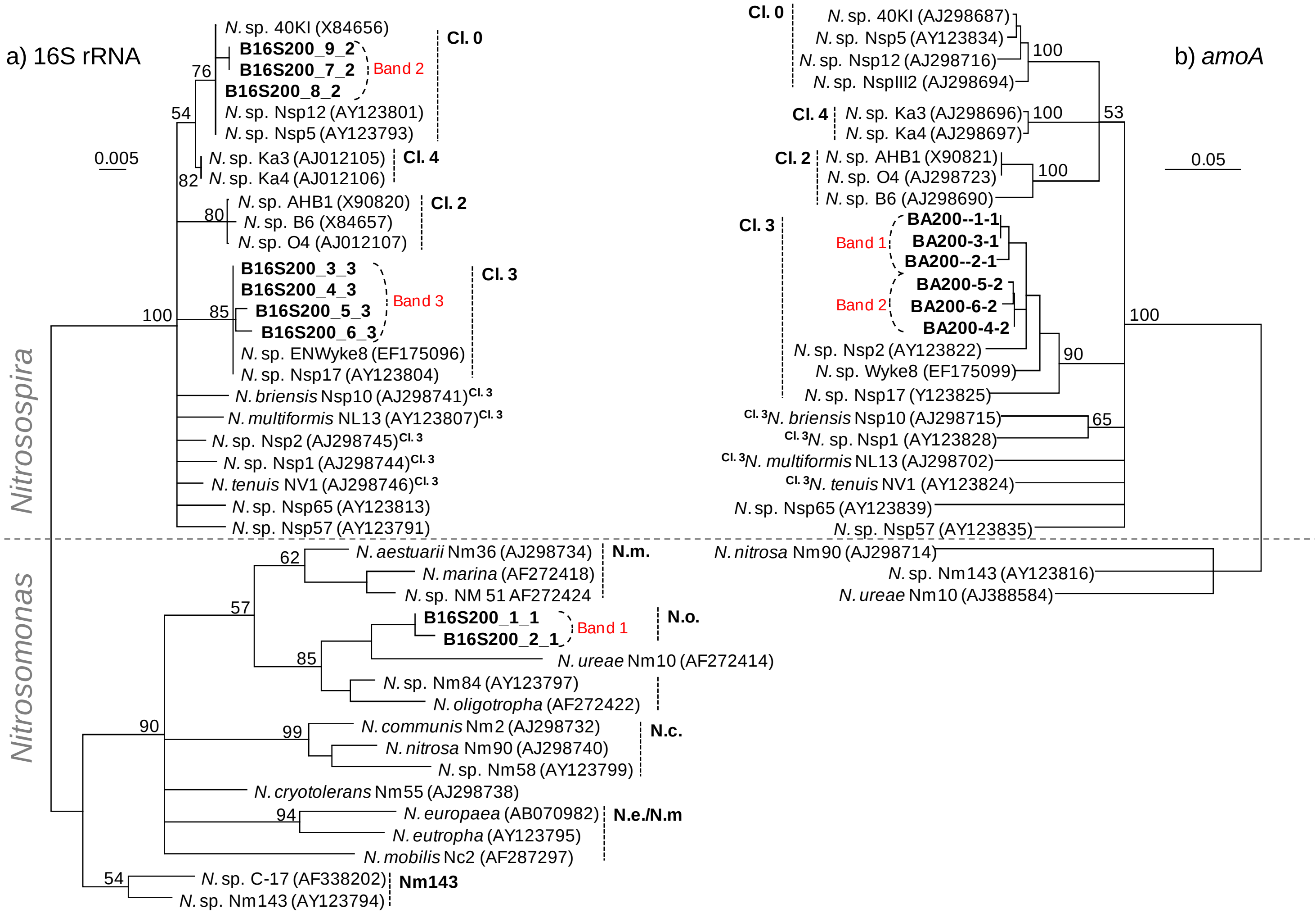

Supplementary Figure 3. Phylogenetic analysis of cloned PCR products from pooled amplicons of AOB 16S rRNA (a) and amoA (b) genes amplified from soil samples incubated for 28 days with 200 µg NH_4^+-N g^{-1} profiled in Figure 2e and 2g respectively. Distance trees were calculated using unambiguously aligned nucleotide positions and ML-estimated variable sites only. Values at nodes represent the most conservative value from bootstrap support of separate ML, parsimony and distance trees (100, 1000 and 1000 replicates respectively). Cluster designations follow that of Purkhold *et al.* (2003) with lineage abbreviations as follows: N.m. – *Nitrosomonas marina,* N.o. – *Nitrosomonas oligotropha*, N.c. - *Nitrosomonas communis*, N.e./N.m. – *Nitrosomonas europaea/Nitrosococcus mobilis*.

Reference Purkhold *et al.* (2003) International Journal of Systematic and Evolutionary Microbiology (2003), 53, 1485–1494.