



Figure S4. Maximum likelihood phylogenetic tree of *nxB* sequences (NOB) 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 and sequenced OTUs are shown in bold. The tree was rooted on the anammox bacterium *Kuenenia stuttgartiensis*. Black and grey circles depict support values above 95 and between 80-95 respectively. Sequence accession numbers are shown in parenthesis