

Supplementary Information on Results

Conversion of methanol and multi-carbon substrates in the Substrate SIP experiment

Methanol was supplemented at low concentrations (1mM daily) resulting in a gradually formation of CO₂ evidently after five days of treatments indicating a utilization of methanol (Figure S4A). Consumption of additionally supplemented methane (200 p.p.m.) was not observed in any treatment (Figure S4B and E) suggesting no stimulation of high affinity methanotrophs. The capacity of active methylotrophs to utilize multi-carbon compounds such as the common intermediate of anaerobic organic matter degradation acetate (C₂) or plant-derived compounds such as xylose (C₅), glucose (C₆) and vanillic acid (C₈) was analysed. The disappearance of supplemented substrates correlated with the formation of CO₂ indicating microbial utilization of substrates (Figure S4E and F). The amount of CO₂ detectable in [¹²C]- and [¹³C]-treatments was similar suggesting no preferential utilization of [¹²C]-substrates. In general, increase of [¹³C]-CO₂ was linear for methanol treatments and exponential for multi-carbon substrate treatments (Figure S4A and F). The corresponding carbon recovery was about 20% for methanol treatments and ranged from 5% (first pulse) to 22% (last pulse) for multi-carbon substrate treatments.

Effect of pH on methanol utilization in the pH shift SIP experiment

The pH did not change in both treatments, i.e. 'pH 4' with *in situ* pH and 'pH 7' with pH adjusted to neutral. CO₂ formation was higher at neutral pH in both, control and methanol treatments (Figure S4C and D). Similar amounts of CO₂ were detected in [¹²C]- and [¹³C]-treatments suggesting no preferential utilization of [¹²C]-methanol. In accordance with [¹³C]-methanol treatments of the Substrate SIP experiment, a continuous formation of [¹³C]-CO₂ per [¹³C]-methanol pulse was observed (Figure S4C and D) with carbon recoveries of 14% (pH4) and 30% (pH7).

Microbial community shaping effect of multi-carbon substrates and pH

Between [¹²C]-, [¹³C]- and combined dataset derived sequences only minor differences were noticeable observed employing in a nMDS analysis (Figure S5). The mean coverage was 98.8±0.66% for 16S rRNA (Figure S6A), 99.08±0.64% for *mxoF* (Figure S7A), and 98.44±0.29% for ITS (Figure S8A). The amount of detected genotypes was for bacterial and fungal phylotypes >100 (Figure S6B and S8B) and for *mxoF* genotypes >50 (Figure S7B). Chao 1 indices indicated higher numbers (Figure S6F, S7F and S8F) and almost no domination of single taxa were observed (Figure S6C,D,E; S7C,D,E and S8C,D,E) indicative for a diverse microbial community at t₀ and the later treatments. Treatments affected the microbial community composition significantly whereas pH had a higher influence on the bacterial community and multi-carbon substrates (i.e. sugars and acetate) showed higher influence on fungal community (Figure S5; Table S13 for 16S, S16 for *mxoF*, S15 for ITS).

Bacterial communities with *in situ* pH (t₀ and treatments) were dominated by *Actinobacteria*, *Planctomycetes* and *Proteobacteria*, with domination of *Gammaproteobacteria* over *Alphaproteobacteria* (abundant in methanol treatments) and *Betaproteobacteria* (abundant in sugar and vanillic acid treatments), and neutral pH communities were dominated by *Bacteroidetes* (Figure S3A, Table S17). Focussing on methylotrophs, *Methylobacterium*-related genotypes decreased and *Hyphomicrobium*-related genotypes increase in *in situ* pH

treatments and at neutral pH the initial low abundant *Methylobacterium*-related genotypes increased (Figure S9, Table S18). Abundance of *Ascomycota* and *Basidiomycota* was balanced in fungal communities with a domination of *Basidiomycota* in acetate and sugar treatments mainly contributed by *Trichosporon*-related genotypes (Figure S3B, Table S12).

Identification of methanol-utilizing bacteria and fungi in the Forest soil – occurrence of *Corynebacterium* and *Rhodanobacter* phylotypes

Analysing all fractions of Substrate SIP experiments revealed the predominance of a *Corynebacterium*-related phylotype (OTU_{16S6}48; sequence identity 93% (Table S2) in acetate, xylose, vanillic acid and CO₂+methanol treatments (Figure S10). Fractions of the treatment pH4 of the pH shift SIP experiment were dominated by a *Rhodanobacter*-related phylotype ((OTU_{16S}300; sequence identity 99% (Table S2). Both phylotypes were highly abundant in both [¹²C]- and [¹³C]-fractions and thus a labelling was not likely. We considered them as artefactual and excluded them from further analyses.

List of supplementary Figures

- Figure S1.** nMDS analyses of bacterial and fungal communities in the 'heavy' and 'middle' fractions of both SIP experiments.
- Figure S2.** Gene numbers of *mmoX* genes of treatments with different pH in the pH shift SIP experiment.
- Figure S3.** Bacterial (A) and fungal (B) phyla composition after different substrate or pH treatments.
- Figure S4.** CO₂ formation and conversion of the different multi-carbon substrates in the soil slurry treatments
- Figure S5.** nMDS analyses of the bacterial community (A), the fungal community (B) and *mxoF* sequences (C) from different substrate or pH treatments.
- Figure S6.** Diversity and richness estimators of 16S rRNA gene sequences from pyrosequencing amplicon pools at similarity level 90.1% (family level).
- Figure S7.** Diversity and richness estimators of *mxoF* sequences from pyrosequencing amplicon pools at similarity level of 90%.
- Figure S8.** Diversity and richness estimators of ITS gene sequences from pyrosequencing amplicon pools at similarity level of 97% (species level).
- Figure S9.** Composition of the various *mxoF* phylotypes after different substrate or pH treatments.
- Figure S10.** Bacterial phyla composition in the 'heavy' fractions after different substrate or pH treatments based on all detected phylotypes.

List of supplementary Tables

- Table S1.** Relative abundances of labeled bacterial taxa (OTU) based on 16S rRNA gene sequences in all fractions (H, heavy; M, middle; L, light) of [¹²C]- and [¹³C₁]-methanol treatment of Substrate SIP experiment.
- Table S2.** Taxonomic affiliation of bacterial phylotypes (OTUs with family-level cut-off 90.0% based on 16S rRNA gene sequences) in numerical order.
- Table S3.** Relative abundances of labeled taxa (OTU) based on *mxoF* gene sequences in all fractions (H, heavy; M, middle; L, light) of [¹²C]- and [¹³C₁]- methanol treatments of Substrate SIP experiment.
- Table S4.** Relative abundances of labeled fungal taxa (OTU) based on ITS gene sequences in all fractions (H, heavy; M, middle; L, light) of [¹²C]- and [¹³C₁]-methanol treatments of Substrate SIP experiment.
- Table S5.** Taxonomic affiliation of fungal phylotypes (ITS gene sequences clustered at species-level 97% similarity cut-off) in numerical order.
- Table S6.** Relative abundances of labeled bacterial taxa (OTU) based on 16S rRNA gene sequences in all fractions (H, heavy; M, middle; L, light) of [¹²C]- and [¹³C₁]-methanol treatment at pH 4 of pH SIP experiment.
- Table S7.** Relative abundances of labeled bacterial taxa (OTU) based on 16S rRNA gene sequences in all fractions (H, heavy; M, middle; L, light) of [¹²C]- and [¹³C₁]-methanol treatment at pH 7 of pH SIP experiment.
- Table S8.** Relative abundances of labeled taxa (OTU) based on *mxoF* gene sequences in all fractions (H, heavy; M, middle; L, light) of [¹²C]- and [¹³C₁]- methanol treatments at pH 4 of pH SIP experiment.
- Table S9.** Relative abundances of labeled taxa (OTU) based on *mxoF* gene sequences in all fractions (H, heavy; M, middle; L, light) of [¹²C]- and [¹³C₁]- methanol treatments at pH 7 of pH SIP experiment.
- Table S10.** Relative abundances of labeled fungal taxa (OTU) based on ITS gene sequences in all fractions (H, heavy; M, middle; L, light) of [¹²C]- and [¹³C₁]- methanol treatments at pH 4 of pH SIP experiment.
- Table S11.** Relative abundances of labeled fungal taxa (OTU) based on ITS gene sequences in all fractions (H, heavy; M, middle; L, light) of [¹²C]- and [¹³C₁]- methanol treatments at pH 7 of pH SIP experiment.
- Table S12.** Relative abundance of fungal taxa based on ITS gene sequences from combined pyrosequencing data sets of [¹²C]- and [¹³C₁]-substrate treatments of both SIP experiments.
- Table S13.** Similarity analyses of bacterial communities (family-level with 90.1% cut-off of 16S rRNA gene sequence) of both SIP experiments based on ANOSIM (Analysis of Similarity) and NPMANOVA (non-parametric multivariate analysis of variance).
- Table S14.** Similarity analyses of fungal communities (family-level with 97.0% cut-off of ITS gene sequence) of both SIP experiments based on ANOSIM (Analysis of Similarity) and NPMANOVA (non-parametric multivariate analysis of variance).

- Table S15.** Similarity analyses of *mxnF*-possessing methylotrophic communities (90% cut-off) of both SIP experiments based on ANOSIM (Analysis of Similarity) and NPMANOVA (non-parametric multivariate analysis of variance).
- Table S16.** Relative abundance of bacterial taxa based on 16S rRNA gene sequences from combined pyrosequencing data sets of [¹²C]- and [¹³C_u]-substrate treatments of both SIP experiments.
- Table S17.** Relative abundance of methylotrophic taxa (OTU) based on *mxnF* gene sequences from combined pyrosequencing data sets of [¹²C]- and [¹³C_u]-substrate treatments of both SIP experiments.

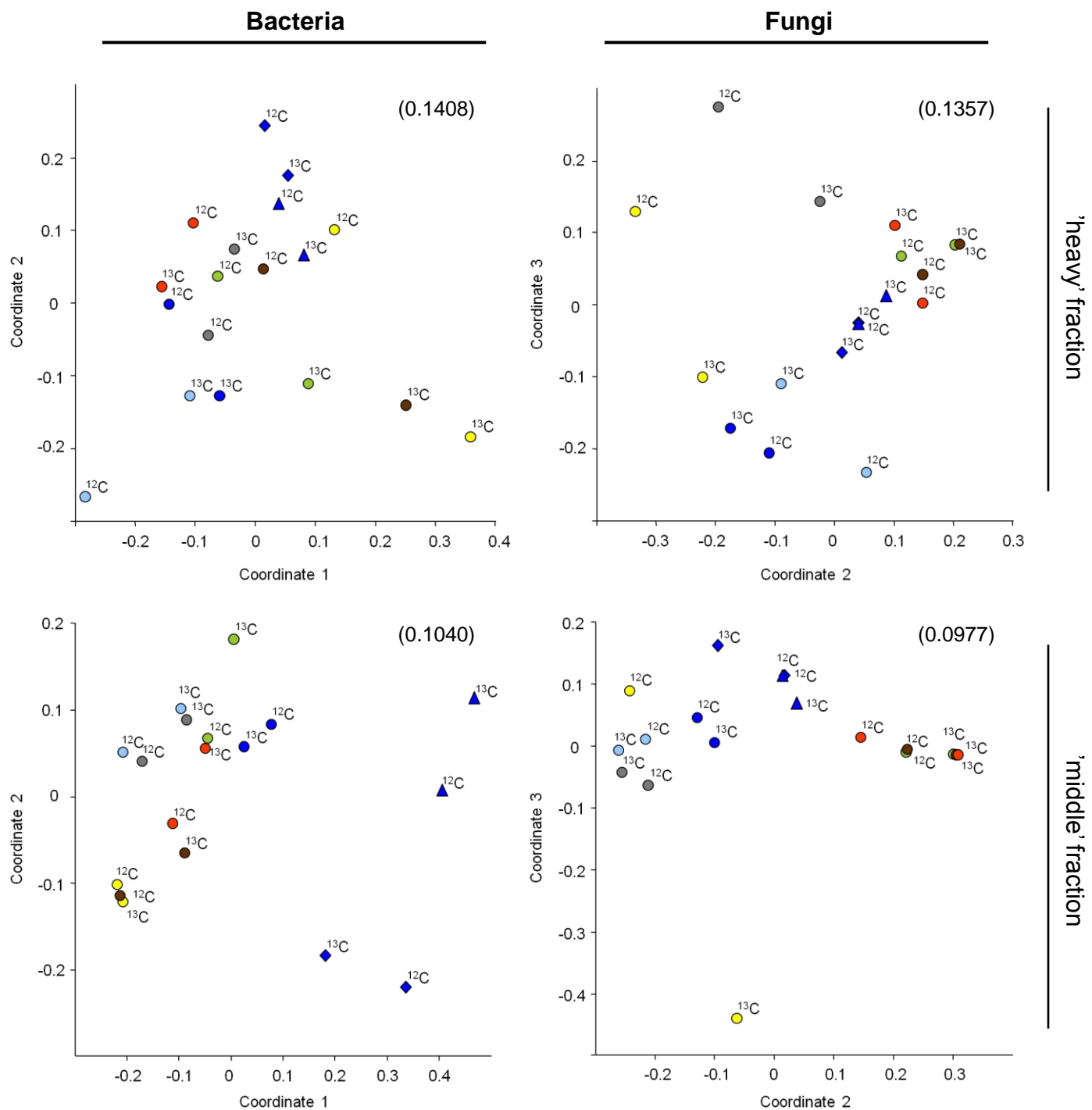


Figure S1. nMDS analyses of bacterial and fungal communities in the 'heavy' and 'middle' fractions of both SIP experiments. Figures show analyses of relative abundances of all sequences in 'heavy' and 'middle' fractions of $[^{12}\text{C}]$ - and $[^{13}\text{C}]$ -treatments with cut-off values of 90.1% for Bacteria (16S rRNA gene sequences, family-level; reduced dataset, for detailed information see Supplemental Materials and Methods) and 97% for Fungi (ITS gene sequences species-level). Stress values are given in brackets. All analyses are based on Bray-Curtis similarity index.

Symbols according to SIP experiment: ○, substrate SIP; ◇, pH 4; △, pH 7. ^{12}C indicates $[^{12}\text{C}]$ -substrates and ^{13}C indicates $[^{13}\text{C}]$ -substrates. Symbols according to supplemented $[^{13}\text{C}]$ -substrate: ●, methanol; ●, acetate +; ●, glucose +; ●, xylose +; ●, vanillic acid +; ●, CO_2 +; ●, CO_2 (cross indicates additional supplementation of $[^{12}\text{C}]$ -methanol in substrate SIP experiment).

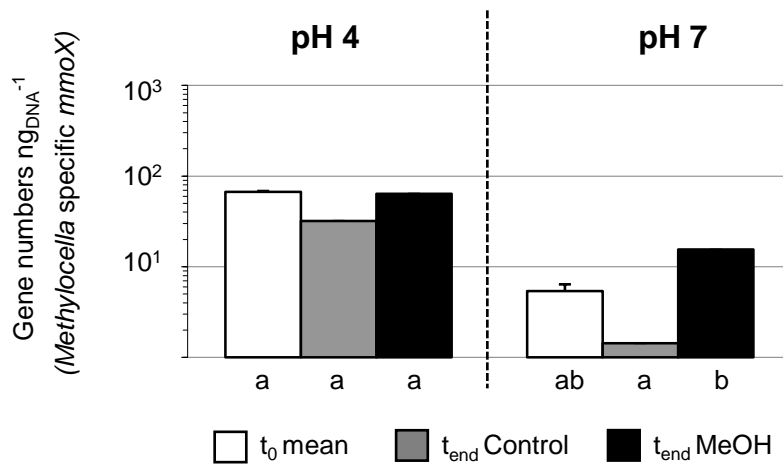
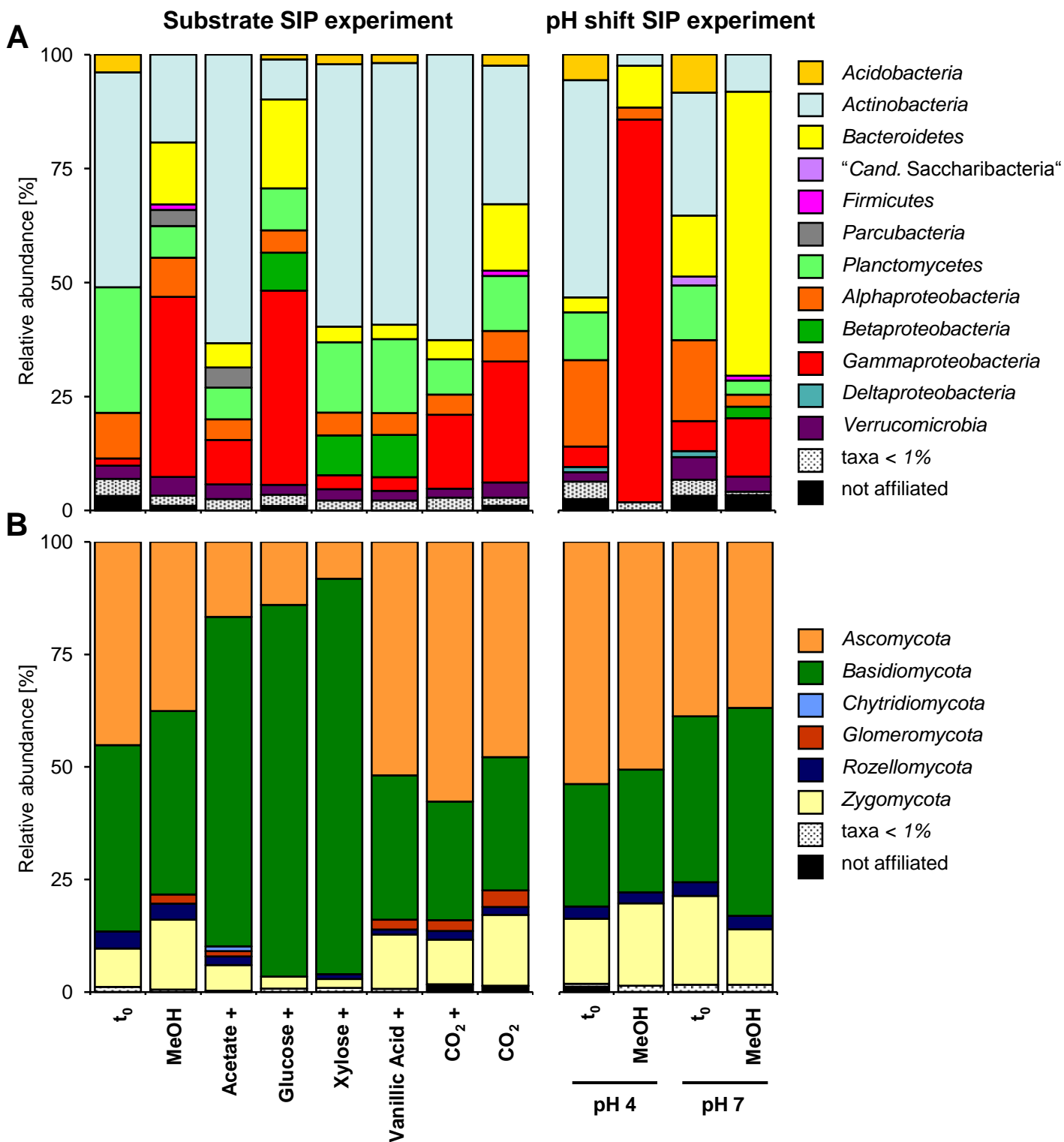


Figure S2. Gene numbers of *mmoX* genes of treatments with different pH in the pH shift SIP experiment. Columns, mean values of the experimental replicates. Error bars, standard deviation; if not visible, the variability between replicates was below 0.5%. Different letters, significant differences between samples (t-test; normal distribution was assumed based on the Shapiro-Wilk-test; n=3).



