Fig. S1 Phylogenetic tree of the *Euryarchaeota*-related 16S rRNA gene sequences from Skan Bay. The tree was constructed by neighbor-joining analysis. The numbers at the branch nodes are bootstrap percentage values based on 1000 iterations and are shown for branches with more than 50% bootstrap support. Sequences from cultivated isolates are in italics, sequences from environmental gene clones are in plain font, and sequences from this study are in bold. GenBank accession numbers are in parentheses. The scale bar represents the number of fixed mutations per nucleotide position.
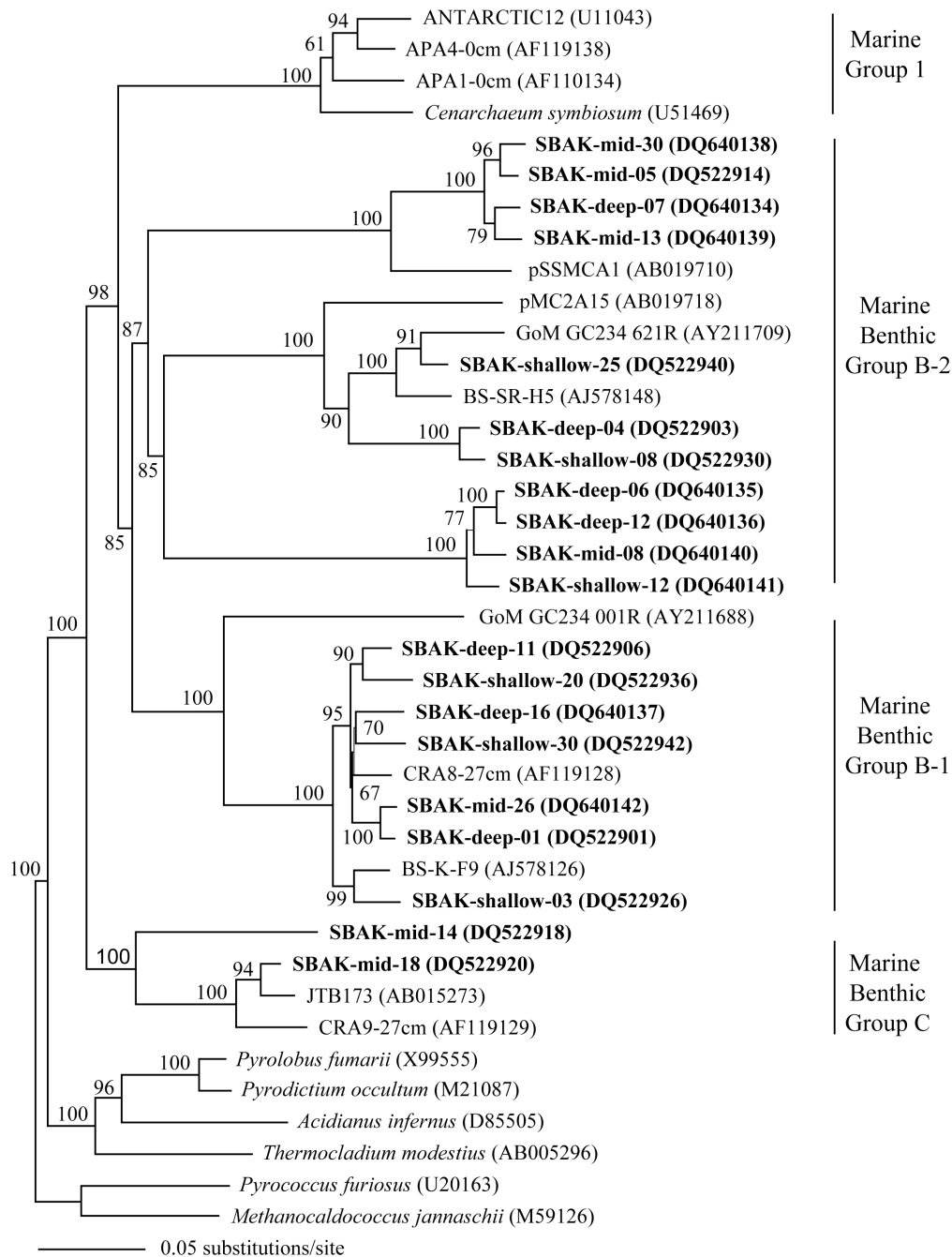
Fig. S2 Phylogenetic tree of the *Crenarchaeota*-related 16S rRNA gene sequences from Skan Bay. The tree was constructed by neighbor-joining analysis. The numbers at the branch nodes are bootstrap percentage values based on 1000 iterations and are shown for branches with more than 50% bootstrap support. Sequences from cultivated isolates are in italics, sequences from environmental gene clones are in plain font, and sequences from this study are in bold. GenBank accession numbers are in parentheses. The scale bar represents the number of fixed mutations per nucleotide position.
