

Supplementary Data

16S rRNA gene sequence amplified by in-house bacterial species specific primers listed in Table 2

- *R. gnavus* PCR amplicon sequence:

GGACTGCATTTGGAAGTGTCTAGGCTAGAGTGTCTGGAGAGGAAAGCGGAATTCCTA
GTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCTT
TCTGGACGATGACTGACGTT

100% identity to *R. gnavus*, closest identity to *Clostridium hylemonae* (96%)

- *R. torques* PCR amplicon sequence

GCTTAGATTCTTCGGATGAAGAGGATTGTGACTGAGCGGCGGACGGGTGAGTAAC
GCGTGGGTAACTGCCTCATACAGGGGGATAACAGTTAGAAATGACTGCTAATAC
CGCATAAGACCACAGCACCGCATGGTGCAGGGGGTAAAACT

100% identity to *R. torques*, closest identity to *Clostridium glycyrrhizinilyticum* (94%)

- *Ba. vulgatus* PCR amplicon sequence

CGTAAGCCGCAAGGCATCTGTGAAGGTGCTGCATGGTTGTCGTCAGCTCGTGCCG
TGAGGTGTCGGCTTAAGTGCCATAACGAGCGCAACCCTTGTTGTCAGTTACTAACA
GGTTATGCTGAGGACTCTGACAAGACT

100% identity to *Ba. vulgatus*, closest identity to *Bacteroides coprocola* (95%)