Supplemental Materials

Tables

Table S1. Pearson correlation analysis between soil physicochemical variables and AOA or AOB abundance or nitrification activity

Table S2. Pearson correlation analysis between soil physicochemical variables and relative abundance of AOA clades (>0.1%)

Table S3. Pearson correlation analysis between soil physicochemical variables and relative abundance of AOB clusters (>0.1%)

Figures

Fig. S1. Measures of soil AOA and AOB *amoA* gene diversity in the treatments. Different letters denote significant differences between treatments at $P < 0.05$. Vertical bars represent SEMs (n = 3)

Fig. S2. Multivariate regression tree analysis of AOA (a), AOB (b) community structure and soil physicochemical variables

Fig. S3. Phylogenetic analysis of AOA *amoA* genes retrieved from soils in different treatments. The dominant OTUs (relative abundance > 0.1%; 92% similarity) and reference sequences available in GenBank were used to construct the phylogenetic tree. Bootstrap values of >50% based on 1000 replicates are shown next to the branches. Bars indicate 0.05 substitutions per position. Relative abundances of specific OTUs are shown following the OTU names and presented in bold in parentheses.

Fig. S4. Phylogenetic analysis of AOB *amoA* genes retrieved from soils in different treatments. The dominant OTUs (relative abundance > 0.1%; 92% similarity) and reference sequences available in GenBank were used to construct the phylogenetic tree. Bootstrap values of >50% based on 1000 replicates are shown next to the branches. Bars indicate 0.05 substitutions per position. Relative abundances of specific OTUs are shown following the OTU names and presented in bold in parentheses.

Fig. S5. Relationship between nitrification activity and AOA (a) and AOB (b) *amoA* gene abundance in the treatments, excluding NL. Shaded area indicates 95% confidence interval of the regression models

Table S1. Pearson correlation analysis between soil physicochemical variables and AOA or AOB abundance or nitrification activity.

	pH	SOC	DOC	TN	DON	NH_4^+-N	NO_3^--N	AP	AK	DC_o
AOA *amoA*	**-0.565****	-0.228	-0.177	-0.356	0.274	0.208	**0.572****	-0.096	**-0.575****	0.261
AOB *amoA*	**0.773*** **	-0.121	-0.124	0.016	**-0.469***	0.031	**-0.638** **	-0.165	**0.548***	0.154
Nitrification activity	**0.942*****	-0.192	-0.088	-0.103	**-0.449***	0.093	**-0.653****	-0.111	0.313	0.096

Values in bold indicate correlations, where ***$P < 0.001$, **$P < 0.01$, and *$P < 0.05$.

Table S2. Pearson correlation analysis between soil physicochemical variables and relative abundance of AOA clades (>0.1%).

