

Additional file 1

Results of the database search using the 16S rRNA gene sequence read.

The nucleotide sequence was compared against the NCBI Bacteria & Archaea Isolate Database, with the statistical significance calculated by BLAST. The closest known bacteria are listed in the table with query cover rates, sequence identity rates and BLAST scores. BLAST: Basic Local Alignment Search Tool; NCBI: National Center for Biotechnology Information

