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Appendix 1

Table A1. The table shows the 50 most abundant OTUs and their mean relative abundance according to QIIME (GreenGenes ver. 13.8) taxonomy. (k = kingdom, p = phylum, c = class, o = order, f = family, g = genus)

OTUs	QIIME OTU ID	Mean relative abundance [%]	QIIME taxonomy						
OTU 1	New.ReferenceOTU512	1.99	K: Bacteria	p: Bacteroidetes	c: Bacteroidia	o: Bacteroidales	f: Prevotellaceae	g: Prevotella	
OTU 2	351812	1.83	K: Bacteria	p: Firmicutes	c: Clostridia	o: Clostridiales	f: Mogibacteriaceae		
OTU 3	585480	1.67	K: Bacteria	p: Firmicutes	c: Clostridia	o: Clostridiales	f: Lachnospiraceae	g: Anaerostipes	
OTU 4	554055	1.35	K: Bacteria	p: Firmicutes	c: Clostridia	o: Clostridiales	f: Ruminococcaceae		
OTU 5	433722	1.33	K: Bacteria	p: Firmicutes	c: Clostridia	o: Clostridiales	f: Ruminococcaceae		
OTU 6	New.ReferenceOTU161	1.30	K: Bacteria	p: Firmicutes	c: Clostridia	o: Clostridiales	f: Mogibacteriaceae		
OTU 7	1110312	1.30	K: Bacteria	p: Firmicutes	c: Clostridia	o: Clostridiales			
OTU 8	265032	1.04	K: Bacteria	p: Firmicutes	c: Clostridia	o: Clostridiales	f: Ruminococcaceae		
OTU 9	331350	0.98	K: Bacteria	p: TM7	c: TM7-3	o: CW040	f: F16		
OTU 10	New.ReferenceOTU276	0.95	K: Bacteria	p: Firmicutes	c: Clostridia	o: Clostridiales	f: Mogibacteriaceae		
OTU 11	816626	0.94	K: Bacteria	p: Firmicutes	c: Clostridia	o: Clostridiales			
OTU 12	New.ReferenceOTU10	0.93	K: Bacteria	p: Firmicutes	c: Clostridia	o: Clostridiales	f: Lachnospiraceae	g: Blautia	
OTU 13	577671	0.92	K: Bacteria	p: TM7	c: TM7-3	o: CW040	f: F16		
OTU 14	461487	0.91	K: Bacteria	p: Firmicutes	c: Clostridia	o: Clostridiales			
OTU 15	555101	0.88	K: Bacteria	p: Firmicutes	c: Clostridia	o: Clostridiales	f: Ruminococcaceae		
OTU 16	New.ReferenceOTU462	0.88	K: Bacteria	p: Bacteroidetes	c: Bacteroidia	o: Bacteroidales	f: Prevotellaceae	g: Prevotella	
OTU 17	New.ReferenceOTU143	0.84	K: Bacteria	p: Bacteroidetes	c: Bacteroidia	o: Bacteroidales	f: Prevotellaceae	g: Prevotella	
OTU 18	New.ReferenceOTU259	0.78	K: Bacteria	p: Firmicutes	c: Clostridia	o: Clostridiales	f: Lachnospiraceae	g: Butyrivibrio	

OTU 19	558599	0.75	K: Bacteria	p: Firmicutes	c: Clostridia	o: Clostridiales	f: Ruminococcaceae	
OTU 20	589920	0.73	K: Bacteria	p: Actinobacteria	c: Coriobacteriia	o: Coriobacteriales	f: Coriobacteriaceae	
OTU 21	New.ReferenceOTU481	0.73	K: Bacteria	p: Bacteroidetes	c: Bacteroidia	o: Bacteroidales	f: Prevotellaceae	g: Prevotella
OTU 22	327282	0.70	K: Bacteria	p: Firmicutes	c: Clostridia	o: Clostridiales		
OTU 23	New.ReferenceOTU199	0.63	K: Bacteria	p: Bacteroidetes	c: Bacteroidia	o: Bacteroidales	f: Prevotellaceae	g: Prevotella
OTU 24	311412	0.61	K: Bacteria	p: Firmicutes	c: Clostridia	o: Clostridiales		
OTU 25	New.ReferenceOTU77	0.59	Unassigned					
OTU 26	355203	0.59	K: Bacteria	p: Firmicutes	c: Clostridia	o: Clostridiales	f: Ruminococcaceae	
OTU 27	New.ReferenceOTU376	0.57	K: Bacteria	p: Firmicutes	c: Clostridia	o: Clostridiales		
OTU 28	571254	0.56	K: Bacteria	p: Bacteroidetes	c: Bacteroidia	o: Bacteroidales		
OTU 29	337289	0.55	K: Bacteria	p: TM7	c: TM7-3	o: CW040	f: F16	
OTU 30	New.ReferenceOTU484	0.54	K: Bacteria	p: Firmicutes	c: Clostridia	o: Clostridiales	f: Lachnospiraceae	
OTU 31	561916	0.48	K: Bacteria	p: Firmicutes	c: Clostridia	o: Clostridiales		
OTU 32	326833	0.47	K: Bacteria	p: Firmicutes	c: Clostridia	o: Clostridiales	f: Lachnospiraceae	g: Coprococcus
OTU 33	153291	0.46	K: Bacteria	p: Firmicutes	c: Clostridia	o: Clostridiales		
OTU 34	New.ReferenceOTU114	0.46	K: Bacteria	p: Firmicutes	c: Clostridia	o: Clostridiales	f: Lachnospiraceae	
OTU 35	589852	0.43	K: Bacteria	p: Firmicutes	c: Clostridia	o: Clostridiales	f: Lachnospiraceae	g: Pseudobutyrvibrio
OTU 36	New.ReferenceOTU433	0.42	K: Bacteria	p: Bacteroidetes	c: Bacteroidia	o: Bacteroidales		
OTU 37	New.ReferenceOTU311	0.41	K: Bacteria	p: Bacteroidetes	c: Bacteroidia	o: Bacteroidales	f: Prevotellaceae	g: Prevotella
OTU 38	300123	0.41	K: Bacteria	p: Firmicutes	c: Clostridia	o: Clostridiales	f: Lachnospiraceae	g: Coprococcus
OTU 39	New.ReferenceOTU152	0.40	K: Bacteria	p: Bacteroidetes	c: Bacteroidia	o: Bacteroidales	f: Prevotellaceae	g: Prevotella
OTU 40	New.ReferenceOTU410	0.39	K: Bacteria	p: Firmicutes	c: Clostridia	o: Clostridiales		
OTU 41	New.ReferenceOTU474	0.39	K: Bacteria	p: Bacteroidetes	c: Bacteroidia	o: Bacteroidales	f: Prevotellaceae	g: Prevotella
OTU 42	173519	0.38	K: Bacteria	p: Firmicutes	c: Clostridia	o: Clostridiales	f: Lachnospiraceae	
OTU 43	New.ReferenceOTU253	0.38	K: Bacteria	p: Firmicutes	c: Clostridia	o: Clostridiales	f: Lachnospiraceae	
OTU 44	581109	0.38	K: Bacteria	p: Firmicutes	c: Clostridia	o: Clostridiales		
OTU 45	New.ReferenceOTU348	0.38	K: Bacteria	p: Actinobacteria	c: Coriobacteriia	o: Coriobacteriales	f: Coriobacteriaceae	
OTU 46	New.ReferenceOTU449	0.37	K: Bacteria	p: Bacteroidetes	c: Bacteroidia	o: Bacteroidales	f: Prevotellaceae	g: Prevotella
OTU 47	533277	0.37	K: Bacteria	p: Firmicutes	c: Bacilli	o: Lactobacillales	f: Streptococcaceae	g: Streptococcus
OTU 48	594330	0.37	K: Bacteria	p: Bacteroidetes	c: Bacteroidia	o: Bacteroidales	f: Prevotellaceae	g: Prevotella
OTU 49	538761	0.36	K: Bacteria	p: Firmicutes	c: Clostridia	o: Clostridiales	f: Lachnospiraceae	g: Butyrivibrio
OTU 50	349539	0.35	K: Bacteria	p: TM7	c: TM7-3	o: CW040	f: F16	