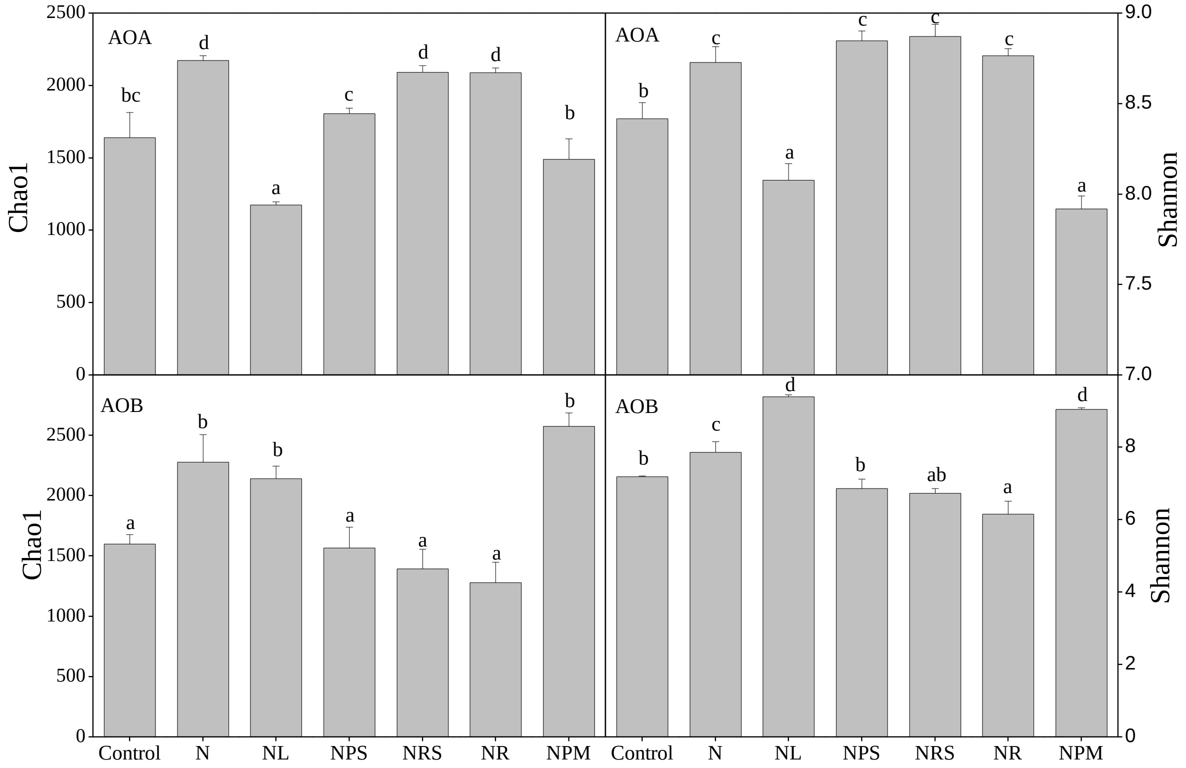
	pH	SOC	DOC	TN	DON	NH_4^+-N	NO_3^--N	AP	AK	DC_o
Clade A	**0.863*** **	**0.468***	**0.533***	0.354	**-0.465***	-0.008	**-0.500***	**0.592****	0.391	**-0.575****
Clade B1	**-0.790*****	**-0.473***	**-0.458***	**-0.454***	**0.436***	0.052	**0.451***	**-0.537***	**-0.485***	**0.588****
Clade B2	-0.348	0.160	-0.124	0.412	-0.024	-0.022	-0.007	-0.040	0.301	-0.128
Clade B3	**-0.511***	**0.448***	0.062	**0.567****	0.227	-0.298	0.278	0.141	0.229	-0.388
Clade B4	**0.942*****	-0.170	-0.014	-0.093	-0.391	0.146	**-0.613****	-0.035	0.272	0.031
Clade C	0.287	0.092	-0.156	0.237	-0.300	0.149	**-0.467***	-0.096	0.412	-0.118
Clade E	-0.188	**0.644****	0.357	**0.658****	-0.010	**-0.482***	0.340	0.273	0.374	**-0.482***
Clade F	**0.911*****	-0.221	-0.093	-0.133	-0.354	0.205	**-0.613****	-0.110	0.279	0.096
Clade *Nitrososphaera*	**-0.905*****	-0.409	**-0.478***	-0.300	**0.475***	0.013	**0.526***	**-0.491***	-0.392	**0.489***

Values in bold indicate correlations, where ******* *P* < 0.001, ****** *P* < 0.01, and ***** *P* < 0.05.

Table S3. Pearson correlation analysis between soil physicochemical variables and relative abundance of AOB clusters (>0.1%).

	pH	SOC	DOC	TN	DON	NH_4^+-N	NO_3^--N	AP	AK	DC_o
Nitrosospira cluster 3a.1	**0.920*****	-0.221	-0.098	-0.140	-0.349	0.190	**-0.627****	-0.120	0.282	0.103
Nitrosospira cluster 3a.2	-0.022	-0.344	-0.300	-0.336	0.403	-0.099	-0.033	-0.349	-0.270	0.383
Nitrosospira cluster 3c	0.081	**0.826*****	**0.876*****	**0.577****	-0.125	-0.154	0.067	**0.951*****	0.064	**-0.910*****
Nitrosospira cluster 8a	**-0.736*****	0.138	-0.000	0.142	0.079	-0.037	**0.492***	0.030	-0.080	-0.053
Nitrosospira cluster 8b	**0.762*****	0.032	0.157	0.049	**-0.436***	-0.005	**-0.461***	0.076	0.256	-0.031

Values in bold indicate correlations, where ******* $P < 0.001$, ****** $P < 0.01$, and ***** $P < 0.05$.