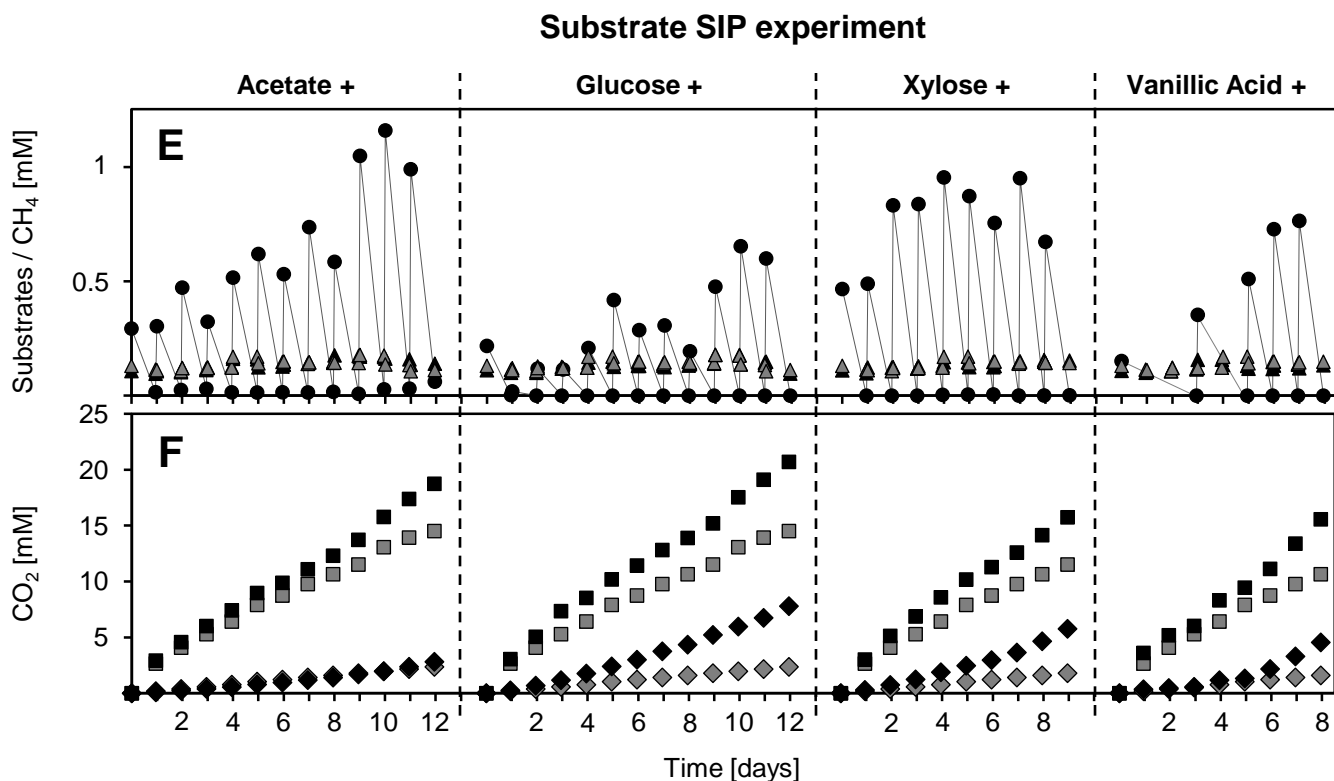
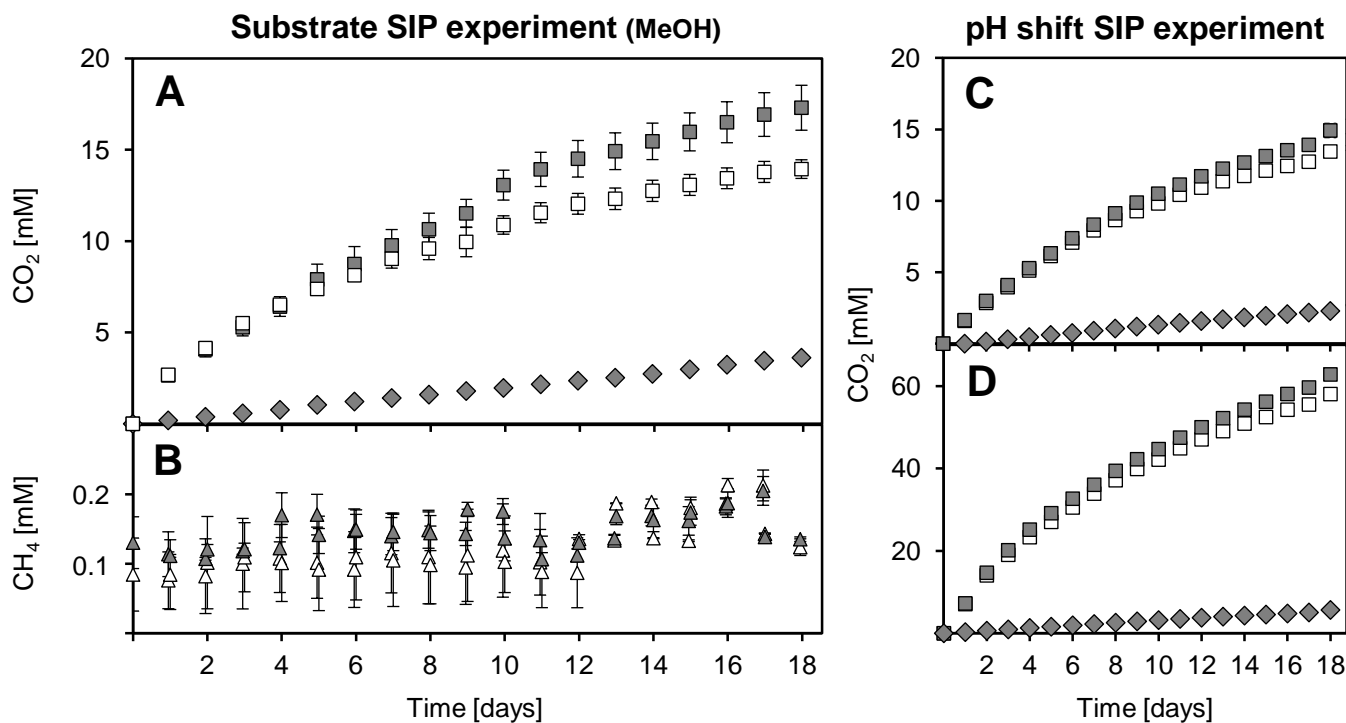


Figure S4. CO_2 formation and conversion of the different multi-carbon substrates in the soil slurry treatments. Shown are cumulative $^{12}CO_2$ and $^{13}CO_2$ concentrations of substrate SIP experiment treatments pulsed with methanol (A) and other multi-carbon substrates (F), and methanol treatments of the pH shift SIP experiment with pH 4 (C) and pH 7 (D). A cross indicates additional methanol supplementation. Substrate utilization is supposed by the conversion of supplemented substrates (E), methane utilization in the substrate SIP experiment treatments is negligible (B, E). Methanol treatments serve as control treatments for supplemented multi-carbon substrate treatments. All values are mean values of replicates; error bars represent standard deviations. White symbols, unsupplemented control; grey symbols, methanol treatments; black symbols, substrate treatments; \diamond , $[^{13}C]-CO_2$; \square , $[^{12}C]-CO_2$; \circ , substrates; \triangle , methane.

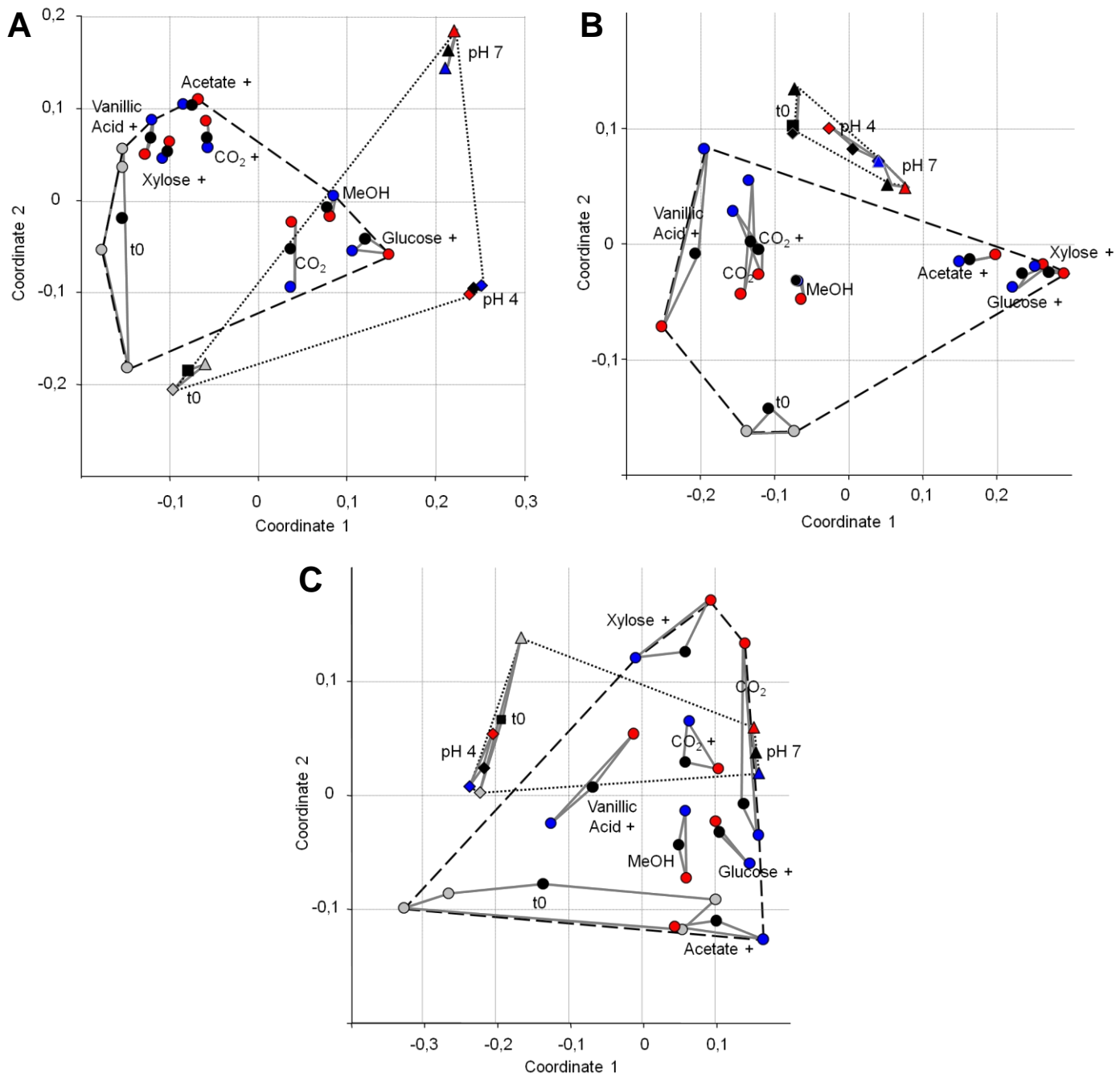


Figure S5. nMDS analyses of the bacterial community (A), the fungal community (B) and *mxa**F* sequences (C) from different substrate or pH treatments.** Figures show analyses of relative abundances of sequences with cut-off values of 90.1% for Bacteria (16S rRNA gene sequences, family-level), 97% for Fungi (ITS gene sequences species-level) and 90% for *mx**a**F*. Stress values are 0.1002 for bacteria, 0.1245 for fungi and 0.1868 for *mx**a**F*. All analyses are based on Bray-Curtis similarity index. Blue, dataset of [¹²C]-replicate; red, dataset of [¹³C]-replicate; black, combined datasets of [¹²C]- and [¹³C]-replicates; grey, *t*₀ replicates; ○, substrate SIP experiment; □, combined *t*₀ datasets of pH shift SIP experiment; ◇, pH 4 treatment; △, pH 7 treatment. A cross indicates additional supplementation of methanol in substrate SIP experiment. Dashed lines indicate convex polygon including all data from substrate SIP experiment. Grey lines indicate convex polygons including all data for each substrate treatment. Dotted lines indicate convex polygon including all data from pH shift SIP experiment.

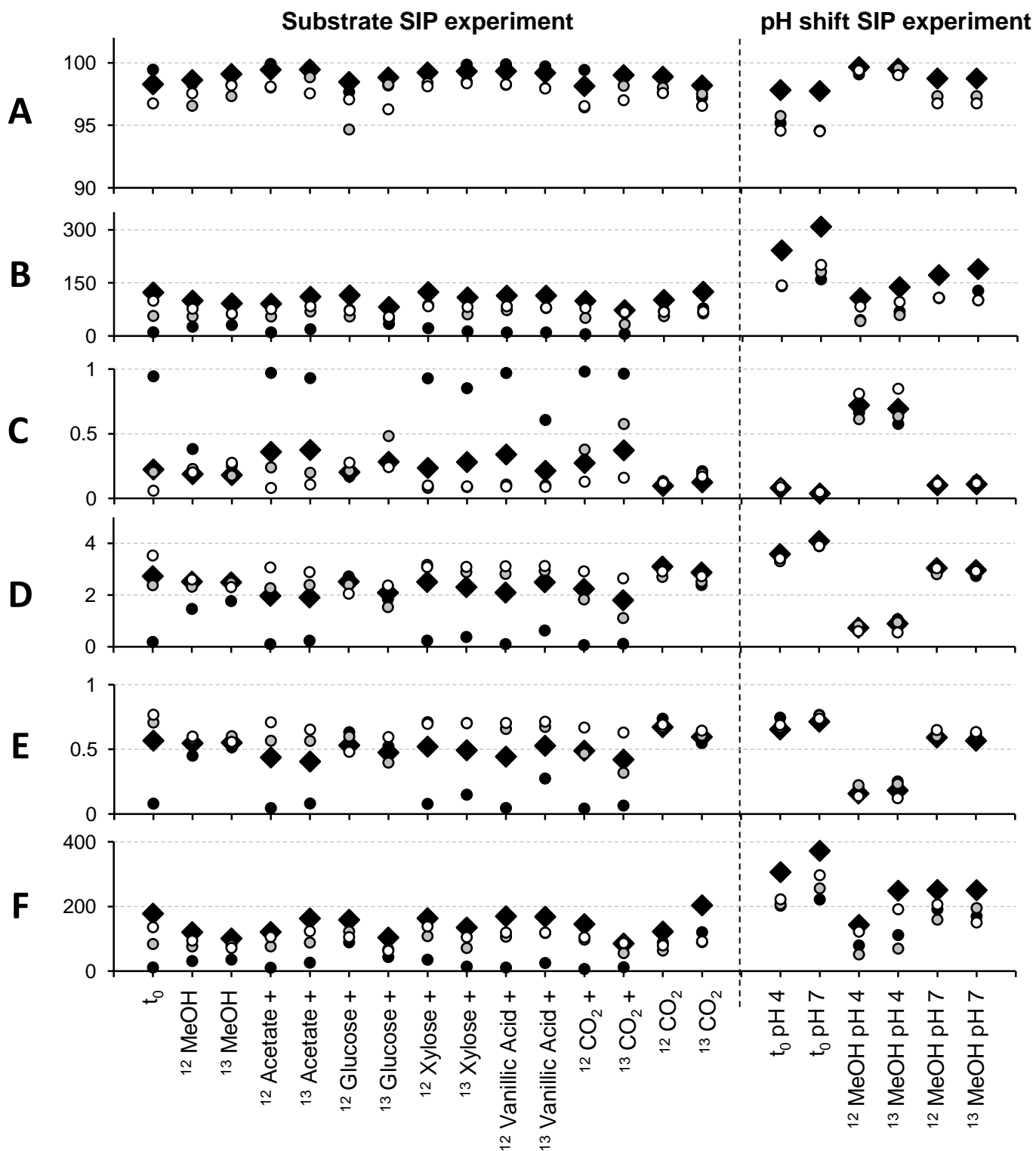


Figure S6. Diversity and richness estimators of 16S rRNA gene sequences from pyrosequencing amplicon pools at similarity level 90.1% (family level). Figures indicating coverage (%) (A), numbers of OTUs (B), dominance D (C), Shannon index H (D), equitability J (E) and Chao1 index (F). Shown are values of t_0 (no treatment, combined data sets of replicates for substrate SIP experiment t_0) and after treatment for both SIP experiments. A ¹² indicates [¹²C]-substrate, ¹³ indicates [¹³C_v]-substrate. A cross indicates additional supplementation of methanol in substrate treatments. Symbols: ◆, combined datasets of ‘heavy’, ‘middle’ and ‘light’ fractions; ●, ‘heavy’ fraction; ◐, ‘middle’ fraction; ○, ‘light’ fraction.

