

Figure S7. Phylogeny analysis of 16S rRNA clones from the PW ETBE-enrichment subculture S3. The Neighbor-Joining tree was constructed based on phylogenetic distances calculated with Kimura-2 parameter (1193 nucleotide positions included in the analysis) inferred from 66 clone sequences and chosen 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.

