

Figure S1: Denitrification and effect of acetylene and supplemental nitrate (1) or nitrite (2) on the production and consumption of N_2O in anoxic microcosms with palsa peat soil. Squares and circles represent 0 to 20 cm and below 20 cm palsa peat soil, respectively. Closed symbols represent microcosms with acetylene, open symbols represent without acetylene. Supplied concentrations of nitrate/nitrite were 0 μM (A), 10 μM (B), 20 μM (C), 50 μM (D), 100 μM (E), 500 μM (F), and 1000 μM (G). Mean values and standard errors of three replicate microcosms are shown.

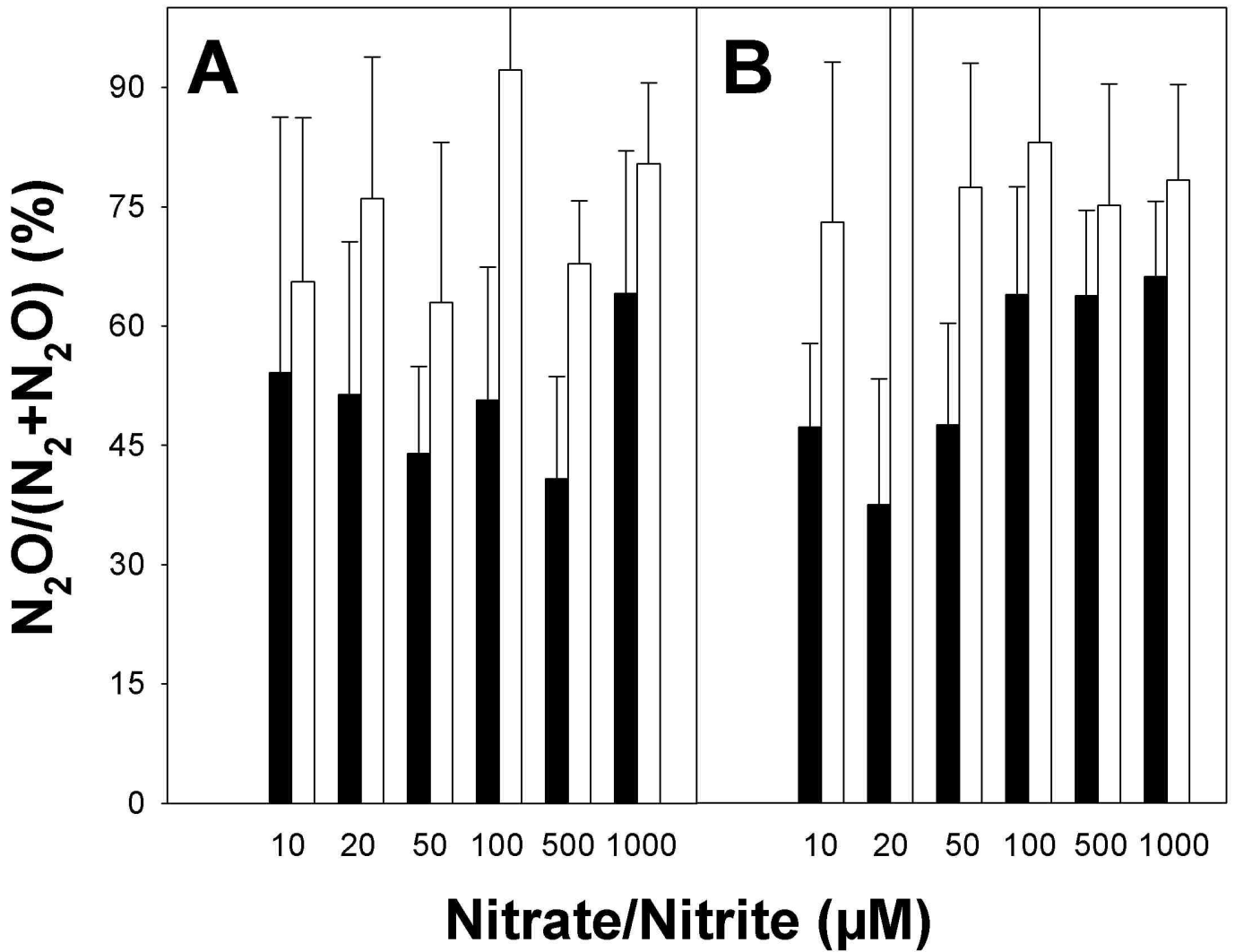


Figure S2: Effect of supplemental nitrate (black) or nitrite (white) on the ratio of N₂O to total N gases in anoxic 0 to 20 cm (A) and below 20 cm (B) peat soil microcosms. Mean values and standard errors of three replicates are shown.

