

Figure S1 (appendix)

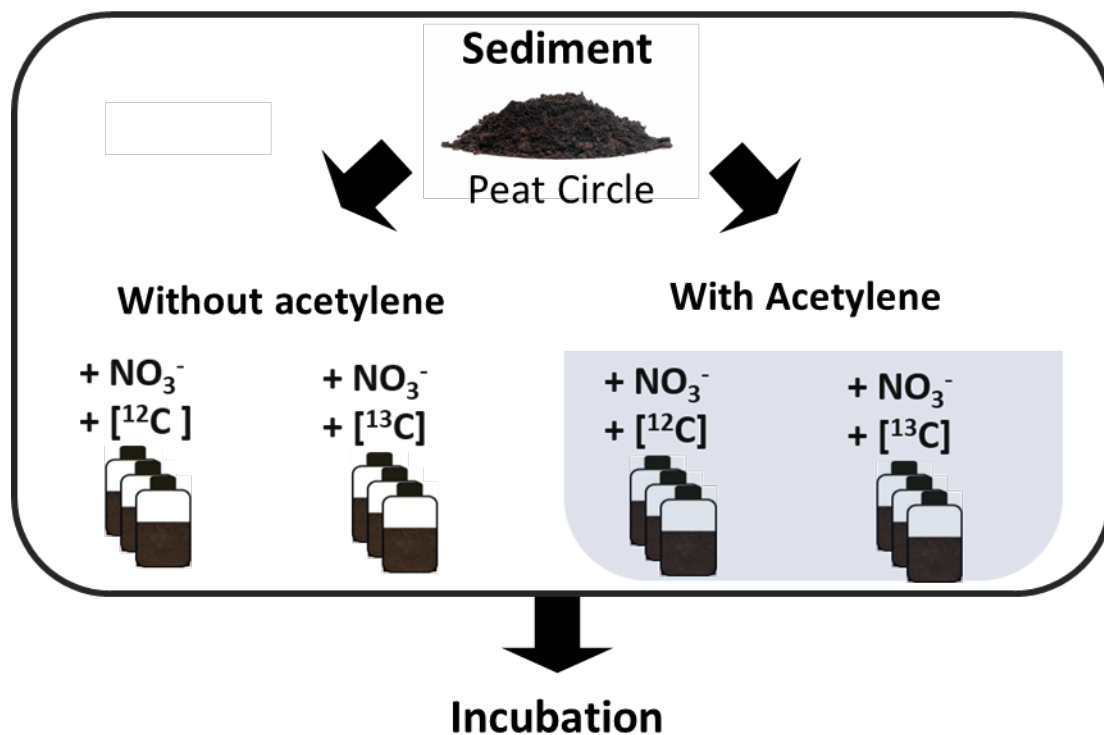


Figure S1. Experimental setup for triplicate anoxic peat circle sediment (pH 4.4) slurries utilized for acetate 16S rRNA stable isotope probing and concomitant analysis of denitrification products and intermediates. Incubations with peat circle sediments containing endogenous nitrate were supplemented with 400 μ M of unlabeled [^{12}C]- or double-labelled [^{13}C]-acetate. Two sets of incubation were set up, one with and one without acetylene (10%-v/v) in the headspace. Only incubations without acetylene were used for total RNA extraction and stable isotope probing. Unlabeled [^{12}C]-acetate treatments served as controls for the stable isotope probing approach to identify labeled taxa, i.e. to account for drift of unlabeled RNA into 'heavy' fractions with a characteristic buoyant density of [^{13}C]-labeled RNA. Acetylene treatments served as process controls to determine denitrification derived N_2 production via the acetylene inhibition method. Nitrate and acetate were re-fed during the course of the incubation upon consumption (see Figure 1). Incubation was at an *in situ* relevant temperature of 15 $^{\circ}\text{C}$ in the dark. Microcosms were rigorously shaken manually twice a day.

Figure S2 (appendix)

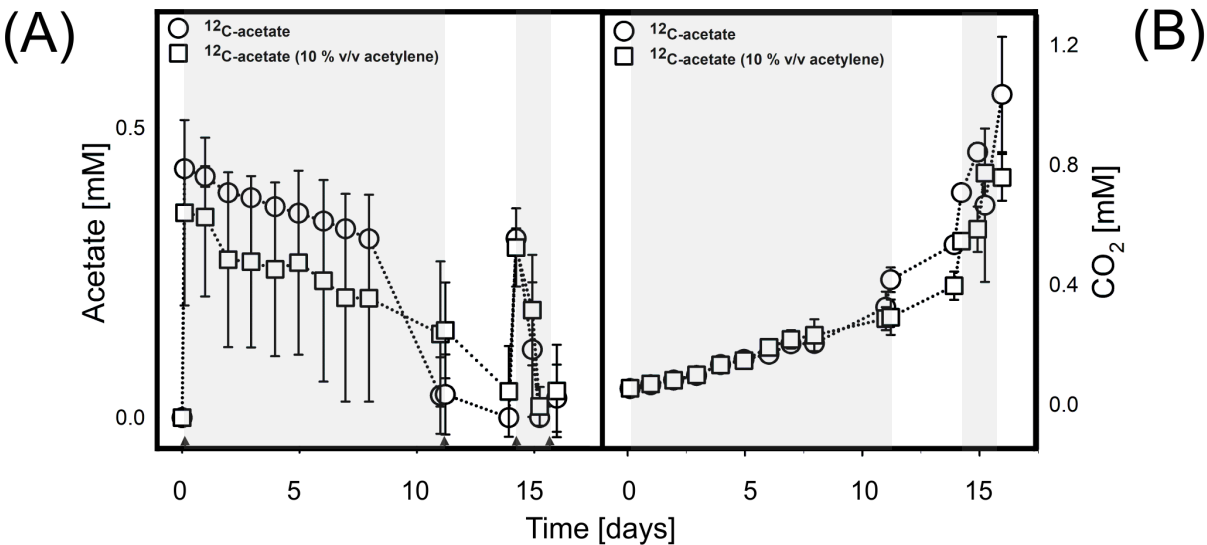


Figure S2. Acetate consumption (A) and CO₂ production (B) in anoxic incubations of ¹²C-acetate supplemented cryoturbated peat circle sediments without and with acetylene. Arrows indicate time of acetate supplementation. Shaded and non-shaded areas highlight different periods of nitrate consumption (Figure 1). Values are means ± standard deviation of triplicate incubations.

