



Fig. S1. Maximum likelihood phylogenetic tree of SSU rRNA gene including *C. subterraneum* and environmental sequences in crenarchaeal lineages using 1020 identical nucleotide positions. Bacterial sequences were used as out-group. Numbers indicate bootstrap values from 100 replications. Accession numbers of GenBank/EMBL/DDBJ were given in parentheses. Bar, 1 substitution per 10 nucleotides.