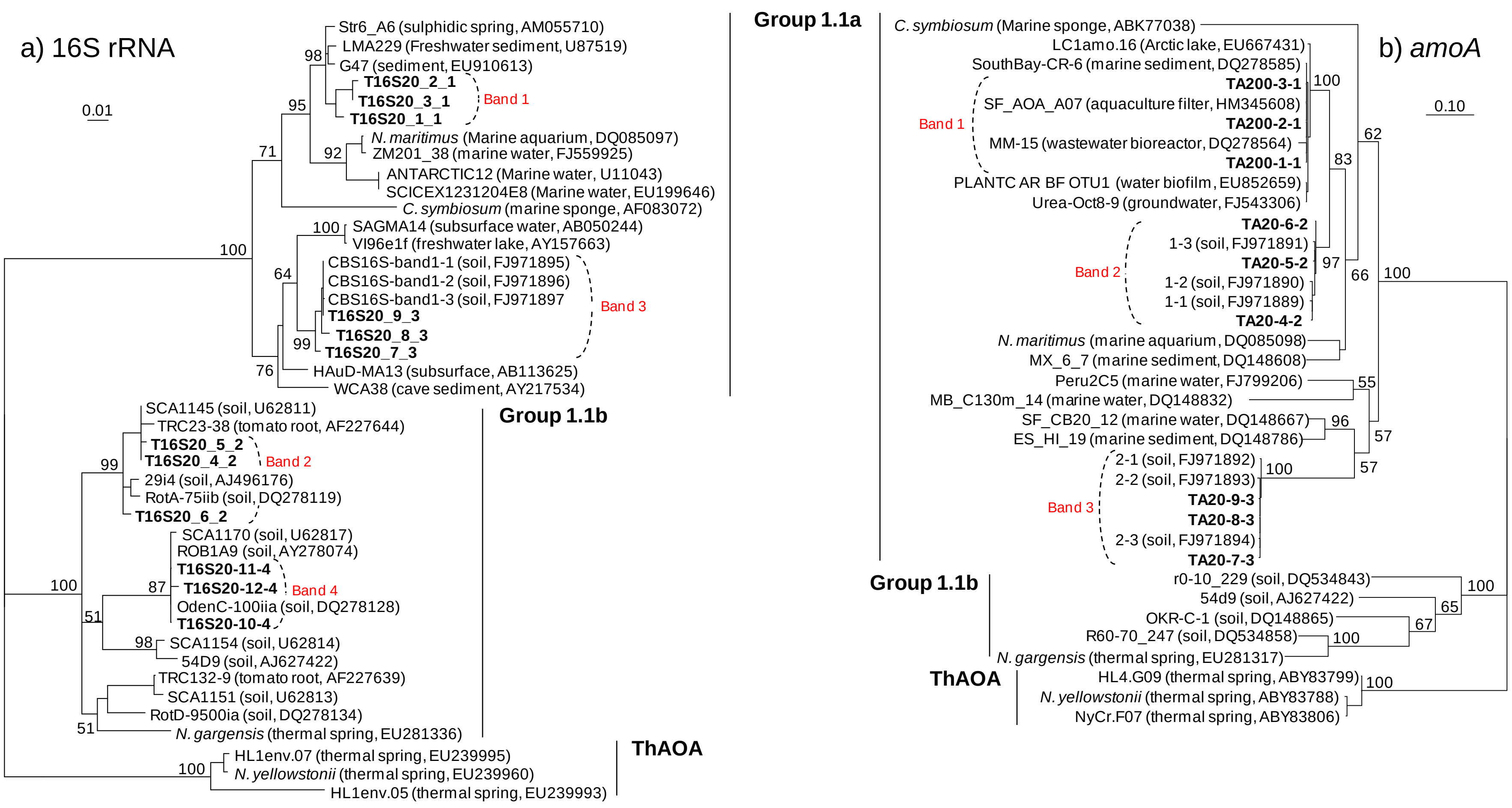

Supplementary Figure 2. Phylogenetic analysis of cloned PCR products of thaumarchaeal genes amplified from soil microcosms incubated for 28 days (Figure 2). Distance trees were calculated using unambiguously aligned nucleotide positions and ML-estimated variable sites only. Values at major nodes represent the most conservative value from bootstrap support of separate ML, parsimony and distance trees (100, 1000 and 1000 replicates respectively). (a) Thaumarchaeal 16S rRNA genes were amplified from pooled PCR products from triplicate microcosms from 20 µg NH_4^+-N g^{-1} microcosms (T16S20) highlighted in Figure 2d. (b) Thaumarchaeal *amoA* genes were amplified from pooled PCR products from either 20 or 200 µg NH_4^+-N g^{-1} microcosms (TA20 and TA200 repectively) highlighted in Figure 2f.