Electronic Supplementary Material (ESI) for Environmental Science: Water Research & Technology.

Supplementary Information (SI)

Methane-driven microbial fuel cells recover energy and mitigate dissolved methane emissions from anaerobic effluents

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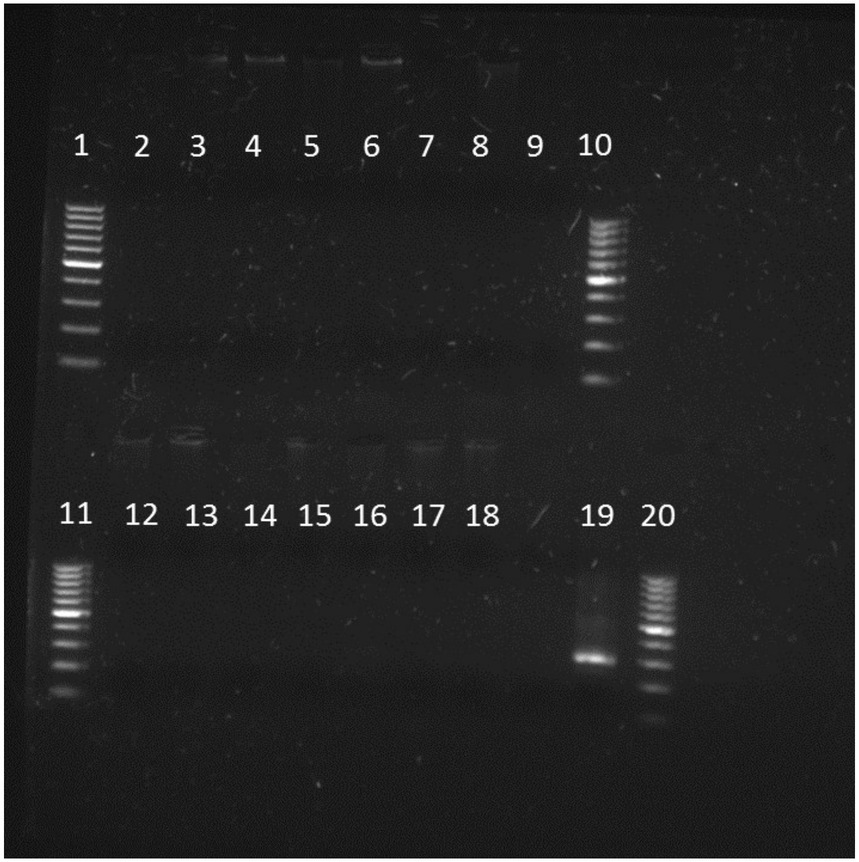
SI Figures

Lane #	Sample
1	DNA ladder
2	Primary effluent

Figure S1. Gel electrophoresis of *Geobacter* 16S rRNA gene PCR products (top) and *pmoA* PCR products (bottom) of reverse transcribed RNA extracts (cDNA) after being treated by Invitrogen DNA-free kit. Bands for *Geobacter* and *pmoA* (faint) are shown in lane 2 and demonstrate that the inoculum contained both *Geobacter* and methanotrophs



Lane #	**Sample**	**Lane #**	**Sample**
1	DNA ladder	11	DNA ladder
2	Reactor A Anode biofilm	12	Reactor A Anode biofilm
3	Reactor A Cathode biofilm	13	Reactor A Cathode biofilm
4	Reactor B Anode biofilm	14	Reactor B Anode biofilm
5	Reactor B Cathode biofilm	15	Reactor B Cathode biofilm
6	Reactor A Anode biofilm	16	Primary effluent
7	Reactor A Cathode biofilm	17	Reactor A Anode biofilm
8	Reactor B Anode biofilm	18	Reactor A Cathode biofilm
9	Reactor B Cathode biofilm	19	Positive control
10	DNA ladder	20	DNA ladder

Figure S2. Gel electrophoresis of 16S rRNA gene PCR products of RNA extracts after being treated by Invitrogen DNA-free kit.