Figure S3 (appendix)

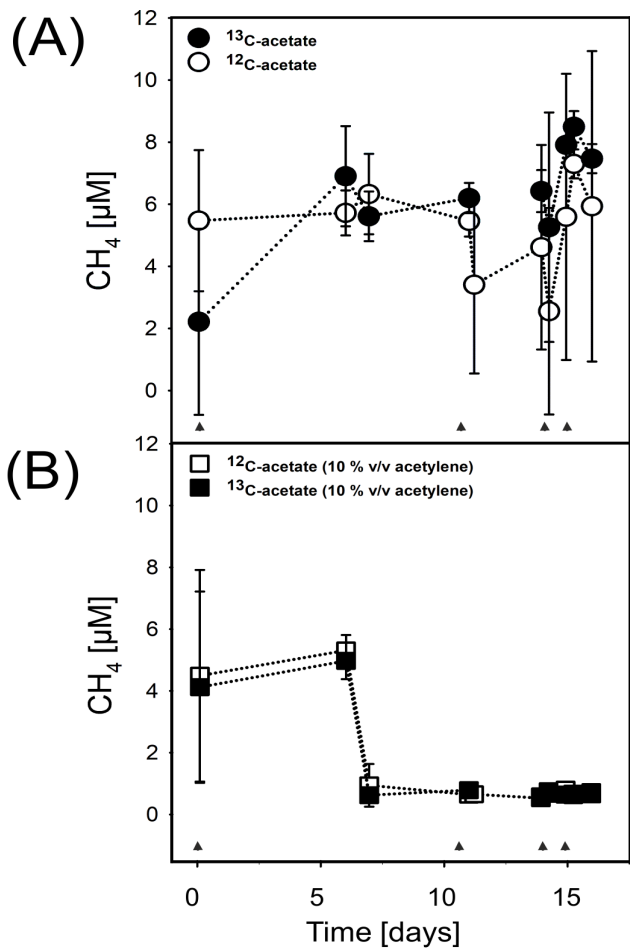


Figure S3. Methane concentrations in anoxic incubations of acetate supplemented cryoturbated peat circle sediments without (A) and with (B) acetylene (Figure 1). Arrows indicate time of acetate supplementation. Values are means $\pm$ standard deviation of triplicate incubations.

Figure S4 (appendix)

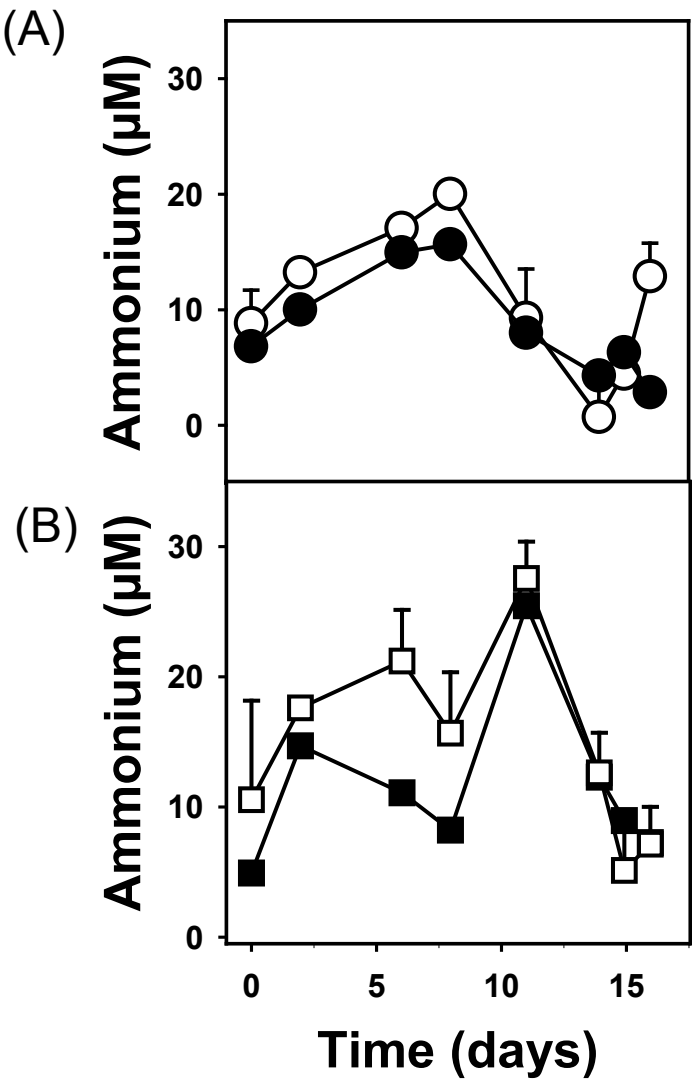


Figure S4. Ammonium concentrations in anoxic incubations of acetate and supplemented cryoturbated peat circle sediments without (A) and with (B) acetylene (Figure 1). Values are means $\pm$ standard deviation of triplicate incubations.

