






















Supplementary Table S1. OTUs identified in the nasopharyngeal, ruminal and vaginal microbiota of at least 60% of samples from virgin yearling heifers.

[illegible]

OTU56 1	[k__Bacteria, p__Firmicutes, c__Clostridia, o__Oscillospirales, f__Oscillospiraceae, g__Colidextribacter, s__NA]	
OTU78	[k__Bacteria, p__Firmicutes, c__Clostridia, o__Oscillospirales, f__Oscillospiraceae, g__NK4A214 group, s__NA]	
OTU37	[k__Bacteria, p__Firmicutes, c__Clostridia, o__Oscillospirales, f__Oscillospiraceae, g__UCG-005, s__NA]	
OTU18 8	[k__Bacteria, p__Firmicutes, c__Clostridia, o__Oscillospirales, f__Ruminococcaceae, g__Ruminococcus, s__NA]	
OTU20 1	[k__Bacteria, p__Firmicutes, c__Clostridia, o__Oscillospirales, f__Ruminococcaceae, g__Ruminococcus, s__NA]	
OTU29	[k__Bacteria, p__Firmicutes, c__Clostridia, o__Oscillospirales, f__Ruminococcaceae, g__Ruminococcus, s__NA]	
OTU30 7	[k__Bacteria, p__Firmicutes, c__Clostridia, o__Oscillospirales, f__Ruminococcaceae, g__Ruminococcus, s__NA]	
OTU44 1	[k__Bacteria, p__Firmicutes, c__Clostridia, o__Oscillospirales, f__Ruminococcaceae, g__Ruminococcus, s__NA]	
OTU83	[k__Bacteria, p__Firmicutes, c__Clostridia, o__Oscillospirales, f__Ruminococcaceae, g__Ruminococcus, s__NA]	
OTU24 4	[k__Bacteria, p__Firmicutes, c__Clostridia, o__Oscillospirales, f__Ruminococcaceae, g__UCG-001, s__NA]	
OTU24 3	[k__Bacteria, p__Firmicutes, c__Clostridia, o__Peptostreptococcales-Tissierellales, f__Anaerovoracaceae, g__Family XIII AD3011 group, s__NA]	
OTU51 8	[k__Bacteria, p__Firmicutes, c__Clostridia, o__Peptostreptococcales-Tissierellales, f__Anaerovoracaceae, g__Family XIII AD3011 group, s__NA]	
OTU37 2	[k__Bacteria, p__Firmicutes, c__Clostridia, o__Peptostreptococcales-Tissierellales, f__Anaerovoracaceae, g__Mogibacterium, s__NA]	
OTU24	[k__Bacteria, p__Firmicutes, c__Clostridia, o__Peptostreptococcales-Tissierellales, f__Peptostreptococcaceae, g__Paeniclostridium, s__NA]	
OTU11	[k__Bacteria, p__Firmicutes, c__Clostridia, o__Peptostreptococcales-Tissierellales, f__Peptostreptococcaceae, g__Romboutsia, s__ilealis]	
OTU16 55	[k__Bacteria, p__Proteobacteria, c__Alphaproteobacteria, o__Acetobacterales, f__Acetobacteraceae, g__Acetobacter, s__pasteurianus]	

Supplementary Table S2. OTUs identified in the nasopharyngeal, ruminal, and vaginal microbiota of at least 60% of samples from pregnant heifers.