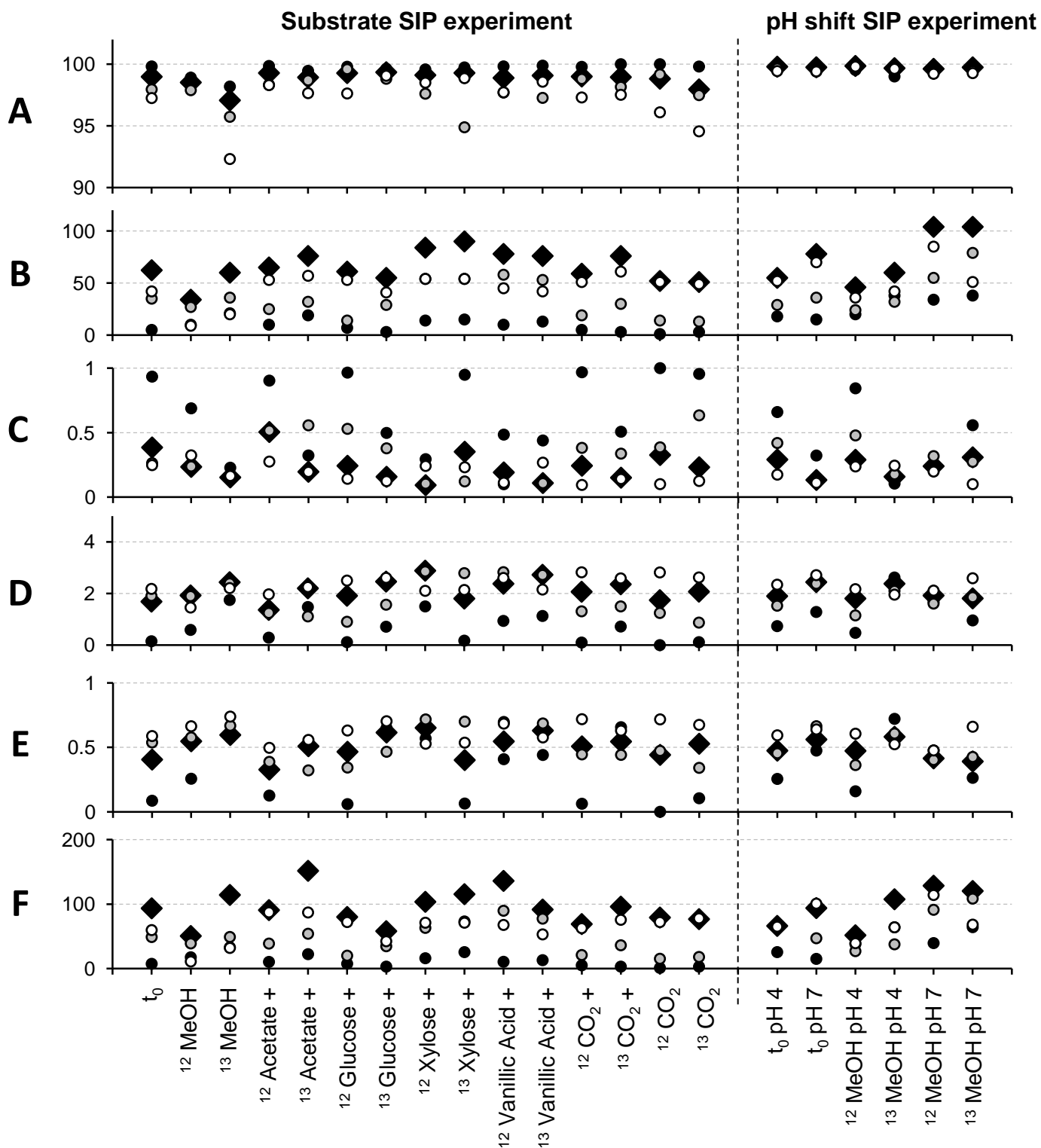


Figure S7. Diversity and richness estimators of *mxrF* sequences from pyrosequencing amplicon pools at similarity level of 90%. Figures indicating coverage (%) (A), numbers of OTUs (B), dominance D (C), Shannon index H (D), equitability J (E) and Chao1 index (F). Shown are values of t_0 (no treatment, combined datasets of replicates for substrate SIP experiment t_0) and after treatment for both SIP experiments. A ¹² indicates [¹²C]-substrate, ¹³ indicates [¹³C_u]-substrate. A cross indicates additional supplementation of methanol in substrate treatments. Symbols: ◆, combined data sets of 'heavy', 'middle' and 'light' fractions; ●, 'heavy' fraction; ●, 'middle' fraction; ○, 'light' fraction.

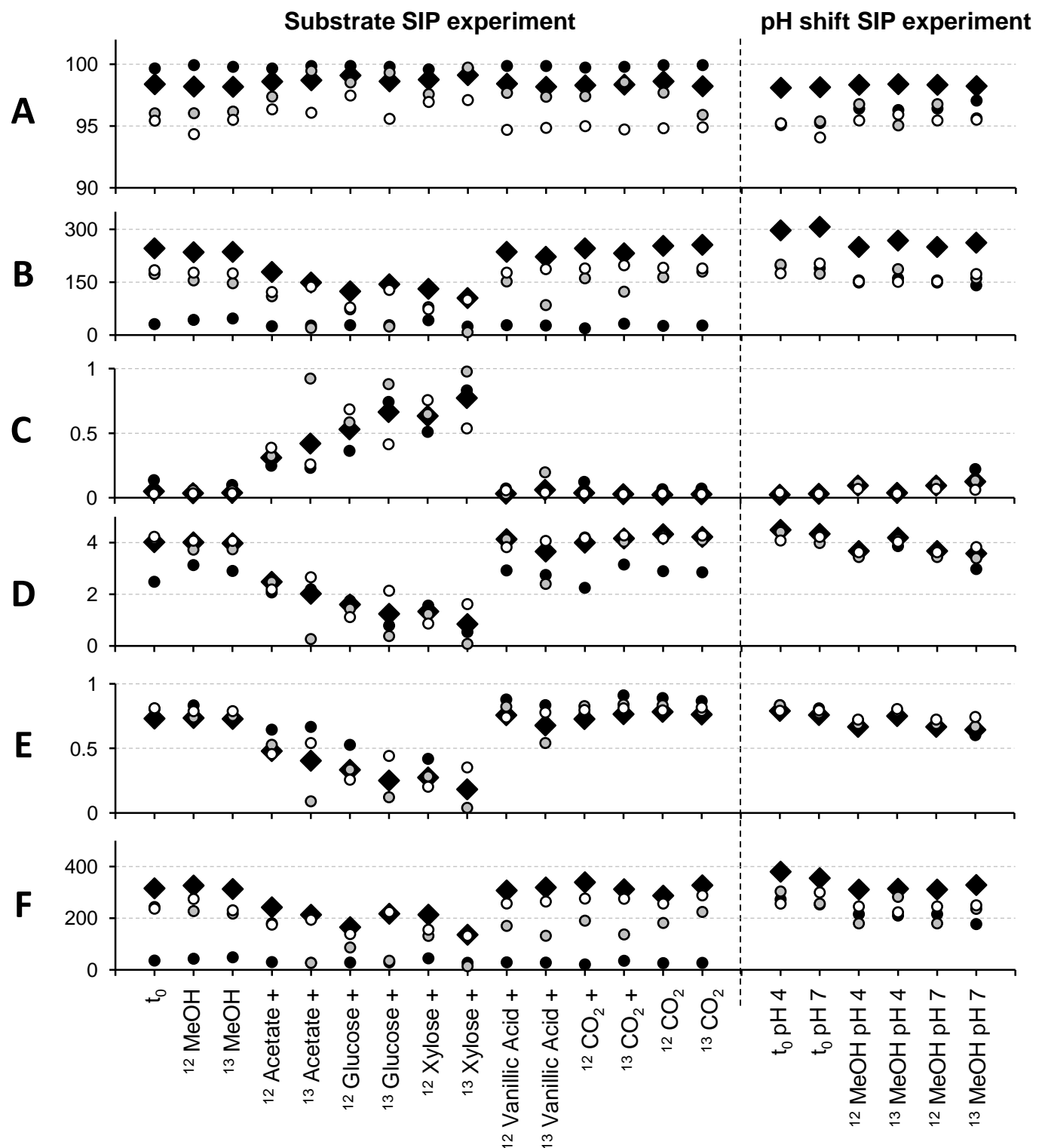


Figure S8. Diversity and richness estimators of ITS gene sequences from pyrosequencing amplicon pools at similarity level of 97% (species level). Figures indicating coverage (%) (A), numbers of OTUs (B), dominance D (C), Shannon index H (D), equitability J (E) and Chao1 index (F). Shown are values of t_0 (no treatment, combined datasets of replicates for substrate SIP experiment t_0) and after treatment for both SIP experiments. A 12 indicates [^{12}C]-substrate, 13 indicates [^{13}C]-substrate. A cross indicates additional supplementation of methanol in substrate treatments. Symbols: \blacklozenge , combined data sets of 'heavy', 'middle' and 'light' fractions; \bullet , 'heavy' fraction; \bullet , 'middle' fraction; \circ , 'light' fraction.

Substrate SIP experiment

pH shift SIP experiment

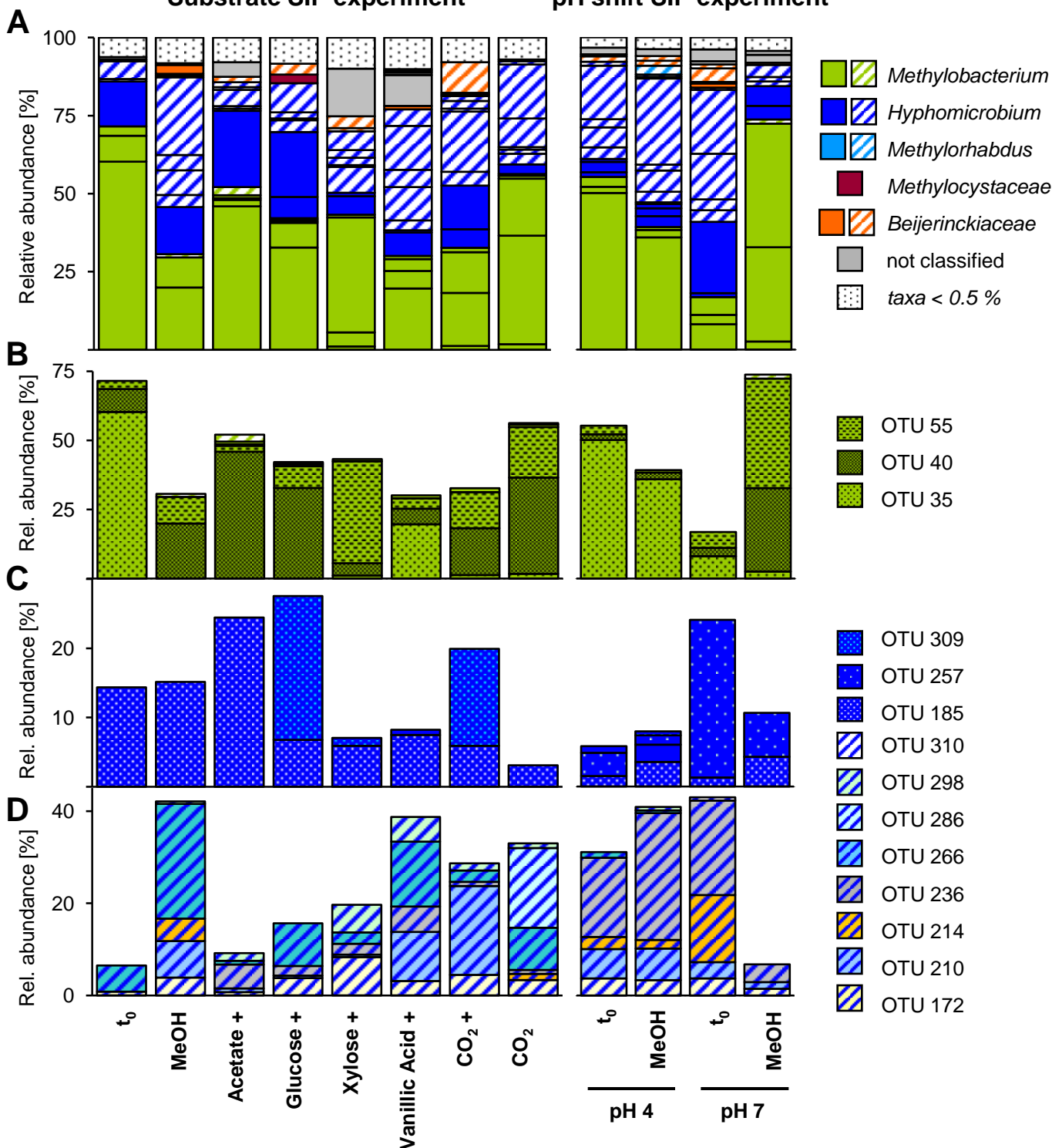


Figure S9. Composition of the various *mxoF* phylotypes after different substrate or pH treatments. Shown are relative abundances of combined (^{12}C and ^{13}C) datasets of all *mxoF*-affiliated phylotypes (A) and in more detail *Methylobacterium*-affiliated (B) and *Hyphomicrobium*-affiliated phylotypes (C, D). Same taxonomic affiliation (family) is indicated by equal colors; ambiguous affiliation (i.e. sequence identity with BLASTn <90% as well as ambiguous position in phylogenetic tree) is indicated by shading. Additional [^{12}C]-methanol supplementation in substrate SIP experiment is indicated by a cross. Shown are phylotypes with relative abundances $\geq 0.5\%$ in combined (^{12}C and ^{13}C) datasets.

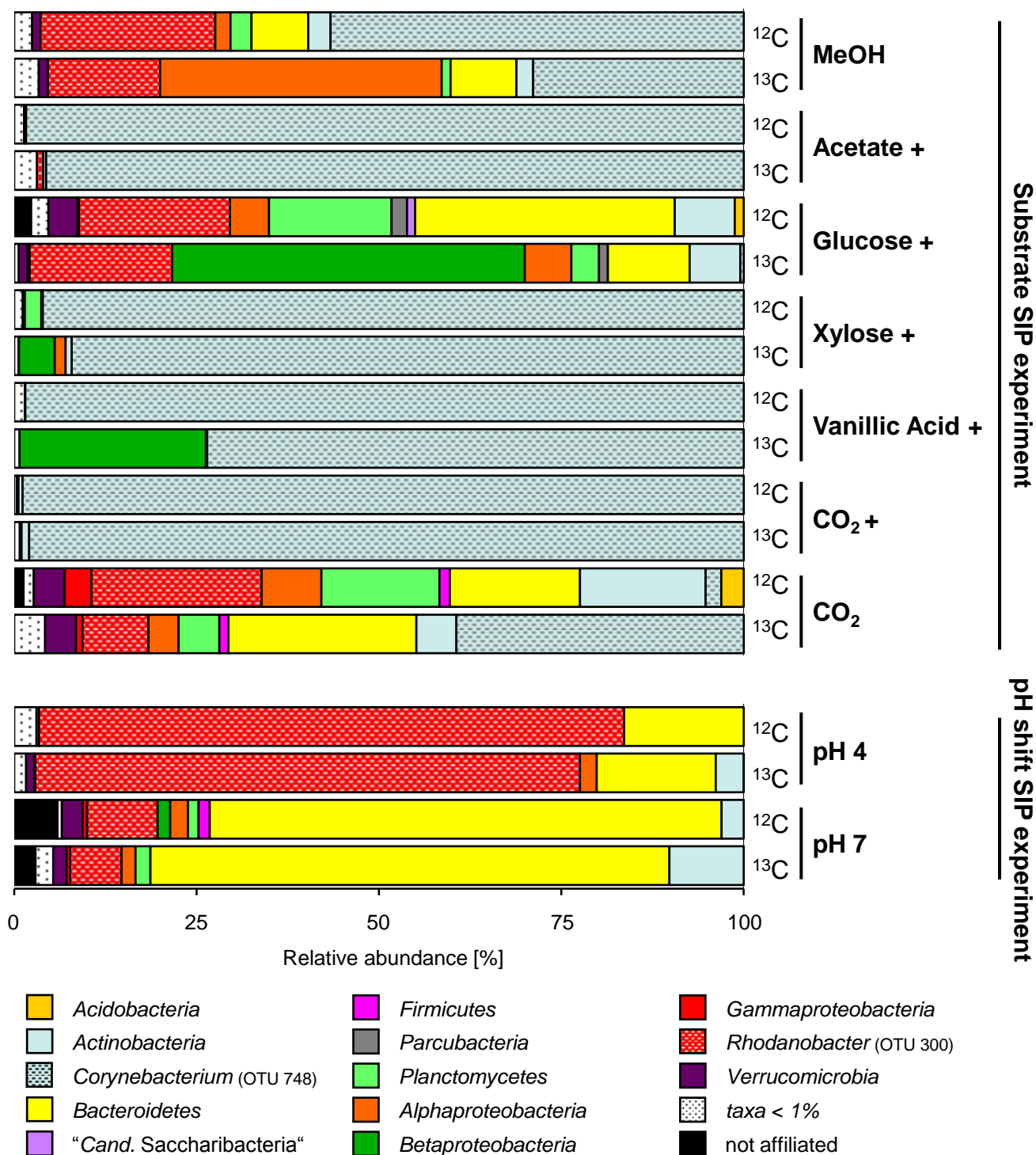


Figure S10. Bacterial phyla composition in the 'heavy' fractions after different substrate or pH treatments based on all detected phlotypes. Shown are relative abundances ($\geq 1\%$) of bacterial phyla based on 16S rRNA gene sequences in the 'heavy' fractions of $[^{12}\text{C}]$ - and $[^{13}\text{C}_u]$ -substrate treatments of both SIP experiments. Hatching indicates dominant families in 'heavy' fractions that were removed for the determination of labelled phlotypes. A cross indicates additional supplementation of methanol in substrate treatments. Phlotypes were clustered with 90.1 % threshold for 16S rRNA genes (family-level) and taxonomic affiliation was confirmed with a GenBank database.