Table A2. Comparison of assigned taxonomy for the 50 most abundant OTUs of the unfed group. Databases used were GreenGenes ver. 13.8, NCBI BLASTn 2.8.0 against 16S ribosomal RNA sequences (Bacteria and Archea) and RDP 11.5 classifier.

Unfed - OTU ID	QIIME taxonomy	BLAST - DESCRIPTION	Accession number	Identity	Habitat	RDP - DESCRIPTION	Accession number	S_ab score	Habitat
New.ReferenceOTU512	K: <i>Bacteria</i> ; p: <i>Bacteroidetes</i> ; c: <i>Bacteroidia</i> ; o: <i>Bacteroidales</i> ; f: <i>Prevotellaceae</i> ; g: <i>Prevotella</i>	<i>Prevotella</i> brevis strain GA33 16S ribosomal RNA, partial sequence	NR_041954.1	91%	Rumen	<i>Prevotella ruminicola</i> ; TC2-28; AF218619	S000365830	0.739	Rumen
351812	K: <i>Bacteria</i> ; p: <i>Firmicutes</i> ; c: <i>Clostridia</i> ; o: <i>Clostridiales</i> ; f: <i>Mogibacteriaceae</i>	<i>Ihubacter massiliensis</i> strain Marseille-P2843 16S ribosomal RNA, partial sequence	NR_144749.1	93%	Feces	<i>Eubacterium</i> sp. WAL 17363; GQ461729	S001611916	0.755	Human feces
New.ReferenceOTU161	K: <i>Bacteria</i> ; p: <i>Firmicutes</i> ; c: <i>Clostridia</i> ; o: <i>Clostridiales</i> ; f: <i>Mogibacteriaceae</i>	<i>Emergencia timonensis</i> strain SN18 16S ribosomal RNA, partial sequence	NR_144737.1	95%	Human feces	<i>Eubacterium</i> sp. WAL 18692; GQ461730	S001611917	0.770	Human feces
554055	K: <i>Bacteria</i> ; p: <i>Firmicutes</i> ; c: <i>Clostridia</i> ; o: <i>Clostridiales</i> ; f: <i>Ruminococcaceae</i>	<i>Flintibacter butyricus</i> strain BLS21 16S ribosomal RNA, partial sequence	NR_144611.1	93%	Mouse intestine	<i>Intestinimonas</i> sp. FSAA-17; KP114242	S004532796	0.751	Sheep
New.ReferenceOTU276	K: <i>Bacteria</i> ; p: <i>Firmicutes</i> ; c: <i>Clostridia</i> ; o: <i>Clostridiales</i> ; f: <i>Mogibacteriaceae</i>	<i>Anaerovorax odorimutans</i> strain NorPut 16S ribosomal RNA gene, partial sequence	NR_028911.1	90%	brackish water sediment	<i>Peptostreptococcaceae bacterium</i> canine oral taxon 097; PO047; JN713261	S003222591	0.689	Dog oral cavity
433722	K: <i>Bacteria</i> ; p: <i>Firmicutes</i> ; c: <i>Clostridia</i> ; o: <i>Clostridiales</i> ; f: <i>Ruminococcaceae</i>	<i>Intestinimonas butyriciproducens</i> strain SRB-521-5-I 16S ribosomal RNA gene, partial sequence	NR_118554.1	93%	Mouse intestine	<i>Rumen bacterium</i> NK4A214; GU324404	S002351043	0.987	Rumen of sheep
555101	K: <i>Bacteria</i> ; p: <i>Firmicutes</i> ; c: <i>Clostridia</i> ; o: <i>Clostridiales</i> ; f: <i>Ruminococcaceae</i>	<i>Sporobacter termitidis</i> strain SYR 16S ribosomal RNA, partial sequence	NR_044972.1	92%	Termite digestive tract	<i>Clostridiales bacterium</i> CIEAF 022; AB702938	S003316343	0.694	Mouse feces
461487	K: <i>Bacteria</i> ; p: <i>Firmicutes</i> ; c: <i>Clostridia</i> ; o: <i>Clostridiales</i>	[<i>Clostridium</i>] <i>cellulolyticum</i> strain H10 16S ribosomal RNA gene, complete sequence	NG_041947.1	87%	Decayed grass in compost pile	<i>Clostridiales bacterium</i> oral taxon F32; VO026; HM099644	S002167974	0.757	Human oral cavity
816626	K: <i>Bacteria</i> ; p: <i>Firmicutes</i> ; c: <i>Clostridia</i> ; o: <i>Clostridiales</i>	<i>Howardella ureilytica</i> strain GPC 589 16S ribosomal RNA, partial sequence	NR_044022.2	94%	Rumen	<i>Howardella ureilytica</i> (T); GPC 589; DQ925472	S000926211	0.708	Rumen
1110312	K: <i>Bacteria</i> ; p: <i>Firmicutes</i> ; c: <i>Clostridia</i> ; o: <i>Clostridiales</i>	[<i>Clostridium</i>] <i>cellulolyticum</i> strain H10	NG_041947.1	88%	Decayed grass in	<i>Clostridiales bacterium</i> oral taxon F32; VO026;	S002167974	0.827	Human oral cavity

