Supplementary TABLE S1. Primers and qPCR protocols[a]

Assay Nr.	Name of Primer	Seq. (5´-3´)[b]	Annealing temp. (℃)	Target gene (taxon)	Product length (bp)	Target seq. (accession nr.)	Non-target seq. (accession nr.)	Reference
Family-Specific Assays [c]								
1	Gm5F Micro1R	CCTACGGGAGGCAGCAG GGA**C**TTTCAC**G**GCAGACG	66.4	16S rRNA (*Micrococcaceae & Cellulomonadaceae*)	270	oxB151 (FN433954)	anoxB58 (FN433940)	this work
2	Gm5F Kin3R	CCTACGGGAGGCAGCAG CAGGCCCG**G**GGTT**A**A	67.5	16S rRNA (*Kineosporiaceae & Nocardioidaceae*)	290	anoxC150 (FN434006)	oxG32 (FN433963)	this work
3	Gm5F CloSac1R	CCTACGGGAGGCAGCAG **A**GAGGTCAT**G**ACAAC	64.0	16S rRNA (Cluster I *Clostridiaceae*)	550	anoxB228 (FN433944)	anoxB112 (FN433943)	this work
4	Pla4F PlaGm5R	GGGAA**C**C**G**GCGTAAGGGGC CTGCAGCCACCCGTGG	67.0	16S rRNA (*Planctomycetaceae*)	250	oxC15 (FN434018)	oxC115 (FR773529)	this work
5	Gm5F Cel4R	CCTACGGGAGGCAGCAG CGATGCTTATTC**A**TACAC	56.0	16S rRNA ('Cellu')[c]	160	anoxC102 (FN433999)	oxC101 (FR773528)	this work
6	Gm5F Sph1R	CCTACGGGAGGCAGCAG C**TG**TCAATTCCGCCT	63.4	16S rRNA ('Sphingo')[c]	350	oxC47 (FN434021)	S. myxococcoides (AJ310654)	this work
7	Gm5F Deh1R	CCTACGGGAGGCAGCAG **C**GACTT**G**AACGACCGCCT	66.3	16S rRNA ('Deha')[c]	260	oxC11 (FN434016)	anoxG57 (FR773527)	this work

Supplementary TABLE S1, continued.

Assay Nr.	Name of Primer	Seq. (5´-3´)[b]	Annealing temp. (℃)	Target gene (taxon)	Product length (bp)	Target seq. (accession nr.)	Non-target seq. (accession nr.)	Reference
Domain-Specific Assay								
8	Eub341F Eub534R	CCTACGGGAGGCAGCAG ATTACCGCGGCTGCTGG	55.7	16S rRNA (*Bacteria*)	190	---	---	2
Inhibition Correction Assays								
9	IhcF IhcR	ATTGGGCCCGACGTC ATTTAGGTGACACTATAGAATA	60.0	pGEM-T vector insert	450	---	---	3
10	T7PromF M13Rev	TAATACGACTATAGGG CAGGAAACAGCTATGACC	61.2	pGEM-T vector insert	450	---	---	3

[a] Numbers in the names of primers indicate the 5'-position of binding sites relative to the reference sequence of *E.coli* [ACCX80725]. Abbreviations: F, forward primer; R, reverse primer. The final concentration of each primer was 750 nM for assay numbers 1, 3, 4, 7, 8, 9, and 10. The final concentration of each primer was 500 nM (forward primer) and 1500 nM (reverse primer) for assay numbers 2, 5, and 6.

[b] Y stands for either C or T. Bold and underlined bases in primer sequence indicate mismatches to non-target control.

[c] Names and affiliation of family-level taxa are as previously published (1).

Supplementary TABLE S2. Numbers of 16S rRNA gene transcripts that were used as reference (set to 100 %) for normalization of relative abundances of sequences of target taxa in Fig. 3.