Figure S5

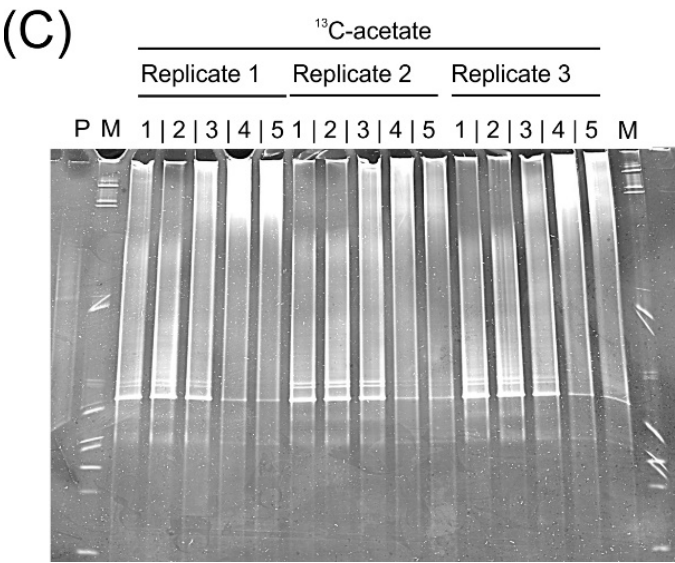
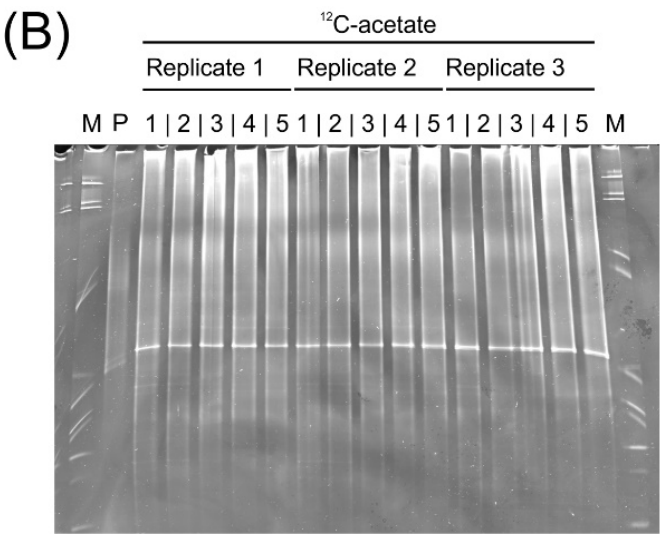
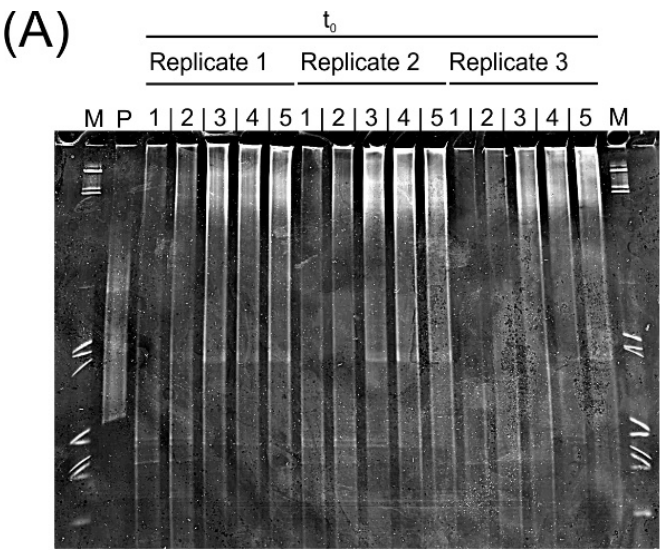


Figure S5. DGGE gels of heavy and light fractions of all replicates (1-3) and treatments. 1 – heaviest fraction; 5 – lightest fraction; M – marker; P – positive control.
A: Heavy and light fractions from all three replicates of t_0 samples.
B: Heavy and light fractions from all three replicates of $^{12}\text{C-acetate}$ treatments.
C: Heavy and light fractions from all three replicates of $^{13}\text{C-acetate}$ treatments.