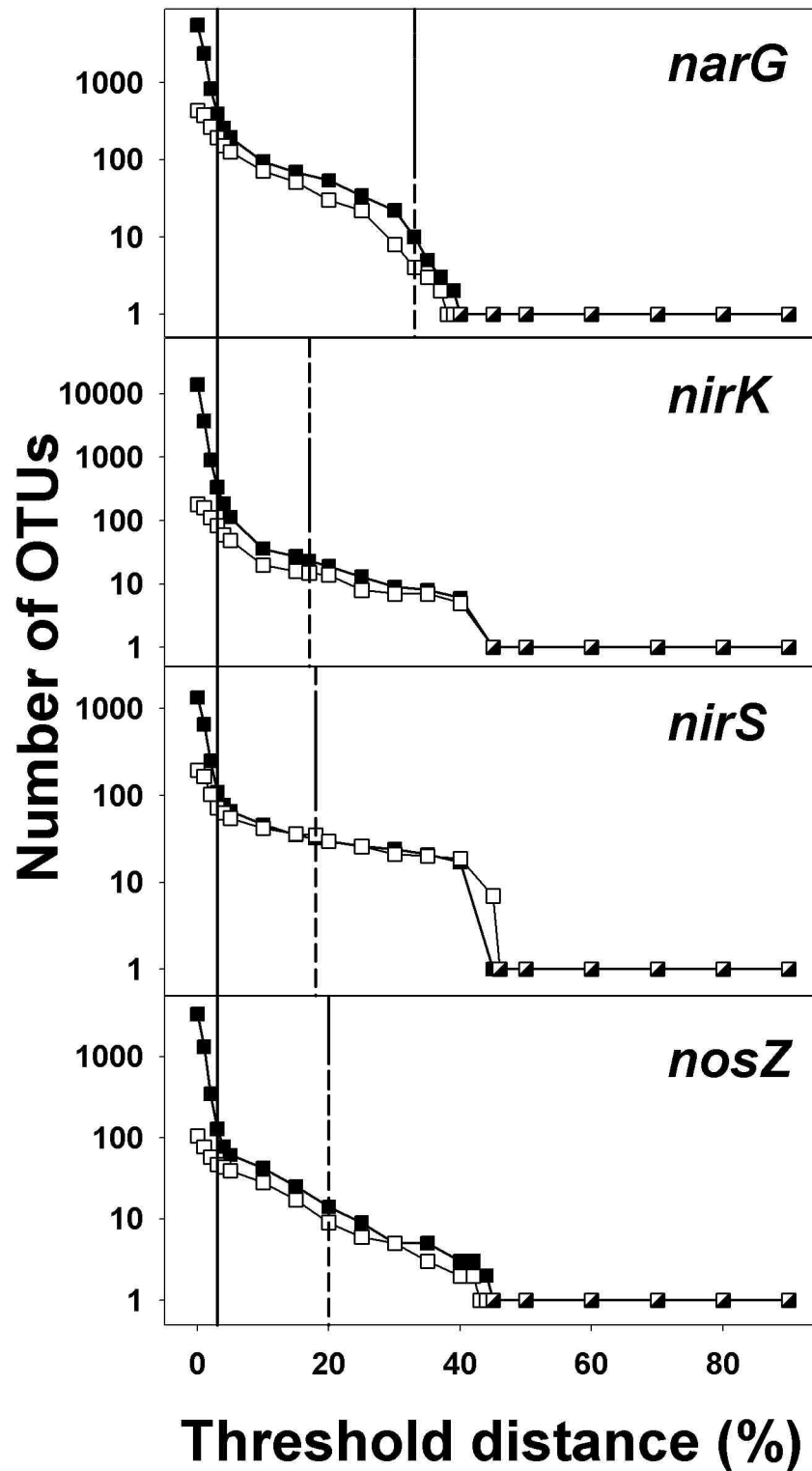


Figure S3: Effect of threshold distance on the number of OTUs obtained before (closed symbols) and after (open symbols) sequence denoising. Solid and dashed lines indicate 3% and species-level threshold distances, respectively.