Target taxon (Phylum)	$16S\ rRNA_{Taxon}\ [16S\ rRNA_{Bacteria}]^{-1}$	Time point (h)
Micrococcaceae & Cellulomonadaceae (*Actinobacteria*)	6.5×10^{-3}	48
Kineosporiaceae & Nocardioidaceae (*Actinobacteria*)	9.3×10^{-7}	0
Cluster I *Clostridiaceae* (*Firmicutes*)	7.9×10^{-5}	192
Planctomycetaceae (Planctomycetes)	1.2×10^{-5}	0
'Cellu' (novel *Bacteroidetes*)	1.8×10^{-6}	168
'Sphingo' (novel *Bacteroidetes*)	1.1×10^{-5}	0
'Deha' (novel *Chloroflexi*)	1.3×10^{-3}	0

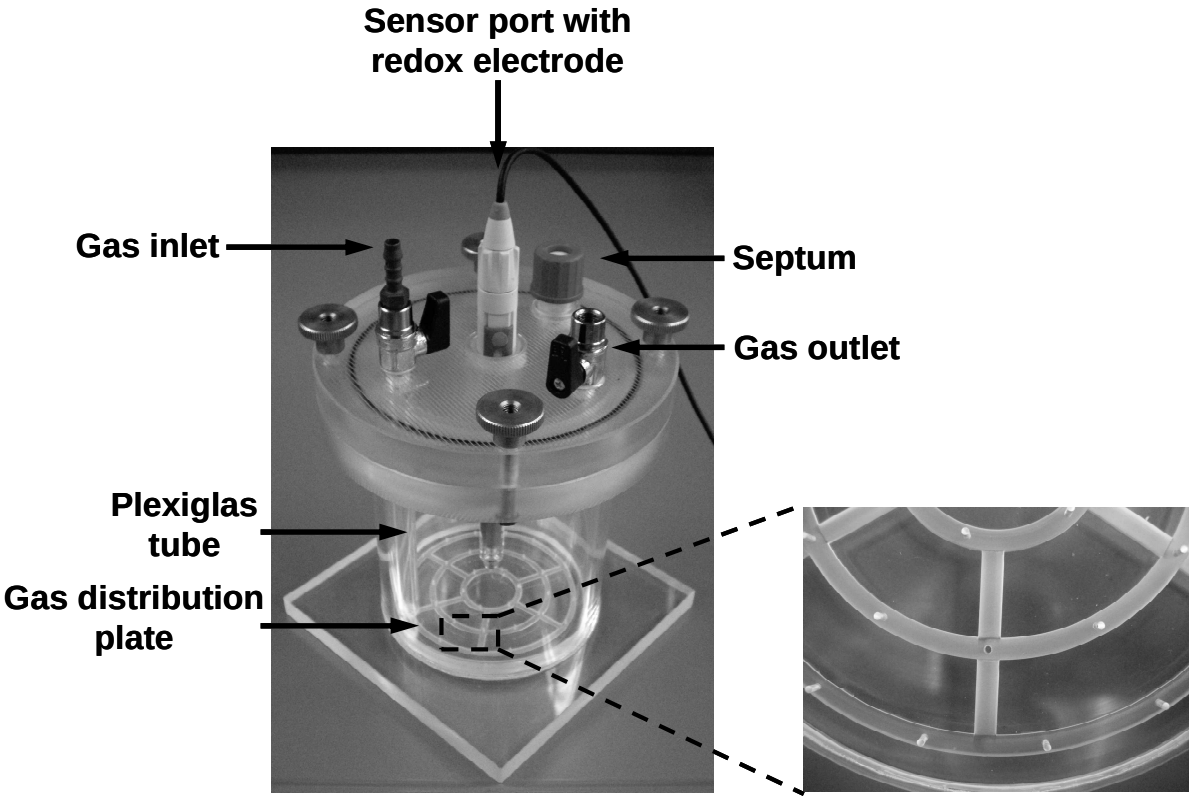
Supplementary Table S3. Numbers of 16S rRNA gene transcripts of detected bacterial taxa in soil slurries[a]

