

Table S3. Rumen microbial compositions of MNFC and LNFC groups (mean value \pm SE; n = 3).

Item	Genus	MNFC \pm SE	LNFC \pm SE
1	Prevotella	38531 \pm 5348	40653 \pm 1013
2	p:Bacteroidetes	8629 \pm 2112	5412 \pm 1241
3	o:Bacteroidales	8214 \pm 414	30450 \pm 4418
4	f:Prevotellaceae	5333 \pm 929	2446 \pm 169
5	Paraprevotella	5238 \pm 2073	896 \pm 126
6	Subdivision5_genera_IS	4423 \pm 458	1086 \pm 673
7	f:Lachnospiraceae	3980 \pm 256	950 \pm 169
8	f:Ruminococcaceae	3341 \pm 611	3140 \pm 157
9	f:Synergistaceae	3270 \pm 2171	42 \pm 33
10	f:Porphyromonadaceae	2973 \pm 1155	1378 \pm 209
11	f:Veillonellaceae	2453 \pm 1439	4473 \pm 212
12	Unclassified_Bacteria	1808 \pm 815	1359 \pm 218
13	Paludibacter	1686 \pm 767	0
14	Barnesiella	1346 \pm 655	260 \pm 17
15	o:Clostridiales	1138 \pm 262	1589 \pm 223
16	Vampirovibrio	927 \pm 482	343 \pm 45
17	Victivallis	784 \pm 204	246 \pm 138
18	Treponema	707 \pm 463	787 \pm 132
19	p:Firmicutes	700 \pm 297	652 \pm 375
20	Ruminococcus	414 \pm 23	152 \pm 13
21	Oscillibacter	405 \pm 111	6 \pm 5
22	c:Lentisphaeria	401 \pm 116	69 \pm 21
23	Clostridium_IV	340 \pm 148	47 \pm 7
24	o:Selenomonadales	323 \pm 139	21 \pm 22
25	Lachnospiracea_IS	310 \pm 36	1018 \pm 15
26	Butyrivibrio	255 \pm 79	176 \pm 56
27	TM7_genera_IS	242 \pm 57	309 \pm 87
28	Synergistes	185 \pm 89	25 \pm 24
29	Anaerovibrio	118 \pm 36	14 \pm 6
30	Salinicoccus	112 \pm 67	0
31	SR1_genera_IS	92 \pm 55	114 \pm 48
32	Hallella	91 \pm 88	19 \pm 20
33	Anaeroplasma	90 \pm 28	324 \pm 78
34	Acetivibrio	87 \pm 28	213 \pm 54
35	c:Alphaproteobacteria	86 \pm 37	516 \pm 154
36	p:Proteobacteria	83 \pm 44	83 \pm 43
37	Elusimicrobium	74 \pm 31	0
38	Anaerovorax	57 \pm 29	47 \pm 19
39	Succinielasticum	55 \pm 41	16 \pm 10
40	Sporobacter	51 \pm 10	14 \pm 12
41	Schwartzia	45 \pm 18	17 \pm 3
42	Fibrobacter	43 \pm 29	123 \pm 30

43	c:Epsilonproteobacteria	37±23	2±4
44	Pseudobutyrvibrio	34±16	21±3
45	Actinomyces	33±21	0
46	Coprococcus	31±14	4±4
47	Guggenheimella	30±22	0
48	Blautia	26±5	0
49	Succinivibrio	25±9	95±41
50	f:Enterobacteriaceae	24±7	18±10
51	Slackia	24±25	4±5
52	o:Actinomycetales	23±7	0
53	f:Coriobacteriaceae	19±17	5±4
54	f:Erysipelotrichaceae	17±7	27±12
55	f:Clostridiales_IS_XI	16±14	0
56	Saccharofermentans	15±4	3±5
57	Nocardioides	15±25	0
58	Petrimonas	14±12	0
59	c:Deltaproteobacteria	12±11	13±5
60	Roseburia	11±5	0
61	Dongia	11±18	0
62	Cerasiococcus	10±10	4±7
63	Howardella	10±9	1±2
64	Virgibacillus	9±8	0
65	Spirochaeta	8±14	1±2
66	Mogibacterium	8±7	0
67	f:Xanthomonadaceae	8±14	0
68	Selenomonas	7±8	1±2
69	Propionibacterium	7±8	0
70	f:Bacillaceae	7±8	0
71	c:Clostridia	6±11	8±8
72	Proteiniphilum	6±6	0
73	Solobacterium	6±6	0
74	Gp1	4±7	0
75	c:Actinobacteria	4±7	0
76	o:Sphingobacteriales	4±6	0
77	Clostridium_XIVa	4±6	0
78	Gemmatimonas	4±7	0
79	Caulobacter	4±8	0
80	f:Comamonadaceae	4±8	0
81	f:Oxalobacteraceae	4±8	0
82	Yaniella	2±3	8±1
83	Streptococcus	2±3	5±5
84	o:Acidimicrobiales	2±3	1±2
85	Desulfobulbus	2±3	1±2
86	Gp3	2±3	0

87	Gp4	2±3	0
88	Actinospica	2±3	0
89	Atopobium	2±3	0
90	Armatimonadetes_gp2	2±3	0
91	Armatimonadetes_gp4	2±3	0
92	Flavisolibacter	2±3	0
93	o:Ktedonobacterales	2±3	0
94	Sphaerobacter	2±3	0
95	p:Chloroflexi	2±3	0
96	Chlorophyta	2±3	0
97	Bacillus	2±3	0
98	Tissierella	2±3	0
99	Acetanaerobacterium	2±3	0
100	Nitrospira	2±3	0
101	Gemmata	2±3	0
102	o:Rhodospirillales	2±3	0
103	Massilia	2±3	0
104	f:Sutterellaceae	2±3	0
105	Ruminobacter	2±3	0
106	Moraxella	2±3	0
107	Pseudomonas	2±3	0
108	Desulfovibrio	0	130±18
109	Olsenella	0	70±23
110	f:Anaerolineaceae	0	31±28
111	Syntrophococcus	0	16±2
112	Rikenella	0	15±6
113	Escherichia/Shigella	0	6±5
114	Oribacterium	0	5±9
115	Bilophila	0	5±5
116	Eubacterium	0	4±4
117	f:Desulfovibrionaceae	0	4±4
118	WS3_genera_IS	0	4±5
119	Rothia	0	1±2
120	Enterorhabdus	0	1±2
121	Pusillimonas	0	1±2

Counts were normalized to the relative abundance of each sample and showed here in a scale of 1/100,000; genera were sorted based on their relative abundance in the rumen microbial community in a descending order; f = Family; o = Order; c = Class; p = Phylum.