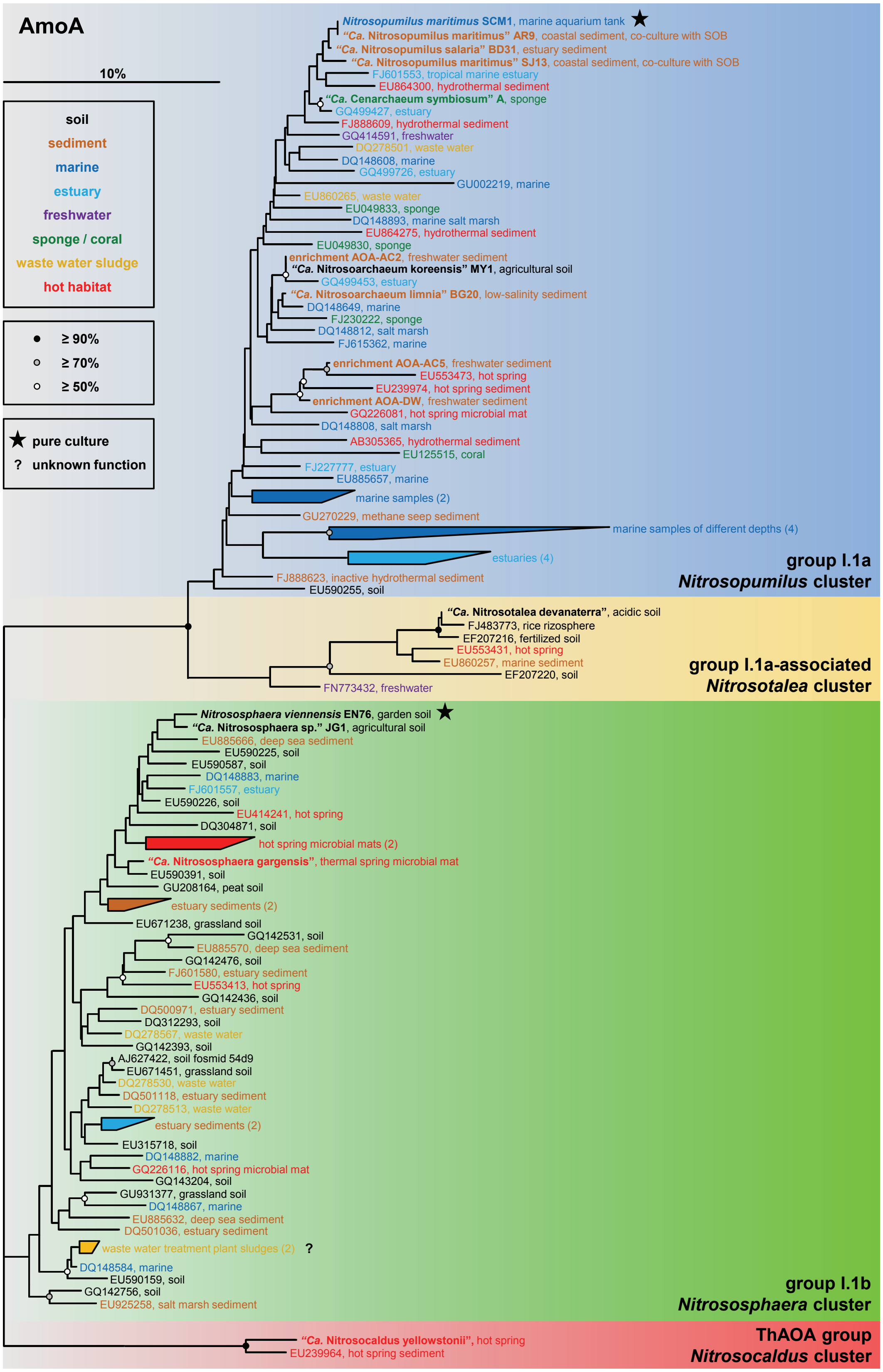
FIGURE S1



Phylogenetic analysis of a representative selection of archaeal ammonia monooxygenase subunit A (AmoA)-like sequences demonstrating the major lineages of *amo*-encoding archaea (AEA) and ammonia-oxidizing archaea (AOA). Note that sequence placement largely does not correlate with habitat type. Group names refer to the traditional names adopted from 16S rRNA phylogeny. Lineage names are derived from the genus name of the first cultured representative of each respective group (following ref. 103). Sequences are colored according to habitat type, and are given in bold if derived from a cultured organism. Asterisks mark AOA available in pure culture. The question-mark indicates sequences obtained from sludge in which *amoA*-encoding and expressing thaumarchaeotes were demonstrated to not engage in autotrophic ammonia oxidation under the tested conditions (92). Numbers in parentheses give the number of sequences within a sequence cluster. The scale bar represents 10% sequence divergence. The basic tree was generated via an evolutionary distance (Fitch) algorithm using an alignment of 198 aligned amino acids. Circles indicate parsimony bootstrap supports from 1,000 iterations. Support below 70 % should be considered unreliable. SOB, sulfur-oxidizing bacteria.