		16S ribosomal RNA gene, complete sequence			compost pile	HM099644			
331350	K: <i>Bacteria</i> ; p: <i>TM7</i> ; c: <i>TM7-3</i> ; o: <i>CW040</i> ; f: <i>F16</i>	<i>Cellulosilyticum ruminicola</i> strain H1 16S ribosomal RNA gene, partial sequence	NR_116001.1	78%	Rumen	<i>TM7 bacterium</i> human oral taxon HOT-870; 4W45; KM018322	S004272182	0.599	Human oral cavity
New.ReferenceOTU10	K: <i>Bacteria</i> ; p: <i>Firmicutes</i> ; c: <i>Clostridia</i> ; o: <i>Clostridiales</i> ; f: <i>Lachnospiraceae</i> ; g: <i>Blautia</i>	<i>Blautia schinkii</i> strain B 16S ribosomal RNA, partial sequence	NR_026312.1	97%	Rumen of suckling lamb	<i>Blautia faecis</i> (T); M25; HM626178	S002232209	0.828	Human feces
New.ReferenceOTU376	K: <i>Bacteria</i> ; p: <i>Firmicutes</i> ; c: <i>Clostridia</i> ; o: <i>Clostridiales</i>	<i>Falcatimonas natans</i> strain WNO11 16S ribosomal RNA, partial sequence	NR_152688.1	90%	Methanogenic reactor	<i>Lachnospiraceae bacterium</i> 14-2; DQ789124	S000891927	0.635	Mouse cecum
561916	K: <i>Bacteria</i> ; p: <i>Firmicutes</i> ; c: <i>Clostridia</i> ; o: <i>Clostridiales</i>	<i>Eubacterium callanderi</i> strain DSM 3662 16S ribosomal RNA gene, partial sequence	NR_026330.1	87%	Anaerobic digester	<i>Rumen bacterium</i> R-7; AB239481	S000607268	0.650	Sheep rumen
577671	K: <i>Bacteria</i> ; p: <i>TM7</i> ; c: <i>TM7-3</i> ; o: <i>CW040</i> ; f: <i>F16</i>	<i>Mogibacterium timidum</i> strain ATCC 33093 16S ribosomal RNA gene, partial sequence	NR_118782.1	79%	Subgingival region of mouth	<i>TM7 bacterium</i> human oral taxon HOT-870; 4W45; KM018322	S004272182	0.598	Human oral cavity
327282	K: <i>Bacteria</i> ; p: <i>Firmicutes</i> ; c: <i>Clostridia</i> ; o: <i>Clostridiales</i>	<i>[Clostridium] clariflavum</i> strain EBR45 16S ribosomal RNA, partial sequence	NR_041235.1	87%	Methanogenic sludge of a bioreactor	<i>Clostridiales bacterium</i> oral taxon F32; VO026; HM099644	S002167974	0.690	Human oral cavity
326833	K: <i>Bacteria</i> ; p: <i>Firmicutes</i> ; c: <i>Clostridia</i> ; o: <i>Clostridiales</i> ; f: <i>Lachnospiraceae</i> ; g: <i>Coprococcus</i>	<i>Anaerostipes butyraticus</i> strain JCM 17466 16S ribosomal RNA gene, partial sequence	NR_113319.1	94%	Cecal content of chicken	<i>Coprococcus</i> sp. DJF_B005; EU728700	S001045992	0.765	Pig intestine
311412	K: <i>Bacteria</i> ; p: <i>Firmicutes</i> ; c: <i>Clostridia</i> ; o: <i>Clostridiales</i>	<i>Geosporobacter ferrireducens</i> strain IRF9 16S ribosomal RNA, partial sequence	NR_148302.1	88%	Petroleum contaminated soil	<i>Clostridiales bacterium</i> RM3; AB730671	S003659390	0.668	Bovine rumen
589920	K: <i>Bacteria</i> ; p: <i>Actinobacteria</i> ; c: <i>Coriobacteriia</i> ; o: <i>Coriobacteriales</i> ; f: <i>Coriobacteriaceae</i>	<i>Raoultibacter timonensis</i> strain Marseille-P3277 16S ribosomal RNA, partial sequence	NR_148574.1	94%	Human feces	<i>Eggerthellaceae bacterium</i> AT8; LN881601	S004508480	0.651	Human feces
New.ReferenceOTU143	K: <i>Bacteria</i> ; p: <i>Bacteroidetes</i> ; c: <i>Bacteroidia</i> ; o: <i>Bacteroidales</i> ; f: <i>Prevotellaceae</i> ; g: <i>Prevotella</i>	<i>Prevotella ruminicola</i> strain Bryant 23 16S ribosomal RNA, partial sequence	NR_102887.1	89%	Bovine rumen	<i>Prevotella</i> sp. 152R-1a; DQ278861	S000650962	0.692	Dairy cow
New.ReferenceOTU259	K: <i>Bacteria</i> ; p: <i>Firmicutes</i> ; c: <i>Clostridia</i> ; o: <i>Clostridiales</i> ; f: <i>Lachnospiraceae</i> ; g: <i>Butyrivibrio</i>	<i>Butyrivibrio proteoclasticus</i> strain B316 16S ribosomal RNA, partial sequence	NR_102893.1	94%	Rumen	<i>Butyrivibrio</i> sp. CA23; AB849434	S004125843	0.741	Bovine rumen
585480	K: <i>Bacteria</i> ; p: <i>Firmicutes</i> ; c: <i>Clostridia</i> ; o: <i>Clostridiales</i> ; f: <i>Lachnospiraceae</i> ; g: <i>Anaerostipes</i>	<i>Eubacterium ventriosum</i> strain ATCC 27560 16S ribosomal RNA gene,	NR_118670.1	98%	Feces	<i>Butyrate-producing bacterium</i> L2-12; AJ270488	S000090760	0.949	Human feces

