

Figure S6. Phylogeny analysis of 16S rRNA clones from the UW ETBE-enrichment subculture S1. The Neighbor-Joining tree was constructed based on phylogenetic distances calculated with Kimura-2 parameter (1126 nucleotide positions included in the analysis) inferred from 74 clone sequences and chosen bacterial strains (high-quality sequences downloaded from RDP). The tree was bootstrapped over 1 000 replicates and the bootstrap values are indicated next to the branches.

