**Supplementary Table 1**: Primers and probes used for the quantitative PCR

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| --- | --- | --- | --- |
| **Bacteria** | **Forward Primer** | **Reverse Primer** | **Probe Sequence** |
| *B. adolescentis* LMG 10502 | TGCTCCAGTTGGATGCATGT  \*nt 150-169 | GCGACCCCATCCCATACC  nt 207-190 | CTTCTGGGAAAGATTC  nt 171-186 |
| *F. prausnitzii*  A2-165 | CCCGGCATCGGGTAGAG  nt 161-177 | GGACGCGAGGCCATCTC  nt 215-199 | AAAAGGAGCAATCCGCT  nt 180-196 |
| *R. gnavus* CCUG 52279 | TGGCGGCGTGCTTAACA  nt 20-36 | TCCGAAGAAATCCGTCAAGGT  nt 56-76 | ATGCAAGTCGAGCGAAG  nt 38-54 |

\*nt= nucleotide; sequences are presented from 5’ to 3’and their position in the corresponding 16S rRNA gene is given

**Supplementary Table 2**: Sequence similarity results of the BLAST identifications per band-class

|  |  |
| --- | --- |
| Band-class 8.55 | 100% match with *Coprococcus comes*  100% match with *Clostridium nexile*  100% match with *Ruminococcus torques* *\** |
| Band-class 9.58 | 100% match with *F. prausnitzii* |
| Band-class 10.79 | 100% match with unknown species of *Clostridium* cluster XIVa |
| Band-class 11.00 | 100% match with *R. gnavus* |
| Band-class 11.35 | 100% match with different members of the *Escherichia coli-Shigella* group |
| Band-class 11.51 | 98% match with *F. prausnitzii* |
| Band-class 14.63 | 100% match with *D. invisus* |
| Band-class 16.24 | 100% match with *B. adolescentis* |
| Band-class 16.89 | 100% match with *C. aerofaciens* |

\*reference sequences of phylogenetic neighbor species (up to 90% similarity) were included for clustering analysis using multiple sequence alignment and the average linking method to confirm allocation of the purified band sequences to the most probable species: in this case: *Ruminococcus torques*