Treatment: Taxon	16S $rRNA_{Taxon}$ $[16S\ rRNA_{Bacteria}]^{-1}$ [b]				
	0 h	48 h	102 h	168 h	192 h
Cellobiose treatment:					
Micrococcaceae & Cellulomonadaceae	$(1.1 \pm 0.1) \times 10^{-4}$	$(6.5 \pm 2.1) \times 10^{-3}$	$(6.0 \pm 1.3) \times 10^{-3}$	$(3.6 \pm 0.6) \times 10^{-3}$	$(4.0 \pm 0.7) \times 10^{-3}$
Kineosporiaceae & Nocardioidaceae	$(9.3 \pm 5.8) \times 10^{-7}$	$(2.5 \pm 0.6) \times 10^{-7}$	$(1.3 \pm 0.6) \times 10^{-7}$	2.0×10^{-7}	$(2.0 \pm 0.5) \times 10^{-7}$
Cluster I *Clostridiaceae*	$(9.4 \pm 3.1) \times 10^{-7}$	$(1.5 \pm 0.7) \times 10^{-6}$	$(1.2 \pm 1.0) \times 10^{-5}$	$(7.5 \pm 6.3) \times 10^{-5}$	$(8.0 \pm 2.5) \times 10^{-5}$
Planctomycetaceae	$(1.2 \pm 0.4) \times 10^{-5}$	$(1.1 \pm 0.5) \times 10^{-6}$	$(1.1 \pm 0.4) \times 10^{-6}$	$(4.5 \pm 2.0) \times 10^{-7}$	$(8.0 \pm 1.3) \times 10^{-7}$
'Cellu'[c]	$(9.0 \pm 2.3) \times 10^{-8}$	$(2.1 \pm 1.0) \times 10^{-7}$	1.6×10^{-6}	1.8×10^{-6}	$(1.6 \pm 0.6) \times 10^{-6}$
'Sphingo'[c]	$(1.1 \pm 0.3) \times 10^{-5}$	$(3.1 \pm 0.9) \times 10^{-6}$	$(2.1 \pm 0.5) \times 10^{-6}$	$(4.5 \pm 0.8) \times 10^{-6}$	$(2.2 \pm 0.3) \times 10^{-6}$
'Deha'[c]	$(1.3 \pm 0.2) \times 10^{-3}$	$(2.8 \pm 0.4) \times 10^{-4}$	$(2.7 \pm 0.5) \times 10^{-4}$	$(2.0 \pm 1.0) \times 10^{-4}$	$(3.1 \pm 0.3) \times 10^{-4}$
Unsupplemented control:					
Micrococcaceae & Cellulomonadaceae	$(2.0 \pm 0.4) \times 10^{-4}$	$(1.2 \pm 0.2) \times 10^{-4}$	$(1.4 \pm 0.4) \times 10^{-4}$	$(1.3 \pm 0.2) \times 10^{-4}$	$(8.7 \pm 3.5) \times 10^{-5}$
Kineosporiaceae & Nocardioidaceae	$(8.6 \pm 4.1) \times 10^{-7}$	$(6.5 \pm 1.4) \times 10^{-7}$	$(6.1 \pm 0.9) \times 10^{-7}$	$(6.4 \pm 1.2) \times 10^{-7}$	$(7.7 \pm 5.9) \times 10^{-7}$
Cluster I *Clostridiaceae*	$(1.0 \pm 0.5) \times 10^{-6}$	$(9.9 \pm 3.5) \times 10^{-7}$	$(8.7 \pm 4.2) \times 10^{-7}$	$(1.4 \pm 0.4) \times 10^{-6}$	$(2.4 \pm 1.3) \times 10^{-6}$
Planctomycetaceae	$(2.4 \pm 0.6) \times 10^{-5}$	$(1.4 \pm 0.3) \times 10^{-5}$	$(8.6 \pm 2.1) \times 10^{-6}$	$(1.3 \pm 0.2) \times 10^{-5}$	$(7.9 \pm 3.4) \times 10^{-6}$
'Cellu'[c]	$(4.2 \pm 1.6) \times 10^{-8}$	$(5.3 \pm 1.1) \times 10^{-8}$	$(4.2 \pm 1.2) \times 10^{-8}$	$(4.6 \pm 1.0) \times 10^{-8}$	$(5.5 \pm 2.8) \times 10^{-8}$
'Sphingo'[c]	$(1.1 \pm 0.9) \times 10^{-5}$	$(7.5 \pm 4.0) \times 10^{-6}$	$(7.4 \pm 2.3) \times 10^{-6}$	$(5.0 \pm 0.2) \times 10^{-6}$	$(6.6 \pm 3.2) \times 10^{-6}$
'Deha'[c]	$(9.2 \pm 0.9) \times 10^{-4}$	$(7.1 \pm 1.3) \times 10^{-4}$	$(6.6 \pm 1.4) \times 10^{-4}$	$(8.2 \pm 0.9) \times 10^{-4}$	$(5.8 \pm 2.3) \times 10^{-4}$