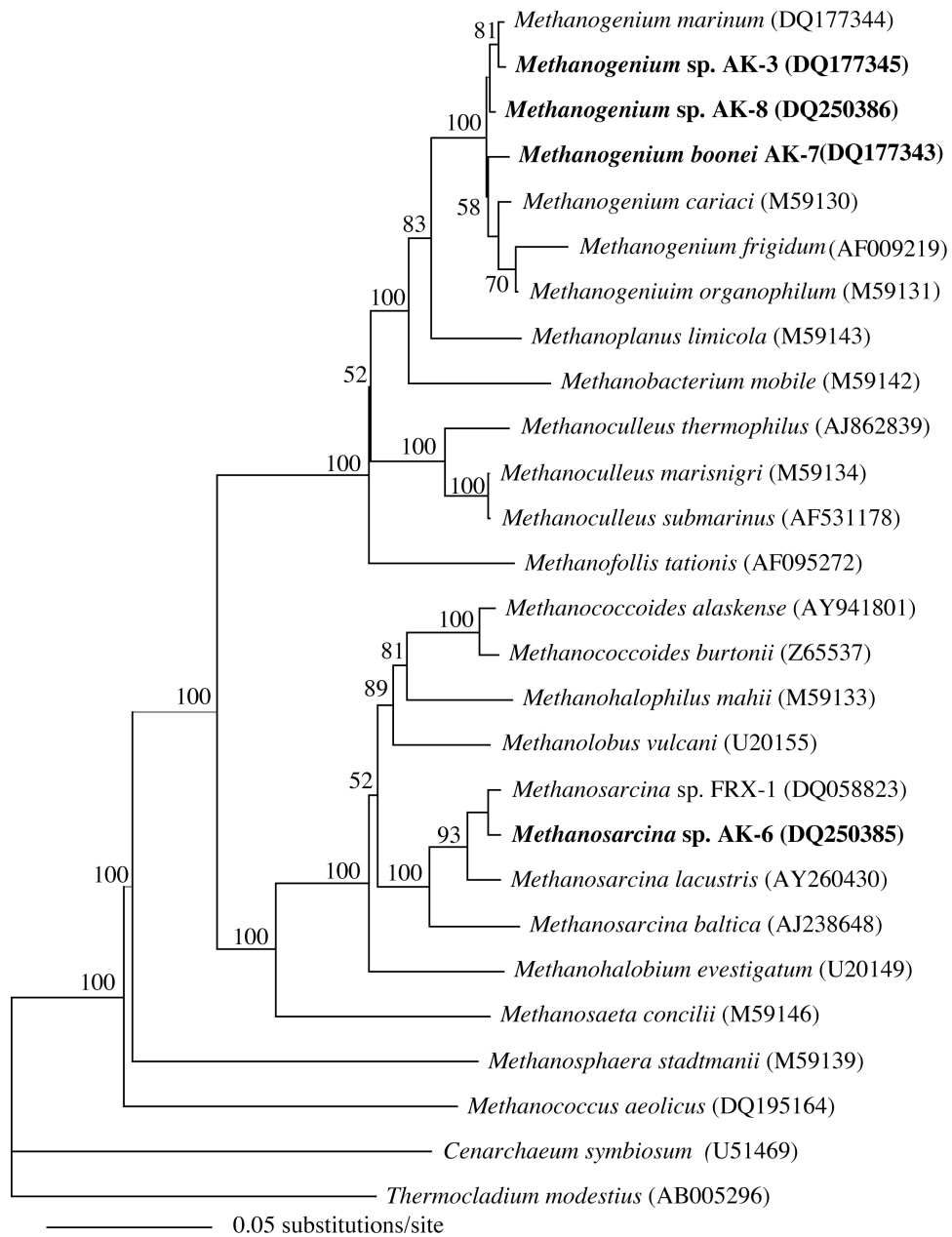
Fig. S3 Phylogenetic tree showing the affiliations of 16S rRNA gene sequences of the strains AK-7, AK-3, AK-8, AK-6. The tree was constructed by using maximum-likelihood analysis. The numbers at the branch nodes are bootstrap values based on 1000 iterations and are shown for branches with more than 50% bootstrap support. The scale bar represents the number of fixed mutations per nucleotide position. GenBank accession numbers are in parentheses.