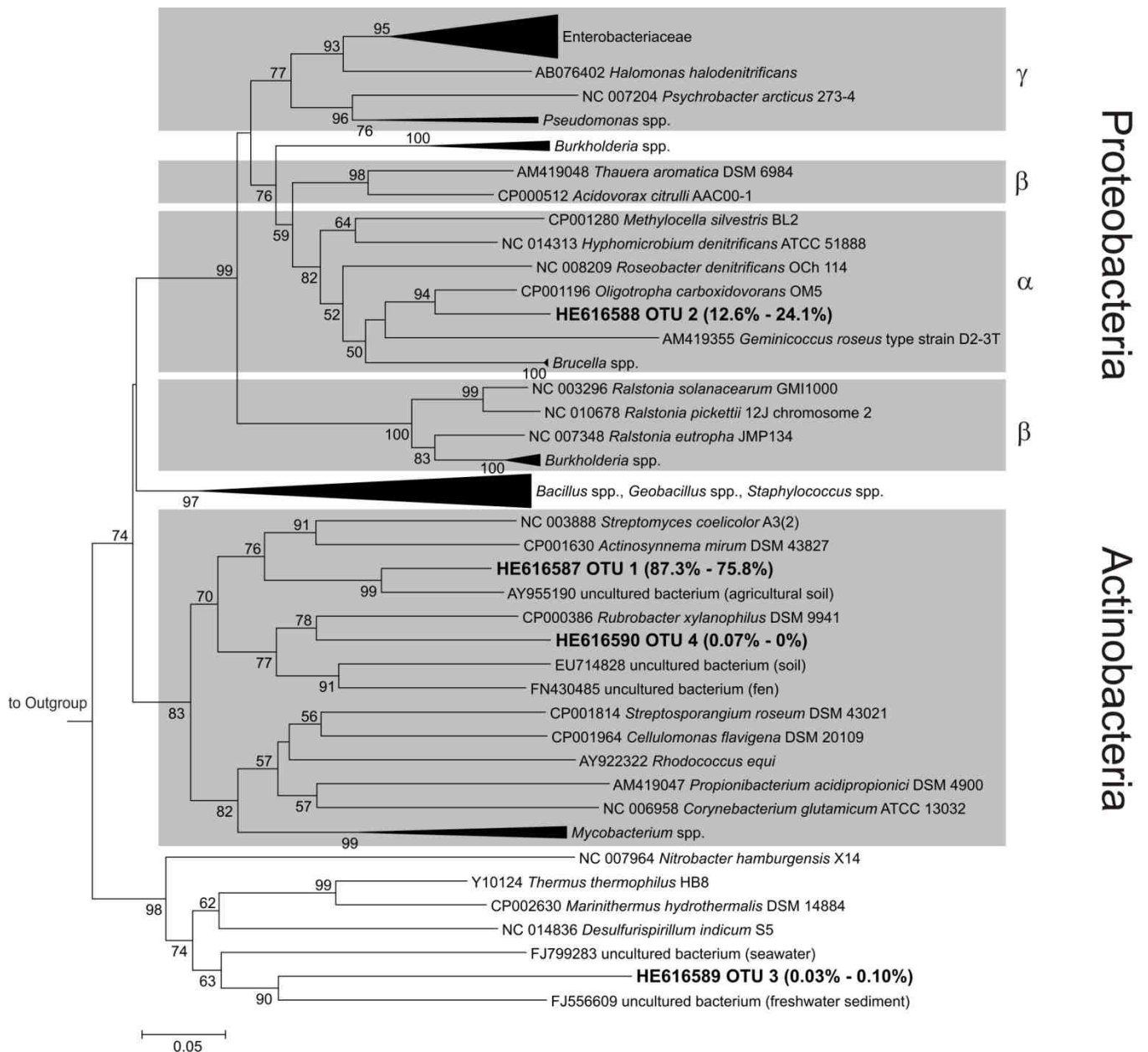


Figure S4: Phylogenetic tree of representative *narG* sequences retrieved from 0 to 20 cm and below 20 cm palsa peat soil. The tree is based on *in silico* translated amino acid sequences. One representative sequence for each OTU generated at 33% threshold distance is shown. Codes preceding sequence names represent sequence accession numbers in public databases. Values in parantheses represent relative abundances of total sequences per OTU from 0 to 20 cm (left) and below 20 cm (right) palsa peat soil. In total, 2 956 and 1 925 denoised sequences from forward reads were obtained from 0 to 20 cm and below 20 cm palsa peat soil, respectively. Grey boxes indicate branches where the majority of sequences are derived from reference strains of a certain phylogenetic class. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (10 000 replicates) are shown next to the branches. Values higher than 50% are shown. The tree was rooted using *narG* of *Haloarcula marismortui* ATCC 43049 as the outgroup (NC 006396).