Table S1. Relative abundances of labeled bacterial taxa (OTU) based on 16S rRNA gene sequences in all fractions (H, heavy; M, middle; L, light) of [¹²C]- and [¹³C₁]-methanol treatment of Substrate SIP experiment. Black faces indicate values that were used for calculating 'labeling proportions' as indicators of relative importance. Bold faces indicate 'labeling proportions' > 5 %.

Taxonomic affiliation ^a	Labeled OTU	Relative abundance [%]						Labeling proportion [%]	
		¹² C			¹³ C			H	M
		H	M	L	H	M	L		
<i>Acidobacteria</i>									
<i>Acidobacteriaceae</i> ^c	OTU 542	0.0	0.2	0.2	0.7	0.3	0.4	1.3	
<i>Acidobacterium</i> ^d	OTU 545	0.0	0.9	0.7	0.5	0.0	0.1	0.9	
<i>Actinobacteria</i>									
<i>Acidimicrobiaceae</i> ^c	OTU 652	0.0	0.2	0.7	0.5	2.0	1.8		12.3
<i>Kineosporiaceae</i> ^c	OTU 703	0.9	2.8	1.7	0.7	4.3	1.3		26.2
<i>Armatimonadetes</i>									
<i>Fimbriimonadaceae</i> ^c	OTU 592	0.0	0.5	0.1	0.0	1.2	0.8		7.4
<i>Chlamydiae</i>									
<i>Parachlamydiaceae</i> ^c	OTU 108	0.0	0.0	0.0	0.5	0.0	0.0	0.9	
<i>Firmicutes</i>									
<i>Bacillus</i> ^d	OTU 202	0.0	0.0	0.2	0.5	0.3	0.0	0.9	
<i>Parcubacteria</i> ^{b,e}	OTU 1155	0.0	0.2	0.0	1.0	0.0	0.1	1.7	
<i>Planctomycetes</i>									
<i>Planctomycetales</i> ^b	OTU 836	0.0	0.0	0.7	0.2	0.5	0.0		3.3
<i>Planctomycetaceae</i> ^c	OTU 968	0.0	0.0	0.2	0.0	0.5	0.9		3.3
<i>Alphaproteobacteria</i>									
<i>Methylovirgula</i> ^d	OTU 438	3.5	0.5	2.5	52.5	3.7	1.8	91.1	22.1
<i>Sphingomonas</i> ^d	OTU 449	0.0	0.0	0.5	0.5	0.1	0.5	0.9	
<i>Acetobacteraceae</i> ^c	OTU 467	0.0	0.5	0.2	0.0	0.8	0.6		4.9
<i>Betaproteobacteria</i>									
<i>Methylophilaceae</i> ^c	OTU 360	0.0	0.0	0.0	0.7	0.0	0.0	1.3	
<i>Verrucomicrobia</i>									
<i>Spartobacteria</i> ^b	OTU 6	0.0	0.9	0.7	0.7	0.4	0.7	1.3	
<i>Verrucomicrobiales</i> ^b	OTU 18	1.8	2.5	1.8	0.7	3.4	1.3		20.5
Percentage of labeled taxa to total fraction [%]					58	17			

^a Taxonomic affiliation was done with BLASTn (November 2015) and is based on the next cultivated hit for each OTU (for further information see Table S8)

^b Sequence identity of next cultured hit < 90 %, phylogenetic affiliation up to order level

^c Sequence identity of next cultured hit < 95 %, phylogenetic affiliation up to family level

^d Sequence identity of next cultured hit ≥ 95 %, phylogenetic affiliation up to genus level

^e known as "Candidate phylum OD1"

Table S2. Taxonomic affiliation of bacterial phylotypes (OTUs with family-level cut-off 90.0% based on 16S rRNA gene sequences) in numerical order. Listed are closest related sequences including cultured and environmental hits (closest related sequences are in grey bold if they are identical with the closest cultured related sequence). BLASTn analyses are based on OTU sequence lengths of 400 – 449 nt.

OTU	closest cultured related sequence ^a					closest related sequence ^b (environmental samples included)				
	Q ^d	Id ^e	Accession ^c	Phylum Class Order	Family	Q ^d	Id ^e	Accession ^c		
6	<i>Chthoniobacter flavus</i>	100	90	NR_115225	Verrucomicrobia Spartobacteria Chthoniobacterales	Chthoniobacteraceae	uncult. <i>Verrucomicrobia</i>	100	97	JQ368535
9	<i>Chthoniobacter flavus</i>	100	89	NR_115225	Verrucomicrobia Spartobacteria Chthoniobacterales	Chthoniobacteraceae	uncult. <i>Verrucomicrobia</i>	100	99	JQ369834
17	<i>Chthoniobacter flavus</i>	100	83	NR_115225	Verrucomicrobia Spartobacteria Chthoniobacterales	Chthoniobacteraceae	uncult. <i>Verrucomicrobia</i>	100	93	JQ366335
18	<i>Prostheco bacter debontii</i>	100	84	AJ966882	Verrucomicrobia Verrucomicrobiae Verrucomicrobiales	Verrucomicrobiaceae	uncult. <i>Verrucomicrobia</i>	100	99	AM945528
54	<i>Terrimicrobium sacchariphilum</i>	99	97	GU129926	Verrucomicrobia Verrucomicrobiae Chthoniobacterales	n.a.	uncult. <i>Verrucomicrobia</i>	99	98	JF168305
93	<i>Parachlamydia acanthamoebae</i>	100	95	JN051144	Chlamydiae Chlamydiae Chlamydiales	Parachlamydiaceae	uncult. <i>Chlamydiae</i>	96	99	AB504668
108	<i>Parachlamydia acanthamoebae</i>	100	91	NR_074972	Chlamydiae Chlamydiae Chlamydiales	Parachlamydiaceae	" <i>Candidatus Metachlamydia lacustris</i> "	99	93	GQ221847
132	<i>Conexibacter woesei</i>	100	94	NR_074830	Actinobacteria Thermoleophilia Solirubrobacterales	Conexibacteraceae	uncult. <i>Bacteria</i>	96	99	LC011356

OTU	closest cultured related sequence ^a					closest related sequence ^b (environmental samples included)				
	Q ^d	Id ^e	Accession ^c	Phylum Class Order	Family	Q ^d	Id ^e	Accession ^c		
142	Gaiella occulta	100	93	NR_118138	Actinobacteria Rubrobacteria Gaiellales	Gaiellaceae	uncult. <i>Bacteria</i>	100	99	JX100028
202	<i>Bacillus</i> sp.	99	99	GU584205	Firmicutes Bacilli Bacillales	Bacillaceae	<i>Bacillus</i> sp.	99	99	GU584205
206	<i>Paenibacillus</i> sp.	100	98	AM162325	Firmicutes Bacilli Bacillales	Paenibacillaceae	uncult. <i>Firmicutes</i>	100	99	EU810868
278	<i>Povalibacter uvarum</i>	100	92	NR_126172	Proteobacteria Gammaproteobacteria Xanthomonadales	Sinobacteraceae	uncult. <i>Gammaproteobacterium</i>	100	99	JF301246
280	<i>Steroidobacter</i> sp.	100	98	KP185148	Proteobacteria Gammaproteobacteria Xanthomonadales	Sinobacteraceae	uncult. <i>Gammaproteobacterium</i>	100	99	HF952308
300	<i>Rhodanobacter</i> sp.	99	99	JX483760	Proteobacteria Gammaproteobacteria Xanthomonadales	Xanthomonadaceae	uncult. <i>Gammaproteobacterium</i>	99	99	HF952332
343	<i>Rhodanobacter</i> sp.	72	98	AF250415	Proteobacteria Gammaproteobacteria Xanthomonadales	Xanthomonadaceae	uncult. <i>Gammaproteobacterium</i> (<i>Xanthomonadales</i>)	72	98	LC016556
358	<i>Methylophilus methylophilus</i>	99	96	KF911346	Proteobacteria Betaproteobacteria Methylophilales	Methylophilaceae	uncult. <i>Betaproteobacterium</i>	99	98	JQ371286
360	<i>Methylophilus</i> sp.	100	91	CP012020	Proteobacteria Betaproteobacteria Methylophilales	Methylophilaceae	uncult. <i>Betaproteobacterium</i>	100	98	HG529147
361	<i>Burkholderia</i> sp.	100	99	AB627009	Proteobacteria Betaproteobacteria Burkholderiales	Burkholderiaceae	uncult. <i>Bacterium</i>	100	99	KP726299

OTU	closest cultured related sequence ^a					closest related sequence ^b (environmental samples included)				
		Q ^d	Id ^e	Accession ^c	Phylum Class Order	Family		Q ^d	Id ^e	Accession ^c
379	<i>Acinetobacter</i> sp.	100	95	JF715439.	Proteobacteria Gammaproteobacteria Pseudomonadales	Moraxellaceae	uncult. <i>Gammaproteobacterium</i>	100	99	HM113016
431	<i>Caulobacter mirabilis</i>	98	95	LN867237	Proteobacteria Alphaproteobacteria Caulobacterales	Caulobacteraceae	uncult. <i>Alphaproteobacterium</i>	94	99	JN032148
438	<i>Methylovirgula ligni</i>	99	98	FM252035	Proteobacteria Alphaproteobacteria Rhizobiales	Beijerinckiaceae	uncult. <i>Alphaproteobacterium</i>	99	99	AM992784
449	<i>Sphingomonas</i> sp.	97	99	KJ654808	Proteobacteria Alphaproteobacteria Sphingomonadales	Sphingomonadaceae	uncult. <i>Alphaproteobacterium</i> (<i>Sphingobium</i> sp.)	97	99	JN860403
450	<i>Paracoccus</i> sp.	100	99	LN879490	Proteobacteria Alphaproteobacteria Rhodobacterales	Rhodobacteraceae	<i>Paracoccus</i> sp.	100	99	LN879490
460	<i>Skermanella</i> sp.	99	94	KF561388	Proteobacteria Alphaproteobacteria Rhodospirillales	Rhodospirillaceae	uncult. <i>Alphaproteobacterium</i>	99	99	EU849340
467	<i>Acidisphaera</i> sp.	100	94	KM369919	Proteobacteria Alphaproteobacteria Rhodospirillales	Acetobacteraceae	uncult. <i>Alphaproteobacterium</i>	100	98	JQ383603
479	<i>Phaeospirillum</i> sp.	97	94	HG417062	Proteobacteria Alphaproteobacteria Rhodospirillales	Rhodospirillaceae	uncult. <i>Alphaproteobacterium</i>	97	97	JQ386981
528	<i>Solibacter usitatus</i>	99	93	CP000473	Acidobacteria Solibacteres Solibacterales	Solibacteraceae	uncult. <i>Acidobacterium</i>	99	99	JX981716
542	<i>Acidipila</i> sp.	100	93	KM083127	Acidobacteria Acidobacteria Acidobacteriales	Acidobacteriaceae	uncult. <i>Acidobacterium</i>	100	99	GU598605

OTU	closest cultured related sequence ^a					closest related sequence ^b (environmental samples included)				
	Q ^d	Id ^e	Accession ^c	Phylum Class Order	Family	Q ^d	Id ^e	Accession ^c		
545	<i>Acidobacterium capsulatum</i>	98	98	AM086241	Acidobacteria Acidobacteria Acidobacteriales	Acidobacteriaceae	uncult. <i>Acidobacterium</i>	98	99	JF300928
592	<i>Fimbriimonas ginsengisoli</i>	100	93	CP007139	Armatimonadetes Fimbriimonadia Fimbriimonadales	Fimbriimonadaceae	uncult. <i>Armatimonadetes</i>	100	98	JN851205
615	<i>Gelria glutamica</i>	99	85	NR_041819	Firmicutes Clostridia Thermoanaerobacterales	Thermo- anaerobacteraceae	uncult. <i>Bacterium</i>	95	99	HQ629022
652	<i>Aciditerrimonas ferrireducens</i>	98	92	NR_112972	Actinobacteria Acidimicrobiia Acidimicrobiales	Acidimicrobiaceae	uncult. <i>Actinobacterium</i>	98	97	HQ845571
654	<i>Aciditerrimonas ferrireducens</i>	99	92	NR_112972	Actinobacteria Acidimicrobiia Acidimicrobiales	Acidimicrobiaceae	uncult. <i>Actinobacterium</i>	99	98	JQ376471
656	<i>Aciditerrimonas ferrireducens</i>	100	93	NR_112972	Actinobacteria Acidimicrobiia Acidimicrobiales	Acidimicrobiaceae	uncult. <i>Actinobacterium</i>	100	99	JQ376189
668	<i>Aciditerrimonas ferrireducens</i>	100	89	NR_112972	Actinobacteria Acidimicrobiia Acidimicrobiales	Acidimicrobiaceae	uncult. <i>Actinobacterium</i>	92	99	JX204369
703	<i>Kineosporia</i> sp.	100	94	FM886845	Actinobacteria Actinobacteria Actinomycetales	Kineosporiaceae	uncult. <i>Actinobacterium</i>	100	99	FJ661525
721	<i>Leifsonia xyli</i>	97	99	HG794292	Actinobacteria Actinobacteria Micrococcales	Microbacteriaceae	<i>Leifsonia xyli</i>	97	99	HG794292
723	<i>Pseudonocardia spinosispora</i>	98	98	NR_025367	Actinobacteria Actinobacteria Pseudonocardiales	Pseudonocardaceae	uncult. <i>Actinobacterium</i>	98	98	JN615726

OTU	closest cultured related sequence ^a					closest related sequence ^b (environmental samples included)				
	Q ^d	Id ^e	Accession ^c	Phylum Class Order	Family	Q ^d	Id ^e	Accession ^c		
748	<i>Corynebacterium nuruki</i>	100	93	NR_117816	Actinobacteria Actinobacteria Corynebacteriales	Corynebacteriaceae	uncult. <i>Actinobacterium</i>	100	94	FN667204
750	<i>Mycobacterium branderi</i>	100	98	JX266696	Actinobacteria Actinobacteria Corynebacteriales	Mycobacteriaceae	uncult. <i>Actinobacterium</i>	100	98	KF530052
752	<i>Corynebacterium nuruki</i>	99	96	NR_117816	Actinobacteria Actinobacteria Corynebacteriales	Corynebacteriaceae	uncult. <i>Actinobacterium</i>	99	97	JF208992
758	<i>Actinospica robiniae</i>	99	99	NR_042364	Actinobacteria Actinobacteria Catenulisporales	Actinospicaceae	uncult. <i>Actinobacterium</i>	99	99	AB180777
796	<i>Tepidisphaera mucosa</i>	99	92	KM052380	Planctomycetes Phycisphaerae	Tepidisphaeraceae	uncult. <i>Bacterium</i>	99	99	KJ407548
800	<i>Tepidisphaera mucosa</i>	100	89	KM052380	Planctomycetes Phycisphaerae	Tepidisphaeraceae	uncult. <i>Planctomycetes</i>	100	98	JQ663701
816	<i>Actinoallomurus</i> sp.	70	92	KR781096	Actinobacteria Actinobacteria Streptosporangiales	Thermomonosporaceae	uncult. <i>Bacterium</i>	71	95	FQ744029
836	<i>Pirellula</i> sp.	99	88	X81947	Planctomycetes Planctomycetia Planctomycetales	Planctomycetaceae	" <i>Candidatus Anammoxi-microbium moscowii</i> "	99	90	KC467065
840	<i>Thermogutta terrifontis</i>	100	86	KC867694	Planctomycetes Planctomycetia Planctomycetales	Planctomycetaceae	uncult. <i>Planctomycetes</i>	100	93	LK025317
844	<i>Thermogutta hypogea</i>	99	88	KC867695	Planctomycetes Planctomycetia Planctomycetales	Planctomycetaceae	uncult. <i>Planctomycetes</i>	99	90	LK025387

OTU	closest cultured related sequence ^a					closest related sequence ^b (environmental samples included)				
	Q ^d	Id ^e	Accession ^c	Phylum Class Order	Family	Q ^d	Id ^e	Accession ^c		
857	<i>Planctopirus limnophilus</i>	100	88	NR_074670	Planctomycetes Planctomycetia Planctomycetales	Planctomycetaceae	<i>Gimesia maris</i>	100	93	KF228168
885	<i>Nostocoida limicola</i> III	100	94	AF244752	Planctomycetes Planctomycetia Planctomycetales	Planctomycetaceae	<i>Nostocoida limicola</i> III	100	94	AF244752
904	<i>Singulisphaera</i> sp.	100	92	GQ889439	Planctomycetes Planctomycetia Planctomycetales	Planctomycetaceae	uncult. <i>Planctomycetes</i>	100	92	HM748671
923	<i>Gemmata</i> sp.	99	90	GQ889476	Planctomycetes Planctomycetia Planctomycetales	Planctomycetaceae	uncult. <i>Planctomycetes</i>	99	95	AB127858
927	<i>Gemmata</i> sp.	100	89	GQ889455	Planctomycetes Planctomycetia Planctomycetales	Planctomycetaceae	uncult. <i>Planctomycetes</i>	100	93	LK025439
939	<i>Gemmata</i> sp.	100	90	GQ889455	Planctomycetes Planctomycetia Planctomycetales	Planctomycetaceae	uncult. <i>Planctomycetes</i>	100	93	LK025552
945	<i>Isosphaera</i> sp.	100	89	GQ889426	Planctomycetes Planctomycetia Planctomycetales	Planctomycetaceae	uncult. <i>Planctomycetes</i>	100	89	FJ405890
951	<i>Gemmata</i> sp.	99	91	GQ889466	Planctomycetes Planctomycetia Planctomycetales	Planctomycetaceae	<i>Gemmata</i> sp.	99	91	GQ889466
968	<i>Zavarzinella formosa</i>	99	90	NR_042465	Planctomycetes Planctomycetia Planctomycetales	Planctomycetaceae	uncult. <i>Planctomycetes</i>	99	98	LK024693
1014	<i>Ferruginibacter lapsinanis</i>	100	97	NR_044589	Bacteroidetes Sphingobacteriia Sphingobacteriales	Chitinophagaceae	<i>Ferruginibacter lapsinanis</i>	100	97	NR_044589

