Roseburia intestinalis L1-82
Roseburia inulinivorans DSM 16841
Shuttleworthia satelles DSM 14600
Lachnospiraceae bacterium 3 1 57FAA CT1
Butyrivibrio proteoclasticus B316
Lachnospiraceae bacterium 2 1 58FAA
Lachnospiraceae bacterium 5 1 57FAA
Dorea longicatena DSM 13814
Marvinbryantia formatexigens DSM 14469
Lachnospiraceae bacterium 6 1 63FAA
Lachnospiraceae bacterium 5 1 63FAA
Catonella morbi ATCC 51271
Clostridium lentocellum DSM 5427
Anaerostipes sp. 3 2 56FAA
Anaerostipes caccae DSM 14662
Lachnospiraceae bacterium 2 1 46FAA
Lachnospiraceae bacterium 4 1 37FAA
Lachnospiraceae bacterium 9 1 43BFAA
Lachnospiraceae bacterium 1 4 56FAA
Lachnospiraceae bacterium 3 1 46FAA
Lachnospiraceae bacterium 8 1 57FAA
Oribacterium sp. oral taxon 078 str. F0262
Oribacterium sp. oral taxon 108 str. F0425
Oribacterium sinus F0268
Butyrivibrio crossotus DSM 2876
Lachnospiraceae oral taxon 107 str. F0167
Lachnospiraceae bacterium 1 1 57FAA
Coprococcus comes ATCC 27758
Dorea formicigenerans ATCC 27755
Coprococcus eutactus ATCC 27759

Supplementary figure 3 - Maximum agreement forest between the 16S and shared gene cluster phylogenetic trees.
SPR operations were used to assess the congruence of phylogenetic trees based upon the 16S gene and the shared gene clusters of all analyzed genomes. The maximum agreement forest displays components that are in present in both trees. Branches are colored based upon listed habitat (yellow = oral; red = sediment; green = rumen; blue = human GI tract).