		partial sequence								
355203	K: <i>Bacteria</i> ; p: <i>Firmicutes</i> ; c: <i>Clostridia</i> ; o: <i>Clostridiales</i> ; f: <i>Ruminococcaceae</i>	<i>Harryflintia acetispora</i> strain V20-281a 16S ribosomal RNA, partial sequence	NR_152059.1	89%	Cecum chicken	<i>Flavonifractor plautii</i> ; MT42; AB693937	S003277052	0.554	Rat feces	
New.ReferenceOTU114	K: <i>Bacteria</i> ; p: <i>Firmicutes</i> ; c: <i>Clostridia</i> ; o: <i>Clostridiales</i> ; f: <i>Lachnospiraceae</i>	<i>Pseudobutyrvibrio ruminis</i> strain DSM 9787 16S ribosomal RNA gene, partial sequence	NR_026315.1	95%	Rumen of cow	<i>Lachnospiraceae bacterium</i> CG34; AB849406	S004125815	0.776	Bovine rumen	
352507	K: <i>Bacteria</i> ; p: <i>Firmicutes</i> ; c: <i>Clostridia</i> ; o: <i>Clostridiales</i> ; f: <i>Lachnospiraceae</i> ; g: <i>Coprococcus</i>	<i>Eubacterium ruminantium</i> strain GA195 16S ribosomal RNA gene, partial sequence	NR_024661.1	95%	Rumen	<i>Lachnospiraceae bacterium</i> CA4; AB849415	S004125824	0.837	Bovine rumen	
New.ReferenceOTU5	K: <i>Bacteria</i> ; p: <i>Firmicutes</i> ; c: <i>Clostridia</i> ; o: <i>Clostridiales</i> ; f: <i>Lachnospiraceae</i>	[<i>Clostridium</i>] <i>clostridioforme</i> strain ATCC 25537 16S ribosomal RNA gene, partial sequence	NR_118128.1	94%	Rumen calf	<i>Butyrvibrio</i> sp. 3; EU714406	S001416389	0.777	Sheep rumen	
589852	K: <i>Bacteria</i> ; p: <i>Firmicutes</i> ; c: <i>Clostridia</i> ; o: <i>Clostridiales</i> ; f: <i>Lachnospiraceae</i> ; g: <i>Pseudobutyrvibrio</i>	<i>Pseudobutyrvibrio ruminis</i> strain DSM 9787 16S ribosomal RNA gene, partial sequence	NR_026315.1	99%	Rumen of cow	<i>Rumen bacterium</i> 1/9293-12; DQ392988	S000650328	0.985	Reindeer on natural pasture	
549866	K: <i>Bacteria</i> ; p: <i>Firmicutes</i> ; c: <i>Clostridia</i> ; o: <i>Clostridiales</i> ; f: <i>Mogibacteriaceae</i>	<i>Emergencia timonensis</i> strain SN18 16S ribosomal RNA, partial sequence	NR_144737.1	94%	Human feces	<i>Eubacterium</i> sp. WAL 17363; GQ461729	S001611916	0.755	Stool sample from autistic individual	
New.ReferenceOTU484	K: <i>Bacteria</i> ; p: <i>Firmicutes</i> ; c: <i>Clostridia</i> ; o: <i>Clostridiales</i> ; f: <i>Lachnospiraceae</i>	<i>Syntrophococcus sucromutans</i> strain S195 16S ribosomal RNA gene, partial sequence	NR_118354.1	97%	Rumen of cattle	<i>Syntrophococcus sucromutans</i> ; S195; JQ346731	S003259700	0.852	Rumen of cattle	
153291	K: <i>Bacteria</i> ; p: <i>Firmicutes</i> ; c: <i>Clostridia</i> ; o: <i>Clostridiales</i>	<i>Anaerobacterium chartisolvens</i> strain T-1-35 16S ribosomal RNA gene, partial sequence	NR_125464.1	87%	Soil of rice field	<i>Clostridiales bacterium</i> oral taxon F32; VO026; HM099644	S002167974	0.789	Human oral cavity	
265032	K: <i>Bacteria</i> ; p: <i>Firmicutes</i> ; c: <i>Clostridia</i> ; o: <i>Clostridiales</i> ; f: <i>Ruminococcaceae</i>	<i>Pseudoflavonifractor capillosus</i> strain ATCC 29799 16S ribosomal RNA gene, partial sequence	NR_025670.1	91%	Human feces	<i>Clostridiales bacterium</i> NK3898; GU324364	S002351003	0.788	Rumen of pasture-grazed sheep	
New.ReferenceOTU142	K: <i>Bacteria</i> ; p: <i>Firmicutes</i> ; c: <i>Clostridia</i> ; o: <i>Clostridiales</i> ; f: <i>Mogibacteriaceae</i>	<i>Eubacterium pyruvativorans</i> strain I-6 16S ribosomal RNA, partial sequence	NR_042074.1	93%	Rumen	<i>Clostridiaceae bacterium</i> FH042; AB298771	S000994706	0.741	Methanogenic reactor	
300123	K: <i>Bacteria</i> ; p: <i>Firmicutes</i> ; c: <i>Clostridia</i> ; o: <i>Clostridiales</i> ; f: <i>Lachnospiraceae</i> ; g: <i>Coprococcus</i>	<i>Eubacterium ruminantium</i> strain GA195 16S ribosomal RNA gene, partial	NR_024661.1	96%	Rumen	<i>Lachnospiraceae bacterium</i> CA4; AB849415	S004125824	0.852	Bovine rumen	

		sequence								
New.ReferenceOTU348	K: <i>Bacteria</i> ; p: <i>Actinobacteria</i> ; c: <i>Coriobacteriia</i> ; o: <i>Coriobacteriales</i> ; f: <i>Coriobacteriaceae</i>	<i>Adlercreutzia equolifaciens</i> strain DSM 19450 16S ribosomal RNA, partial sequence	NR_121696.1	92%	Human feces	Coriobacteriaceae bacterium 68-1-3; CP009302	S004444305	0.729	Pig small intestine	
558599	K: <i>Bacteria</i> ; p: <i>Firmicutes</i> ; c: <i>Clostridia</i> ; o: <i>Clostridiales</i> ; f: <i>Ruminococcaceae</i>	<i>Intestinimonas butyriciproducens</i> strain SRB-521-5-1 16S ribosomal RNA gene, partial sequence	NR_118554.1	93%	mouse cecum	<i>Rumen bacterium</i> NK4A214; GU324404	S002351043	1000	Rumen of sheep	
570471	K: <i>Bacteria</i> ; p: <i>Firmicutes</i> ; c: <i>Clostridia</i> ; o: <i>Clostridiales</i> ; f: <i>Mogibacteriaceae</i>	<i>Emergencia timonensis</i> strain SN18 16S ribosomal RNA, partial sequence	NR_144737.1	93%	Human feces	<i>Clostridiaceae bacterium</i> FH042; AB298771	S000994706	0.730	Methanogenic reactor	
New.ReferenceOTU152	K: <i>Bacteria</i> ; p: <i>Bacteroidetes</i> ; c: <i>Bacteroidia</i> ; o: <i>Bacteroidales</i> ; f: <i>Prevotellaceae</i> ; g: <i>Prevotella</i>	<i>Prevotella ruminicola</i> strain Bryant 23 16S ribosomal RNA, partial sequence	NR_102887.1	93%	Bovine rumen	<i>Prevotella</i> sp. RM13; AB730677	S003659396	0.805	Bovine rumen	
New.ReferenceOTU317	K: <i>Bacteria</i> ; p: <i>Bacteroidetes</i> ; c: <i>Bacteroidia</i> ; o: <i>Bacteroidales</i>	<i>Alistipes shahii</i> strain JCM 16773 16S ribosomal RNA gene, partial sequence	NR_113153.1	84%	Human specimens	<i>Bacteroidetes bacterium</i> CA45; AB849455	S004125864	0.615	Bovine rumen	
102017	K: <i>Bacteria</i> ; p: <i>Firmicutes</i> ; c: <i>Clostridia</i> ; o: <i>Clostridiales</i> ; f: <i>Lachnospiraceae</i> ; g: <i>Pseudobutyrvibrio</i>	<i>Pseudobutyrvibrio ruminis</i> strain DSM 9787 16S ribosomal RNA gene, partial sequence	NR_026315.1	99%	Rumen of cow	<i>Butyrvibrio fibrisolvens</i> ; OB192; U41171	S000437587	1000	Rumen	
New.ReferenceOTU131	K: <i>Bacteria</i> ; p: <i>Firmicutes</i> ; c: <i>Clostridia</i> ; o: <i>Clostridiales</i> ; f: <i>Ruminococcaceae</i>	<i>Flintibacter butyricus</i> strain BLS21 16S ribosomal RNA, partial sequence	NR_144611.1	94%	Mouse	<i>Rumen bacterium</i> NK4A214; GU324404	S002351043	0.714	Rumen of sheep	
335793	K: <i>Bacteria</i> ; p: <i>TM7</i> ; c: <i>TM7-3</i> ; o: <i>CW040</i> ; f: <i>F16</i>	<i>Mogibacterium timidum</i> strain ATCC 33093 16S ribosomal RNA gene, partial sequence	NR_118782.1	78%	Human oral cavity	<i>TM7 bacterium</i> human oral taxon HOT-870; 4W45; KM018323	S004272182	0.634	Human oral cavity	
349539	K: <i>Bacteria</i> ; p: <i>TM7</i> ; c: <i>TM7-3</i> ; o: <i>CW040</i> ; f: <i>F16</i>	[<i>Clostridium</i>] <i>fimetarium</i> strain Z-2189 16S ribosomal RNA gene, partial sequence	NR_024993.1	79%	cattle manure	<i>TM7 bacterium</i> human oral taxon HOT-870; 4W45; KM018322	S004272182	0.596	Human oral cavity	
New.ReferenceOTU434	K: <i>Bacteria</i> ; p: <i>Firmicutes</i> ; c: <i>Clostridia</i> ; o: <i>Clostridiales</i> ; f: <i>Lachnospiraceae</i>	<i>Fusicatenibacter saccharivorans</i> strain HT03-11 16S ribosomal RNA gene, partial sequence	NR_114326.1	91%	Human feces	<i>Lachnospiraceae bacterium</i> CG18; AB849442	S004125851	0.682	Bovine rumen	
New.ReferenceOTU254	K: <i>Bacteria</i> ; p: <i>Firmicutes</i> ; c: <i>Clostridia</i> ; o: <i>Clostridiales</i>	<i>Anaerobacterium chartisolvens</i> strain T-1-35 16S ribosomal RNA gene, partial sequence	NR_125464.1	88%	soil of rice field	<i>Clostridiales bacterium</i> oral taxon F32; VQ026; HM099644	S002167974	0.702	Human oral cavity	
337289	K: <i>Bacteria</i> ; p: <i>TM7</i> ; c: <i>TM7-3</i> ; o: <i>CW040</i> ; f:	<i>Cellulosilyticum</i>	NR_116001.1	79%	rumen	<i>TM7 bacterium</i> human	S004272182	0.651	Human oral	

