

Table S1. Proportion of microbial taxa among total sequences in the rumen samples of the three groups.

Phylum	Genus	Mean proportion of each taxon identified among the total sequences ¹			SEM	P-value ²
		Stomach tube (n = 3)	Dorsal sac (n = 3)	Ventral sac (n = 3)		
Bacteroidetes		0.616	0.509	0.551	0.046	0.320
	<i>Prevotella</i>	0.417	0.255	0.321	0.064	0.274
	YRC22	0.015	0.012	0.016	0.005	0.893
	CF231	0.010	0.012	0.011	0.001	0.613
	BF311	0.002	0.003	0.003	0.001	0.238
	Family Prevotellaceae	0.418	0.256	0.321	0.064	0.274
	Family Paraprevotellaceae	0.030	0.029	0.032	0.007	0.945
	Family S24-7	0.015 ^b	0.036 ^a	0.027 ^b	0.004	0.039
	Family BS11	0.009	0.015	0.012	0.006	0.789
	Family RF16	0.015	0.009	0.010	0.003	0.269
	Family Bacteroidaceae	0.002	0.004	0.003	0.001	0.220
Firmicutes		0.318	0.416	0.381	0.032	0.178
	<i>Succiniclasticum</i>	0.061	0.039	0.047	0.009	0.317
	<i>Butyrivibrio</i>	0.020	0.048	0.045	0.016	0.466
	<i>Ruminococcus</i>	0.013	0.020	0.013	0.006	0.659
	<i>Selenomonas</i>	0.016	0.007	0.011	0.006	0.619
	RFN20	0.008 ^a	0.005 ^b	0.006 ^b	0.000	0.027
	<i>Anaerostipes</i>	0.005	0.005	0.006	0.001	0.888
	<i>Anaerovibrio</i>	0.005	0.003	0.006	0.002	0.623
	<i>Pseudobutyrvibrio</i>	0.003	0.005	0.006	0.001	0.053
	<i>Clostridium</i>	0.003	0.003	0.003	0.002	0.996
	<i>Moryella</i>	0.002	0.003	0.002	0.001	0.363
	p-75-a5	0.002	0.002	0.003	0.000	0.758
	<i>Coprococcus</i>	0.002	0.002	0.003	0.000	0.332
	<i>Oscillospira</i>	0.001	0.003	0.002	0.001	0.198
	<i>Blautia</i>	0.001 ^b	0.002 ^a	0.002 ^b	0.000	0.017
	Family Lachnospiraceae	0.068	0.118	0.110	0.022	0.288
	Family Veillonellaceae	0.107	0.070	0.088	0.010	0.091
	Family Ruminococcaceae	0.062	0.095	0.076	0.009	0.109
	Family Erysipelotrichaceae	0.012	0.011	0.011	0.001	0.476
	Family Christensenellaceae	0.008	0.015	0.011	0.004	0.565
	Family Mogibacteriaceae	0.006	0.013	0.009	0.002	0.175
	Family Clostridiaceae	0.006	0.008	0.007	0.003	0.823
Verrucomicrobia		0.023	0.016	0.016	0.009	0.857
	Family RFP12	0.010	0.008	0.008	0.002	0.798
TM7		0.007	0.008	0.008	0.001	0.854
	Family F16	0.007	0.008	0.008	0.001	0.857
Proteobacteria		0.007	0.007	0.007	0.001	0.897

	<i>Desulfovibrio</i>	0.003	0.004	0.003	0.001	0.569
	Family Desulfovibrionaceae	0.003	0.004	0.003	0.001	0.534
	Family Succinivibrionaceae	0.002	0.001	0.002	0.001	0.685
Actinobacteria		0.004	0.009	0.006	0.002	0.423
	Family Coriobacteriaceae	0.004	0.008	0.006	0.002	0.372
Spirochaetes		0.005	0.006	0.006	0.001	0.862
	<i>Treponema</i>	0.003	0.004	0.004	0.001	0.713
	Family Spirochaetaceae	0.003	0.005	0.005	0.001	0.663
Tenericutes		0.005	0.005	0.006	0.001	0.476
	<i>Anaeroplasma</i>	0.002	0.002	0.003	0.001	0.510
	Family Anaeroplasmataceae	0.002	0.002	0.003	0.001	0.528
Chloroflexi		0.003 ^b	0.008 ^a	0.005 ^b	0.001	0.004
	SHD-231	0.003 ^b	0.008 ^a	0.005 ^b	0.001	0.004
	Family Anaerolinaceae	0.003 ^b	0.008 ^a	0.005 ^b	0.001	0.004
Planctomycetes		0.004	0.007	0.005	0.001	0.217
	Family Pirellulaceae	0.004	0.007	0.005	0.001	0.217
Synergistetes		0.003	0.004	0.003	0.001	0.907
	TG5	0.003	0.004	0.003	0.001	0.898
	Family Dethiosulfovibrionaceae	0.003	0.004	0.003	0.001	0.905
WPS-2		0.001	0.002	0.002	0.001	0.777

^{a,b}Means with different superscript lowercase letters within a row are significantly different ($P < 0.05$).

¹Values indicate least-square means.

²Bold P -values indicate groups that significantly differ ($P < 0.05$)