Supplementary data Fig. S1. Maximum-likelihood (ML) phylogenetic tree calculated in ARB with major OTUs in Figure 2 based on 493 position of the 16S rRNA from Methanosaeta concilli (Acc. No. X51423) as an outgroup. A Neibor-joining (NJ) tree was also constructed (not shown). Sequences from this study are in bold. Bootstrap values for ≥ 60 replicate trees are indicated at the nodes.