

b.

Subject	Identity	E-value	Bitscore
D19_AOB-968-133;size=1352	100	0	828
D12_AOB-26-1125;size=21	100	0	828
D16_AOB-75-722;size=8	100	0	828
D8_AOB-80-2013;size=13	100	0	828
D16_AOB-7-539;size=54	100	0	828
D21_AOB-7-796;size=16	100	0	828
D12_AOB-910-11289;size=5	91.071	2.23-174	606
D12_AOB-490-2083;size=3	95.759	0	723
D7_AOB-149-3286;size=12	98.214	0	784
D2_AOB-910-338;size=51	100	0	828
D9_Nitrosospira_spL115_(AY123817)	99.517	0	754
D12_AOB-49-12128;size=2	93.304	0	662
D8_AOB-7-83;size=257	99.33	0	808
	D19_AOB-968-133;size=1352 D12_AOB-26-1125;size=21 D16_AOB-75-722;size=8 D8_AOB-80-2013;size=13 D16_AOB-7-539;size=54 D21_AOB-7-796;size=16 D12_AOB-910-11289;size=5 D12_AOB-910-11289;size=3 D7_AOB-149-3286;size=12 D2_AOB-910-338;size=51 D9_Nitrosospira_spL115_(AY123817) D12_AOB-49-12128;size=2	D19_AOB-968-133;size=1352 100   D12_AOB-26-1125;size=21 100   D16_AOB-75-722;size=8 100   D8_AOB-80-2013;size=13 100   D16_AOB-7-539;size=54 100   D21_AOB-7-796;size=16 100   D12_AOB-910-11289;size=5 91.071   D12_AOB-910-11289;size=3 95.759   D7_AOB-149-3286;size=12 98.214   D2_AOB-910-338;size=51 100   D9_Nitrosospira_spL115_(AY123817) 99.517   D12_AOB-49-12128;size=2 93.304	D19_AOB-968-133;size=1352 100 0   D12_AOB-26-1125;size=21 100 0   D16_AOB-75-722;size=8 100 0   D8_AOB-80-2013;size=13 100 0   D16_AOB-7-539;size=54 100 0   D11_AOB-7-796;size=16 100 0   D12_AOB-910-11289;size=5 91.071 2.23 <sup>-174</sup> D12_AOB-490-2083;size=3 95.759 0   D7_AOB-149-3286;size=12 98.214 0   D2_AOB-910-338;size=51 100 0   D9_Nitrosospira_spL115_(AY123817) 99.517 0   D12_AOB-49-12128;size=2 93.304 0

**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.