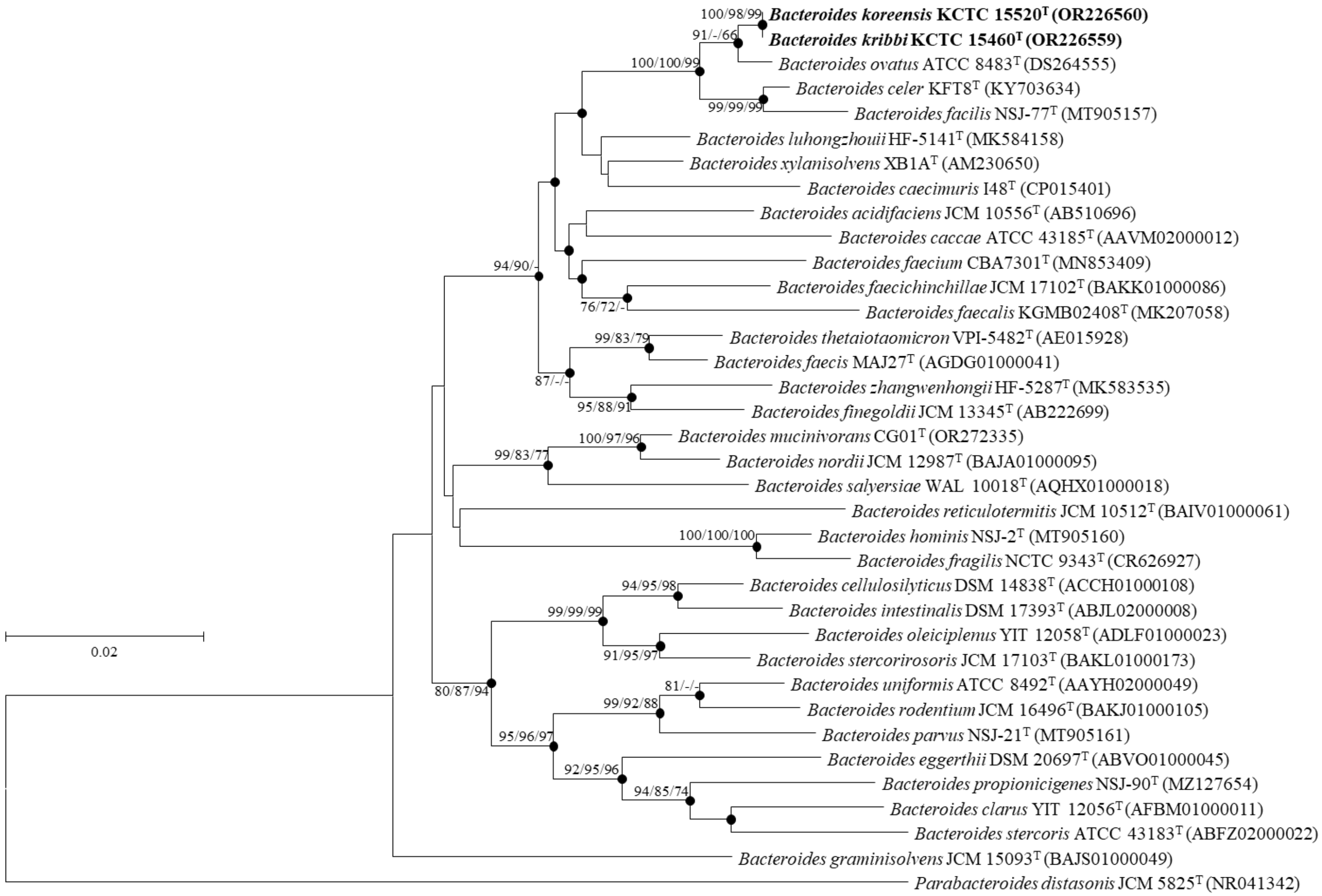

Fig. S1. Phylogenetic tree was constructed based on 16S rRNA gene sequences using NJ algorithms with the addition of *B. koreensis* KCTC 15520^{T} and *B. kribbi* KCTC 15460^{T}. Bootstrap values over 70% based on NJ/ML/MP algorithms are shown at nodes as a percentage of 1,000 replicates. Filled circles represent branches consistently recovered in all three algorithms. Scale bar indicates 0.02 substitutions per nucleotide.