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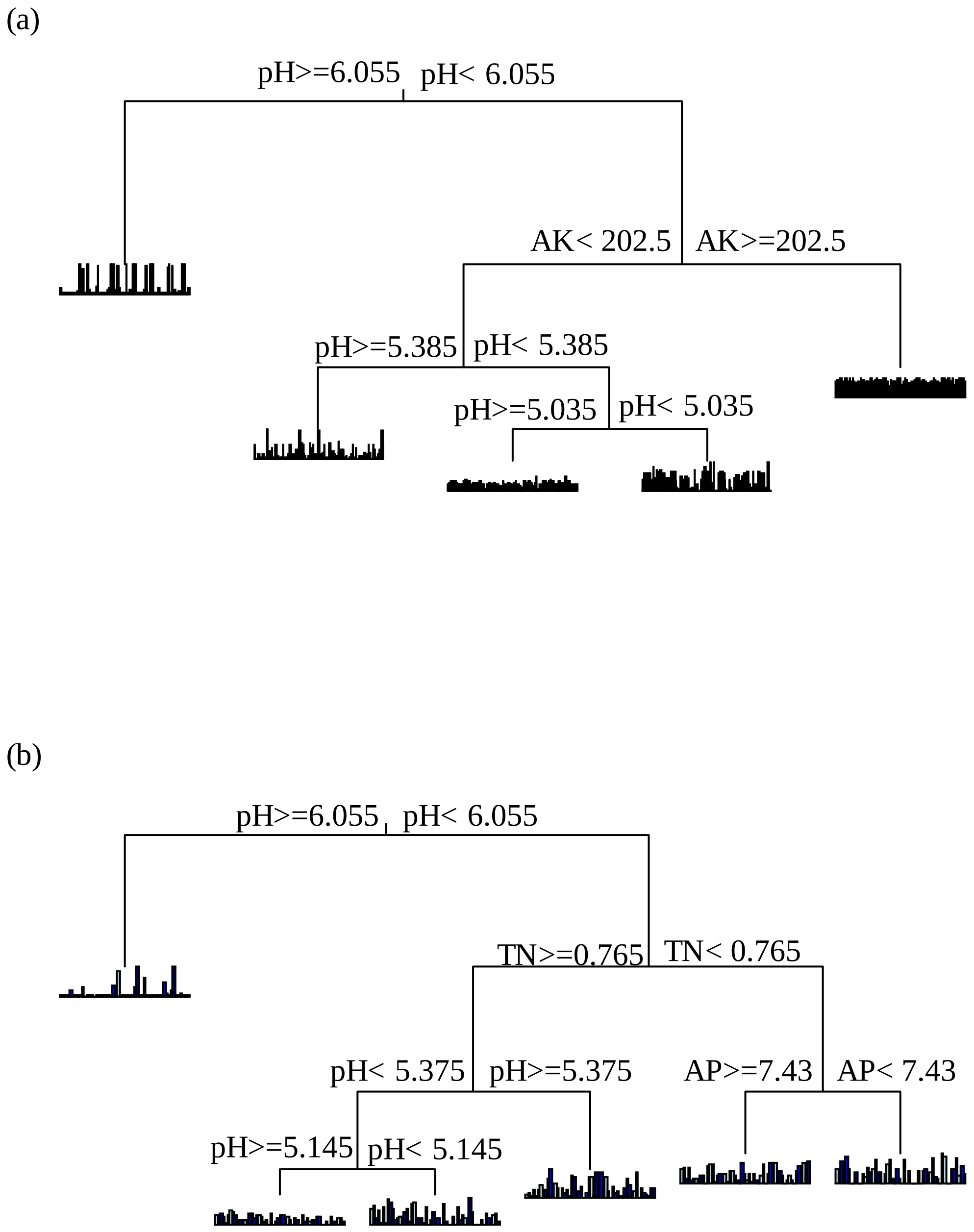

