



Supplementary Figure S2. Phylogenetic trees of bacterial 16S crDNA sequences obtained from the MUC8 and Dive 203 PC8 sediment cores. Clones noted in red represent sequences obtained in this study. The tree was constructed based on a subset of ~600 bp sequences using the neighbor-joining method. Only one representative of each sequence group with >97% identity is shown. Bootstrap values are expressed as percentages determined from 1,000 trials; the values at the nodes are the values that were greater than 50%. Scale bar represents 10% estimated sequence divergence.