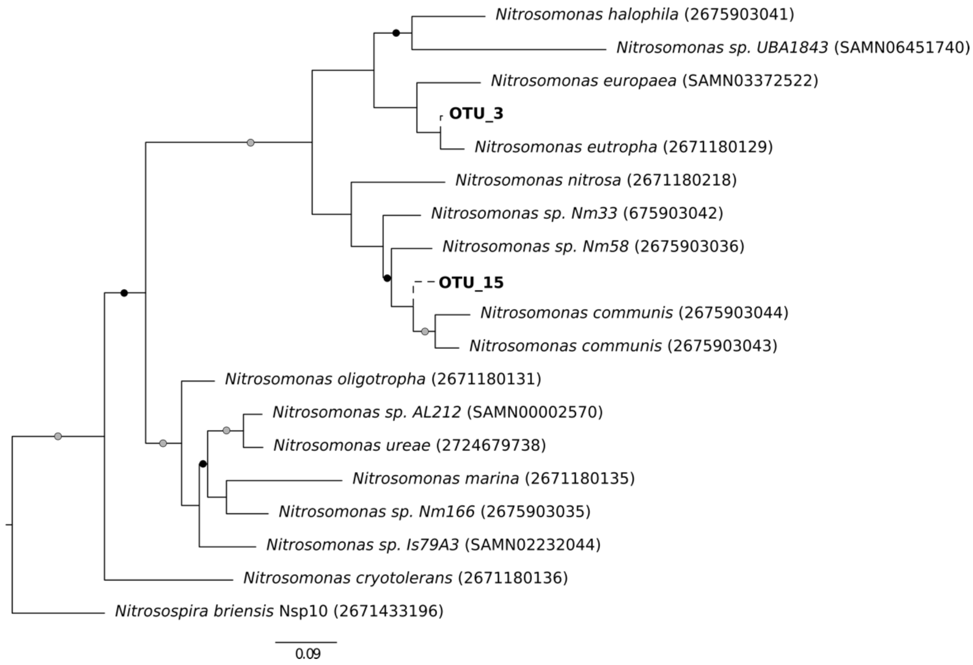
a.



b.

Query	Subject	Identity	E-value	Bitscore
OTU_1	D19_AOB-968-133;size=1352	100	0	828
OTU_2	D12_AOB-26-1125;size=21	100	0	828
OTU_4	D16_AOB-75-722;size=8	100	0	828
OTU_5	D8_AOB-80-2013;size=13	100	0	828
OTU_6	D16_AOB-7-539;size=54	100	0	828
OTU_9	D21_AOB-7-796;size=16	100	0	828
OTU_10	D12_AOB-910-11289;size=5	91.071	2.23^{-174}	606
OTU_11	D12_AOB-490-2083;size=3	95.759	0	723
OTU_12	D7_AOB-149-3286;size=12	98.214	0	784
OTU_14	D2_AOB-910-338;size=51	100	0	828
OTU_24	D9_Nitrosospira_sp._L115_(AY123817)	99.517	0	754
OTU_28	D12_AOB-49-12128;size=2	93.304	0	662
OTU_34	D8_AOB-7-83;size=257	99.33	0	808

Figure S3: Taxonomic classification of bacterial *amoA* OTUs from genera a) *Nitrosospira* and b) *Nitrosomonas*. *Nitrosospira amoA* OTUs were classified by blastn against a reference database. Maximum likelihood phylogenetic tree of *Nitrosomonas amoA* gene sequences were constructed using RAxML v. 8.2.12 with 100 rapid bootstraps and GTRGAMMA model of nucleotide evolution. Query sequences were inserted into the reference tree using the EPA algorithm implemented in RAxML after manual inspection of the alignment. Inserted short reads are depicted in dashed lines. The tree was rooted on *Nitrosospira briensis*. Black and grey circles depict support values above 95 and between 80-95 respectively. Sequence accession numbers are shown in parenthesis. For details regarding tree construction and OTU classification, see Material and Methods.