	<i>F16</i>	<i>ruminicola</i> strain H1 16S ribosomal RNA gene, partial sequence				oral taxon HOT-870; 4W45; KM018322				cavity
New.ReferenceOTU458	K: <i>Bacteria</i> ; p: <i>Bacteroidetes</i> ; c: <i>Bacteroidia</i> ; o: <i>Bacteroidales</i> ; f: <i>Prevotellaceae</i> ; g: <i>Prevotella</i>	<i>Prevotella baroniae</i> strain JCM 13447 16S ribosomal RNA gene, partial sequence	NR_113094.1	92%	Human oral cavity	<i>Prevotella baroniae</i> ; JCM 13447; AB547671	S002235853	0.716		Human oral cavity
New.ReferenceOTU536	K: <i>Bacteria</i> ; p: <i>Firmicutes</i> ; c: <i>Bacilli</i> ; o: <i>Lactobacillales</i> ; f: <i>Streptococcaceae</i> ; g: <i>Streptococcus</i>	<i>Streptococcus suis</i> strain ATCC 43765 16S ribosomal RNA gene, partial sequence	NR_117504.1	97%	Pig	<i>Streptococcus porcorum</i> ; 1792-03; FN908165	S002222559	0.877		Pig lung
New.ReferenceOTU105	K: <i>Bacteria</i> ; p: <i>Firmicutes</i> ; c: <i>Clostridia</i> ; o: <i>Clostridiales</i> ; f: <i>Mogibacteriaceae</i>	<i>Pseudobutyrvibrio ruminis</i> strain DSM 9787 16S ribosomal RNA gene, partial sequence	NR_026315.1	96%	Rumen of cow	<i>Butyrvibrio</i> sp. 3; EU714406	S001416389	0.805		Sheep rumen
New.ReferenceOTU410	K: <i>Bacteria</i> ; p: <i>Firmicutes</i> ; c: <i>Clostridia</i> ; o: <i>Clostridiales</i>	<i>[Eubacterium] hallii</i> strain ATCC 27751 16S ribosomal RNA gene, partial sequence	NR_118673.1	95%	Human feces	<i>Butyrate-producing bacterium</i> SM6/1; AY305318	S000406444	0.788		Human feces
251961	K: <i>Bacteria</i> ; p: <i>Firmicutes</i> ; c: <i>Clostridia</i> ; o: <i>Clostridiales</i>	<i>Irregularibacter muris</i> strain 2PG-426-CC-4.2 16S ribosomal RNA, partial sequence	NR_144613.1	87%	Mouse gut	<i>Clostridiales bacterium</i> RM3; AB730671	S003659390	0.678		Bovine rumen

Table A3. Comparison of assigned taxonomy for the 50 most abundant OTUs of the fed group. Databases used were GreenGenes ver. 13.8, NCBI BLASTn 2.8.0 against 16S ribosomal RNA sequences (Bacteria and Archaea) and RDP 11.5 classifier.

Fed - OTU ID	QIIME taxonomy	BLAST - DESCRIPTION	Accession number	Identity	Habitat	RDP - DESCRIPTION	Accession number	S_ab score	Habitat
585480	K: <i>Bacteria</i> ; p: <i>Firmicutes</i> ; c: <i>Clostridia</i> ; o: <i>Clostridiales</i> ; f: <i>Lachnospiraceae</i> ; g: <i>Anaerostipes</i>	<i>Eubacterium ventriosum</i> strain ATCC 27560 16S ribosomal RNA gene, partial sequence	NR_118670.1	98%	Feces	<i>Butyrate-producing bacterium</i> L2-12; AJ270488	S000090760	0.949	Human feces
New.ReferenceOTU462	K: <i>Bacteria</i> ; p: <i>Bacteroidetes</i> ; c: <i>Bacteroidia</i> ; o: <i>Bacteroidales</i> ; f: <i>Prevotellaceae</i> ; g: <i>Prevotella</i>	<i>Prevotella oralis</i> strain JCM 12251 16S ribosomal RNA gene, partial sequence	NR_113117.1	90%	Human oral cavity	<i>Prevotella oralis</i> (T); ATCC 33269; AY323522	S000546838	0.711	Human oral cavity
265032	K: <i>Bacteria</i> ; p: <i>Firmicutes</i> ; c: <i>Clostridia</i> ; o: <i>Clostridiales</i> ; f: <i>Ruminococcaceae</i>	<i>Pseudoflavonifractor capillosus</i> strain ATCC 29799 16S ribosomal RNA gene, partial sequence	NR_025670.1	91%	Human feces	<i>Clostridiales bacterium</i> NK3B98; GU324364	S002351003	0.788	Rumen of pasture-grazed sheep
New.ReferenceOTU481	K: <i>Bacteria</i> ; p: <i>Bacteroidetes</i> ; c: <i>Bacteroidia</i> ; o: <i>Bacteroidales</i> ; f: <i>Prevotellaceae</i> ; g: <i>Prevotella</i>	<i>Prevotella brevis</i> strain GA33 16S ribosomal RNA, partial sequence	NR_041954.1	90%	Rumen	<i>Rumen bacterium</i> NK4C107; GU324396	S002351035	0.695	Rumen of sheep
1110312	K: <i>Bacteria</i> ; p: <i>Firmicutes</i> ; c: <i>Clostridia</i> ; o: <i>Clostridiales</i>	[<i>Clostridium</i>] <i>cellulolyticum</i> strain H10 16S ribosomal RNA gene, complete sequence	NG_041947.1	88%	Decayed grass in compost pile	<i>Clostridiales bacterium</i> oral taxon F32; VO026; HM099644	S002167974	0.827	Human oral cavity
New.ReferenceOTU199	K: <i>Bacteria</i> ; p: <i>Bacteroidetes</i> ; c: <i>Bacteroidia</i> ; o: <i>Bacteroidales</i> ; f: <i>Prevotellaceae</i> ; g: <i>Prevotella</i>	<i>Prevotella loescheii</i> strain JCM 8530 16S ribosomal RNA gene, partial sequence	NR_113109.1	87%	Human oral cavity	<i>Prevotella</i> sp. RS2; AY158021	S000398586	0.604	Pig colon mucosa
433722	K: <i>Bacteria</i> ; p: <i>Firmicutes</i> ; c: <i>Clostridia</i> ; o: <i>Clostridiales</i> ; f: <i>Ruminococcaceae</i>	<i>Intestinimonas butyriciproducens</i> strain SRB-521-5-I 16S ribosomal RNA gene, partial sequence	NR_118554.1	93%	Mouse caecum	<i>Rumen bacterium</i> NK4A214; GU324404	S002351043	0.987	Rumen of sheep
351812	K: <i>Bacteria</i> ; p: <i>Firmicutes</i> ; c: <i>Clostridia</i> ; o: <i>Clostridiales</i> ; f: <i>Mogibacteriaceae</i>	<i>Emergencia timonensis</i> strain SN18 16S ribosomal RNA, partial sequence	NR_144737.1	93%	Human feces	<i>Eubacterium</i> sp. WAL 17363; GQ461729	S001611916	0.755	Human feces
New.ReferenceOTU77	Unassigned	<i>Prevotella dentalis</i> strain DSM 3688 16S ribosomal RNA, partial sequence	NR_102481.1	89%	Human oral cavity	<i>Rumen bacterium</i> NK3B31; GU324411	S002351050	0.646	Rumen of sheep
571254	K: <i>Bacteria</i> ; p: <i>Bacteroidetes</i> ; c: <i>Bacteroidia</i> ; o: <i>Bacteroidales</i>	<i>Lentimicrobium saccharophilum</i> strain TBC1 16S ribosomal RNA, partial sequence	NR_149795.1	85%	Anaerobic wastewater treatment sludge	<i>Bacteroidales bacterium</i> TBC1; LC049960	S004501385	0.591	Anaerobic wastewater treatment sludge

