

Supplementary information

	QSB	QMI	OS	RBBC	PCB
Bacteroidia; Bacteroidales -	46.6	16.8	18.4	60.1	39.2
Clostridia; Clostridiales -	21.1	51.1	37.4	28	34.9
Fibrobacteria; Fibrobacterales -	14.2	0	24.4	0	9.4
Saccharimonadia; Saccharimonadales -	0	10.1	1.6	3	2.6
Negativicutes; Selenomonadales -	0	2.6	3	0.1	5.6
Erysipelotrichia; Erysipelotrichales -	0.1	2	4.7	2.3	1.8
Gracilibacteria; Absconditabacteriales (SR1) -	3.9	1.7	1	2.4	1.7
Coriobacteriia; Coriobacteriales -	0.2	6.3	2.9	0.1	0.1
Mollicutes; Mollicutes RF39 -	2.1	3.2	1.3	0	0
Kiritimatiellae; WCHB1-41 -	2.3	0	0	0	2.1
Lentisphaeria; Victivallales -	1.8	0.1	0	1.1	1.1
Mollicutes; Anaeroplasmatales -	3.8	0	0	0	0
k__No blast hit_OTU_000244; k__No blast hit_OTU_000244 -	0.8	0.8	0.9	0	0
Alphaproteobacteria; Rhodospirillales -	0.9	0	0	0.4	0.5
Anaerolineae; Anaerolineales -	0	1.7	0	0	0
Remaining taxa (36) -	2.2	3.7	4.3	2.5	1.1

Figure S1. Heatmap of relative abundance of bacterial order (a) and eukaryotic phyla (b) of ruminal complete sample preparations using different extraction methods; QSB; QMI; OS; RBBC; PCB.

	QSB	QMI	OS	RBBC	PCB
Ciliophora; Litostomatea -	71.2	0.3	57.3	53.8	76.1
Streptophyta; Embryophyceae -	2.1	93.8	11.1	11	1
Fungi; Chytridiomycota -	11.1	4.8	27.6	32.3	18.6
Conosa; Archamoebae -	7.5	0	1.6	1.1	2
Metamonada; Parabasalia -	4.9	0	1.1	1.2	1.2
Apicomplexa; Apicomplexa_X -	2.4	0	0.4	0.3	0.6
Metazoa; Craniata -	0	0.3	0.6	0	0
Fungi; Basidiomycota -	0	0.5	0.1	0	0.2
k__No blast hit_OTU_000130; k__No blast hit_OTU_000130 -	0.2	0	0.1	0.1	0
k__No blast hit_OTU_000155; k__No blast hit_OTU_000155 -	0.1	0	0	0.2	0
Remaining taxa (28) -	0.4	0.2	0.1	0.1	0.2

Figure S2. Heatmap of relative abundance of eukaryotic phyla of ruminal complete sample preparations using different extraction methods; QSB; QMI; OS; RBBC; PCB.

	Oral	Liquid	Complete	Solid	Faecal
Bacteroidia; Bacteroidales -	0.6	39.2	57.1	56.9	38.8
Clostridia; Clostridiales -	1.1	17.5	17	21.3	51.6
Gammaproteobacteria; Pasteurellales -	65.6	0	0	0	0
Bacilli; Lactobacillales -	26.6	0	0	0	0
Fibrobacteria; Fibrobacterales -	0.1	9.7	11.4	0	0
Spirochaetia; Spirochaetales -	0	3	0.2	8.2	0
Erysipelotrichia; Erysipelotrichales -	0	7.6	0.1	2.9	0.8
Mollicutes; Anaeroplasmatales -	0	7.6	3	0	0
Gracilibacteria; Absconditabacteriales (SR1) -	0.2	0	3.1	3.7	0
Lentisphaeria; Victivallales -	0	3.5	1.5	0.2	0
Mollicutes; Mollicutes RF39 -	0	3.3	1.7	0	0
Saccharimonadia; Saccharimonadales -	0	3.1	0	1.6	0
Negativicutes; Selenomonadales -	0	0.6	0	2	1.4
Kiritimatiellae; WCHB1-41 -	0	0	1.8	0	2
Melainabacteria; Gastranaerophilales -	0	1.2	0	0.7	1.7
Remaining taxa (43) -	5.8	3.7	3.1	2.6	3.8

Figure S3. Heatmap of relative abundance of bacterial order sample preparations from different sample sites; Oral swab; Rumen fraction (liquid); Rumen fraction (complete); Rumen fraction (Solid); Faecal collection.