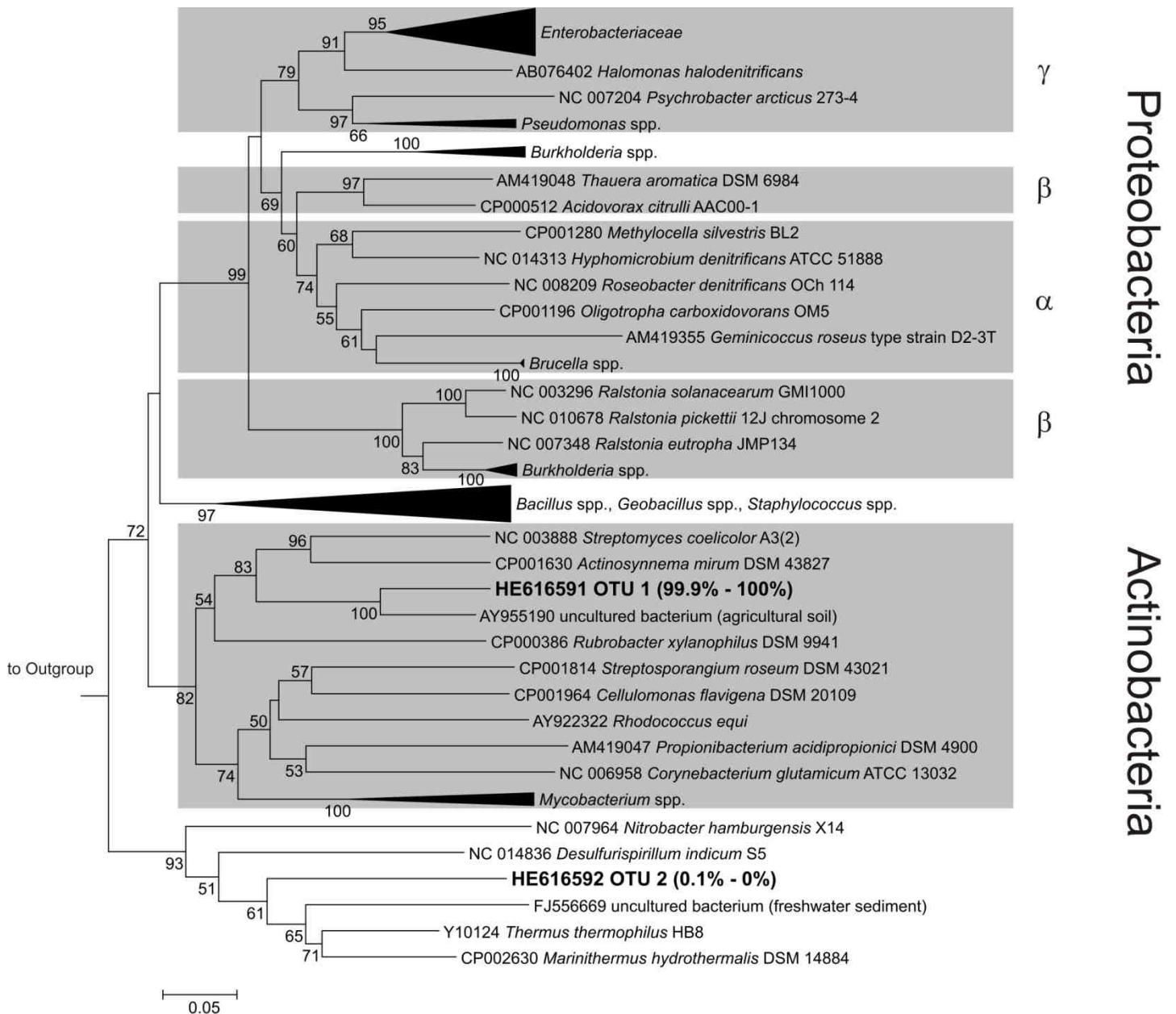


Figure S5: Phylogenetic tree of *narG* reverse reads retrieved from 0 to 20 cm and below 20 cm peat soil. The tree is based on *in silico* translated amino acid sequences. Representatives for each OTU are shown. Relative abundances of sequences from 0 to 20 cm and below 20 cm palsa peat soil are shown in parentheses per OTU. Codes preceding sequence names represent sequence accession numbers in public databases. In total, 3 541 and 1 774 sequences from reverse reads were obtained from 0 to 20 cm and below 20 cm palsa peat soil, respectively. Grey boxes indicate branches where the majority of sequences are derived from reference strains of a certain phylogenetic class. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (10 000 replicates) are shown next to the branches. Values below 50% have been omitted. The outgroup was *narG* of *Haloarcula marismortui* ATCC 43049 (NC 006396).

