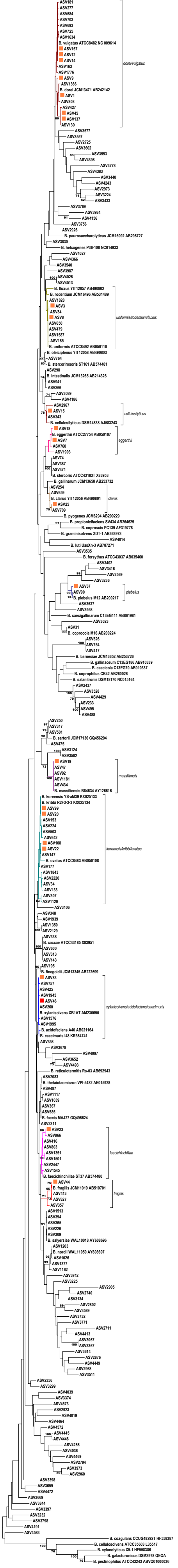

Additional file 4: Figure S2. A tree showing the inferred relationship between the 225 ASVs classified in the genus *Bacteroides* and the 16S rRNA genes sequences from the type strain for each of the recognised species in the genus *Bacteroides*. Phylogeny Groups of related taxa shown and named according to the species of the type strain sequence included in the group, Phylogeny Group names are shown in italics. Those ASVs with relative abundance greater than 0.5% are indicated by an orange box next to the taxon label. The evolutionary history was inferred using the Minimum Evolution method [1]. The optimal tree with the sum of branch length = 4.96440154 is shown. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (100 replicates, only branches present in >70 are replicates) are shown next to the branches [2]. The tree is drawn to scale, with branch lengths in the same units as those of the evolutionary distances used to infer the phylogenetic tree. The evolutionary distances were computed using the Maximum Composite Likelihood method [3] and are in the units of the number of base substitutions per site. The ME tree was searched using the Close-Neighbor-Interchange (CNI) algorithm [4] at a search level of 1. The Neighbor-joining algorithm [5] was used to generate the initial tree. The analysis involved 268 nucleotide sequences. All positions containing gaps and missing data were eliminated. There were a total of 388 positions in the final dataset. Evolutionary analyses were conducted in MEGA7 [6].

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