Supplementary Figure 1. Phylogenetic tree showing relationships of DSA OTU and ESA OTU phylotypes from South Chamorro Seamount showing lineages within the *Lokiarchaeota* (formerly Marine Benthic Group B), *Thaumarchaeota* (formerly Marine Group I), and *Crenarchaeota* as determined by maximum likelihood analysis of aligned SSU rDNA sequences. Numbers at nodes represent bootstrap values based on 500 bootstrap resamplings. The outgroup is represented by bacterium *Aquifex pyrophilus*. The scale bar represents 0.10 fixed mutations per nucleotide position. Bootstrap values are shown for frequencies at or above a threshold of 50% (adapted from Curtis *et al.*, 2013, reference [14] in main text).