OTU	closest cultured related sequence ^a					closest related sequence ^b (environmental samples included)				
	Q ^d	Id ^e	Accession ^c	Phylum Class Order	Family	Q ^d	Id ^e	Accession ^c		
1018	<i>Heliimonas saccharivorans</i>	100	95	JX458466	Bacteroidetes Sphingobacteriia Sphingobacteriales	Chitinophagaceae	<i>Heliimonas saccharivorans</i>	100	95	JX458466
1020	<i>Chitinophaga</i> sp.	99	96	JF806524	Bacteroidetes Sphingobacteriia Sphingobacteriales	Chitinophagaceae	<i>Chitinophaga</i> sp.	99	96	JF806524
1045	<i>Chryseobacterium</i> sp.	100	99	JF700394	Bacteroidetes Flavobacteriia Flavobacteriales	Flavobacteriaceae	<i>Chryseobacterium</i> sp.	100	99	JF700394
1073	<i>Mucilaginibacter mallensis</i>	100	98	NR_116978	Bacteroidetes Sphingobacteriia Sphingobacteriales	Sphingobacteriaceae	<i>Mucilaginibacter mallensis</i>	100	98	NR_116978
1078	<i>Sphingobacterium</i> sp.	100	99	LN867309	Bacteroidetes Sphingobacteriia Sphingobacteriales	Sphingobacteriaceae	<i>Sphingobacterium</i> sp.	100	99	LN867309
1094	<i>Pedobacter westerhofensis</i>	97	91	NR_042602	Bacteroidetes Sphingobacteriia Sphingobacteriales	Sphingobacteriaceae	<i>Pedobacter westerhofensis</i>	97	91	NR_042602
1098	<i>Solitalea koreensis</i>	100	86	NR_044568	Bacteroidetes Sphingobacteriia Sphingobacteriales	Sphingobacteriaceae	uncult. <i>Bacteroidetes</i>	95	90	HQ663372
1108	<i>Cytophaga hutchinsonii</i>	100	99	NR_102866	Bacteroidetes Cytophagia Cytophagales	Cytophagaceae	<i>Cytophaga hutchinsonii</i>	100	99	NR_102866
1116	" <i>Candidatus Saccharimonas aalborgensis</i> "	99	86	CP005957	Candidatus Saccharibacteria <i>Candidatus Saccharimonas</i>	n.a.	uncult. <i>Bacterium</i>	99	90	EF197025
1136	" <i>Candidatus Saccharimonas aalborgensis</i> "	99	83	KC495062	Parcubacteria <i>Candidatus Sonnebornia</i> .	n.a.	uncult. <i>Parcubacterium</i>	99	87	HQ290495

OTU	closest cultured related sequence ^a					closest related sequence ^b (environmental samples included)				
	Q ^c	Id ^d	Accession ^e	Phylum Class Order	Family	Q ^d	Id ^e	Accession ^c		
1140	" <i>Candidatus</i> <i>Saccharimonas</i> <i>aalborgensis</i> "	100	85	KC495062	Parcubacteria <i>Campbellbacteria</i> .	n.a.	" <i>Candidatus</i> <i>Saccharimonas</i> <i>aalborgensis</i> "	100	85	KC495062
1155	" <i>Candidatus</i> <i>Saccharimonas</i> <i>aalborgensis</i> "	100	83	KC495061	Parcubacteria <i>Campbellbacteria</i> .	n.a.	uncult. <i>Parcubacterium</i>	98	86	CP011215
1158	<i>Parcubacterium</i>	100	84	CP011215	<i>Parcubacterium</i>	n.a.	uncult. <i>Parcubacterium</i>	100	95	JN128702

^a Closest cultured sequences includes validly published names of bacterial species with known strains. No Candidates are listed here with the exception for the candidates' phyla *Saccharibacteria* (OTU_{16S}1116) and *Parcubacteria* (OTU_{16S}1136, OTU_{16S}1140, OTU_{16S}1155).

^b Closest related sequences includes uncultured hits and are affiliated at least to phylum level using NCBI and SILVA SSU databases.

^c Query values of sequences [%].

^d Maximum sequence identity [%] in BLASTn.

^e Accession number of closest sequence hit.

^f n.a. – no further details available

Table S3. Relative abundances of labeled taxa (OTU) based on *mxnF* gene sequences in all fractions (H, heavy; M, middle; L, light) of [¹²C]- and [¹³C₁]-methanol treatments of Substrate SIP experiment. Black faces indicate values that were used for calculating ‘labeling proportions’ as indicators of relative importance. Bold faces indicate ‘labeling proportions’ > 5 %.

Taxonomic affiliation ^a	Labeled OTU	Relative abundance [%]						Labeling proportion [%]	
		¹² C			¹³ C			H	M
		H	M	L	H	M	L		
<i>Methylobacteriaceae</i>	OTU 40	0.2	35.3	7.5	24.9	32.4	3.1	25.6	
	OTU 58	0.0	0.0	0.0	0.0	1.5	0.0		3.6
	OTU 79	0.0	0.0	1.9	0.0	0.6	0.0		1.4
	OTU 107	0.0	0.8	0.0	0.0	1.2	0.0		2.9
	OTU 108	0.0	0.2	0.0	0.6	0.9	0.0	0.6	2.1
	OTU 153	0.0	0.0	1.9	0.0	0.9	0.0		2.1
<i>ambiguous^b</i>	OTU 0	0.0	0.0	0.0	0.6	0.0	0.0	0.6	
	OTU 2	0.0	0.0	0.0	0.6	0.0	0.0	0.6	
	OTU 9	0.0	0.0	0.0	0.2	1.5	0.0		3.6
	OTU 222	0.0	2.1	1.9	1.6	0.6	0.0	1.7	
<i>Hyphomicrobiaceae</i>	OTU 185	0.4	10.6	47.2	30.2	20.2	11.6	31.0	47.1
	OTU 202	0.2	0.0	1.9	0.0	2.1	0.0		5.0
<i>ambiguous^b</i>	OTU 177	0.0	0.4	0.0	0.0	0.6	0.0		1.4
	OTU 197	0.0	0.2	0.0	0.0	0.9	0.0		2.1
	OTU 210	0.0	1.3	30.2	25.4	4.0	0.0	26.0	9.3
	OTU 289	0.0	0.0	0.0	0.0	0.9	0.0		2.1
	OTU 316	0.0	0.0	0.0	0.0	0.9	0.0		2.1
<i>Methylorhabdus</i>	OTU 190	0.0	0.0	0.0	2.2	0.0	0.0	2.3	
<i>ambiguous^b</i>	OTU 18	0.0	0.0	0.0	1.8	0.0	0.0	1.9	
<i>Beijerinckiaceae</i>	OTU 144	0.2	0.0	0.0	9.5	2.8	0.8	9.7	6.4
	OTU 152	0.0	0.0	0.0	0.4	0.6	0.0		1.4
	OTU 374	0.0	0.0	0.0	0.0	0.6	0.0		1.4
<i>ambiguous^b</i>	OTU 352	0.0	0.0	0.0	0.0	0.9	0.0		2.1
<i>not classified</i>	OTU 275	0.0	0.0	0.0	0.0	1.5	0.0		3.6
Percentage of labeled taxa to total fraction [%]					97	43			

- ^a Taxonomic affiliation was done with BLASTn (December 2015; (for further information see Table S2) and confirmed by positioning in phylogenetic tree (data not shown)
- ^b Sequence identity with BLASTn < 90 % as well as ambiguous position in phylogenetic tree (for further information see Table S2)

Table S4. Relative abundances of labeled fungal taxa (OTU) based on ITS gene sequences in all fractions (H, heavy; M, middle; L, light) of [¹²C]- and [¹³C₁]-methanol treatments of Substrate SIP experiment. Black faces indicate values that were used for calculating ‘labeling proportions’ as indicators of relative importance. Bold faces indicate ‘labeling proportions’ > 5 %.

Taxonomic affiliation ^a	Labeled OTU	Relative abundance [%]						Labeling proportion [%]		
		¹² C			¹³ C			H	M	
		H	M	L	H	M	L			
Ascomycota										
<i>Saccharomyces</i>	OTU 2	0.0	14.2	5.2	7.6	8.6	5.1	9.9		
<i>Oidiodendron</i>	OTU 9	0.0	0.7	1.0	0.6	0.0	0.4	0.8		
<i>Penicillium</i>	OTU 10	0.0	1.1	3.2	14.7	0.8	4.1	19.2		
<i>Paecilomyces</i>	OTU 14	0.0	0.1	0.4	2.5	0.0	0.1	3.3		
<i>Bionectria</i>	OTU 24	0.0	0.4	0.7	0.0	0.7	1.2		4.3	
<i>Oidiodendron</i>	OTU 32	4.1	0.3	0.9	5.4	0.1	1.0	7.1		
<i>Geomyces</i>	OTU 55	0.0	0.3	0.8	0.1	0.6	0.3		3.5	
<i>Hyaloscyphaceae</i>	OTU 135	0.0	0.1	0.1	0.0	1.1	0.1		7.0	
<i>Penicillium</i>	OTU 188	0.0	0.0	0.0	2.9	0.0	0.0	3.8		
Basidiomycota										
<i>Leucosporiales</i>	OTU 15	0.0	4.4	2.6	1.2	3.3	2.4	1.6		
<i>Syzygospora</i>	OTU 22	0.0	2.5	1.7	0.5	2.9	1.4	0.7	18.3	
<i>Laccaria</i>	OTU 27	0.5	0.9	0.3	0.6	1.3	0.3		8.3	
<i>Cortinarius</i>	OTU 44	0.0	0.0	0.1	0.8	0.4	0.1	1.1		
<i>Cryptococcus</i>	OTU 46	0.0	0.0	0.0	23.6	0.0	0.0	30.9		
Glomeromycota										
<i>Glomeromycetes</i>	OTU 25	0.0	0.8	0.4	3.4	0.3	0.2	4.5		
Rozellomycota										
	OTU 29	0.0	0.4	1.1	2.2	0.1	1.5	2.9		
	OTU 38	0.8	1.2	0.7	2.0	0.5	0.3	2.6		
	OTU 153	0.0	0.0	0.0	2.3	0.1	0.0	3.0		
Zygomycota										
<i>Mortierella</i>	OTU 5	2.8	5.0	4.6	5.1	5.7	5.8	6.7	35.7	
<i>Mortierella</i>	OTU 33	0.0	0.6	1.3	1.1	0.7	1.0	1.4	4.3	
<i>Mortierella</i>	OTU 53	0.0	0.5	0.3	0.0	0.6	0.1		3.9	
<i>Mortierella</i>	OTU 112	0.0	0.8	0.6	0.4	2.4	0.4	0.5	14.8	
Percentage of labeled taxa to total fraction [%]					77	16				

^a Taxonomic affiliation is based on the dynamic UNITE database (v7, release 01.08.2015) and was done with a bayesian classifier implied with MOTUHR based on the best hit of consensus taxonomy after 100 bootstrapped assignments (for further reference sequences based on ‘massBLASTer’ of UNITE see Table S12)

Table S5. Taxonomic affiliation of fungal phylotypes (ITS gene sequences clustered at species-level 97% similarity cut-off) in numerical order. Listed are reference sequences of the UNITE database (<https://unite.ut.ee/analysis.php>) and their phylogenetic affiliation based on the dynamic UNITE database (v7 release 1.08.2015) using MOTHUR.

OTU	Reference sequence ^a					Taxonomy ^b				
		Accession ^c	SH code ^d	Q ^e	Id ^f	Phyl ^g	Class	Order	Family	Genus
1	<i>Trichosporon porosum</i>	NR_073209	SH196641.07FU	100	100	Baso	Tremellomycetes	Trichosporonales	Trichosporonaceae	Trichosporon
2	<i>Saccharomycetales</i>	FN610974	SH180919.07FU	100	100	Asco	Saccharomycetes	NA	NA	NA
4	<i>Mortierella humilis</i>	KP772755		100	100	Zygo	Incertae sedis	Mortierellales	Mortierellaceae	Mortierella
5	<i>Mortierella</i>	JQ312759		99	98	Zygo	Incertae sedis	Mortierellales	Mortierellaceae	Mortierella
6	<i>Cryptococcus terricola</i>	NR_073221	SH190017.07FU	100	100	Baso	Tremellomycetes	Tremellales	Incertae sedis	Cryptococcus
7	<i>Ganoderma applanatum</i>	KJ857258	SH187220.07FU	100	100	Baso	Agaricomycetes	Polyporales	Ganodermataceae	Ganoderma
8	<i>Trichoderma viride</i>	X93980	SH187755.07FU	100	100	Asco	Sordariomycetes	Hypocreales	Hypocreaceae	Trichoderma
9	<i>Oidiodendron</i>	HM488481	SH216993.07FU	100	100	Asco	Leotiomycetes	Incertae sedis	Myxotrichaceae	Oidiodendron
10	<i>Penicillium</i>	FJ379809	SH182493.07FU	100	100	Asco	Eurotiomycetes	Eurotiales	Trichocomaceae	Penicillium
11	<i>Tomentella radiosa</i>	UDB017828	SH184517.07FU	100	100	Baso	Agaricomycetes	Thelephorales	Thelephoraceae	Tomentella
12	<i>Hyaloriaceae</i>	HQ021773	SH021770.07FU	97	96	Baso	Agaricomycetes	NA	NA	NA
13	<i>Cryptococcus podzolicus</i>	NR_073213	SH181879.07FU	100	100	Baso	Tremellomycetes	Tremellales	Incertae sedis	Cryptococcus
14	<i>Paecilomyces</i>	LN886697		98	97	Asco	Eurotiomycetes	Eurotiales	Trichocomaceae	Paecilomyces
15	<i>Leucosporidiales</i>	FN565254	SH193764.07FU	100	100	Baso	Microbotryomycetes	Leucosporidiales	NA	NA
16	<i>Tolypocladium cylindrosporum</i>	KJ028796	SH184933.07FU	100	99	Asco	Sordariomycetes	Hypocreales	Ophiocordycipitaceae	Elaphocordyceps
17	<i>Oidiodendron</i>	KF212286	SH217009.07FU	98	98	Asco	Leotiomycetes	Incertae sedis	Myxotrichaceae	Oidiodendron
18	<i>Nectria ramulariae</i>	FR717232	SH217194.07FU	100	100	Asco	Sordariomycetes	Hypocreales	Nectriaceae	Nectria
19	<i>Mortierellales</i>	GU366727	SH026735.07FU	100	100	Zygo	Incertae sedis	Mortierellales	Mortierellaceae	Mortierella
20	<i>Elaphomyces</i>	HQ021974	SH190236.07FU	100	100	Asco	Eurotiomycetes	Eurotiales	Elaphomycetaceae	Elaphomyces
21	<i>Dermateaceae</i>	HQ021920	SH196224.07FU	99	98	Asco	Leotiomycetes	Helotiales	Dermateaceae	NA

OTU	Reference sequence ^a				Taxonomy ^b					
	Accession ^c	SH code ^d	Q ^e	Id ^f	Phyl ^g	Class	Order	Family	Genus	
22	<i>Syzygospora</i>	HQ211619	SH182180.07FU	100	100	Baso	Tremellomycetes	Cystofilobasidiales	Incertae sedis	<i>Syzygospora</i>
23	<i>Mortierella gamsii</i>	AJ878509	SH193938.07FU	100	100	Zygo	Incertae sedis	Mortierellales	Mortierellaceae	<i>Mortierella</i>
24	<i>Bionectria</i>	GQ219910	SH211202.07FU	100	100	Asco	Sordariomycetes	Hypocreales	Bionectriaceae	<i>Bionectria</i>
25	<i>Glomeromycetes</i>	JF300543	SH462390.07FU	98	96	Glom	Glomeromycetes	NA	NA	NA
26	<i>Glomeromycetes</i>	JF300543	SH462390.07FU	97	95	Glom	Glomeromycetes	NA	NA	NA
27	<i>Laccaria amethystina</i>	HM189774	SH220959.07FU	100	100	Baso	Agaricomycetes	Agaricales	Hydnangiaceae	<i>Laccaria</i>
28	<i>Cryptococcus podzolicus</i>	DQ069015	SH181879.07FU	97	96	Baso	Tremellomycetes	Tremellales	Incertae sedis	<i>Cryptococcus</i>
29	<i>Rozellomycota</i>	AF504877	SH211778.07FU	100	99	Roz	NA	NA	NA	NA
30	<i>Trechispora</i>	FJ820706	SH009022.07FU	99	99	Baso	Agaricomycetes	Trechisporales	Hydnodontaceae	<i>Trechispora</i>
31	<i>Inocybe napipes</i>	AM882927	SH196058.07FU	100	100	Baso	Agaricomycetes	Agaricales	Inocybaceae	<i>Inocybe</i>
32	<i>Oidiodendron</i>	FJ475564	SH216991.07FU	99	99	Asco	Leotiomycetes	Incertae sedis	Myxotrichaceae	<i>Oidiodendron</i>
33	<i>Mortierellaceae</i>	JQ666581	SH208762.07FU	100	100	Zygo	Incertae sedis	Mortierellales	Mortierellaceae	<i>Mortierella</i>
35	<i>Volutella</i>	HM136667	SH474556.07FU	100	100	Asco	Sordariomycetes	Hypocreales	Nectriaceae	<i>Volutella</i>
37	<i>Mycena cinerella</i>	UDB021984	SH220720.07FU	100	100	Baso	Agaricomycetes	Agaricales	Mycenaceae	<i>Mycena</i>
38	<i>Rozellomycota</i>	JQ666464	SH001662.07FU	99	99	Roz	NA	NA	NA	NA
39	<i>Leptodontidium trabinellum</i>	GU934588	SH019513.07FU	100	100	Asco	Leotiomycetes	Helotiales	Incertae sedis	<i>Leptodontidium</i>
40	<i>Chaunopycnis</i>	GQ302677	SH184950.07FU	99	98	Asco	Sordariomycetes	Hypocreales	Ophiocordycipitaceae	<i>Chaunopycnis</i>
41	<i>Bulgaria inquinans</i>	JN033386	SH194396.07FU	100	100	Asco	Leotiomycetes	Leotiales	Bulgariaceae	<i>Bulgaria</i>
42	<i>Mortierella simplex</i>	JX975982	SH189943.07FU	99	98	Zygo	Incertae sedis	Mortierellales	Mortierellaceae	<i>Mortierella</i>
44	<i>Cortinarius diasemospermus</i>	UDB000066	SH188559.07FU	100	100	Baso	Agaricomycetes	Agaricales	Cortinariaceae	<i>Cortinarius</i>
45	<i>Fungi</i>	KF297116	SH032387.07FU	98	95	Baso	NA	NA	NA	NA
46	<i>Cryptococcus oeirensis</i>	NR_077106	SH197623.07FU	100	100	Baso	Tremellomycetes	Tremellales	Incertae sedis	<i>Cryptococcus</i>
48	<i>Pochonia</i>	HM439557	SH012122.07FU	100	100	Asco	Sordariomycetes	Hypocreales	Clavicipitaceae	NA