Figure S6

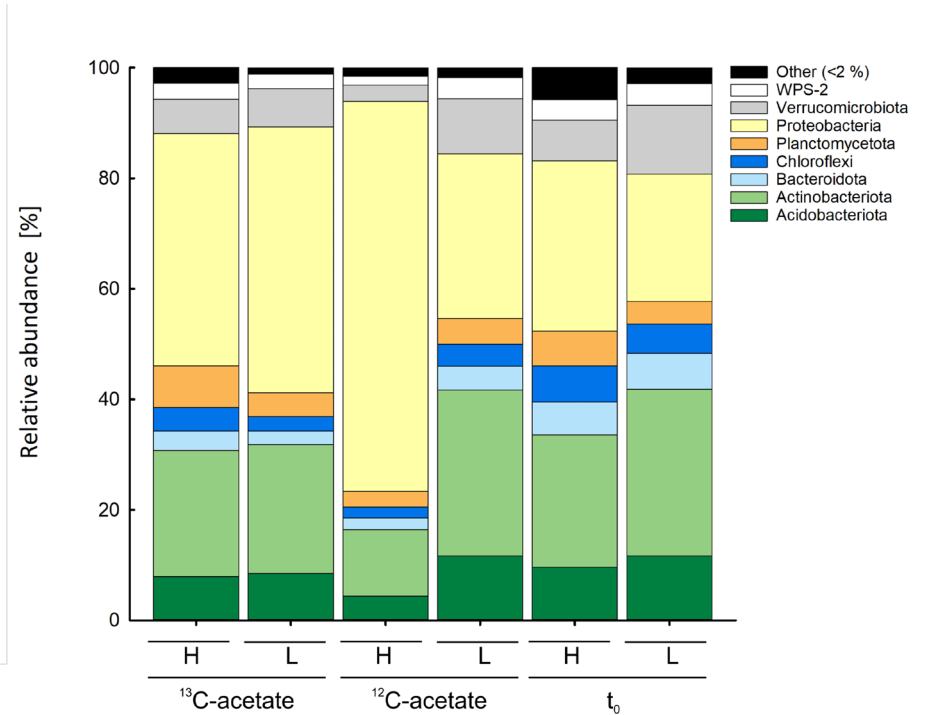
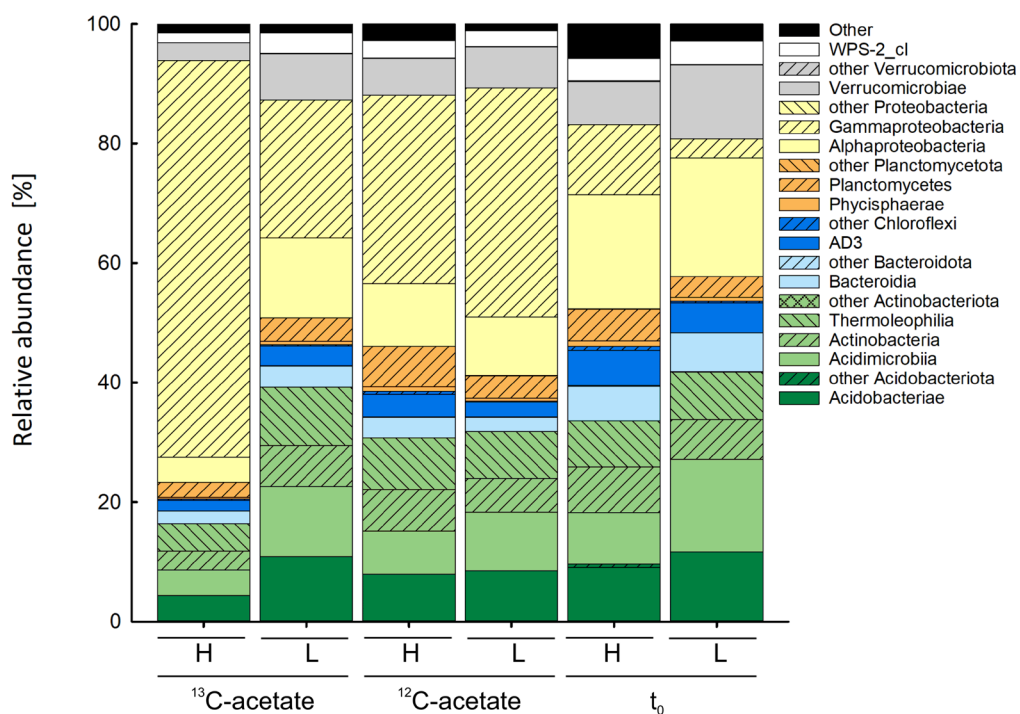


Figure S6. Mean relative abundance of bacterial phyla (>2% of relative abundance in at least one sample) delineated from analysis of density resolved 16S rRNA retrieved from cryoturbated peat circle sediments prior to and after 16 days of anoxic incubation (see Figure 1). Values are means of triplicate incubations. Heavy (H) and Light (L) indicate fractions representing ^{13}C -labeled and unlabeled 16S rRNA after isopycnic centrifugation (see Materials and Methods for further details) where sequences have been retrieved from. ^{13}C - and ^{12}C -acetate refer to treatments with ^{13}C - and ^{12}C -acetate, respectively. t_0 indicates peat circle sediments prior to incubation.

Figure S7
(A)



(B)