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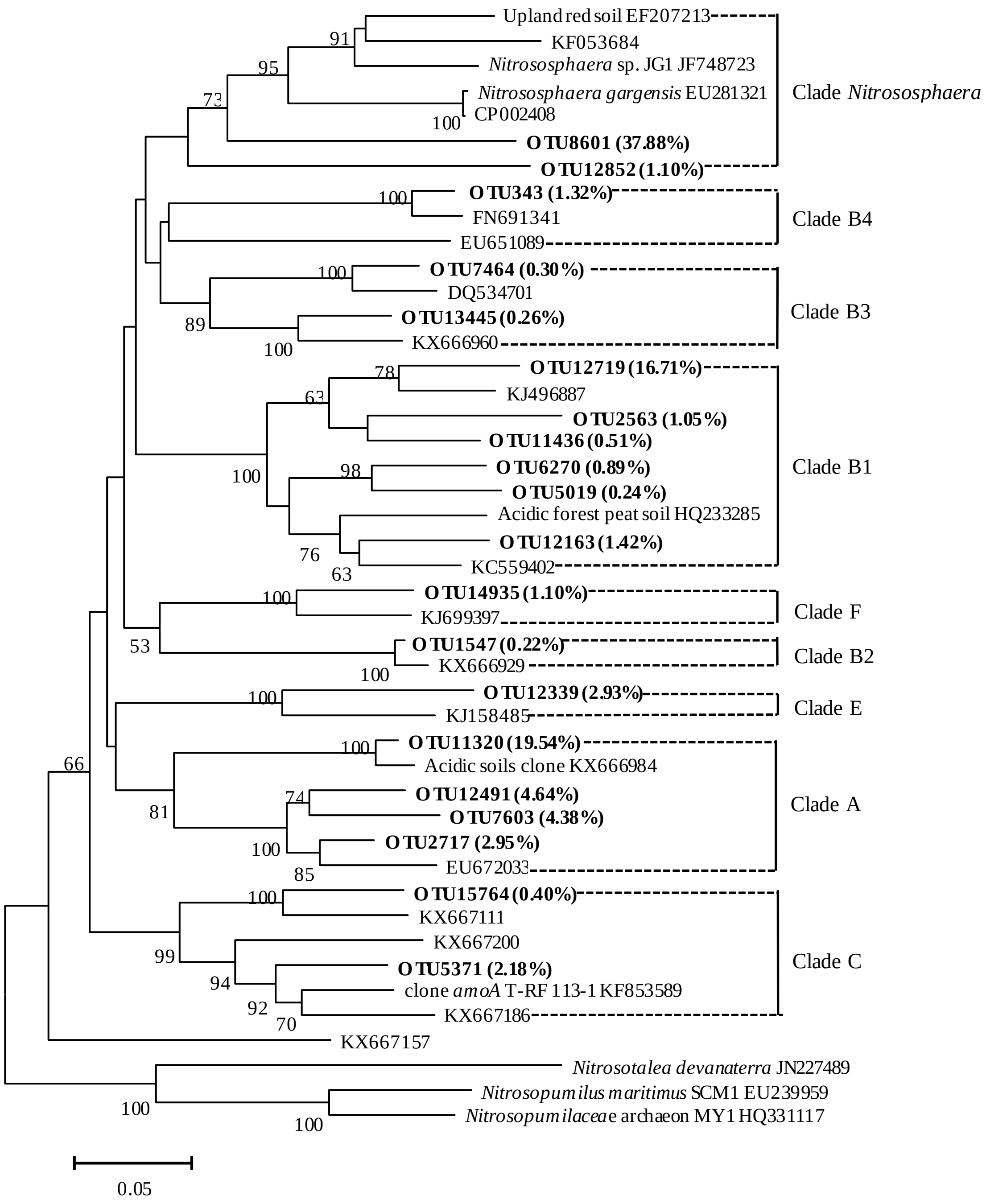