558599	K: <i>Bacteria</i> ; p: <i>Firmicutes</i> ; c: <i>Clostridia</i> ; o: <i>Clostridiales</i> ; f: <i>Ruminococcaceae</i>	<i>Intestinimonas butyrificiproducens</i> strain SRB-521-5-1 16S ribosomal RNA gene, partial sequence	NR_118554.1	93%	Mouse caecum	<i>Rumen bacterium</i> NK4A214; GU324404	S002351043	1000	Rumen of sheep
331350	K: <i>Bacteria</i> ; p: <i>TM7</i> ; c: <i>TM7-3</i> ; o: <i>CW040</i> ; f: <i>F16</i>	<i>Cellulosilyticum ruminicola</i> strain H1 16S ribosomal RNA gene, partial sequence	NR_116001.1	78%	Rumen	<i>TM7 bacterium</i> human oral taxon HOT-870; 4W45; KM018322	S004272182	0.599	Human oral cavity
New.ReferenceOTU143	K: <i>Bacteria</i> ; p: <i>Bacteroidetes</i> ; c: <i>Bacteroidia</i> ; o: <i>Bacteroidales</i> ; f: <i>Prevotellaceae</i> ; g: <i>Prevotella</i>	<i>Prevotella ruminicola</i> strain Bryant 23 16S ribosomal RNA, partial sequence	NR_102887.1	89%	Bovine rumen	<i>Prevotella</i> sp. 152R-1a; DQ278861	S000650962	0.692	Dairy cow
577671	K: <i>Bacteria</i> ; p: <i>TM7</i> ; c: <i>TM7-3</i> ; o: <i>CW040</i> ; f: <i>F16</i>	<i>Mogibacterium timidum</i> strain ATCC 33093 16S ribosomal RNA gene, partial sequence	NR_118782.1	79%	Subgingival region of mouth	<i>TM7 bacterium</i> human oral taxon HOT-870; 4W45; KM018322	S004272182	0.598	Human oral cavity
New.ReferenceOTU10	K: <i>Bacteria</i> ; p: <i>Firmicutes</i> ; c: <i>Clostridia</i> ; o: <i>Clostridiales</i> ; f: <i>Lachnospiraceae</i> ; g: <i>Blautia</i>	<i>Blautia schinkii</i> strain B 16S ribosomal RNA, partial sequence	NR_026312.1	97%	Rumen of suckling lamb	<i>Blautia faecis</i> (T); M25; HM626178	S002232209	0.828	Human feces
554055	K: <i>Bacteria</i> ; p: <i>Firmicutes</i> ; c: <i>Clostridia</i> ; o: <i>Clostridiales</i> ; f: <i>Ruminococcaceae</i>	<i>Flintibacter butyricus</i> strain BLS21 16S ribosomal RNA, partial sequence	NR_144611.1	93%	Mouse intestine	<i>Intestinimonas</i> sp. FSAA-17; KP114242	S004532796	0.751	Sheep
New.ReferenceOTU259	K: <i>Bacteria</i> ; p: <i>Firmicutes</i> ; c: <i>Clostridia</i> ; o: <i>Clostridiales</i> ; f: <i>Lachnospiraceae</i> ; g: <i>Butyrivibrio</i>	<i>Butyrivibrio proteoclasticus</i> strain B316 16S ribosomal RNA, partial sequence	NR_102893.1	94%	Rumen	<i>Butyrivibrio</i> sp. CA23; AB849434	S004125843	0.741	Bovine rumen
New.ReferenceOTU311	K: <i>Bacteria</i> ; p: <i>Bacteroidetes</i> ; c: <i>Bacteroidia</i> ; o: <i>Bacteroidales</i> ; f: <i>Prevotellaceae</i> ; g: <i>Prevotella</i>	<i>Prevotella marshii</i> strain JCM 13450 16S ribosomal RNA gene, partial sequence	NR_113111.1	91%	Human oral cavity	<i>Prevotella</i> sp. RM13; AB730677	S003659396	0.692	Bovine rumen
589920	K: <i>Bacteria</i> ; p: <i>Actinobacteria</i> ; c: <i>Coriobacteriia</i> ; o: <i>Coriobacteriales</i> ; f: <i>Coriobacteriaceae</i>	<i>Raoultibacter timonensis</i> strain Marseille-P3277 16S ribosomal RNA, partial sequence	NR_148574.1	94%	Human feces	<i>Eggerthellaceae bacterium</i> AT8; LN881601	S004508480	0.651	Human feces
594330	K: <i>Bacteria</i> ; p: <i>Bacteroidetes</i> ; c: <i>Bacteroidia</i> ; o: <i>Bacteroidales</i> ; f: <i>Prevotellaceae</i> ; g: <i>Prevotella</i>	<i>Prevotella ruminicola</i> strain Bryant 23 16S ribosomal RNA, partial sequence	NR_102887.1	91%	Bovine rumen	<i>Prevotella brevis</i> (T); GA33; AJ011682	S000021675	0.724	Rumen
337289	K: <i>Bacteria</i> ; p: <i>TM7</i> ; c: <i>TM7-3</i> ; o: <i>CW040</i> ; f: <i>F16</i>	<i>Cellulosilyticum ruminicola</i> strain H1 16S ribosomal RNA gene, partial sequence	NR_116001.1	79%	Rumen	<i>TM7 bacterium</i> human oral taxon HOT-870; 4W45; KM018322	S004272182	0.651	Human oral cavity
816626	K: <i>Bacteria</i> ; p: <i>Firmicutes</i> ; c: <i>Clostridia</i> ; o: <i>Clostridiales</i>	<i>Howardella ureilytica</i> strain GPC 589 16S ribosomal RNA, partial sequence	NR_044022.2	94%	Rumen	<i>Howardella ureilytica</i> (T); GPC 589; DQ925472	S000926211	0.708	Rumen