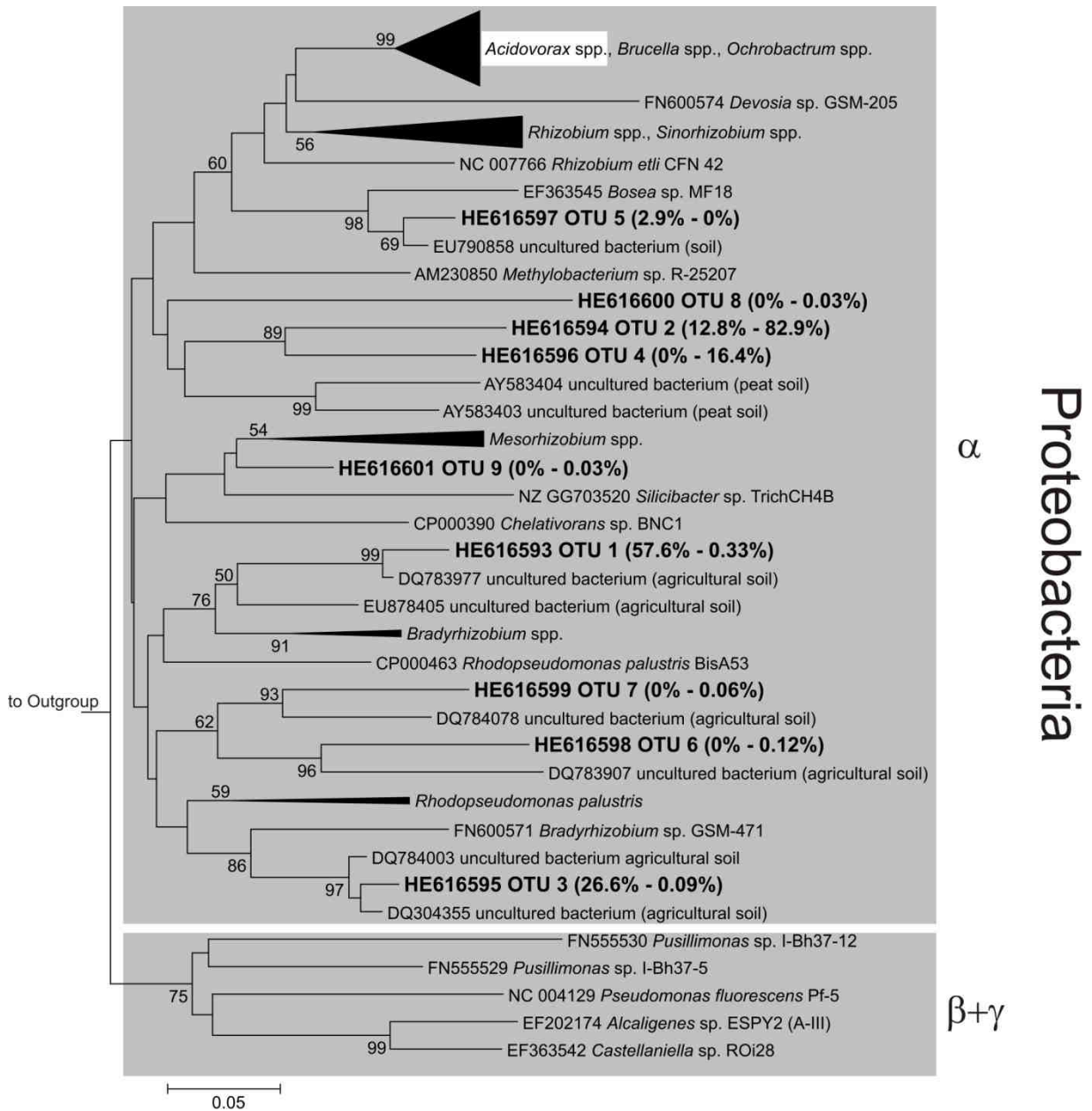


Figure S6: Phylogenetic tree of representative *nirK* sequences retrieved from 0 to 20 cm and below 20 cm palsa peat soil. The tree is based on *in silico* translated amino acid sequences. One representative sequence for each OTU generated at 17% threshold distance is shown. Codes preceding sequence names represent sequence accession numbers in public databases. Values in parantheses represent relative abundances of total sequences per OTU from 0 to 20 cm (left) and below 20 cm (right) palsa peat soil. In total, 8 313 and 3 299 denoised sequences were obtained from 0 to 20 cm and below 20 cm palsa peat soil, respectively. Grey boxes indicate branches where the majority of sequences are derived from reference strains of a certain phylogenetic class; white boxes indicate minority sequences from genera not affiliated with the indicated class. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (10 000 replicates) are shown next to the branches. Values below 50% have been omitted. The tree was rooted using *nirK* of *Nitrosomonas* sp. C-56 as the outgroup (AF339044).