OTU	Taxa	60%	65%	70%	75%	80%	85%	90%	95%	100%
OTU 23	[k__Archaea, p__Euryarchaeota, c__Methanobacteria, o__Methanobacteriales, f__Methanobacteriaceae, g__Methanobrevibacter, s__ruminantium]									
OTU 56	[k__Bacteria, p__Actinobacteriota, c__Actinobacteria, o__Bifidobacteriales, f__Bifidobacteriaceae, g__Bifidobacterium, s__merycicum]									
OTU 68	[k__Bacteria, p__Actinobacteriota, c__Actinobacteria, o__Bifidobacteriales, f__Bifidobacteriaceae, g__Bifidobacterium, s__pseudolongum]									
OTU 105	[k__Bacteria, p__Actinobacteriota, c__Actinobacteria, o__Corynebacteriales, f__Corynebacteriaceae, g__Corynebacterium, s__crudilactis]									
OTU 147	[k__Bacteria, p__Actinobacteriota, c__Actinobacteria, o__Corynebacteriales, f__Corynebacteriaceae, g__Corynebacterium, s__marinum]									
OTU 26	[k__Bacteria, p__Actinobacteriota, c__Actinobacteria, o__Corynebacteriales, f__Corynebacteriaceae, g__Corynebacterium, s__NA]									
OTU 3812	[k__Bacteria, p__Actinobacteriota, c__Actinobacteria, o__Corynebacteriales, f__Corynebacteriaceae, g__Corynebacterium, s__NA]									
OTU 272	[k__Bacteria, p__Actinobacteriota, c__Actinobacteria, o__Corynebacteriales, f__Corynebacteriaceae, g__Corynebacterium, s__provencense]									
OTU 160	[k__Bacteria, p__Actinobacteriota, c__Actinobacteria, o__Micrococcales, f__Intrasporangiaceae, g__Ornithinimicrobium, s__NA]									
OTU 20	[k__Bacteria, p__Actinobacteriota, c__Actinobacteria, o__Micrococcales, f__Micrococcaceae, g__Arthrobacter, s__castelli]									
OTU 14	[k__Bacteri, p__Actinobacteriota, c__Actinobacteria, o__Micrococcales, f__Micrococcaceae, g__Arthrobacter, s__pigmenti]									
OTU 352	[k__Bacteria, p__Actinobacteriota, c__Actinobacteria, o__Micrococcales, f__Micrococcaceae, g__Paeniglutamicibacter, s__NA]									
OTU 76	[k__Bacteria, p__Actinobacteriota, c__Actinobacteria, o__Propionibacteriales, f__Nocardioidaceae, g__Marmoricola, s__NA]									
OTU 80	[k__Bacteria, p__Actinobacteriota, c__Actinobacteria, o__Propionibacteriales, f__Nocardioidaceae, g__Nocardioides, s__jensenii]									
OTU 377	[k__Bacteria, p__Actinobacteriota, c__Actinobacteria, o__Propionibacteriales, f__Propionibacteriaceae, g__Cutibacterium, s__acnes]									
OTU 35	[k__Bacteria, p__Actinobacteriota, c__Actinobacteria, o__Streptomycetales, f__Streptomycetaceae, g__Streptomyces, s__NA]									
OTU 370	[k__Bacteria, p__Firmicutes, c__Clostridia, o__Clostridia UCG-014, f__NA, g__NA, s__NA]									
OTU 927	[k__Bacteria, p__Firmicutes, c__Clostridia, o__Clostridia UCG-014, f__NA, g__NA, s__NA]									
OTU 119	[k__Bacteria, p__Firmicutes, c__Clostridia, o__Clostridiales, f__Clostridiaceae, g__Clostridium sensu stricto 1, s__NA]									
OTU 43	[k__Bacteria, p__Firmicutes, c__Clostridia, o__Hungateiclostridiaceae, f__Saccharofermentans, g__NA, s__NA]									
OTU 97	[k__Bacteria, p__Firmicutes, c__Clostridia, o__Hungateiclostridiaceae, f__Saccharofermentans, g__NA, s__NA]									
OTU 489	[k__Bacteria, p__Firmicutes, c__Clostridia, o__Lachnospirales, f__Lachnospiraceae, g__[Eubacterium] hallii group, s__NA]									
OTU 90	[k__Bacteria, p__Firmicutes, c__Clostridia, o__Lachnospirales, f__Lachnospiraceae, g__Dorea, s__NA]									
OTU 62	[k__Bacteria, p__Firmicutes, c__Clostridia, o__Lachnospirales, f__Lachnospiraceae, g__Lachnospiraceae NK3A20 group, s__NA]									
OTU 295	[k__Bacteria, p__Firmicutes, c__Clostridia, o__Lachnospirales, f__Lachnospiraceae, g__Lachnospiraceae NK3A20 group, s__NA]									