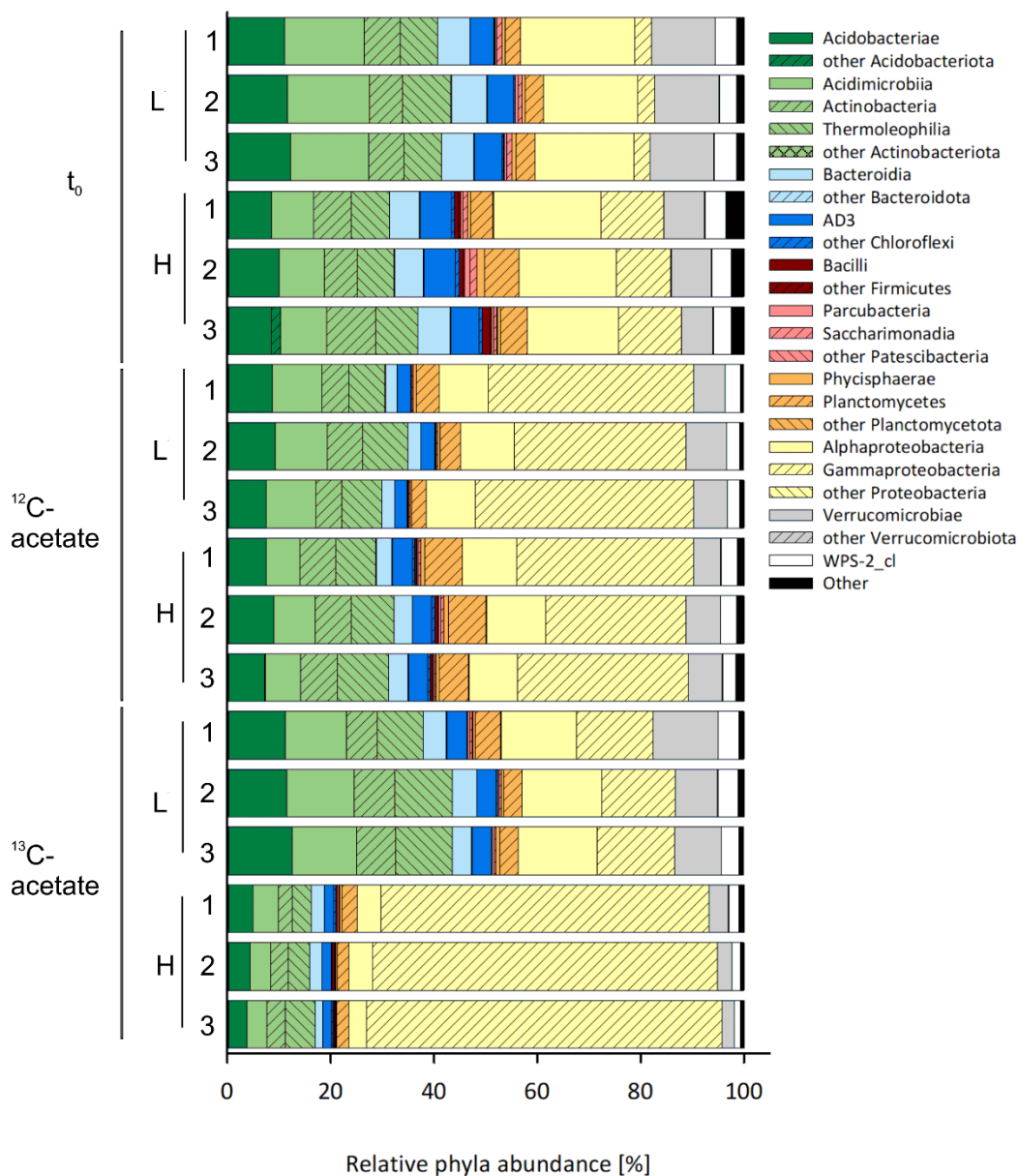


Figure S7. Mean relative abundance of bacterial classes (>2% of relative abundance in at least one sample) delineated from analysis of density resolved 16S rRNA retrieved from cryoturbated peat circle sediments prior to and after 16 days of anoxic incubation (see Figure 1). Values are means of triplicate incubations (A) or indicate single replicates (B). Heavy (H) and Light (L) indicate fractions representing ^{13}C -labeled and unlabeled 16S rRNA after isopycnic centrifugation (see Materials and Methods for further details) where sequences have been retrieved from. ^{13}C - and ^{12}C -acetate refer to treatments with ^{13}C - and ^{12}C -acetate, respectively. t_0 indicates peat circle sediments prior to incubation.

