078476	0
<i>Lachnospiraceae</i> ND3007 group	0.000348782	0
<i>Pelistega</i>	0	0.000518953
<i>Fibrobacter</i>	0	0.000518953
<i>Helicobacter</i>	0	0.000518953
Unclassified genus within family <i>Rhizobiaceae</i>	0.000348782	0
<i>Tumebacillus</i>	0.000261587	0
<i>Butyricimonas</i>	0.000261587	0
<i>Brachybacterium</i>	0.000261587	0
<i>Clostridium sensu stricto</i> 18	0	0.000389215
<i>Candidatus Endomicrobium</i>	0.000261587	0
<i>Brevundimonas</i>	0.000174391	0
<i>Arcanobacterium</i>	0.000174391	0
<i>Lachnoclostridium</i> 12	0	0.000259476
Unclassified genus within family <i>Solirubrobacteraceae</i>	0	0.000259476
Unclassified genus within family <i>Fusobacteriaceae</i>	0.000174391	0

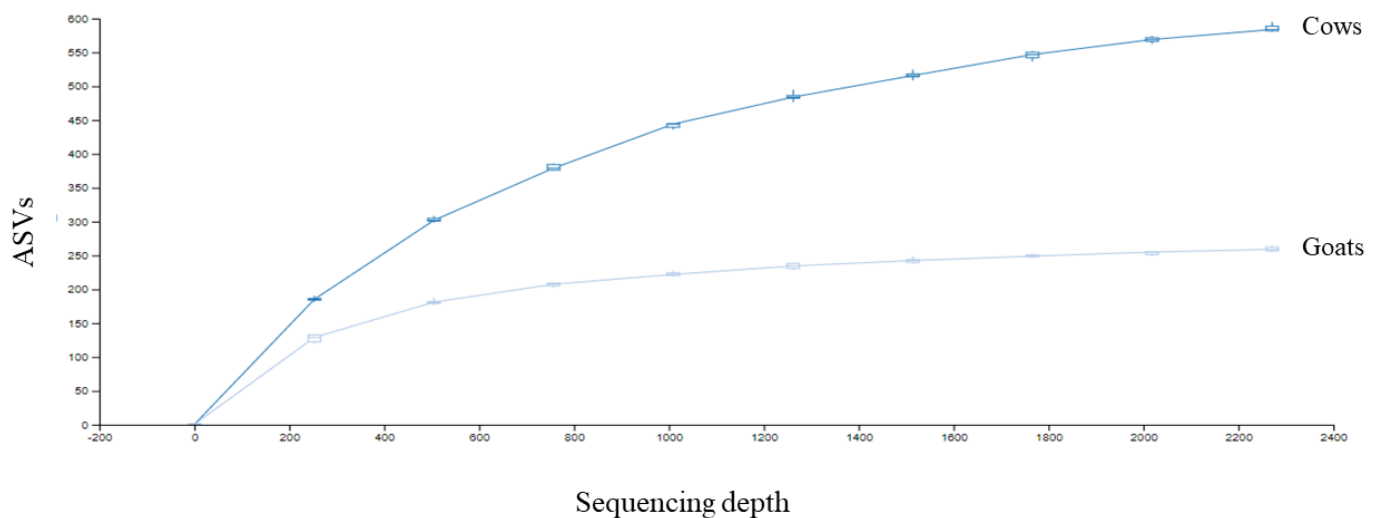


Figure S1. Rarefaction curves representing the sequencing depth (number of reads) and the number of ASVs (sequence variants) found in feces of goats and cows.

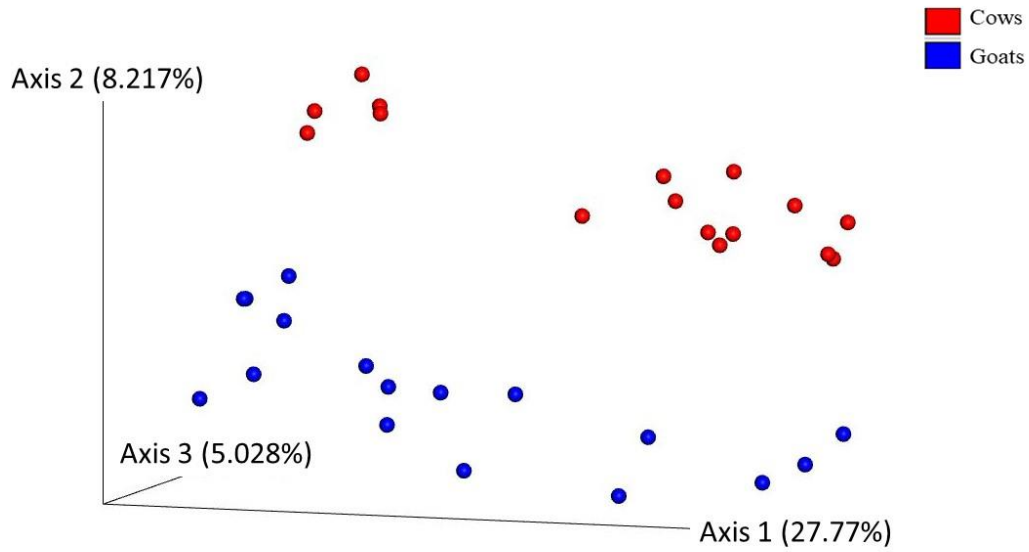


Figure S2. Principal Coordinate Analysis (PCoA) showing the unweighted UniFrac distance matrix of bacterial 16S rRNA amplicons from fecal samples of cow (red color) and goat (blue color) groups. Each dot represents one sample. The percentage of variation explained by the plotted principal coordinates is indicated on the axes.