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

|  |  |  |  |
| --- | --- | --- | --- |
| **Bacteria** | **Forward Primer** | **Reverse Primer** | **Probe Sequence** |
| *B. adolescentis* LMG 10502 | TGCTCCAGTTGGATGCATGT\*nt 150-169 | GCGACCCCATCCCATACCnt 207-190 | CTTCTGGGAAAGATTCnt 171-186 |
| *F. prausnitzii* A2-165 | CCCGGCATCGGGTAGAGnt 161-177            | GGACGCGAGGCCATCTCnt 215-199 | AAAAGGAGCAATCCGCTnt 180-196            |
| *R. gnavus* CCUG 52279 | TGGCGGCGTGCTTAACAnt 20-36 | TCCGAAGAAATCCGTCAAGGTnt 56-76 | ATGCAAGTCGAGCGAAGnt 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*