OTU	Reference sequence ^a				Taxonomy ^b				
		Accession ^c	SH code ^d	Q ^e Id ^f	Phyl ^g Class	Order	Family	Genus	
49	<i>Tomentella</i>	KM576633		100 100	Baso Agaricomycetes	Thelephorales	Thelephoraceae	<i>Tomentella</i>	
50	<i>Mortierella longigemmata</i>	JX976055	SH180129.07FU	99 99	Zygo Incertae sedis	Mortierellales	Mortierellaceae	<i>Mortierella</i>	
51	<i>Penicillium daleae</i>	GU981583	SH182497.07FU	100 100	Asco Eurotiomycetes	Eurotiales	Trichocomaceae	<i>Penicillium</i>	
53	<i>Mortierella macrocystis</i>	JQ272448	SH187863.07FU	100 100	Zygo Incertae sedis	Mortierellales	Mortierellaceae	<i>Mortierella</i>	
55	<i>Geomyces auratus</i>	KF039895	SH183331.07FU	100 100	Asco Leotiomycetes	Incertae sedis	Incertae sedis	<i>Geomyces</i>	
56	<i>Hyaloriaceae</i>	FJ475763	SH207620.07FU	100 100	Baso Agaricomycetes	NA	NA	NA	
57	<i>Lactarius camphoratus</i>	KF432971	SH220116.07FU	100 100	Baso Agaricomycetes	Russulales	Russulaceae	<i>Lactarius</i>	
58	<i>Pochonia bulbilosa</i>	JX535180	SH192574.07FU	100 100	Asco Sordariomycetes	Hypocreales	Clavicipitaceae	<i>Pochonia</i>	
59	<i>Trichoderma hamatum</i>	X93975	SH177682.07FU	100 100	Asco Sordariomycetes	Hypocreales	Hypocreaceae	<i>Trichoderma</i>	
60	<i>Humicola</i>	KF981440	SH195345.07FU	99 99	Asco Sordariomycetes	Sordariales	Chaetomiaceae	NA	
61	<i>Mortierella</i>	KC009383		98 96	Zygo Incertae sedis	Mortierellales	Mortierellaceae	<i>Mortierella</i>	
62	<i>Hyaloscyphaceae</i>	AB476538	SH196230.07FU	98 97	Asco Leotiomycetes	Helotiales	NA	NA	
64	<i>Pezizomycotina</i>	KF359573	SH217842.07FU	100 100	Asco Eurotiomycetes	Chaetothyriales	NA	NA	
66	<i>Aspergillus versicolor</i>	LN482531	SH186265.07FU	100 100	Asco Eurotiomycetes	Eurotiales	Trichocomaceae	<i>Aspergillus</i>	
67	<i>Russula cyanoxantha</i>	KF432956	SH186707.07FU	100 100	Baso Agaricomycetes	Russulales	Russulaceae	<i>Russula</i>	
69	<i>Oidiodendron</i>	JX456904	SH216990.07FU	99 99	Asco Leotiomycetes	Incertae sedis	Myxotrichaceae	<i>Oidiodendron</i>	
71	<i>Penicillium arianeae</i>	KC773833	SH005531.07FU	100 100	Asco Eurotiomycetes	Eurotiales	Trichocomaceae	NA	
72	<i>Volutella</i>	JX507700	SH217585.07FU	100 100	Asco Sordariomycetes	Hypocreales	Nectriaceae	NA	
73	<i>Trichosporon moniliiforme</i>	NR_073240	SH196643.07FU	100 100	Baso Tremellomycetes	Trichosporonales	Trichosporonaceae	<i>Trichosporon</i>	
77	<i>Tremella fibulifera</i>	KP986518		93 89	Baso NA	NA	NA	NA	
81	<i>Luellia recondita</i>	JF519380	SH179954.07FU	100 100	Baso Agaricomycetes	Trechisporales	Hydnodontaceae	<i>Luellia</i>	
83	<i>Chaetosphaeria myriocarpa</i>	AF178552	SH198584.07FU	97 97	Asco Sordariomycetes	Chaetosphaeriales	Chaetosphaeriaceae	<i>Chaetosphaeria</i>	
85	<i>Microbotryomycetes</i>	HM036653	SH180664.07FU	99 99	Baso Microbotryomycetes	NA	NA	NA	

OTU	Reference sequence ^a				Taxonomy ^b					
		Accession ^c	SH code ^d	Q ^e	Id ^f	Phyl ^g	Class	Order	Family	Genus
86	<i>Cladosporium cladosporioides</i>	LN482458	SH216250.07FU	100	100	Asco	Dothideomycetes	Capnodiales	Davidiellaceae	NA
88	<i>Cladophialophora chaetospora</i>	KF359558	SH213266.07FU	97	97	Asco	Eurotiomycetes	Chaetothyriales	Herpotrichiellaceae	<i>Cladophialophora</i>
91	<i>Exophiala</i>	HM439556	SH197643.07FU	100	100	Asco	Eurotiomycetes	Chaetothyriales	Herpotrichiellaceae	<i>Exophiala</i>
94	<i>Helotiales</i>	HQ021923	SH201613.07FU	99	99	Asco	Leotiomycetes	Helotiales	NA	NA
96	<i>Bionectria ochroleuca</i>	JX967106	SH182678.07FU	100	100	Asco	Sordariomycetes	Hypocreales	Bionectriaceae	NA
98	<i>Fungi</i>	KT194869		99	98	NA	NA	NA	NA	NA
103	<i>Trechispora araneosa</i>	AF347084		99	99	Baso	Agaricomycetes	Trechisporales	Hydnodontaceae	<i>Trechispora</i>
108	<i>Chytridiomycota</i>	EF619656	SH462789.07FU	98	95	NA	NA	NA	NA	NA
111	<i>Capronia fungicola</i>	AF050246	SH015749.07FU	97	94	Asco	Eurotiomycetes	Chaetothyriales	Herpotrichiellaceae	NA
112	<i>Mortierella gemmifera</i>	JX976121	SH185196.07FU	100	100	Zygo	<i>Incertae sedis</i>	Mortierellales	Mortierellaceae	<i>Mortierella</i>
113	<i>Capnodiales</i>	KF617528	SH472617.07FU	98	98	Asco	NA	NA	NA	NA
114	<i>Fungi</i>	JX675128	SH216421.07FU	95	93	Chyt	NA	NA	NA	NA
121	<i>Saccharomycetales</i>	FN610974	SH180919.07FU	97	95	Asco	Saccharomycetes	NA	NA	NA
128	<i>Helotiales</i>	HQ850140	SH215245.07FU	98	97	Asco	Leotiomycetes	NA	NA	NA
130	<i>Lycoperdon pyriforme</i>	DQ112557	SH175879.07FU	100	100	Baso	Agaricomycetes	Agaricales	Agaricaceae	<i>Lycoperdon</i>
131	<i>Lactarius quietus</i>	UDB015797	SH220118.07FU	100	100	Baso	Agaricomycetes	Russulales	Russulaceae	<i>Lactarius</i>
135	<i>Helotiales</i>	AY969487	SH195228.07FU	100	100	Asco	Leotiomycetes	Helotiales	Hyaloscyphaceae	NA
138	<i>Dermateaceae</i>	FN610995	SH014516.07FU	99	99	Asco	Leotiomycetes	Helotiales	NA	NA
140	<i>Exophiala moniliae</i>	HE605213	SH199199.07FU	100	100	Asco	Eurotiomycetes	Chaetothyriales	Herpotrichiellaceae	<i>Exophiala</i>
141	<i>Rozellomycota</i>	HM069428	SH025237.07FU	99	99	Roz	NA	NA	NA	NA
153	<i>Rozellomycota</i>	HM069429	SH025236.07FU	98	97	Roz	NA	NA	NA	NA
154	<i>Rozellomycota</i>	JQ666484	SH020528.07FU	98	96	Roz	NA	NA	NA	NA
157	<i>Helotiales</i>	AY394669	SH025727.07FU	95	95	Asco	Leotiomycetes	NA	NA	NA

OTU	Reference sequence ^a				Taxonomy ^b			
		Accession ^c	SH code ^d	Q ^e Id ^f	Phyl ^g Class	Order	Family	Genus
161	<i>Crocicreas</i>	AY969794		99 99	Asco Leotiomyces	Helotiales	Helotiaceae	<i>Crocicreas</i>
177	<i>Ilyonectria crassa</i>	KJ475469	SH202967.07FU	100 100	Asco Sordariomyces	Hypocreales	<i>Incertae sedis</i>	<i>Ilyonectria</i>
185	<i>Pleosporales</i>	GU083188	SH200451.07FU	98 96	Asco Dothideomyces	Pleosporales	NA	NA
187	<i>Cenococcum geophilum</i>	AM087244	SH199613.07FU	100 100	Asco Dothideomyces	Hysteriales	Gloniaceae	<i>Cenococcum</i>
188	<i>Penicillium corylophilum</i>	KF170363	SH207150.07FU	99 99	Asco Eurotiomyces	Eurotiales	Trichocomaceae	<i>Penicillium</i>
190	<i>Glomeromyces</i>	JF300543	SH462390.07FU	90 82	Glom Glomeromyces	NA	NA	NA
198	<i>Cladophialophora</i>	HQ211891	SH193233.07FU	97 95	Asco Eurotiomyces	Chaetothyriales	Herpotrichiellaceae	<i>Cladophialophora</i>
199	<i>Xenasmatella</i>	JQ272394	SH026877.07FU	100 100	Baso Agaricomycetes	Polyporales	<i>Incertae sedis</i>	<i>Phlebiella</i>
256	<i>Hypocreales</i>	JF449629	SH203174.07FU	100 100	Asco Sordariomyces	Hypocreales	NA	NA
265	<i>Helotiales</i>	HM044632	SH013010.07FU	95 95	Asco Leotiomyces	Helotiales	NA	NA
302	<i>Mortierella parvispora</i>	AB476418	SH193938.07FU	99 99	Zygo <i>Incertae sedis</i>	Mortierellales	Mortierellaceae	<i>Mortierella</i>
304	<i>Rhodotorula diffluens</i>	NR_073289	SH213958.07FU	94 90	Baso Microbotryomyces	Sporidiobolales	<i>Incertae sedis</i>	NA
350	<i>Mucor</i>	JQ676211	SH188380.07FU	100 100	Zygo <i>Incertae sedis</i>	Mucorales	Mucoraceae	<i>Mucor</i>

^a Reference sequences based on 'massBLASTer' of the UNITE database including sequences from the International Nucleotide Sequence Database (GenBank, EMBL, DDBJ) and environmental samples (isolated from soil, ectomycorrhizal roots, orchids etc.) in UNITE.

^b Taxonomy is based on the dynamic UNITE database (v7, release 01.08.2015) and was done with a bayesian classifier implied with MOTHR based on the best hit of consensus taxonomy after 100 bootstrapped assignments (implementation of Wang *et al.* 2007). 'NA' (not applicable) indicates no further affiliation possible based on consensus taxonomy.

^c Accession number of reference sequence applicable in International Nucleotide Sequence Database.

^d SH code provided by UNITE considering species hypothesis (comprise any species level group of individuals sharing a given set of observed characteristics).

^e Query [%] of the BLAST alignment calculated with the number of mismatches over a 355 nt long input sequence and the corresponding section of the reference sequence.

^f Maximum sequence identity [%] over the BLAST alignment.

^g Fungal phyla using the following abbreviations: 'Asco', *Ascomycota*; 'Baso', *Basidiomycota*; 'Chyt', *Chytridiomycota*; 'Glom', *Glomeromycota*; 'Roz', *Rozellomycota*; 'Zygo', *Zygomycota*.

Table S6. Relative abundances of labeled bacterial taxa (OTU) based on 16S rRNA gene sequences in all fractions (H, heavy; M, middle; L, light) of [¹²C]- and [¹³C₁]-methanol treatment at pH 4 of pH SIP experiment. Black faces indicate values that were used for calculating 'labeling proportions' as indicators of relative importance. Bold faces indicate 'labeling proportions' > 5 %.

Taxonomic affiliation ^a	Labeled OTU	Relative abundance [%]						Labeling proportion [%]	
		¹² C			¹³ C			H	M
		H	M	L	H	M	L		
Actinobacteria									
<i>Leifsonia</i> ^d	OTU 721	0.4	0.54	2.5	10.8	7.0	1.2	45.0	13.9
Bacteroidetes									
<i>Chitinophaga</i> ^d	OTU 1020	3.5	11.5	1.7	5.3	9.2	2.1	22.3	
<i>Sphingobacteriales</i> ^b	OTU 1098	0.0	0.5	0.5	0.5	0.1	0.2	2.2	
Firmicutes									
<i>Paenibacillus</i> ^d	OTU 206	0.2	0.4	0.8	0.6	0.2	0.0	2.6	
Alphaproteobacteria									
<i>Methylovirgula</i> ^d	OTU 438	1.0	0.4	3.1	6.7	42.3	3.5	27.9	83.5
<i>Sphingomonas</i> ^d	OTU 449	0.2	0.0	1.7	0.7	0.6	3.0		1.2
Gammaproteobacteria									
<i>Rhodanobacter</i> ^{d,e}	OTU 343	0.2	0.0	0.2	0.1	0.7	0.7		1.4
Percentage of labeled taxa to total fraction [%]					24	51			

^a Taxonomic affiliation was done with BLASTn (November 2015) and is based on the next cultivated hit for each OTU (for further information see Table S8)

^b Sequence identity of next cultured hit < 90 %, phylogenetic affiliation up to order level

^d Sequence identity of next cultured hit ≥ 95 %, phylogenetic affiliation up to genus level

^e Query of next cultured hit was only 72 % with BLASTn analysis

Table S7. Relative abundances of labeled bacterial taxa (OTU) based on 16S rRNA gene sequences in all fractions (H, heavy; M, middle; L, light) of [¹²C]- and [¹³C₁]-methanol treatment at pH 7 of pH SIP experiment. Black faces indicate values that were used for calculating 'labeling proportions' as indicators of relative importance. Bold faces indicate 'labeling proportions' > 5 %.

Taxonomic affiliation ^a	Labeled OTU	Relative abundance [%]						Labeling proportion [%]	
		¹² C			¹³ C			H	M
		H	M	L	H	M	L		
Actinobacteria									
<i>Leifsonia</i> ^d	OTU 721	1.0	1.7	2.7	8.5	9.3	2.9	19.7	19.4
Bacteroidetes									
<i>Chryseobacterium</i> ^d	OTU 1045	8.5	11.6	5.0	32.5	23.1	23.5	75.1	48.1
<i>Sphingobacterium</i> ^d	OTU 1078	1.7	0.4	0.5	0.9	1.0	0.8		2.1
<i>Sphingobacteriaceae</i> ^c	OTU 1094	0.3	0.6	0.5	0.5	0.6	0.1	1.3	
<i>Cytophaga</i> ^d	OTU 1108	0.1	0.4	0.4	0.3	0.5	0.1		1.1
Alphaproteobacteria									
<i>Caulobacter</i> ^d	OTU 431	0.8	0.3	1.6	1.0	0.1	0.6	2.3	
<i>Paracoccus</i> ^d	OTU 450	0.0	0.0	0.0	0.1	0.8	0.0		1.6
Betaproteobacteria									
<i>Methylophilus</i> ^d	OTU 358	0.6	0.2	0.5	0.4	9.8	0.0		20.4
Verrucomicrobia									
<i>Terrimicrobium</i> ^d	OTU 54	0.3	0.1	0.6	0.7	3.5	0.0	1.7	7.2
Percentage of labeled taxa to total fraction [%]					43	48			

^a Taxonomic affiliation was done with BLASTn (November 2015) and is based on the next cultivated hit for each OTU (for further information see Table S8)

^c Sequence identity of next cultured hit < 95 %, phylogenetic affiliation up to family level

^d Sequence identity of next cultured hit ≥ 95 %, phylogenetic affiliation up to genus level

Table S8. Relative abundances of labeled taxa (OTU) based on *mxnF* gene sequences in all fractions (H, heavy; M, middle; L, light) of [¹²C]- and [¹³C₁]-methanol treatments at pH 4 of pH SIP experiment. Black faces indicate values that were used for calculating 'labeling proportions' as indicators of relative importance. Bold faces indicate 'labeling proportions' > 5 %.