Figure S8

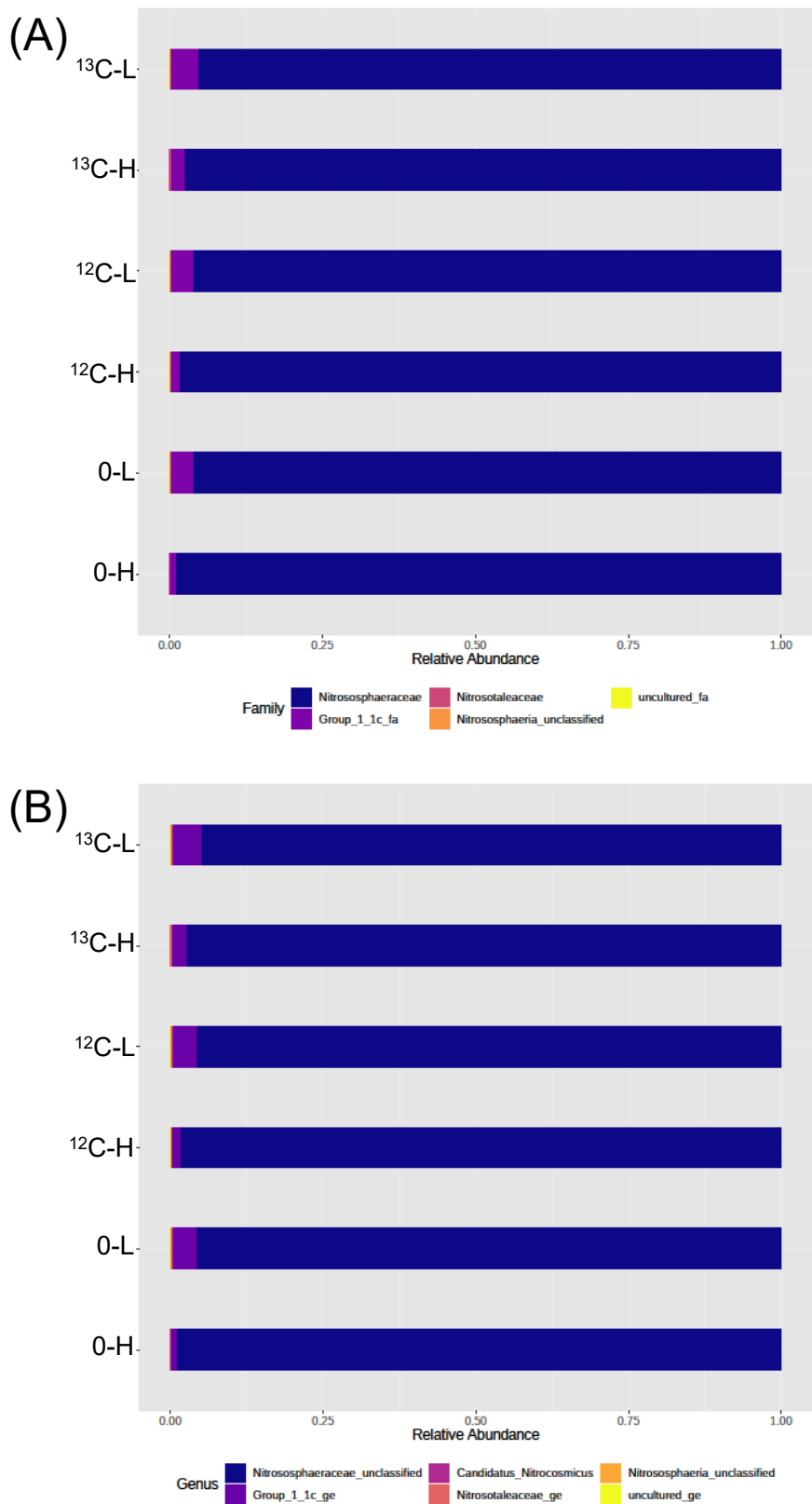


Figure S8. Mean relative abundance of archaeal families (A) and genera (B) delineated from analysis of density resolved 16S rRNA retrieved from cryoturbated peat circle sediments prior to and after 16 days of anoxic incubation (see Figure 1). Values are means of triplicate incubations. Sample code: H and L indicate heavy and light fractions, respectively; 0, ^{13}C - and ^{12}C - represent peat circle sediments prior to incubation, ^{13}C - and ^{12}C -acetate treatments, respectively.

Figure S9

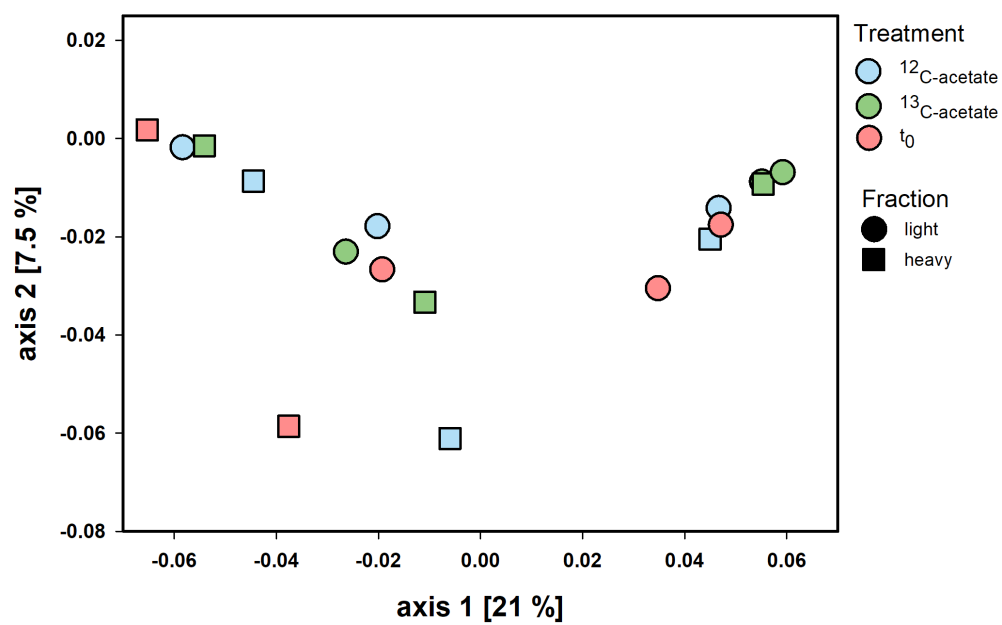


Figure S9. Principal Coordinates Analysis (PCoA) based on Bray-Curtis dissimilarity calculated from relative abundance data of archaeal species-level OTUs from density resolved 16S rRNA retrieved from cryoturbated peat circle sediments prior to (t_0) and after 16 days of anoxic incubation (see Figure 1).

Table S1. Correlation table of network analysis on bacterial genus level using SparCC algorithm (Figure 5A). Significant correlations of *Burkholderia-Caballeronia-Paraburkholderia* and *Rhodanobacter* spp. affiliating sequences are shown.

