



**Supplementary Fig. S1.** Neighbour-joining tree based on 16S rRNA gene sequences available from the databases (accession numbers in parentheses). Bootstrap values based on 1000 replications are given as percentages at branching points. The tree was calculated using *Flexibacter flexilis* ATCC 23079<sup>T</sup> as an outgroup. Bar, 0.02 substitutions per nucleotide position.