

The following supplement accompanies the article

Response of an archaeal community from anoxic coastal marine sediments to experimental petroleum contamination

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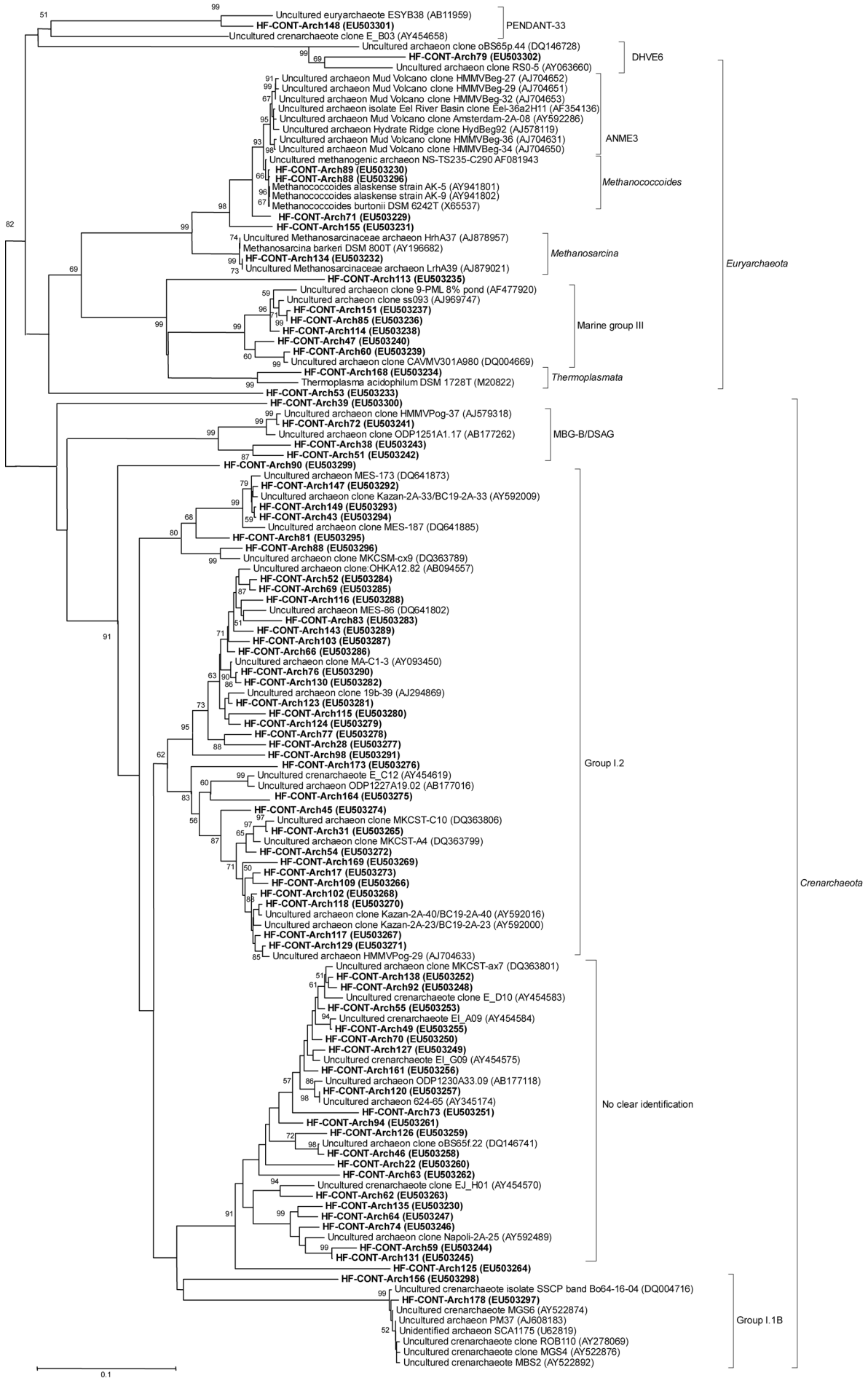
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Aquatic Microbial Ecology 59:25–31 (2010)

Supplement 1. Phylogenetic trees showing affiliation of CONT (control sediment, Fig. S1) and OIL (Oiled sediment, Fig. S2) clones to closest related sequences

Fig. S1. (Following page.) Phylogenetic tree calculated by neighbor joining showing affiliation of CONT clones to closest related sequences from either cultivated or cloned members of different archaeal groups. Representative clones of different phylotypes obtained by RFLP analysis are indicated in **bold**. Comparisons were made using 568 positions. Percentages of 1000 bootstrap resamplings that support the branching orders are shown above or near the relevant nodes (only values >50% are shown). Scale bar indicates 10% estimated sequence divergence. DHVE6: deep sea hydrothermal vent *Euryarchaeota* cluster 6; ANME3: anaerobic methane oxidizing *Archaea* cluster 3; MBG-B/ DSAG: marine benthic group B/deep sea archaeal group