Genus-level Taxon 1	Genus-level Taxon 2	Correlation	p-value
<i>Burkholderia_Caballeronia_Paraburkholderia</i>	37_13_ge	-0.5083	0.0297
<i>Burkholderia_Caballeronia_Paraburkholderia</i>	Acetobacteraceae_unclassified	0.8124	0.0099
<i>Burkholderia_Caballeronia_Paraburkholderia</i>	Acidipila	0.4913	0.0495
<i>Burkholderia_Caballeronia_Paraburkholderia</i>	Acidobacteriaceae_(Subgroup_1)_unclassified	0.5336	0.0396
<i>Burkholderia_Caballeronia_Paraburkholderia</i>	Acidocella	0.5518	0.0198
<i>Burkholderia_Caballeronia_Paraburkholderia</i>	Acidothermus	0.7593	0.0099
<i>Burkholderia_Caballeronia_Paraburkholderia</i>	Aquisphaera	0.9022	0.0099
<i>Burkholderia_Caballeronia_Paraburkholderia</i>	Asticcacaulis	0.5135	0.0396
<i>Burkholderia_Caballeronia_Paraburkholderia</i>	B12_WMSP1_ge	0.7295	0.0099
<i>Burkholderia_Caballeronia_Paraburkholderia</i>	Bacteroidota_unclassified	0.6141	0.0099
<i>Burkholderia_Caballeronia_Paraburkholderia</i>	Burkholderiaceae_unclassified	0.5359	0.0198
<i>Burkholderia_Caballeronia_Paraburkholderia</i>	Candidatus_Nostocoida	0.9138	0.0099
<i>Burkholderia_Caballeronia_Paraburkholderia</i>	Candidatus_Ovatusbacter	-0.5198	0.0099
<i>Burkholderia_Caballeronia_Paraburkholderia</i>	Conexibacter	0.8632	0.0099
<i>Burkholderia_Caballeronia_Paraburkholderia</i>	Frankiales_unclassified	0.7387	0.0297
<i>Burkholderia_Caballeronia_Paraburkholderia</i>	Gemmata	0.5819	0.0198
<i>Burkholderia_Caballeronia_Paraburkholderia</i>	Gemmatimonadaceae_unclassified	0.6845	0.0099
<i>Burkholderia_Caballeronia_Paraburkholderia</i>	Gemmatimonas	0.4979	0.0495
<i>Burkholderia_Caballeronia_Paraburkholderia</i>	Granulicella	0.6775	0.0198
<i>Burkholderia_Caballeronia_Paraburkholderia</i>	IMCC26256_ge	0.5904	0.0198
<i>Burkholderia_Caballeronia_Paraburkholderia</i>	Isosphaeraceae_unclassified	0.9104	0.0099
<i>Burkholderia_Caballeronia_Paraburkholderia</i>	Jatrophihabitans	0.7261	0.0099
<i>Burkholderia_Caballeronia_Paraburkholderia</i>	Legionella	-0.6195	0.0297
<i>Burkholderia_Caballeronia_Paraburkholderia</i>	Mucilaginibacter	0.5412	0.0297
<i>Burkholderia_Caballeronia_Paraburkholderia</i>	Novosphingobium	0.5869	0.0396
<i>Burkholderia_Caballeronia_Paraburkholderia</i>	Occallatibacter	0.7075	0.0099
<i>Burkholderia_Caballeronia_Paraburkholderia</i>	Pajaroellobacter	-0.5466	0.0396
<i>Burkholderia_Caballeronia_Paraburkholderia</i>	Pedosphaeraceae_ge	0.6921	0.0099
<i>Burkholderia_Caballeronia_Paraburkholderia</i>	Phenylobacterium	0.6286	0.0396
<i>Burkholderia_Caballeronia_Paraburkholderia</i>	RCP2_54_ge	0.7328	0.0198
<i>Burkholderia_Caballeronia_Paraburkholderia</i>	Rhodanobacter	0.6159	0.0099
<i>Burkholderia_Caballeronia_Paraburkholderia</i>	Rickettsiaceae_unclassified	-0.5811	0.0297
<i>Burkholderia_Caballeronia_Paraburkholderia</i>	Solirubrobacteraceae_unclassified	0.6492	0.0297
<i>Burkholderia_Caballeronia_Paraburkholderia</i>	Solirubrobacterales_unclassified	0.487	0.0396
<i>Burkholderia_Caballeronia_Paraburkholderia</i>	Subgroup_13_ge	0.5191	0.0198
<i>Burkholderia_Caballeronia_Paraburkholderia</i>	Subgroup_2_ge	0.8369	0.0198
<i>Burkholderia_Caballeronia_Paraburkholderia</i>	Tepidisphaerales_unclassified	0.7028	0.0099
<i>Burkholderia_Caballeronia_Paraburkholderia</i>	Tundrisphaera	0.8681	0.0099
<i>Burkholderia_Caballeronia_Paraburkholderia</i>	WD2101_soil_group_ge	0.5906	0.0396
<i>Burkholderia_Caballeronia_Paraburkholderia</i>	WPS_2_ge	0.6062	0.0099

Table S1 (continued). Correlation table of network analysis on bacterial genus level using SparCC algorithm (see Figure 5A). Significant correlations of *Burkholderia-Caballeronia-Paraburkholderia* and *Rhodanobacter* spp. affiliating sequences are shown.