Taxonomic affiliation ^a	Labeled OTU	Relative abundance [%]						Labeling proportion [%]	
		¹² C			¹³ C			H	M
		H	M	L	H	M	L		
<i>Methylobacteriaceae</i>	OTU 7	0.0	0.1	0.0	0.0	1.1	0.0		1.3
	OTU 55	1.1	1.3	0.9	2.1	0.1	0.7	2.7	
<i>ambiguous^b</i>	OTU 0	0.0	0.0	0.2	0.2	1.9	0.1		2.2
<i>Hyphomicrobiaceae</i>	OTU 185	0.6	0.4	1.9	9.9	3.7	7.4	12.2	4.3
	OTU 186	0.0	0.0	0.1	0.7	0.2	0.4	0.9	
	OTU 243	0.0	0.0	1.6	0.2	11.7	0.1		13.7
	OTU 257	0.3	0.5	2.0	7.4	0.2	0.8	9.1	
	OTU 308	0.0	0.0	0.6	0.5	0.0	0.7	0.7	
<i>ambiguous^b</i>	OTU 309	0.1	0.0	0.5	5.3	0.0	0.1	6.5	
	OTU 172	0.1	0.2	8.2	8.7	0.0	2.8	10.8	
	OTU 210	0.1	2.6	6.2	3.0	19.9	5.5	3.7	23.1
	OTU 214	0.5	0.2	2.2	3.5	1.6	3.2	4.4	1.9
	OTU 236	1.6	19.5	46.0	22.1	31.7	25.4	27.3	36.9
	OTU 266	0.4	0.0	1.4	1.4	0.1	0.3	1.7	
	OTU 310	0.0	0.1	0.2	0.1	0.5	0.3		0.6
<i>Methylorhabdus</i>									
<i>ambiguous^b</i>	OTU 18	0.0	0.8	2.4	8.0	8.2	0.0	10.0	9.6
<i>Beijerinckiaceae</i>									
<i>ambiguous^b</i>	OTU 144	0.0	0.0	1.3	1.0	0.0	0.2	1.2	
	OTU 337	0.0	0.0	0.1	1.5	0.1	0.0	1.8	
	OTU 338	0.1	0.1	0.3	4.1	0.0	0.3	5.1	
	OTU 340	0.1	0.7	2.3	1.5	3.8	0.6	1.9	4.5
	OTU 349	0.1	0.6	2.9	0.5	1.7	1.4		2.0
Percentage of labeled taxa to total fraction [%]					81	86			

^a Taxonomic affiliation was done with BLASTn (December 2015; for further information see Table S2) and confirmed by positioning in phylogenetic tree (data not shown)

^b Sequence identity with BLASTn < 90 % as well as ambiguous position in phylogenetic tree (for further information see S2)

Table S9. Relative abundances of labeled taxa (OTU) based on *mxnF* gene sequences in all fractions (H, heavy; M, middle; L, light) of [¹²C]- and [¹³C_u]-methanol treatments at pH 7 of pH SIP experiment. Black faces indicate values that were used for calculating 'labeling proportions' as indicators of relative importance. Bold faces indicate 'labeling proportions' > 5 %.

Taxonomic affiliation ^a	Labeled OTU	Relative abundance [%]						Labeling proportion [%]	
		¹² C			¹³ C			H	M
		H	M	L	H	M	L		
<i>Methylobacteriaceae</i>	OTU 55	27.0	37.4	25.8	72.0	39.7	9.0	95.4	80.1
	OTU 107	0.1	0.2	0.4	0.1	0.6	0.0		1.2
<i>ambiguous^b</i>	OTU 141	0.0	0.7	1.0	3.5	1.3	0.4	4.6	2.7
<i>Hyphomicrobiaceae</i>	OTU 185	1.4	1.9	5.8	0.9	7.3	12.7		14.7
	OTU 213	0.0	0.3	0.4	0.0	0.7	0.2		1.3
Percentage of labeled taxa to total fraction [%]					75	50			

^a Taxonomic affiliation was done with BLASTn (December 2015; for further information see Table S2) and confirmed by positioning in phylogenetic tree (data not shown)

^b Sequence identity with BLASTn < 90 % as well as ambiguous position in phylogenetic tree (for further information see Table S2)

Table S10. Relative abundances of labeled fungal taxa (OTU) based on ITS gene sequences in all fractions (H, heavy; M, middle; L, light) of [¹²C]- and [¹³C₁]-methanol treatments at pH 4 of pH SIP experiment. Black faces indicate values that were used for calculating 'labeling proportions' as indicators of relative importance. Bold faces indicate 'labeling proportions' > 5 %.

Taxonomic affiliation ^a	Labeled OTU	Relative abundance [%]						Labeling proportion [%]		
		¹² C			¹³ C			H	M	
		H	M	L	H	M	L			
Ascomycota										
<i>Bionectria</i>	OTU 24	1.3	1.0	0.6	1.8	0.8	1.4	3.8		
<i>Chaenopycnis</i>	OTU 40	0.2	0.3	0.8	0.8	0.6	1.0	1.7		
<i>Clavicipitaceae</i>	OTU 48	0.3	0.2	1.3	0.7	0.3	0.8	1.4		
<i>Penicillium</i>	OTU 51	0.3	0.4	0.5	0.6	0.1	1.4	1.2		
<i>Trichoderma</i>	OTU 59	0.3	0.0	1.0	0.7	0.5	1.3	1.4		
<i>Chaetomiaceae</i>	OTU 60	0.6	0.4	1.9	1.3	1.2	3.1	2.7	6.9	
<i>Trichocomaceae</i>	OTU 71	0.0	0.3	0.2	0.1	0.6	0.8		3.3	
<i>Ascomycota</i>	OTU 113	0.4	0.6	0.6	0.6	0.4	0.1	1.3		
<i>Helotiales</i>	OTU 265	0.0	0.0	0.0	0.0	0.8	0.0		4.5	
Basidiomycota										
<i>Ganoderma</i>	OTU 7	2.0	2.7	3.4	2.9	3.3	2.0	5.9	19.5	
<i>Tomentella</i>	OTU 11	0.1	0.3	0.5	0.4	0.6	0.0		3.7	
<i>Agaricomycetes</i>	OTU 12	0.5	0.5	1.0	2.4	1.5	1.1	5.1	8.5	
<i>Cryptococcus</i>	OTU 13	1.3	0.8	1.2	1.9	1.2	0.6	3.9	6.9	
<i>Leucosporidiales</i>	OTU 15	1.1	3.0	1.4	3.9	2.8	1.5	8.1		
<i>Laccaria</i>	OTU 27	0.7	1.4	0.8	1.0	1.0	0.6	2.0		
<i>Trechispora</i>	OTU 30	1.6	2.0	2.1	2.9	1.8	2.0	5.9		
<i>Mycena</i>	OTU 37	0.1	0.1	0.0	0.7	0.1	0.1	1.4		
<i>Basidiomycota</i>	OTU 45	0.5	1.0	0.1	0.8	0.1	0.5	1.7		
<i>Microbotryomycetes</i>	OTU 85	0.0	0.2	0.3	0.6	0.2	0.1	1.2		
<i>Lycoperdon</i>	OTU 130	0.2	0.1	0.3	0.6	0.6	0.4	1.2	3.3	
<i>Phlebiella</i>	OTU 199	0.1	0.1	0.1	0.6	0.4	0.1	1.2		
Rozellomycota	OTU 38	0.6	1.2	0.3	1.6	1.0	0.6	3.3		
Zygomycota										
<i>Mortierella</i>	OTU 4	6.5	11.8	9.5	14.8	11.7	6.7	30.6		
<i>Mortierella</i>	OTU 5	3.4	3.2	2.3	3.6	3.9	1.8	7.5	22.8	
<i>Mortierella</i>	OTU 19	0.7	0.9	1.0	1.6	1.4	1.2	3.3	8.1	
<i>Mortierella</i>	OTU 23	0.5	0.1	0.1	0.8	0.3	0.2	1.6		
<i>Mortierella</i>	OTU 33	0.4	0.5	0.1	1.3	1.1	0.7	2.6	6.5	
<i>Mortierella</i>	OTU 50	0.6	0.5	0.5	0.6	1.0	0.2		6.1	
Percentage of labeled taxa to total fraction [%]					48	17				

^a Taxonomic affiliation is based on the dynamic UNITE database (v7, release 01.08.2015) and was done with a bayesian classifier implied with MOTUHR based on the best hit of consensus taxonomy after 100 bootstrapped assignments (for further reference sequences based on 'massBLASTer' of UNITE see Table S5)

Table S11. Relative abundances of labeled fungal taxa (OTU) based on ITS gene sequences in all fractions (H, heavy; M, middle; L, light) of [¹²C]- and [¹³C₁]-methanol treatments at pH 7 of pH SIP experiment. Black faces indicate values that were used for calculating 'labeling proportions' as indicators of relative importance. Bold faces indicate 'labeling proportions' > 5 %.

Taxonomic affiliation ^a	Labeled OTU	Relative abundance [%]						Labeling proportion [%]		
		¹² C			¹³ C			H	M	
		H	M	L	H	M	L			
Ascomycota										
<i>Saccharomyces</i>	OTU 2	1.3	0.6	0.3	1.9	0.4	0.2	3.0		
<i>Paecilomyces</i>	OTU 14	1.6	1.0	1.0	2.7	6.6	4.8	4.2	13.5	
<i>Bionectria</i>	OTU 24	1.3	1.0	0.6	1.8	1.1	2.7	2.8		
<i>Chaetothyriales</i>	OTU 64	0.0	0.1	0.0	0.1	0.6	0.0		1.3	
Basidiomycota										
<i>Trichosporon</i>	OTU 1	32.4	29.9	21.0	46.4	34.7	20.1	72.7	71.0	
<i>Cryptococcus</i>	OTU 6	0.9	0.9	0.2	2.3	1.6	1.5	3.6	3.3	
<i>Ganoderma</i>	OTU 7	2.0	2.7	3.4	2.1	3.5	1.3		7.3	
<i>Leucosporidiales</i>	OTU 15	1.1	3.0	1.4	2.0	2.2	0.2	3.1		
<i>Syzygospora</i>	OTU 22	1.4	0.1	0.1	1.9	0.8	0.6	3.0	1.7	
<i>Trichosporon</i>	OTU 73	0.4	0.1	0.0	1.8	0.5	0.7	2.9		
<i>Basidiomycota</i>	OTU 77	1.0	0.4	0.1	1.4	0.5	0.3	2.2		
Rozellomycota	OTU 154	0.2	0.0	0.0	0.9	0.2	0.2	1.4		
Zygomycota										
<i>Mortierella</i>	OTU 23	0.5	0.1	0.1	0.7	1.0	0.1	1.1	2.0	
Percentage of labeled taxa to total fraction [%]					64	49				

^a Taxonomic affiliation is based on the dynamic UNITE database (v7, release 01.08.2015) and was done with a bayesian classifier implied with MOTUHR based on the best hit of consensus taxonomy after 100 bootstrapped assignments (for further reference sequences based on 'massBLASter' of UNITE see Table S5)

Table S12. Relative abundance of fungal taxa based on ITS gene sequences from combined pyrosequencing data sets of [¹²C]- and [¹³C_u]-substrate treatments of both SIP experiments. Only taxa with a relative abundance ≥ 0.5% are listed, abundance < 0.5% is indicated by *, no presence is indicated by -. Percentages are always related to filtered datasets of ITS gene sequence of pyrosequencing amplicon libraries.

	Substrate SIP experiment ^c								pH shift SIP experiment ^d			
									pH 4		pH 7	
	t ₀	MeOH	Ace +	Glu +	Xyl +	Van +	CO ₂ +	CO ₂	t ₀	MeOH	t ₀	MeOH
number of sequences combined data sets & singletons removed	8619	8535	8670	8833	8860	8516	8647	8526	4301	8612	4251	8673
Taxonomic affiliation^a	Relative abundance [%]											
Ascomycota	45.16	37.56	16.68	14.00	8.18	51.89	47.84	57.71	53.80	38.76	50.60	36.87
<i>Dothideomycetes</i>	1.13	*	*	*	*	*	1.41	1.38	1.74	*	1.11	*
<i>Eurotiomycetes</i>	5.80	9.31	4.35	5.38	2.61	10.24	13.81	12.68	17.41	9.72	24.84	11.54
<i>Chaetothyriales</i>	*	0.71	0.60	1.23	*	4.20	*	*	*	0.82	*	0.65
<i>Eurotiales</i>	5.53	8.60	3.75	4.14	2.44	6.04	13.58	12.30	16.93	8.89	24.35	10.90
<i>Trichocomaceae</i>	3.03	8.54	3.70	4.11	2.42	5.86	12.83	11.93	14.76	8.69	13.67	10.80
<i>Elaphomycetaceae</i>	2.49	*	*	*	*	*	0.75	*	2.16	*	10.63	*
<i>Leotiomycetes</i>	10.85	10.03	4.86	2.94	2.00	11.16	12.41	18.21	10.72	8.19	8.52	7.11
<i>Helotiales</i>	2.84	5.21	1.30	1.31	0.63	5.28	7.49	7.95	2.53	2.04	2.35	2.08
<i>Leotiales</i>	*	*	1.23	*	*	*	*	2.50	*	*	-	*
<i>Incertae sedis</i>	7.08	4.18	2.16	1.06	1.08	4.94	3.99	6.69	8.07	5.84	5.01	4.77
<i>Saccharomycetes</i>	18.49	7.05	2.70	2.34	0.80	6.11	6.27	7.86	1.86	0.60	2.49	0.90
<i>Sordariomycetes</i>	6.89	9.82	4.12	2.62	2.51	22.91	12.17	15.66	19.81	18.32	11.46	15.81
<i>Chaetosphaeriales</i>	0.68	1.65	*	*	*	0.72	0.87	1.02	3.30	4.30	1.91	3.46
<i>Hypocreales</i>	5.70	7.44	3.44	1.64	2.12	21.54	10.48	13.65	15.02	11.83	7.60	10.73
<i>Nectriaceae</i>	0.70	1.07	*	*	0.51	9.63	2.73	2.78	1.05	1.45	0.73	1.25
<i>Ophiocordycipitaceae</i>	*	*	1.03	*	*	5.97	1.33	3.19	2.58	1.58	1.51	1.52

	Substrate SIP experiment ^c								pH shift SIP experiment ^d			
									pH 4		pH 7	
	t ₀	MeOH	Ace +	Glu +	Xyl +	Van +	CO ₂ +	CO ₂	t ₀	MeOH	t ₀	MeOH
<i>Chytridiomycota</i>	*	*	1.06	*	-	-	*	*	-	*	*	*
<i>Glomeromycota</i>	0.52	2.03	1.18	*	0.55	2.21	3.70	2.40	0.65	0.52	*	0.62
<i>Rozellomycota</i>	3.78	3.55	1.89	*	1.07	1.10	1.73	1.94	2.70	3.04	2.42	2.97
<i>Zygomycota</i>	8.54	15.51	5.76	2.68	1.95	12.09	15.74	9.90	14.46	19.71	18.30	12.30
<i>Mortierellales</i> (<i>Mortierellaceae</i>) ^b	8.24	15.22	5.61	2.66	1.94	11.91	15.64	9.75	14.35	19.66	18.14	12.11
not affiliated	0.60	0.54	*	*	*	0.68	1.33	1.58	1.16	0.92	0.87	0.84

^a Taxonomic affiliation is based on the dynamic UNITE database (v7, release 01.08.2015) and was done with a bayesian classifier implied with MOTUHR based on the best hit of consensus taxonomy after 100 bootstrapped assignments (for further reference sequences based on 'massBLASter' of UNITE see Table S5)

^b Taxa in brackets dominated fungal order or family

^c Treatment with methanol (MeOH), acetate (Ace), glucose (Glu), xylose (Xyl), vanillic acid (Van) and carbon dioxide (CO₂); cross (+) indicates additional methanol supplementation

^d Treatment with methanol at different pH conditions (pH 4 and pH 7)

Table S13. Similarity analyses of bacterial communities (family-level with 90.1% cut-off of 16S rRNA gene sequence) of both SIP experiments based on ANOSIM (Analysis of Similarity) and NPMANOVA (non-parametric multivariate analysis of variance). Values of total analyses in bold, pairwise analyses in cursive.

ANOSIM **R 0.75/ p 0.0001**

Substrate SIP experiment^a R 0.55 / p 0.001							pH SIP experiment^b R 1.00 / p 0.02		t₀ R 0.48 / p 0.06		
MeOH	Ace +	Glu +	Xyl +	Van +	CO ₂ +	CO ₂	pH4	pH7	Sub vs pH4 ^c	Sub vs pH7 ^c	pH4 vs pH7 ^c
<i>t₀ vs t_{End}</i>							<i>t₀ vs t₀</i>				
<i>1.00</i>	<i>0.21</i>	<i>1.00</i>	<i>0.04</i>	<i>0.11</i>	<i>0.18</i>	<i>0.61</i>	<i>1.00</i>	<i>1.00</i>	<i>0.58</i>	<i>0.67</i>	<i>2.00</i>
<i>t_{End} MeOH vs t_{End} Substrate</i>							<i>t_{End} pH4 vs t_{End} pH7</i>				
<i>-</i>	<i>1.00</i>	<i>0.50</i>	<i>1.00</i>	<i>1.00</i>	<i>1.00</i>	<i>0.50</i>	<i>1.00</i>				

NPMANOVA **F 8.23 / p 0.0001**

Substrate SIP experiment^a F 5.31 / p 0.0001							pH SIP experiment^b F 19.71 / p 0.02		t₀ F 1.75 / p 0.07		
MeOH	Ace +	Glu +	Xyl +	Van +	CO ₂ +	CO ₂	pH4	pH7	Sub vs pH4 ^c	Sub vs pH7 ^c	pH4 vs pH7 ^c
<i>t₀ vs t_{End}</i>							<i>t₀ vs t₀</i>				
<i>6.31</i>	<i>3.63</i>	<i>6.85</i>	<i>1.66</i>	<i>1.90</i>	<i>2.80</i>	<i>3.57</i>	<i>262.50</i>	<i>8.94</i>	<i>2.02</i>	<i>1.98</i>	<i>28.69</i>
<i>t_{End} MeOH vs t_{End} Substrate</i>							<i>t_{End} pH4 vs t_{End} pH7</i>				
<i>-</i>	<i>23.69</i>	<i>2.22</i>	<i>24.74</i>	<i>21.60</i>	<i>18.36</i>	<i>3.93</i>	<i>23.99</i>				

^a Treatment with methanol (MeOH), acetate (Ace), glucose (Glu), xylose (Xyl), vanillic acid (Van) and carbon dioxide (CO₂); cross (+) indicates additional methanol supplementation

^b Treatment with methanol at different pH conditions (pH 4 and pH 7)

^c Comparison between t₀ of Substrate SIP experiment and pH-SIP experiment (Sub vs pH) and between both t₀ of pH-SIP (pH4 vs pH7)

Table S14. Similarity analyses of fungal communities (family-level with 97.0% cut-off of ITS gene sequence) of both SIP experiments based on ANOSIM (Analysis of Similarity) and NPMANOVA (non-parametric multivariate analysis of variance). Values of total analyses in bold, pairwise analyses in cursive.

