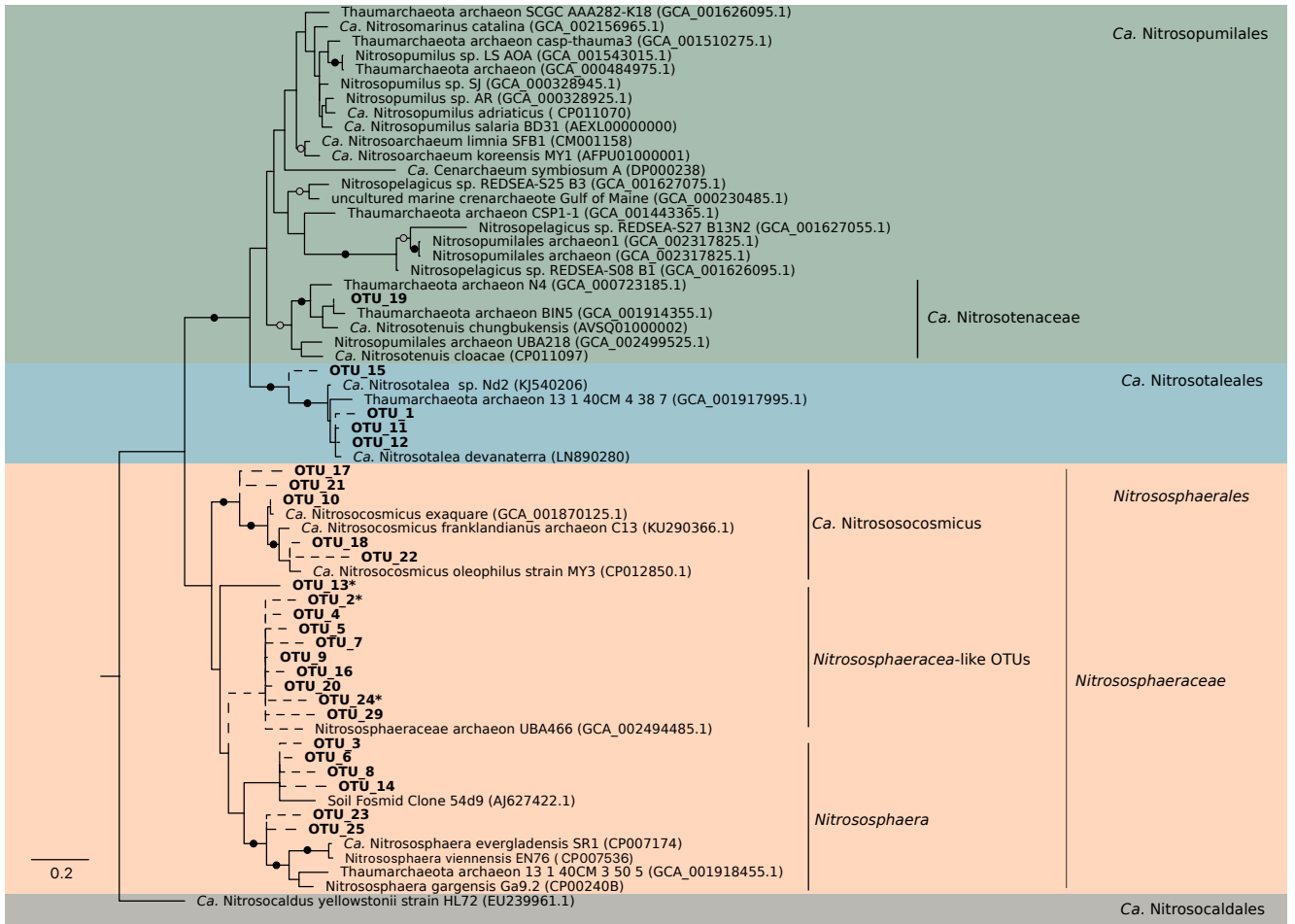
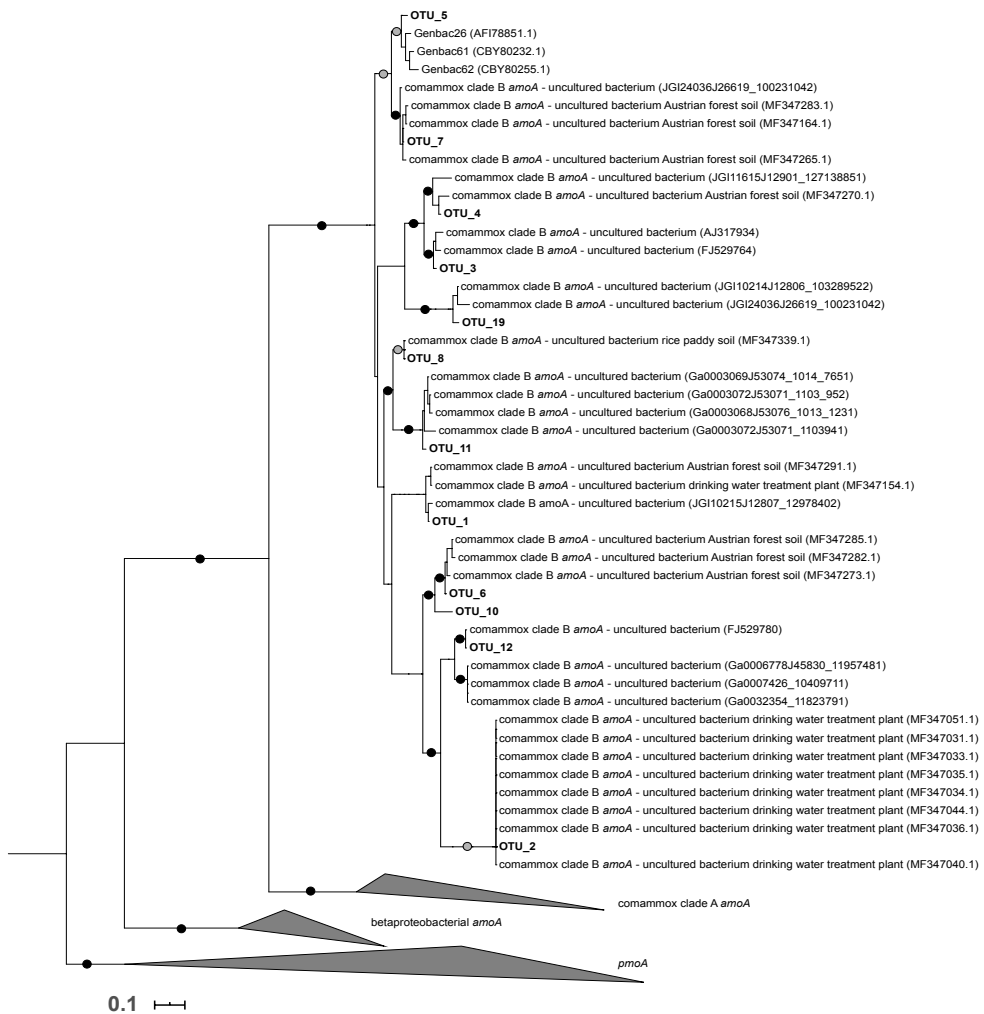


a.



b.



**Figure S2:** Rooted maximum likelihood phylogenetic tree of a) archaeal *amoA* and b) CMX *amoA* gene and transcript sequences. Inserted short reads are depicted in dashed lines and sequenced OTUs are shown in bold. Asterisks depict archaeal OTUs retrieved by sequencing, but not covered by the qPCR primer pair. The AOA maximum likelihood tree was constructed using RAxML v. 8.2.12 with 100 rapid bootstraps and GTRGAMMA model of nucleotide evolution and rooted on *Ca. Nitrosocaldus yellowstonni*. Query sequences were inserted using the EPA algorithm implemented in RAxML after manual inspection of the alignment. Black and grey circles depict support values above 95 and between 80-95 respectively. The CMX tree was constructed from an alignment of query and reference sequences using W-IQ-Tree with 1000 bootstrap iterations and ModelFinder to determine the best fitting base substitution model. The tree was rooted on particulate methane monooxygenase (*pmoA*) gene sequences. Sequence accession numbers are shown in parenthesis. For details regarding tree construction, see Material and Methods.