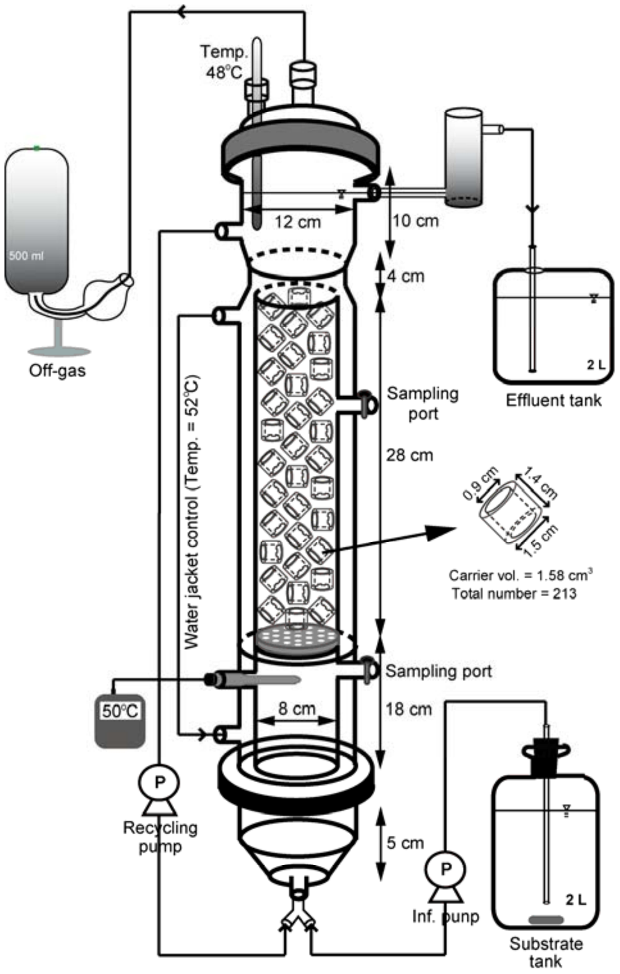

Supplementary Figure. S1

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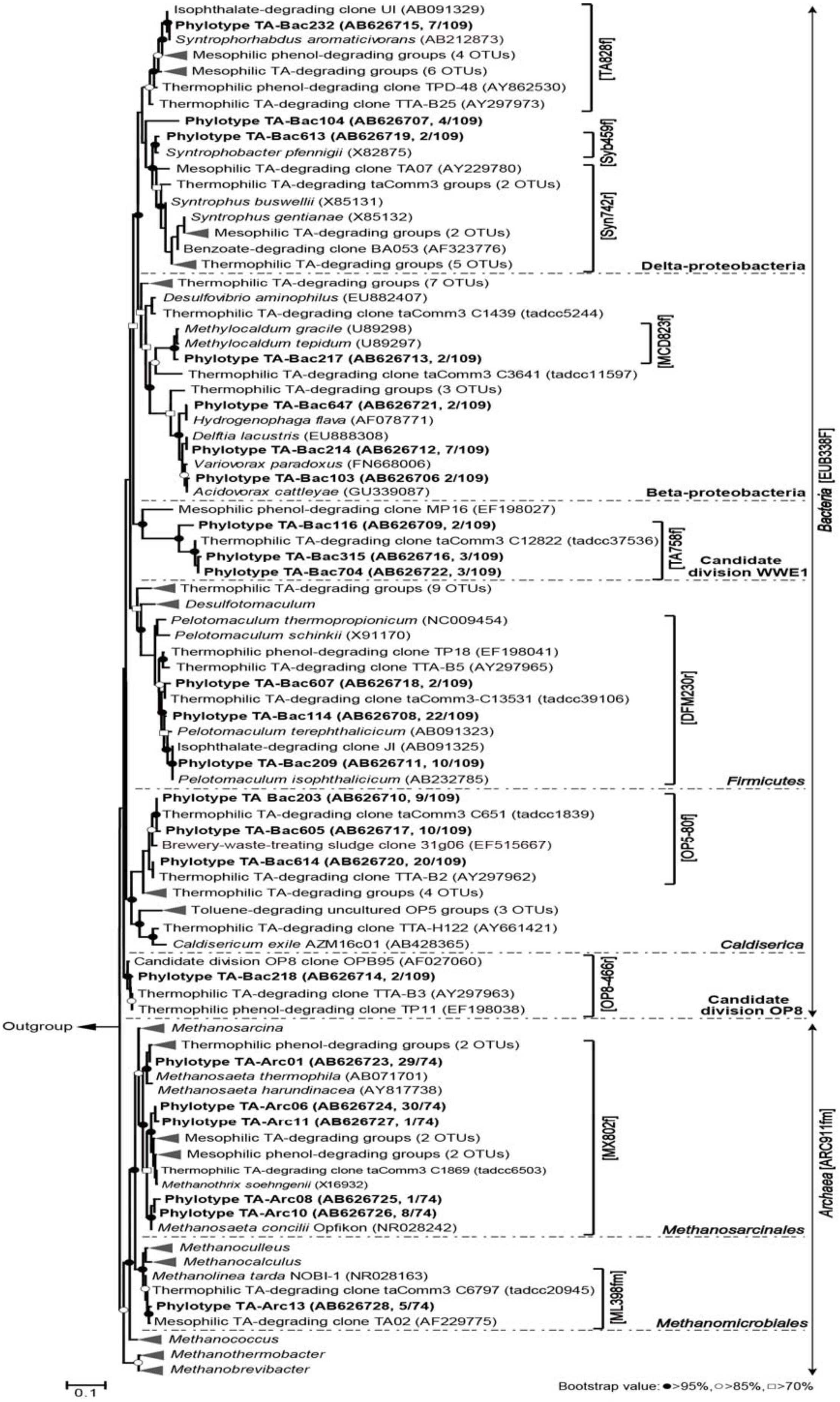