ANOSIM R 0.82 / p 0.0001

		<u>Substrate SIP experiment^a</u> R 0.78 / p 0.0001					<u>pH SIP experiment^b</u> R 0.69 / p 0.07		<u>t₀</u> R 0.60 / p 0.33				
		MeOH	Ace +	Glu +	Xyl +	Van +	CO ₂ +	CO ₂	pH4	pH7	Sub vs pH4 ^c	Sub vs pH7 ^c	pH4 vs pH7 ^c
		t ₀ vs t _{End}							t ₀ vs t ₀				
<i>R</i>		<i>1.00</i>	<i>1.00</i>	<i>1.00</i>	<i>1.00</i>	<i>1.00</i>	<i>1.00</i>	<i>1.00</i>	<i>1.00</i>	<i>1.00</i>	<i>1.00</i>	<i>1.00</i>	<i>2.00</i>
		t _{End} MeOH vs t _{End} Substrate					t _{End} pH4 vs t _{End} pH7						
<i>R</i>		<i>-</i>	<i>1.00</i>	<i>1.00</i>	<i>1.00</i>	<i>0</i>	<i>0.75</i>	<i>1.00</i>	<i>0.00</i>				

NPMANOVA F 8.11 / p 0.0001

		<u>Substrate SIP experiment^a</u> F 9.41 / p 0.0001					<u>pH SIP experiment^b</u> F 2.98 / p 0.09		<u>t₀</u> F 8.21 / p 0.0001				
		MeOH	Ace +	Glu +	Xyl +	Van +	CO ₂ +	CO ₂	pH4	pH7	Sub vs pH4 ^c	Sub vs pH7 ^c	pH4 vs pH7 ^c
		t ₀ vs t _{End}							t ₀ vs t ₀				
<i>F</i>		<i>7.23</i>	<i>13.17</i>	<i>24.93</i>	<i>30.91</i>	<i>3.58</i>	<i>3.64</i>	<i>2.69</i>	<i>2.95</i>	<i>4.62</i>	<i>3.39</i>	<i>3.79</i>	<i>0.99</i>
		t _{End} MeOH vs t _{End} Substrate					t _{End} pH4 vs t _{End} pH7						
<i>F</i>		<i>-</i>	<i>19.50</i>	<i>47.01</i>	<i>65.45</i>	<i>1.82</i>	<i>2.55</i>	<i>2.77</i>	<i>1.46</i>				

^a Treatment with methanol (MeOH), acetate (Ace), glucose (Glu), xylose (Xyl), vanillic acid (Van) and carbon dioxide (CO₂); cross (+) indicates additional methanol supplementation

^b Treatment with methanol at different pH conditions (pH 4 and pH 7)

^c Comparison between t₀ of Substrate SIP experiment and pH-SIP experiment (Sub vs pH) and between both t₀ of pH-SIP (pH4 vs pH7)

Table S15. Similarity analyses of *mxoF*-possessing methylotrophic communities (90% cut-off) of both SIP experiments based on ANOSIM (Analysis of Similarity) and NPMANOVA (non-parametric multivariate analysis of variance). Values of total analyses in bold, pairwise analyses in cursive.

ANOSIM R 0.33 / p 0.02

		<u>Substrate SIP experiment^a</u> R 0.18 / p 0.13					<u>pH SIP experiment^b</u> R 0.85 / p 0.02		<u>t₀</u> R -0.04 / p 0.66				
		MeOH	Ace +	Glu +	Xyl +	Van +	CO ₂ +	CO ₂	pH4	pH7	Sub vs pH4 ^c	Sub vs pH7 ^c	pH4 vs pH7 ^c
		t ₀ vs t _{End}							t ₀ vs t ₀				
R		0.14	0.14	0.11	0.14	-0.11	0.14	0.11	0.00	1.00	0.00	0.00	2.00
		t _{End} MeOH vs t _{End} Substrate					t _{End} pH4 vs t _{End} pH7						
R		-	0.25	0.25	1.00	0.25	-0.5	0.00	1.00				

NPMANOVA F 2.02 / p 0.0023

		<u>Substrate SIP experiment^a</u> F 1.49 / p 0.07					<u>pH SIP experiment^b</u> F 7.52 / p 0.04		<u>t₀</u> F 1.59 / p 0.03				
		MeOH	Ace +	Glu +	Xyl +	Van +	CO ₂ +	CO ₂	pH4	pH7	Sub vs pH4 ^c	Sub vs pH7 ^c	pH4 vs pH7 ^c
		t ₀ vs t _{End}							t ₀ vs t ₀				
F		1.30	1.47	1.63	2.01	0.90	1.56	1.53	0.99	7.19	0.77	1.50	1.97
		t _{End} MeOH vs t _{End} Substrate					t _{End} pH4 vs t _{End} pH7						
F		-	1.46	1.13	2.20	1.23	0.81	1.13	15.43				

^a Treatment with methanol (MeOH), acetate (Ace), glucose (Glu), xylose (Xyl), vanillic acid (Van) and carbon dioxide (CO₂); cross (+) indicates additional methanol supplementation

^b Treatment with methanol at different pH conditions (pH 4 and pH 7)

^c Comparison between t₀ of Substrate SIP experiment and pH-SIP experiment (Sub vs pH) and between both t₀ of pH-SIP (pH4 vs pH7)

Table S16. Relative abundance of bacterial taxa based on 16S rRNA gene sequences from combined pyrosequencing data sets of [¹²C]- and [¹³C_u]-substrate treatments of both SIP experiments. Only taxa with a relative abundance ≥ 0.5% are listed, abundance < 0.5% is indicated by *, no presence is indicated by -. Percentages are always related to filtered datasets of 16S rRNA gene sequence of pyrosequencing amplicon libraries.

	Substrate SIP experiment ^c								pH shift SIP experiment ^d			
	t ₀	MeOH	Ace +	Glu +	Xyl +	Van +	CO ₂ +	CO ₂	pH 4		pH 7	
									t ₀	MeOH	t ₀	MeOH
number of sequences combined data sets & singletons removed	11979	4405	10105	4744	8098	10145	4203	5023	3796	26042	4281	11188
Taxonomic affiliation^a	Relative abundance [%]											
<i>Acidobacteria</i>	3.89	0.98	0.89	1.05	2.09	1.86	0.88	2.43	5.64	*	8.36	*
<i>Actinobacteria</i>	47.14	19.25	63.29	8.79	57.56	57.38	62.62	30.38	47.63	2.49	26.98	8.13
<i>Actinomycetales</i>	7.89	1.98	2.11	4.22	2.84	3.44	5.19	11.09	25.66	0.89	14.48	1.47
<i>Kineosporiaceae</i> (<i>Kineosporia</i> . OTU 703) ^b	7.61	1.82	2.04	3.96	2.80	3.40	4.83	10.55	23.29	0.70	11.42	0.88
<i>Corynebacteriales</i>	33.32	15.12	59.72	0.51	52.14	51.10	54.15	10.23	1.24	*	*	*
<i>Corynebacteriaceae</i> (<i>Corynebacterium</i> . OTU 748) ^b	32.62	14.71	59.31	*	51.67	50.63	53.91	9.06	-	-	-	-
<i>Mycobacteriaceae</i> (<i>Mycobacterium</i> . OTU 750) ^b	0.63	*	*	*	*	*	*	1.17	1.24	*	*	*
<i>Micrococcales</i>												
<i>Microbacteriaceae</i> (<i>Leifsonia</i> . OTU 721) ^b	*	*	*	*	*	*	*	*	*	0.78	*	4.45
<i>Streptosporangiales</i>	0.99	*	*	0.53	*	*	*	1.19	2.29	*	1.40	*
<i>other Actinobacteria</i>	12.39	3.70	3.27	6.91	5.08	5.81	7.71	18.12	41.07	1.33	21.16	2.57

	Substrate SIP experiment ^c								pH shift SIP experiment ^d			
	t ₀	MeOH	Ace +	Glu +	Xyl +	Van +	CO ₂ +	CO ₂	pH 4		pH 7	
									t ₀	MeOH	t ₀	MeOH
Bacteroidetes	*	13.62	5.31	19.50	3.42	3.13	4.21	14.57	3.29	9.15	13.38	62.34
<i>Flavobacteriales</i>	-	-	-	-	-	-	-	-	-	-	*	18.25
<i>Flavobacteriaceae</i>	-	-	-	-	-	-	-	-	-	-	*	17.31
(<i>Chryseobacterium</i> , OTU 1045) ^b												
<i>Sphingobacteriales</i>	*	13.55	5.18	19.39	3.30	3.03	4.07	14.19	1.21	9.02	8.11	38.63
<i>Chitinophagaceae</i>	-	*	*	*	*	*	0.57	2.29	*	-	*	12.14
(<i>Ferruginibacter</i> , OTU 1014) ^b												
<i>Sphingobacteriaceae</i>	-	13.14	4.86	18.82	3.03	2.79	3.50	11.83	0.76	7.96	6.73	15.99
(<i>Mucilaginibacter</i> ; OTU 1073) ^b												
other Bacteroidetes	*	*	*	*	*	*	*	*	2.08	*	5.21	5.13
“Cand. Saccharibacteria”	0.63	*	*	*	*	*	*	*	0.61	*	1.94	*
Chlamydiae	0.86	*	*	*	*	*	-	*	0.74	*	0.96	*
Firmicutes	0.51	1.20	*	0.53	0.68	0.78	*	1.17	0.53	*	0.93	1.04
<i>Bacilli</i>	*	*	*	*	*	*	*	*	*	*	*	0.76
Parcubacteria	*	3.50	4.46	0.84	*	*	*	*	*	*	*	-
Planctomycetes	27.53	6.97	6.95	9.19	15.46	16.25	7.73	12.06	10.48	*	12.01	3.12
<i>Planctomycetia</i>	16.13	4.31	4.74	5.35	10.40	11.21	4.71	7.76	7.03	*	6.82	2.61

	Substrate SIP experiment ^c								pH shift SIP experiment ^d			
	t ₀	MeOH	Ace +	Glu +	Xyl +	Van +	CO ₂ +	CO ₂	pH 4		pH 7	
									t ₀	MeOH	t ₀	MeOH
Proteobacteria	12.62	48.42	14.66	56.11	16.84	17.13	20.99	33.76	25.37	86.68	26.26	18.10
Alphaproteobacteria	10.03	8.58	4.50	4.93	5.01	4.77	4.43	6.67	18.97	2.61	17.75	2.61
<i>Rhizobiales</i>	6.09	6.61	1.92	3.35	3.87	3.59	2.78	4.38	11.01	2.03	8.25	0.92
<i>Beijerinckiaceae</i>												
(<i>Methylovirgula</i> . OTU 438) ^b	6.04	6.61	1.92	2.91	3.87	3.58	2.78	4.38	10.96	2.03	8.11	0.86
<i>Rhodospirillales</i>	2.59	0.54	1.16	*	*	*	0.64	1.39	4.37	*	4.51	*
<i>Acetobacteraceae</i>	0.98	*	1.03	*	*	*	*	0.86	2.00	*	2.27	*
<i>Sphingomonadales</i>	0.55	*	*	0.89	*	*	*	*	1.77	*	2.31	0.73
other <i>Alphaproteobacteria</i>	0.79	1.09	0.98	*	*	*	0.59	*	1.82	*	2.69	0.72
Betaproteobacteria	*	*	*	8.31	8.74	9.31	*	*	0.76	*	0.61	2.53
<i>Burkholderiales</i>	*	-	*	8.31	8.74	9.29	*	*	0.71	*	*	0.79
<i>Burkholderiaceae</i>												
(<i>Burkholderia</i> . OTU 361) ^b	*	-	*	8.26	8.74	9.29	*	*	0.55	*	*	*
<i>Methylophilales</i>												
(<i>Methylophilus</i> . OTU 358) ^b	-	-	-	-	-	-	-	*	*	-	-	1.73
Gammaproteobacteria	1.58	39.50	9.77	42.58	3.03	2.97	16.23	26.54	4.45	83.98	6.59	12.80
<i>Xanthomonadales</i>	0.60	37.25	9.61	42.22	2.69	2.63	15.92	25.24	3.53	83.70	4.18	12.27
<i>Xanthomonadaceae</i>												
(<i>Rhodanobacter</i> . OTU 300) ^b	0.58	37.09	9.45	42.12	2.62	2.57	15.92	25.20	3.45	83.65	4.09	12.16
other <i>Gammaproteobacteria</i>	0.98	2.25	*	*	*	*	*	0.72	0.87	*	2.29	*
Deltaproteobacteria	0.83	*	*	*	*	*	*	*	1.19	*	1.31	*

	Substrate SIP experiment ^c								pH shift SIP experiment ^d			
	t ₀	MeOH	Ace +	Glu +	Xyl +	Van +	CO ₂ +	CO ₂	pH 4		pH 7	
									t ₀	MeOH	t ₀	MeOH
<i>Verrucomicrobia</i>	2.88	4.09	3.19	2.19	2.49	2.13	1.95	3.30	2.03	0.56	4.93	3.31
<i>Methylacidiphilales</i>	*	*	*	*	*	*	*	*	-	*	0.56	-
<i>Spartobacteria</i>	*	0.59	1.02	*	*	*	*	0.58	*	*	0.77	2.65
<i>Verrucomicrobiae</i>	1.56	2.07	1.46	1.05	1.52	1.29	1.24	2.07	1.21	*	3.01	0.50
<i>other Verrucomicrobia</i>	*	1.18	0.50	*	0.54	*	*	*	*	*	*	*
<i>not affiliated bacteria</i>	3.19	1.04	0.75	1.01	*	*	0.67	1.08	2.48	*	3.22	3.36

^a Taxonomic affiliation was done with JAguc2 and is based on GenBank Release (GenBank release 209, 14.08.2015)

^b Genera in brackets dominated bacterial taxa

^c Treatment with methanol (MeOH), acetate (Ace), glucose (Glu), xylose (Xyl), vanillic acid (Van) and carbon dioxide (CO₂); cross (+) indicates additional methanol supplementation

^d Treatment with methanol at different pH conditions (pH 4 and pH 7)

Table S17. Relative abundance of methylotrophic taxa (OTU) based on *mxoF* gene sequences from combined pyrosequencing data sets of [¹²C]- and [¹³C_u]-substrate treatments of both SIP experiments. Only taxa with a relative abundance ≥ 0.5% are listed, abundance < 0.5% is indicated by *, no presence is indicated by -. Percentages are always related to filtered datasets of *mxoF* gene sequence of pyrosequencing amplicon libraries.

	Substrate SIP experiment ^c								pH shift SIP experiment ^d			
	t ₀	MeOH	Ace +	Glu +	Xyl +	Van +	CO ₂ +	CO ₂	pH 4		pH 7	
									t ₀	MeOH	t ₀	MeOH
number of sequences combined data sets & singletons removed	13602	2036	6963	4604	7568	5372	4862	3004	8364	16826	11167	29321
Taxonomic affiliation^a	Relative abundance [%]											
<i>Methylobacteriaceae</i>	72.43	31.14	50.29	43.22	44.37	31.24	33.63	56.79	55.26	39.24	16.79	72.92
OTU 35	60.23	-	*	*	1.10	19.62	1.25	1.76	50.12	35.88	8.08	2.56
OTU 40	8.34	19.94	45.91	32.78	4.47	5.64	16.97	34.79	2.00	2.41	3.00	30.17
OTU 55	2.98	9.63	2.11	7.84	36.87	3.80	13.00	18.28	3.13	0.90	5.71	39.61
OTU 76	*	*	*	0.52	*	*	*	*	-	-	-	*
OTU 78	*	*	0.56	*	0.81	1.01	1.44	0.93	-	-	-	*
OTU 79	*	*	*	0.52	*	*	*	0.53	-	*	-	*
OTU 107	*	*	*	0.52	*	*	*	*	*	-	-	*
OTU 108	*	*	0.95	*	*	*	*	*	-	*	-	*
ambiguous ^b	*	1.33	2.77	*	*	*	*	*	*	*	*	1.44
OTU 9	-	*	2.56	-	*	-	-	-	*	*	*	-
OTU 141	-	-	-	-	-	-	-	-	-	-	-	1.39
OTU 222	*	1.03	*	*	*	*	*	*	*	-	-	*

	Substrate SIP experiment ^c								pH shift SIP experiment ^d			
	t ₀	MeOH	Ace +	Glu +	Xyl +	Van +	CO ₂ +	CO ₂	pH 4		pH 7	
									t ₀	MeOH	t ₀	MeOH
<i>Beijerinckiaceae</i>	*	2.85	*	*	*	1.04	0.51	-	*	*	1.33	0.69
OTU 144	*	2.85	*	*	*	1.04	0.51	-	*	*	1.33	0.69
ambiguous ^b	*	*	1.82	4.17	4.78	0.86	10.51	0.87	2.76	3.55	6.12	0.34
OTU 338	*	*	*	*	1.03	*	0.58	*	*	*	0.55	*
OTU 340	*	-	1.77	3.50	3.74	*	*	0.60	1.69	1.60	4.32	*
OTU 349	-	-	-	*	*	-	9.79	-	0.62	1.47	1.25	*
<i>not affiliated</i>	1.53	0.54	4.87	0.76	15.86	11.93	0.76	0.80	2.28	2.29	5.01	3.91
OTU 21	0.76	-	4.64	-	15.31	9.94	*	-	2.18	2.20	1.01	*
OTU 90	*	-	*	*	*	0.74	*	*	-	-	-	-
OTU 200	*	0.54	*	*	*	*	*	*	-	-	-	*
OTU 234	*	-	-	*	-	0.54	*	*	-	*	-	*
OTU 268	*	-	*	*	*	0.58	*	*	-	-	-	-
OTU 282	*	-	-	-	-	-	-	-	*	*	*	2.58
OTU 325	-	-	-	-	*	-	-	-	*	*	3.81	1.27

^a Taxonomic affiliation was done with BLASTn (December 2015; for further information see Table S2) and confirmed by positioning in phylogenetic tree (data not shown)

^b Sequence identity with BLASTn <90% as well as ambiguous position in phylogenetic tree (for further information see Table S2)

^c Treatment with methanol (MeOH), acetate (Ace), glucose (Glu), xylose (Xyl), vanillic acid (Van) and carbon dioxide (CO₂); cross (+) indicates additional methanol supplementation

^d Treatment with methanol at different pH conditions (pH 4 and pH 7)