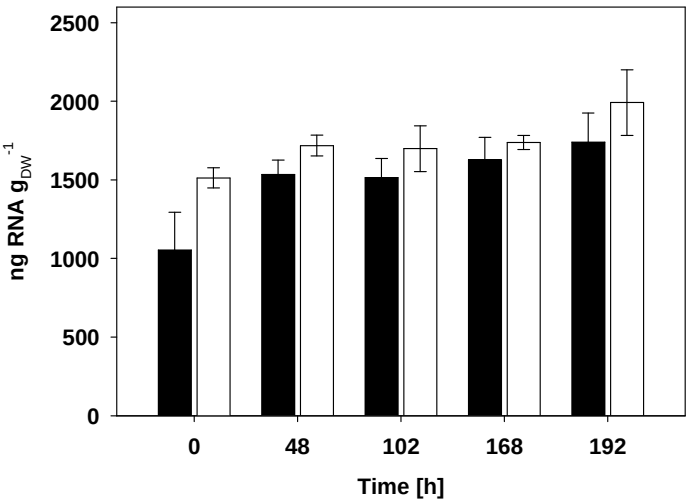
[a] Assignment to a family was based on a minimal 16S rRNA gene similarity of 87% (4).

[b] Values are the means of two replicates (without standard deviation) or three replicates (with standard deviation).

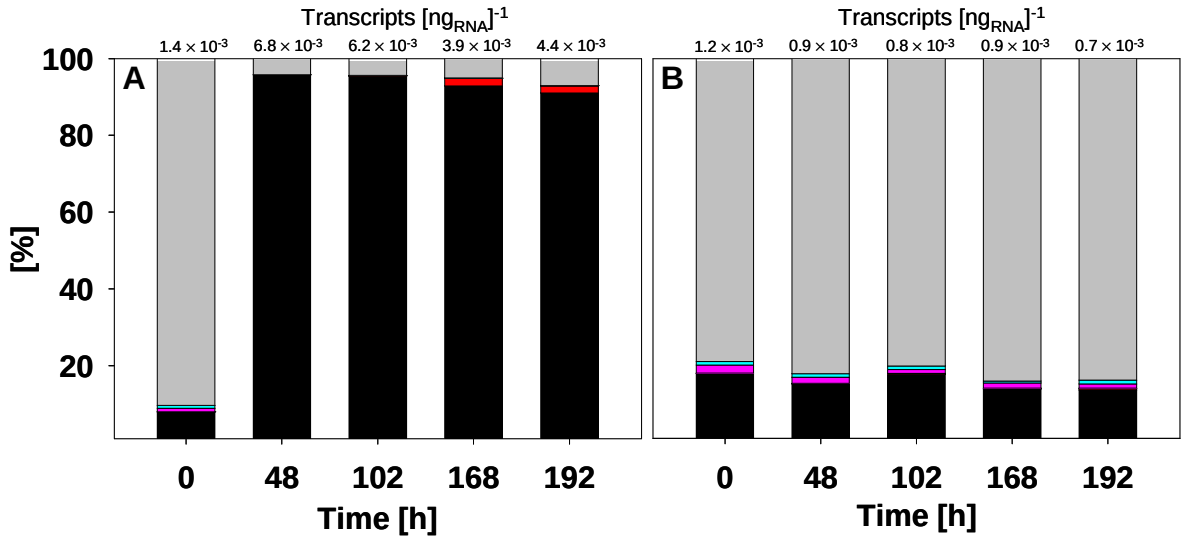
[c] Name and affiliation as defined elsewhere (1).



Supplemental FIG. S1. Incubation chamber. Sensor port was used for pH and redox potential measurements. Sterile synthetic air or N_2 were supplied at a gas inlet, and slurries were aerated from below by a gas distribution plate. Liquid samples were taken at the septum with a sterile syringe. Gas was released from the gas outlet. Valves of gas inlet and outlet were closed during anoxic incubation, but at the oxic phases synthetic air was permanently flushed through the soil slurry.



Supplemental FIG. S2. Total RNA extracted from each sampling period of each treatment exposed to fluctuating availabilities of O_2. Filled bars, cellobiose treatments; empty bars, unsupplemented control treatments.



Supplemental FIG. S3. Relative abundances of taxa in (A) cellobiose treatments, and (B) unsupplemented control treatments. 100 % corresponds to the total number of transcripts of all taxa.

'Deha' (*Chloroflexi*) *Planctomycetaceae* *Micrococcaceae & Cellulomonadaceae*
Clostridia I 'Cellu' (*Bacteroidetes*) *Kineosporiaceae & Nocardioidaceae*
'Sphingo' (*Bacteroidetes*)

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