Supplementary Figure. S2

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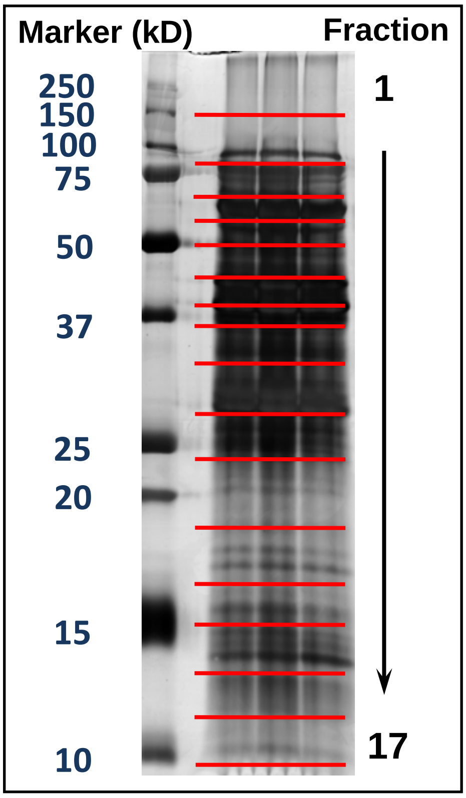

Supplementary Figure. S3

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Legends for Supplementary Figures

Figure. S1. The schematic configuration of laboratory-scale anaerobic fixed-film bioreactor fed with synthetic medium that contained terephthalate as the sole substrate at 50^{o}C.

Figure. S2. Phylogenetic tree of the 16S rRNA gene sequences of *Bacteria* and *Archaea* members in the anaerobic terephthalate-degrading biofilm under 50^{o}C conditions. Total community DNA subjected to the microbial community analysis was obtained from biofilms sampled at Day 99. The tree was reconstructed based on the neighour-joining method with 1000-time bootstrapping and rooted with *Voromonas pontica* (AF280076). Bootstrap values that were greater than 70% were shown at branch nodes. The scale bar corresponds to 10 nucleotide substitutions per 100 nucleotide positions. The accession numbers and abundances of cloned phylotypes (in bold) in the clone libraries were indicated in parentheses. The 16S rRNA sequences of the close relatives in the tree were retrieved from NCBI and IMG/M. The inference of taxonomic phyla for the phylotypes and the names of primers (i.e., specificity) in brackets were showed on the right of the tree. The 16S rRNA gene sequences obtained in the study were deposited in GenBank under the accession number of AB626706-AB626728.

Figure. S3. Electrophoregram of sodium dodecyl sulfate polyacrylamide gel electrophoresis on total proteins recovered from syntrophic terephthalate-degrading biofilm at Day 464. Lane 1 represented the distribution of marker proteins with different sizes (10-250 kD), and lane 2-4 showed the electrophoresis of triplicate samples. The numbers (1-17) on the right indicted the sections cut for the nanoLC MS/MS analysis.