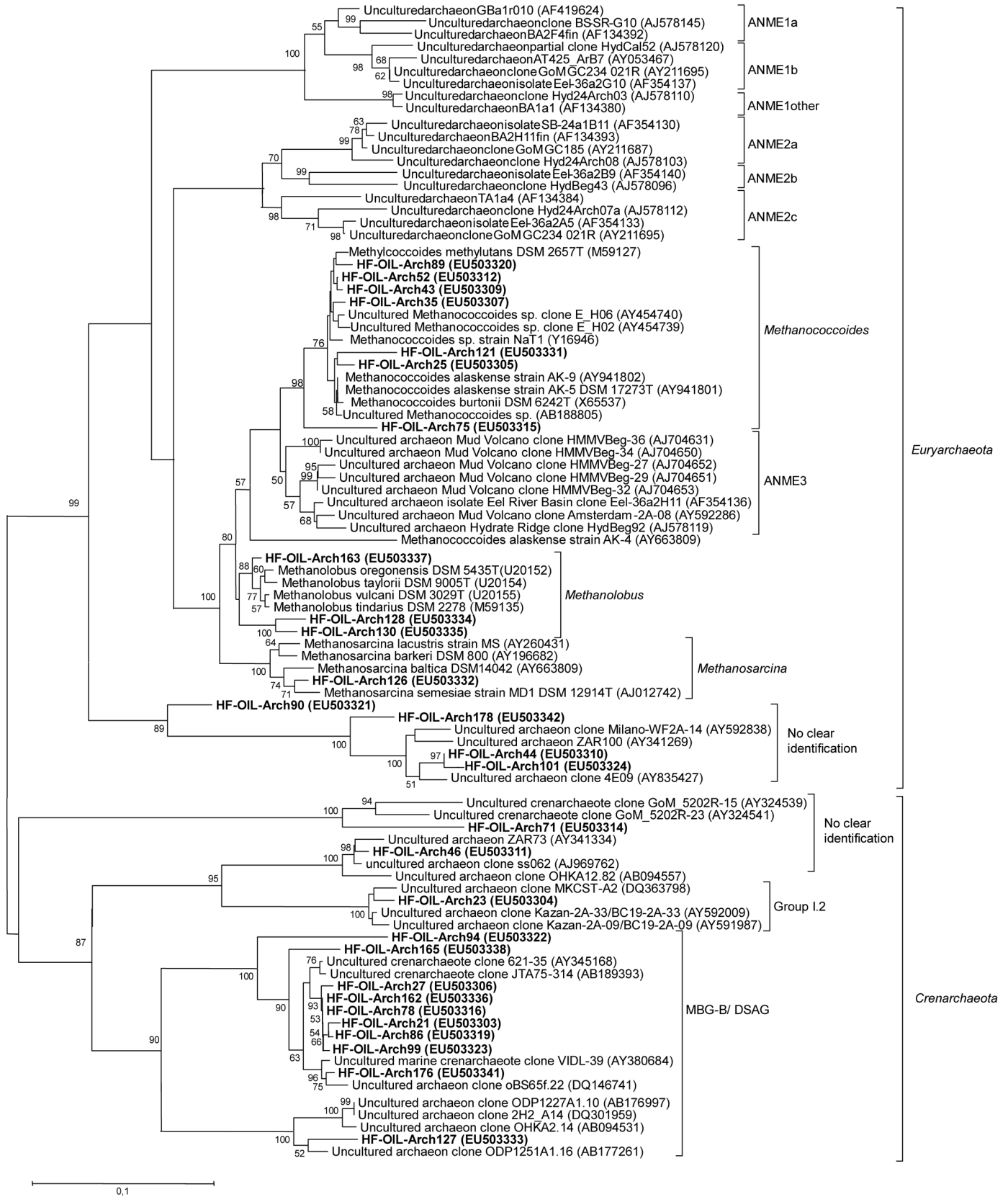


Fig. S2. Phylogenetic tree calculated by neighbor joining showing affiliation of OIL clones to closest related sequences from either cultivated or cloned members of different archaeal groups. Representative clones of different phylotypes obtained by RFLP analysis are indicated in **bold**. Comparisons were made using 524 positions. Percentages of 1000 bootstrap resamplings that support the branching orders are shown above or near the relevant nodes (only values >50% are shown). Scale bar indicates 10% estimated sequence divergence. ANME3: anaerobic methane oxidizing *Archaea* cluster 3; MBG-B/ DSAG: marine benthic group B/deep sea archaeal group