

*Oribacterium* sp. oral taxon 108 str. F0425

*Oribacterium* sinus F0268

*Oribacterium* sp. oral taxon 078 str. F0262

*Lachnospiraceae* 9 1 43BFAA  
*Lachnospiraceae* bacterium 4 1 37FAA

*Lachnospiraceae* bacterium 3 1 46FAA  
*Lachnospiraceae* bacterium 1 1 57FAA  
*Lachnospiraceae* bacterium 8 1 57FAA

*Roseburia inulinivorans* DSM 16841  
*Roseburia intestinalis* L1-82

*Lachnospiraceae* bacterium 5 1 57FAA  
*Dorea formicifenerans* ATCC 27755  
*Dorea longicatena* DSM 13814

*Clostridium lentoceullum*  
DSM 5427    *Coprococcus comes*  
ATCC 27758

Anaerostipes sp. 3 2 56FAA    Anaerostipes caccae DSM 14662

*Lachnospiraceae* bacterium 6 1 63FAA  
*Butyrivibrio crossotus* DSM 2876  
*Coprococcus eutactus* ATCC 27759  
*Lachnospiraceae* bacterium 3 1 57FAA CT1  
*Lachnospiraceae* bacterium 2 1 46FAA  
*Lachnospiraceae* bacterium 1 4 56FAA  
*Catonella morbi* ATCC 51271  
*Lachnospiraceae* oral taxon 107 str. F0167  
*Shuttleworthia satelles* DSM 14600  
*Marvinbryantia formaticigens* DSM 14469  
*Butyrivibrio proteoclasticus* B316

**Supplementary figure 4- Phylogenetic network of shared gene clusters based upon individual gene tree topologies.**

The gene trees of 91 family-wide shared gene clusters were input to SplitsTree4 to construct an unrooted phylogenetic network that best represented all the individual relationships. Most gene trees were found to disagree, resulting in a star-like topology. Branch coloring is based upon listed habitat (yellow = oral; red = sediment; green = rumen; blue = human GI tract).