OTU 373	[k__Bacteria, p__Firmicutes, c__Clostridia, o__Lachnospirales, f__Lachnospiraceae, g__Lachnospiraceae NK3A20 group, s__NA]	
OTU 986	[k__Bacteria, p__Firmicutes, c__Clostridia, o__Lachnospirales, f__Lachnospiraceae, g__Lachnospiraceae NK3A20 group, s__NA]	
OTU 1688	[k__Bacteria, p__Firmicutes, c__Clostridia, o__Lachnospirales, f__Lachnospiraceae, g__Lachnospiraceae NK3A20 group, s__NA]	
OTU 897	[k__Bacteria, p__Firmicutes, c__Clostridia, o__Lachnospirales, f__Lachnospiraceae, g__Syntrophococcus, s__NA]	
OTU 25	[k__Bacteria, p__Firmicutes, c__Clostridia, o__Oscillospirales, f__[Eubacterium] coprostanoligenes group, g__NA, s__NA]	
OTU 78	[k__Bacteria, p__Firmicutes, c__Clostridia, o__Oscillospirales, f__Oscillospiraceae, g__NK4A214 group, s__NA]	
OTU 37	[k__Bacteria, p__Firmicutes, c__Clostridia, o__Oscillospirales, f__Oscillospiraceae, g__UCG-005, s__NA]	
OTU 54	[k__Bacteria, p__Firmicutes, c__Clostridia, o__Oscillospirales, f__Oscillospiraceae, g__UCG-005, s__NA]	
OTU 360	[k__Bacteria, p__Firmicutes, c__Clostridia, o__Oscillospirales, f__Ruminococcaceae, g__NA, s__NA]	
OTU 29	[k__Bacteria, p__Firmicutes, c__Clostridia, o__Oscillospirales, f__Ruminococcaceae, g__Ruminococcus, s__NA]	
OTU 83	[k__Bacteria, p__Firmicutes, c__Clostridia, o__Oscillospirales, f__Ruminococcaceae, g__Ruminococcus, s__NA]	
OTU 188	[k__Bacteria, p__Firmicutes, c__Clostridia, o__Oscillospirales, f__Ruminococcaceae, g__Ruminococcus, s__NA]	
OTU 201	[k__Bacteria, p__Firmicutes, c__Clostridia, o__Oscillospirales, f__Ruminococcaceae, g__Ruminococcus, s__NA]	
OTU 244	[k__Bacteria, p__Firmicutes, c__Clostridia, o__Oscillospirales, f__Ruminococcaceae, g__UCG-001, s__NA]	
OTU 243	[k__Bacteria, p__Firmicutes, c__Clostridia, o__Peptostreptococcales-Tissierellales, f__Anaerovoracaceae, g__Family XIII AD3011 group, s__NA]	
OTU 518	[k__Bacteria, p__Firmicutes, c__Clostridia, o__Peptostreptococcales-Tissierellales, f__Anaerovoracaceae, g__Family XIII AD3011 group, s__NA]	
OTU 372	[k__Bacteria, p__Firmicutes, c__Clostridia, o__Peptostreptococcales-Tissierellales, f__Anaerovoracaceae, g__Mogibacterium, s__NA]	
OTU 24	[k__Bacteria, p__Firmicutes, c__Clostridia, o__Peptostreptococcales-Tissierellales, f__Peptostreptococcaceae, g__Paeniclostridium, s__NA]	
OTU 11	[k__Bacteria, p__Firmicutes, c__Clostridia, o__Peptostreptococcales-Tissierellales, f__Peptostreptococcaceae, g__Romboutsia, s__ilealis]	
OTU 32	[k__Bacteria, p__Firmicutes, c__Clostridia, o__Peptostreptococcales-Tissierellales, f__Peptostreptococcaceae, g__Romboutsia, s__NA]	
OTU 96	[k__Bacteria, p__Firmicutes, c__Clostridia, o__Peptostreptococcales-Tissierellales, f__Peptostreptococcaceae, g__Romboutsia, s__NA]	
OTU 1655	[k__Bacteria, p__Proteobacteria, c__Alphaproteobacteria, o__Acetobacterales, f__Acetobacteraceae, g__Acetobacter, s__pasteurianus]	