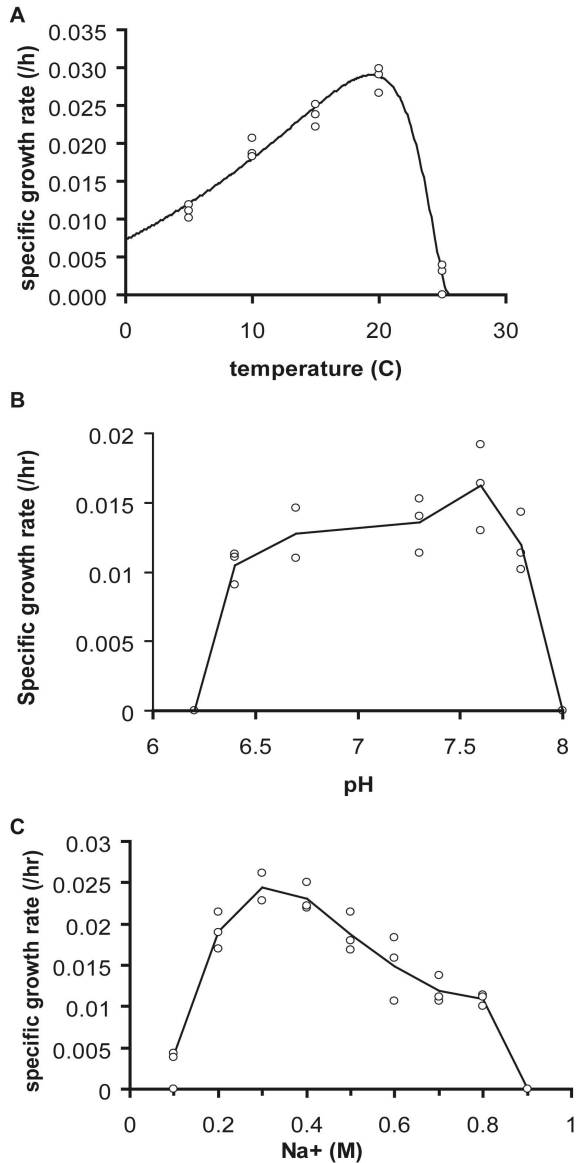
Fig. S4. Effect of environmental factors on the growth of strain AK-7. (A) Specific growth rate at various temperatures. Data points (circles) were fitted with the square-root equation (solid curve). The square-root equation describes bacterial growth throughout the entire temperature range and can be used to extrapolate a T_{min} value where the growth rate is equal to zero [1]. (B) Specific growth rate at various pH values. (C) Specific growth rate in media with various salinities.

[1] Ratkowsky, D. A., R. K. Lowry, T. A. McMeekin, A. N. Stokes, and R. E. Chandler. 1983. Model for bacterial culture growth rate throughout the entire biokinetic temperature range. J. Bacteriol. 154:1222-1226
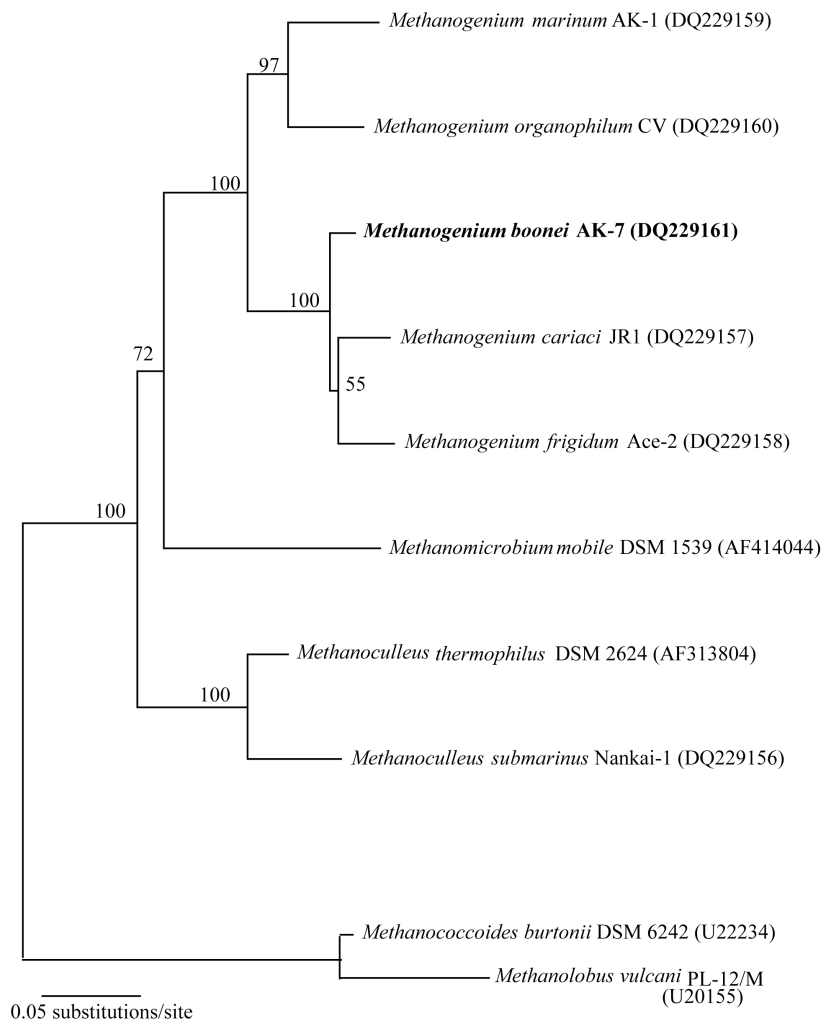
Fig. S5. Phylogenetic tree showing the affiliations of *mcr*A gene sequences between strain AK-7 and members of the genus *Methanogenium* and the family *Methanomicrobiaceae*. The tree was constructed by using maximum-likelihood analysis in combination with filters excluding highly variable positions. The numbers at the branch nodes are bootstrap values based on 1000 iterations. The scale bar represents the number of fixed mutations per nucleotide position.