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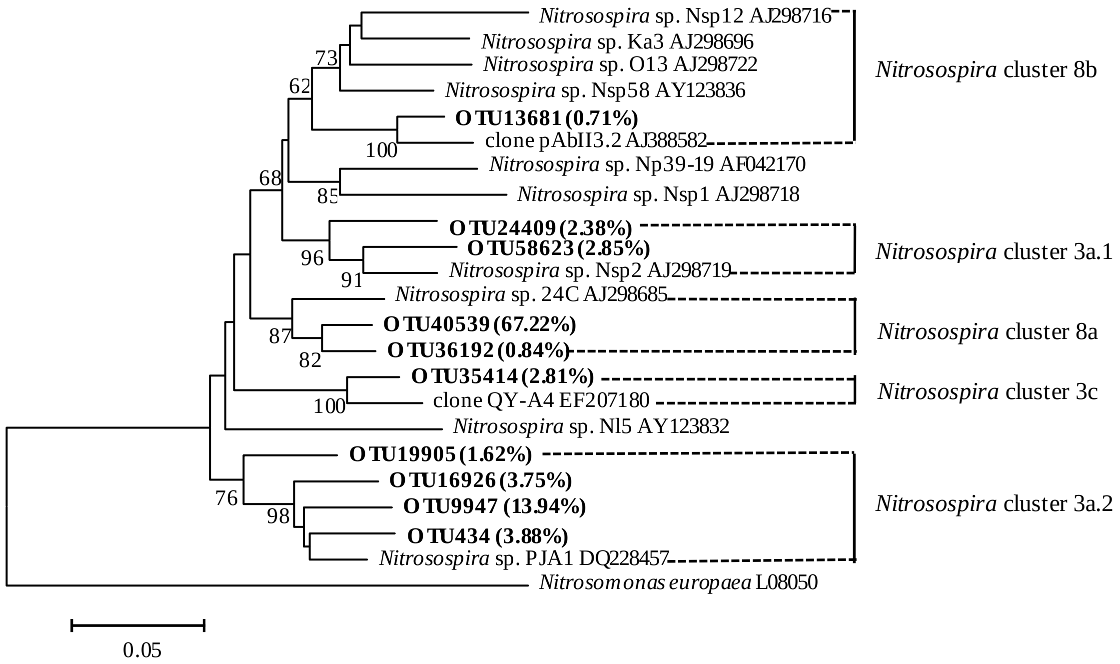
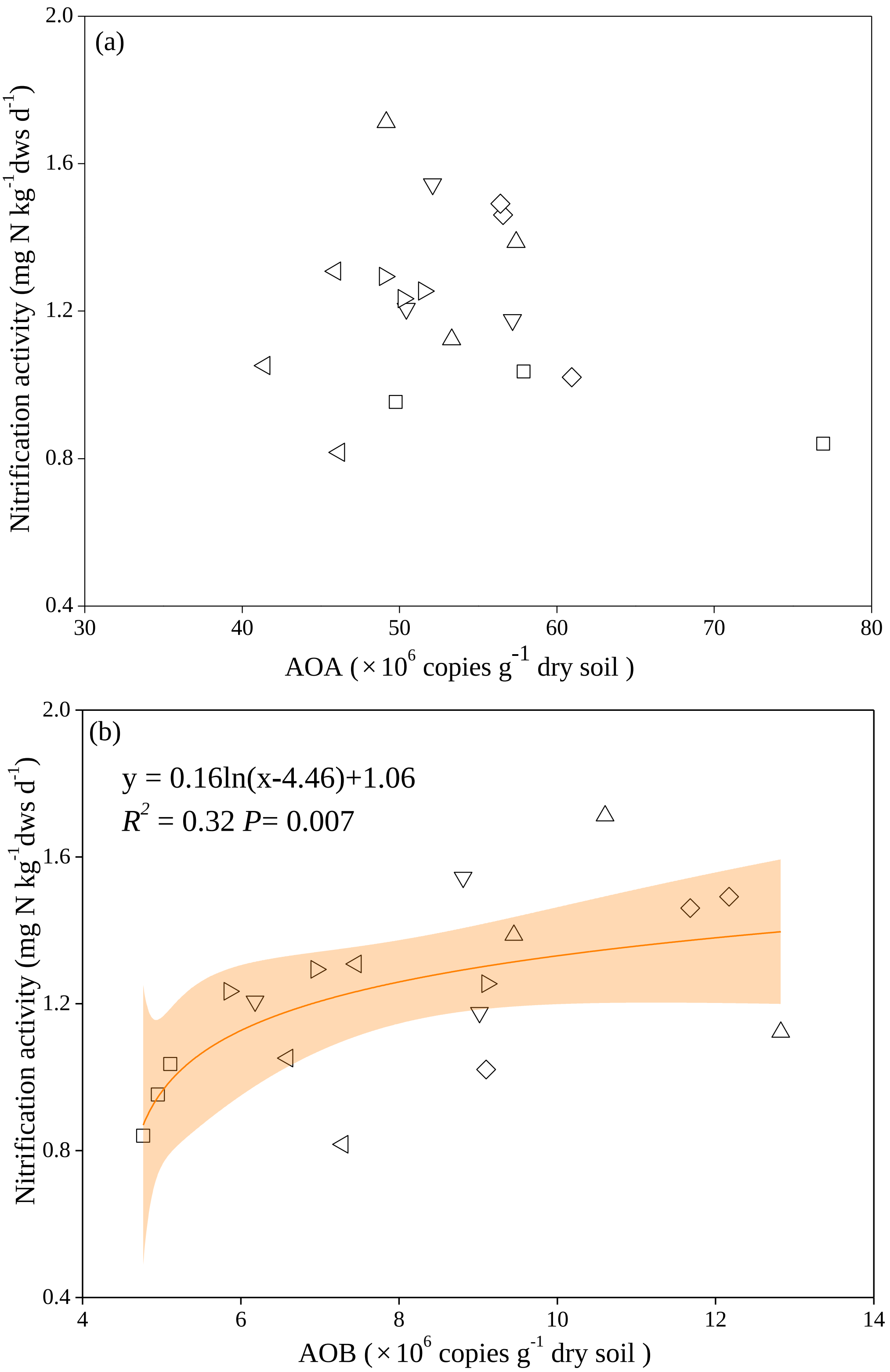


Fig. S4. Phylogenetic analysis of AOB *amoA* genes retrieved from soils in different treatments. The dominant OTUs (relative abundance > 0.1%; 92% similarity) and reference sequences available in GenBank were used to construct the phylogenetic tree. Bootstrap values of >50% based on 1000 replicates are shown next to the branches. Bars indicate 0.05 substitutions per position. Relative abundances of specific OTUs are shown following the OTU names and presented in bold in parentheses.



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