355203	K: <i>Bacteria</i> ; p: <i>Firmicutes</i> ; c: <i>Clostridia</i> ; o: <i>Clostridiales</i> ; f: <i>Ruminococcaceae</i>	<i>Harryflintia acetispora</i> strain V20-281a 16S ribosomal RNA, partial sequence	NR_152059.1	89%	Cecum chicken	<i>Flavonifractor plautii</i> ; MT42; AB693937	S003277052	0.554	Rat feces
461487	K: <i>Bacteria</i> ; p: <i>Firmicutes</i> ; c: <i>Clostridia</i> ; o: <i>Clostridiales</i>	[<i>Clostridium</i>] <i>cellulolyticum</i> strain H10 16S ribosomal RNA gene, complete sequence	NG_041947.1	87%	Decayed grass in compost pile	<i>Clostridiales</i> bacterium oral taxon F32; VO026; HM099644	S002167974	0.757	Human oral cavity
538761	K: <i>Bacteria</i> ; p: <i>Firmicutes</i> ; c: <i>Clostridia</i> ; o: <i>Clostridiales</i> ; f: <i>Lachnospiraceae</i> ; g: <i>Butyrivibrio</i>	<i>Butyrivibrio fibrisolvens</i> strain ATCC 19171 16S ribosomal RNA gene, partial sequence	NR_025981.1	92%	Rumen	<i>Butyrivibrio fibrisolvens</i> (T); ATCC 19171; U41172	S000437588	0.674	Rumen (deer)
New.ReferenceOTU433	K: <i>Bacteria</i> ; p: <i>Bacteroidetes</i> ; c: <i>Bacteroidia</i> ; o: <i>Bacteroidales</i>	<i>Capnocytophaga cynodegmi</i> strain ATCC 49044 16S ribosomal RNA, partial sequence	NR_119226.1	85%	Dog mouth	<i>Bacteroidales</i> bacterium P13; AB730729	S003659448	0.527	Bovine rumen
New.ReferenceOTU31	K: <i>Bacteria</i> ; p: <i>Bacteroidetes</i> ; c: <i>Bacteroidia</i> ; o: <i>Bacteroidales</i>	<i>Lentimicrobium saccharophilum</i> strain TBC1 16S ribosomal RNA, partial sequence	NR_149795.1	85%	Anaerobic wastewater treatment sludge	<i>Bacteroidales</i> bacterium TBC1; LC049960	S004501385	0.570	Anaerobic wastewater treatment sludge
327282	K: <i>Bacteria</i> ; p: <i>Firmicutes</i> ; c: <i>Clostridia</i> ; o: <i>Clostridiales</i>	[<i>Clostridium</i>] <i>clariflavum</i> strain DSM 19732 16S ribosomal RNA, partial sequence	NR_102987.1	87%	Methanogenic sludge of a bioreactor	<i>Clostridiales</i> bacterium oral taxon F32; VO026; HM099644	S002167974	0.690	Human oral cavity
534926	K: <i>Bacteria</i> ; p: <i>Firmicutes</i> ; c: <i>Clostridia</i> ; o: <i>Clostridiales</i> ; f: <i>Lachnospiraceae</i> ; g: <i>Anaerostipes</i>	<i>Eubacterium ventriosum</i> strain ATCC 27560 16S ribosomal RNA gene, partial sequence	NR_118670.1	97%	Feces	<i>Rumen bacterium</i> 2/9293-25; DQ382351	S000650250	0.842	Reindeer
581109	K: <i>Bacteria</i> ; p: <i>Firmicutes</i> ; c: <i>Clostridia</i> ; o: <i>Clostridiales</i>	<i>Geosporobacter subterraneus</i> strain VNs68 16S ribosomal RNA gene, partial sequence	NR_115818.1	87%	Water-producing deep artesian well	<i>Clostridiales</i> bacterium RM3; AB730671	S003659390	0.663	Bovine rumen
New.ReferenceOTU484	K: <i>Bacteria</i> ; p: <i>Firmicutes</i> ; c: <i>Clostridia</i> ; o: <i>Clostridiales</i> ; f: <i>Lachnospiraceae</i>	<i>Syntrophococcus sucromutans</i> strain S195 16S ribosomal RNA gene, partial sequence	NR_118354.1	97%	Rumen of cattle	<i>Syntrophococcus sucromutans</i> ; S195; JQ346731	S003259700	0.852	Rumen of cattle
New.ReferenceOTU253	K: <i>Bacteria</i> ; p: <i>Firmicutes</i> ; c: <i>Clostridia</i> ; o: <i>Clostridiales</i> ; f: <i>Lachnospiraceae</i>	<i>Pseudobutyrvibrio ruminis</i> strain DSM 9787 16S ribosomal RNA gene, partial sequence	NR_026315.1	94%	Rumen of cow	<i>Pseudobutyrvibrio ruminis</i> ; M80; AY699284	S000380156	0.774	Camel digestive system
New.ReferenceOTU161	K: <i>Bacteria</i> ; p: <i>Firmicutes</i> ; c: <i>Clostridia</i> ; o: <i>Clostridiales</i> ; f: <i>Mogibacteriaceae</i>	<i>Emergencia timonensis</i> strain SN18 16S ribosomal RNA, partial sequence	NR_144737.1	95%	Feces (human)	<i>Eubacterium</i> sp. WAL 18692; GQ461730	S001611917	0.770	Human feces
New.ReferenceOTU84	K: <i>Bacteria</i> ; p: <i>Bacteroidetes</i> ; c: <i>Bacteroidia</i> ; o: <i>Bacteroidales</i> ; f: <i>Prevotellaceae</i> ; g: <i>Prevotella</i>	<i>Prevotella ruminicola</i> strain Bryant 23 16S ribosomal RNA, partial sequence	NR_102887.1	90%	Bovine rumen	<i>Rumen bacterium</i> R-9; AB239482	S000607269	0.709	Sheep rumen