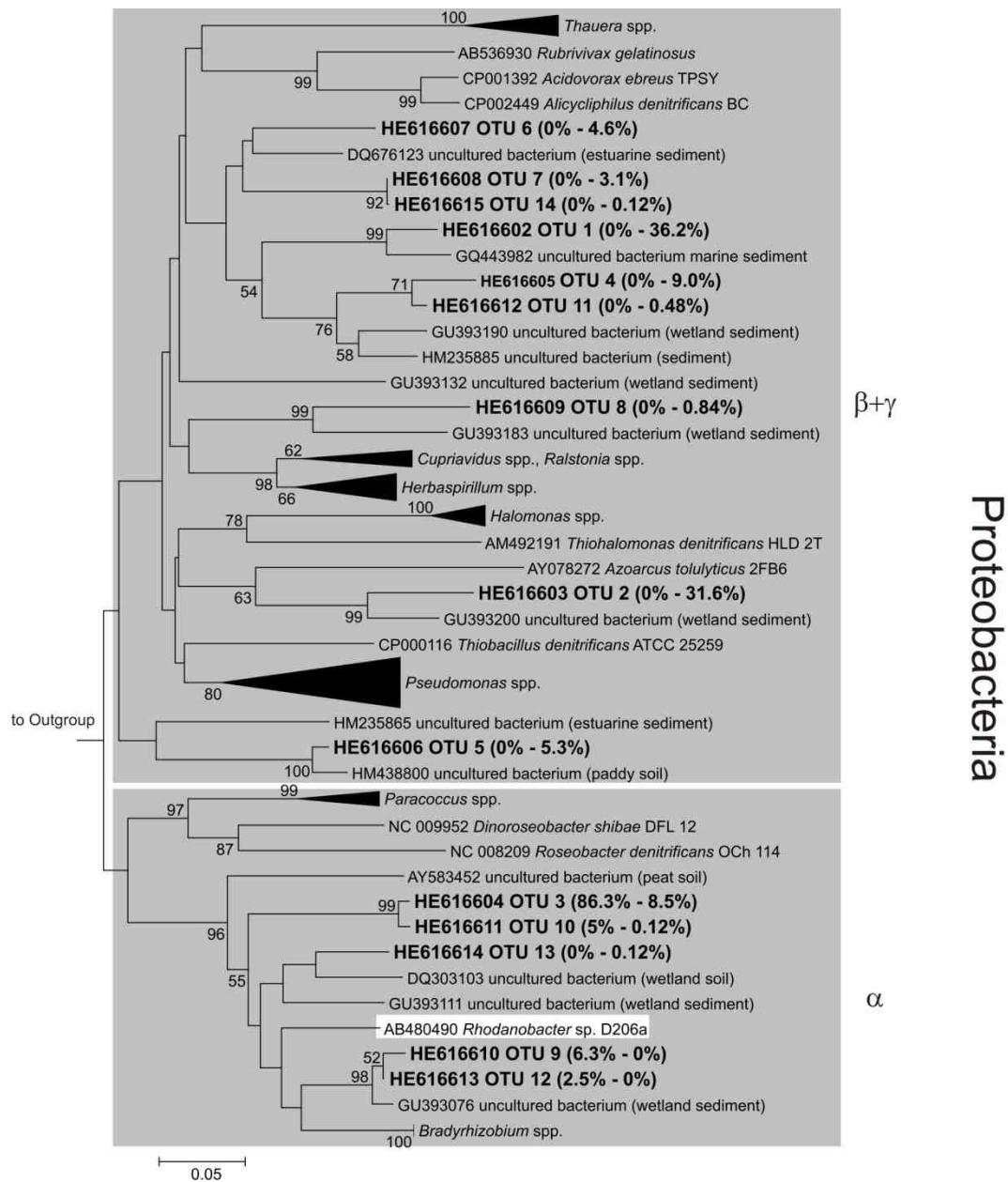


Figure S7: Phylogenetic tree of representative *nirS* sequences retrieved from 0 to 20 cm and below 20 cm palsa peat soil. The tree is based on *in silico* translated amino acid sequences. One representative sequence for each OTU generated at 18% threshold distance is shown. Codes preceding sequence names represent sequence accession numbers in public databases. Values in parantheses represent relative abundances of total sequences per OTU from 0 to 20 cm (left) and below 20 cm (right) palsa peat soil. In total, 85 and 833 denoised sequences were obtained from 0 to 20 cm and below 20 cm palsa peat soil, respectively. Grey boxes indicate branches where the majority of sequences are derived from reference strains of a certain phylogenetic class; white boxes indicate minority sequences from genera not affiliated with the indicated class. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (10 000 replicates) are shown next to the branches. Values below 50% have been omitted. The tree was rooted using *nirS* of *Rhodothermus marinus* DSM 4252 as the outgroup (CP001807).