Genus-level Taxon 1	Genus-level Taxon 2	Correlation	p-value
<i>Rhodanobacter</i>	67_14_ge	0.7189	0.0099
<i>Rhodanobacter</i>	<i>Acetobacteraceae_unclassified</i>	0.6952	0.0099
<i>Rhodanobacter</i>	<i>Acidicaldus</i>	0.6046	0.0297
<i>Rhodanobacter</i>	<i>Acidimicrobiia_unclassified</i>	0.8753	0.0099
<i>Rhodanobacter</i>	<i>Acidiphilium</i>	0.565	0.0396
<i>Rhodanobacter</i>	<i>Acidipila</i>	0.8737	0.0099
<i>Rhodanobacter</i>	<i>Acidobacteriaceae_(Subgroup_1)_unclassified</i>	0.8053	0.0099
<i>Rhodanobacter</i>	<i>Acidothermus</i>	0.8716	0.0099
<i>Rhodanobacter</i>	AD3_ge	0.8077	0.0099
<i>Rhodanobacter</i>	<i>Anaerococcus</i>	-0.5117	0.0297
<i>Rhodanobacter</i>	<i>Aquisphaera</i>	0.715	0.0198
<i>Rhodanobacter</i>	<i>Asticcacaulis</i>	0.6313	0.0198
<i>Rhodanobacter</i>	B10_SB3A_ge	-0.7032	0.0099
<i>Rhodanobacter</i>	<i>Bacteria_unclassified</i>	0.6577	0.0495
<i>Rhodanobacter</i>	<i>Bacteroidota_unclassified</i>	0.6721	0.0297
<i>Rhodanobacter</i>	<i>Bauldia</i>	0.6846	0.0198
<i>Rhodanobacter</i>	<i>Beijerinckiaceae_unclassified</i>	0.6147	0.0198
<i>Rhodanobacter</i>	<i>Bryobacter</i>	0.6329	0.0198
<i>Rhodanobacter</i>	<i>Burkholderia_Caballeronia_Paraburkholderia</i>	0.6159	0.0099
<i>Rhodanobacter</i>	<i>Burkholderiaceae_unclassified</i>	0.7673	0.0099
<i>Rhodanobacter</i>	<i>Candidatus_Solibacter</i>	0.5734	0.0099
<i>Rhodanobacter</i>	<i>Caulobacteraceae_unclassified</i>	0.7944	0.0099
<i>Rhodanobacter</i>	<i>Chloroflexi_unclassified</i>	-0.4809	0.0495
<i>Rhodanobacter</i>	<i>Conexibacter</i>	0.8495	0.0297
<i>Rhodanobacter</i>	<i>Cutibacterium</i>	-0.6078	0.0099
<i>Rhodanobacter</i>	<i>Devosiaceae_unclassified</i>	0.8543	0.0099
<i>Rhodanobacter</i>	<i>Edaphobacter</i>	0.801	0.0099
<i>Rhodanobacter</i>	<i>Enterobacteriaceae_unclassified</i>	-0.6285	0.0198
<i>Rhodanobacter</i>	<i>Frankiales_unclassified</i>	0.8164	0.0099
<i>Rhodanobacter</i>	<i>Gaiellales_unclassified</i>	0.7761	0.0099
<i>Rhodanobacter</i>	<i>Galbitalea</i>	0.8499	0.0099
<i>Rhodanobacter</i>	<i>Gemmataceae_unclassified</i>	0.4778	0.0396
<i>Rhodanobacter</i>	<i>Granulicella</i>	0.9096	0.0099
<i>Rhodanobacter</i>	<i>Iamia</i>	0.8828	0.0099
<i>Rhodanobacter</i>	IMCC26256_ge	0.8993	0.0099
<i>Rhodanobacter</i>	<i>Isosphaeraceae_unclassified</i>	0.6114	0.0198
<i>Rhodanobacter</i>	<i>Janthinobacterium</i>	-0.7784	0.0099
<i>Rhodanobacter</i>	<i>Jatrophihabitans</i>	0.7414	0.0297
<i>Rhodanobacter</i>	KF_JG30_B3_ge	0.7278	0.0198
<i>Rhodanobacter</i>	<i>Lawsonella</i>	-0.56	0.0198
<i>Rhodanobacter</i>	<i>Leuconostoc</i>	-0.4848	0.0297
<i>Rhodanobacter</i>	<i>Micropepsaceae_unclassified</i>	0.8316	0.0099
<i>Rhodanobacter</i>	<i>Mucilaginibacter</i>	0.784	0.0099
<i>Rhodanobacter</i>	<i>Ocellatibacter</i>	0.9115	0.0099
<i>Rhodanobacter</i>	<i>Paracoccus</i>	-0.5079	0.0495
<i>Rhodanobacter</i>	<i>Pedosphaeraceae_ge</i>	0.8516	0.0099
<i>Rhodanobacter</i>	<i>Phenylobacterium</i>	0.7777	0.0297
<i>Rhodanobacter</i>	<i>Pseudolabrys</i>	0.6153	0.0099
<i>Rhodanobacter</i>	<i>Pseudomonas</i>	-0.5055	0.0396
<i>Rhodanobacter</i>	RCP2_54_ge	0.8097	0.0099
<i>Rhodanobacter</i>	<i>Roseiarcus</i>	0.7133	0.0198
<i>Rhodanobacter</i>	<i>Saccharimonadales_unclassified</i>	0.455	0.0396
<i>Rhodanobacter</i>	<i>Solirubrobacteraceae_unclassified</i>	0.8568	0.0198
<i>Rhodanobacter</i>	<i>Solirubrobacterales_unclassified</i>	0.8588	0.0099
<i>Rhodanobacter</i>	<i>Sphingomonadaceae_unclassified</i>	0.4842	0.0297
<i>Rhodanobacter</i>	<i>Staphylococcus</i>	-0.5193	0.0198
<i>Rhodanobacter</i>	Subgroup_13_ge	0.5406	0.0396
<i>Rhodanobacter</i>	Subgroup_2_ge	0.8628	0.0495
<i>Rhodanobacter</i>	<i>Tepidisphaerales_unclassified</i>	0.6729	0.0297
<i>Rhodanobacter</i>	<i>Thermoleophilia_unclassified</i>	0.7003	0.0099
<i>Rhodanobacter</i>	<i>Tundrisphaera</i>	0.6042	0.0099
<i>Rhodanobacter</i>	uncultured	0.8411	0.0099
<i>Rhodanobacter</i>	uncultured_ge	0.8642	0.0099
<i>Rhodanobacter</i>	<i>Verrucomicrobiaceae_unclassified</i>	-0.5151	0.0297
<i>Rhodanobacter</i>	WD2101_soil_group_ge	0.6635	0.0297
<i>Rhodanobacter</i>	WD260_ge	0.6857	0.0099
<i>Rhodanobacter</i>	WPS_2_ge	0.8374	0.0099
<i>Rhodanobacter</i>	<i>Xanthobacteraceae_unclassified</i>	0.5919	0.0495