New.ReferenceOTU474	K: <i>Bacteria</i> ; p: <i>Bacteroidetes</i> ; c: <i>Bacteroidia</i> ; o: <i>Bacteroidales</i> ; f: <i>Prevotellaceae</i> ; g: <i>Prevotella</i>	<i>Prevotella buccalis</i> strain JCM 12246 16S ribosomal RNA gene, partial sequence	NR_113098.1	90%	Dental plaque	<i>Prevotella</i> sp. AN 5135; KP334252	S004537769	0.748	Tracheal-aspirate (horse)
533277	K: <i>Bacteria</i> ; p: <i>Firmicutes</i> ; c: <i>Bacilli</i> ; o: <i>Lactobacillales</i> ; f: <i>Streptococcaceae</i> ; g: <i>Streptococcus</i>	<i>Streptococcus alactolyticus</i> strain ATCC 43077 16S ribosomal RNA gene, partial sequence	NR_041781.1	100%	Pig intestine	<i>Streptococcus</i> sp. LRC 0253; AF298197	S000390926	1000	Bovine rumen and feces
356394	K: <i>Bacteria</i> ; p: <i>Firmicutes</i> ; c: <i>Clostridia</i> ; o: <i>Clostridiales</i> ; f: <i>Ruminococcaceae</i>	<i>Flintibacter butyricus</i> strain BLS21 16S ribosomal RNA, partial sequence	NR_144611.1	93%	Mouse	<i>Rumen bacterium</i> NK4A214; GU324404	S002351043	0.924	Sheep rumen
New.ReferenceOTU276	K: <i>Bacteria</i> ; p: <i>Firmicutes</i> ; c: <i>Clostridia</i> ; o: <i>Clostridiales</i> ; f: <i>Mogibacteriaceae</i>	<i>Anaerovorax odorimutans</i> strain NorPut 16S ribosomal RNA gene, partial sequence	NR_028911.1	90%	Brackish water sediment	<i>Peptostreptococcaceae bacterium</i> canine oral taxon 097; PO047; JN713261	S003222591	0.689	Dog oral cavity
New.ReferenceOTU449	K: <i>Bacteria</i> ; p: <i>Bacteroidetes</i> ; c: <i>Bacteroidia</i> ; o: <i>Bacteroidales</i> ; f: <i>Prevotellaceae</i> ; g: <i>Prevotella</i>	<i>Prevotella ruminicola</i> strain Bryant 23 16S ribosomal RNA, partial sequence	NR_102887.1	90%	Bovine rumen	<i>Rumen bacterium</i> R-9; AB239482	S000607269	0.686	Sheep rumen
153291	K: <i>Bacteria</i> ; p: <i>Firmicutes</i> ; c: <i>Clostridia</i> ; o: <i>Clostridiales</i>	<i>Anaerobacterium chartisolvens</i> strain T-1-35 16S ribosomal RNA gene, partial sequence	NR_125464.1	87%	Soil of rice field	<i>Clostridiales bacterium</i> oral taxon F32; VO026; HM099644	S002167974	0.789	Human oral cavity
555101	K: <i>Bacteria</i> ; p: <i>Firmicutes</i> ; c: <i>Clostridia</i> ; o: <i>Clostridiales</i> ; f: <i>Ruminococcaceae</i>	<i>Sporobacter termitidis</i> strain SYR 16S ribosomal RNA, partial sequence	NR_044972.1	92%	Termite digestive tract	<i>Clostridiales bacterium</i> CIEAF 022; AB702938	S003316343	0.694	Mouse feces
331740	K: <i>Bacteria</i> ; p: <i>Bacteroidetes</i> ; c: <i>Bacteroidia</i> ; o: <i>Bacteroidales</i>	<i>Prevotella ruminicola</i> strain Bryant 23 16S ribosomal RNA, partial sequence	NR_102887.1	90%	Bovine rumen	<i>Bacteroidales bacterium</i> P13; AB730729	S003659448	0.752	Bovine rumen
New.ReferenceOTU410	K: <i>Bacteria</i> ; p: <i>Firmicutes</i> ; c: <i>Clostridia</i> ; o: <i>Clostridiales</i>	<i>[Eubacterium] hallii</i> strain ATCC 27751 16S ribosomal RNA gene, partial sequence	NR_118673.1	95%	Human feces	<i>Butyrate-producing bacterium</i> SM6/1; AY305318	S000406444	0.788	Human feces
173519	K: <i>Bacteria</i> ; p: <i>Firmicutes</i> ; c: <i>Clostridia</i> ; o: <i>Clostridiales</i> ; f: <i>Lachnospiraceae</i>	<i>Stomatobaculum longum</i> strain ACC2 16S ribosomal RNA gene, partial sequence	NR_117792.1	91%	Human oral cavity	<i>Clostridium polysaccharolyticum</i> (T); DSM 1801; X77839	S000260417	0.586	Rumen of sheep
4480176	K: <i>Bacteria</i> ; p: <i>Firmicutes</i> ; c: <i>Clostridia</i> ; o: <i>Clostridiales</i>	<i>Vallitalea pronyensis</i> strain FatNI3 16S ribosomal RNA gene, partial sequence	NR_125677.1	87%	Alkaline hydrothermal chimney	<i>Clostridiales bacterium</i> oral taxon F32; VO026; HM099644	S002167974	0.743	Human oral cavity
311412	K: <i>Bacteria</i> ; p: <i>Firmicutes</i> ; c: <i>Clostridia</i> ; o: <i>Clostridiales</i>	<i>Geosporobacter ferrireducens</i> strain IRF9 16S ribosomal RNA, partial sequence	NR_148302.1	88%	Petroleum contaminated soil	<i>Clostridiales bacterium</i> RM3; AB730671	S003659390	0.668	Bovine rumen

277519	K: <i>Bacteria</i> ; p: <i>TM7</i> ; c: <i>TM7-3</i> ; o: <i>CW040</i> ; f: <i>F16</i>	<i>Ruminococcus champanellensis</i> strain 18P13 16S ribosomal RNA, partial sequence	NR_102884.1	79%	Human feces	<i>TM7 phylum</i> sp. canine oral taxon 363; 2A026; JN713533	S003222863	0.652	Dog oral cavity
593008	K: <i>Bacteria</i> ; p: <i>Firmicutes</i> ; c: <i>Clostridia</i> ; o: <i>Clostridiales</i>	<i>Geosporobacter ferrireducens</i> strain IRF9 16S ribosomal RNA, partial sequence	NR_148302.1	87%	Petroleum contaminated soil	<i>Clostridiales bacterium</i> RM3; AB730671	S003659390	0.622	Bovine rumen
New.ReferenceOTU152	K: <i>Bacteria</i> ; p: <i>Bacteroidetes</i> ; c: <i>Bacteroidia</i> ; o: <i>Bacteroidales</i> ; f: <i>Prevotellaceae</i> ; g: <i>Prevotella</i>	<i>Prevotella ruminicola</i> strain Bryant 23 16S ribosomal RNA, partial sequence	NR_102887.1	93%	Bovine rumen	<i>Prevotella</i> sp. RM13; AB730677	S003659396	0.805	Bovine rumen
152450	k: <i>Archaea</i> ; p: <i>Euryarchaeota</i> ; c: <i>Methanobacteria</i> ; o: <i>Methanobacteriales</i> ; f: <i>Methanobacteriaceae</i> ; g: <i>Methanobrevibacter</i>	<i>Methanobrevibacter millerae</i> strain ZA-10 16S ribosomal RNA gene, partial sequence	NR_042785.1	99%	Bovine rumen fluid	<i>Methanobrevibacter</i> sp. 1Y; DQ135988	S000587031	1000	Rumen