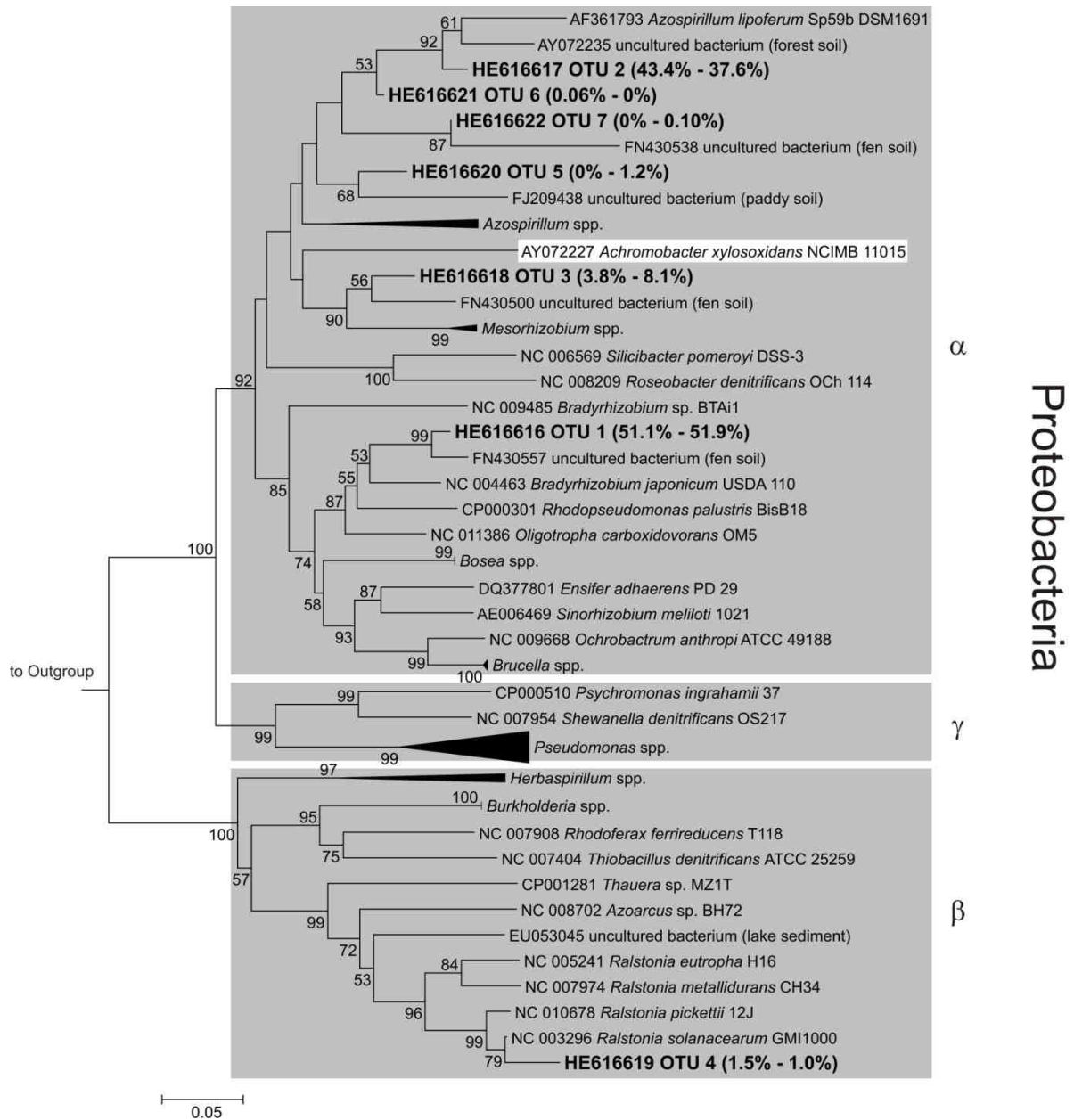


Figure S8: Phylogenetic tree of representative *nosZ* sequences - retrieved from 0 to 20 cm and below 20 cm palsa peat soil. The tree is based on *in silico* translated amino acid sequences. One representative sequence for each OTU generated at 20% threshold distance is shown. Codes preceding sequence names represent sequence accession numbers in public databases. Values in parantheses represent relative abundances of total sequences per OTU from 0 to 20 cm (left) and below 20 cm (right) palsa peat soil. In total, 1 563 and 1 044 denoised sequences from forward reads were obtained from 0 to 20 cm and below 20 cm palsa peat soil, respectively. Grey boxes indicate branches where the majority of sequences are derived from reference strains of a certain phylogenetic class; white boxes indicate minority sequences from genera not affiliated with the indicated class. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (10 000 replicates) are shown next to the branches. Values below 50% have been omitted. The tree was rooted using *nosZ* of *Haloarcula marismortui* ATCC 43049 as the outgroup (NC 006396).

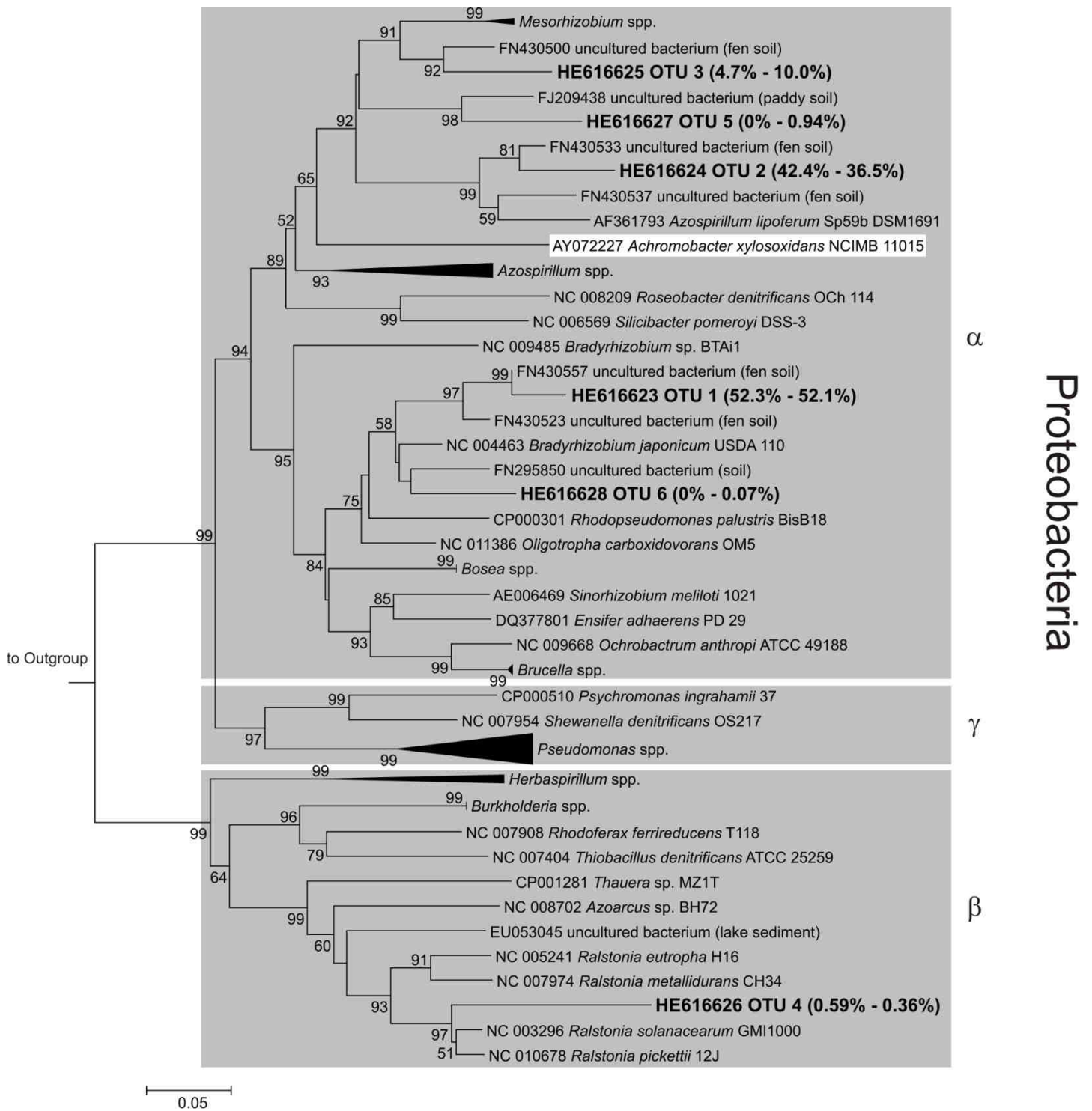


Figure S9: Phylogenetic tree of *nosZ* reverse reads retrieved from 0 to 20 cm and below 20 cm palsa peat soil. The tree is based on *in silico* translated amino acid sequences. Representatives for each OTU are shown. Relative abundances of sequences from 0 to 20 cm and below 20 cm palsa peat soil are shown in parentheses per OTU. Codes preceding sequence names represent sequence accession numbers in public databases. In total, 1 856 and 1 381 sequences from reverse reads were obtained from unturbated and cryoturbated peat soil, respectively. Grey boxes indicate branches where the majority of sequences are derived from reference strains of a certain phylogenetic class; white boxes indicate minority sequences from genera not affiliated with the indicated class. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (10 000 replicates) are shown next to the branches. Values below 50% have been omitted. The outgroup was *nosZ* of *Haloarcula marismortui* ATCC 43049 (NC 006396).