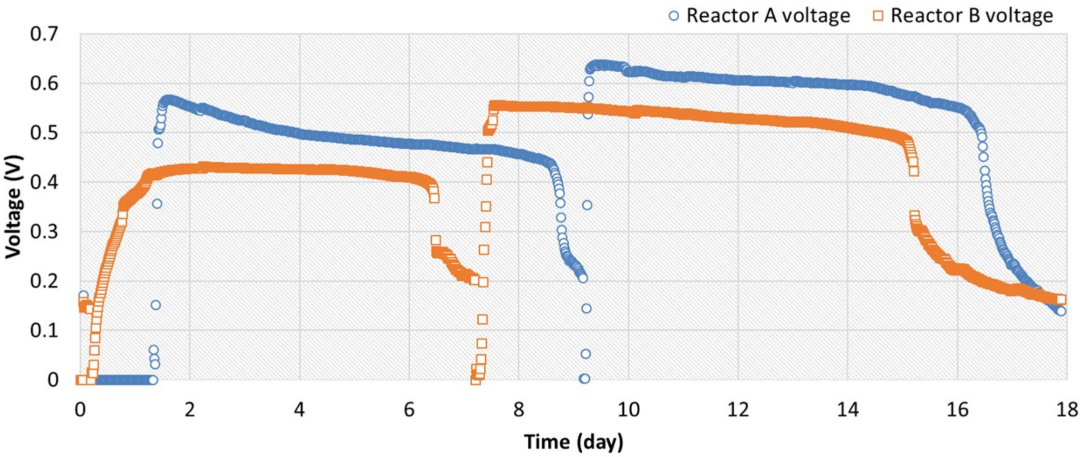


Figure S3. 2 cycles of voltage production while MFCs were operated in fed-batch mode on acetate containing media.

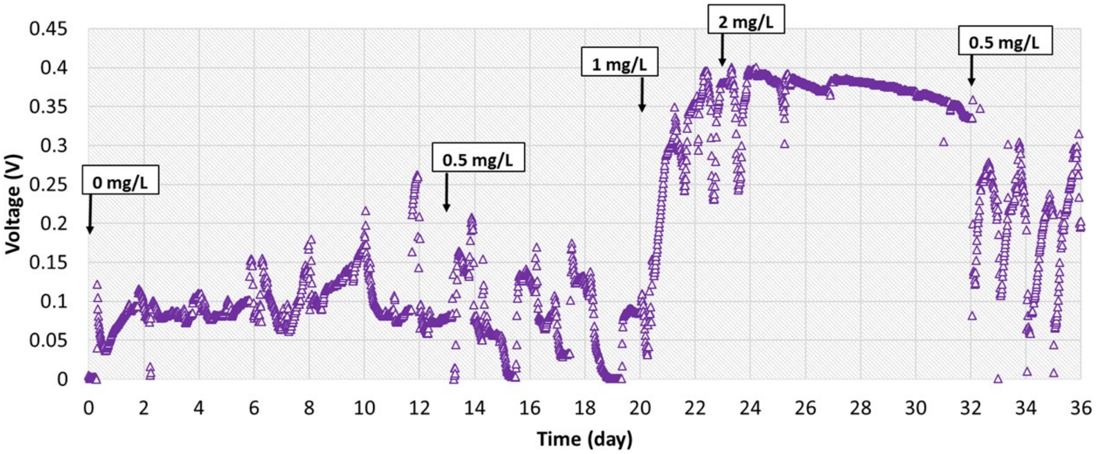


Figure S4. Voltage production while double-chamber MFCs were operated in continuous mode on methane containing media with different dissolved oxygen concentration

SI Tables

Table S1. Influent media recipe

Substrate		**Trace metals solution (mg/L)**	
80% methane saturation / 1 g/L acetate solution		Chromium Nitrate [$Cr(NO_3)_3 \cdot 9H_2O$]	1.00
Chemical compounds (mg/L)		Copper Chloride [$CuCl_2$]	0.500
Calcium Chloride [$CaCl_2$]	75.1	Manganese Sulfate [$MnSO_4$]	1.13
Ferric phosphate [$FePO_4$]	27.2	Nickel Sulfate [$NiSO_4$]	0.230
Phosphate buffer solution (50mM PBS) (mg/L)		Zinc Chloride [$ZnCl_2$]	0.380
Sodium phosphate dibasic anhydrous [Na_2HPO_4]	3949	Lead Chloride [$PbCl_2$]	0.130
Sodium dihydrogen phosphate monohydrate [$NaH_2PO_4 \bullet H_2O$]	2112		
Potassium chloride [KCl]	112		
Ammonium Chloride [NH_4Cl]	267		

Table S2. PCR and qPCR temperature cycling for primer sets 564F/840R (*Geobacter* 16S rRNA), A189F/mb661R (*pmoA*), and 515F/806R (total 16S rRNA)

	Primer set	**Initial denaturation**	**Cycles**	**Denaturation**	**Annealing**	**Extension**	**Final extension**	**High-resolution melting**	**Serial dilution**	**R^2, standards**	**Amplification efficiency**
PCR	564F/840R	99°C 900s	25	94°C 60s	50°C 60s	72°C 60s	72°C 60s				
	A189F/mb661R	96°C 300s	30	94°C 60s	50°C 60s	72°C 60s	72°C 300s				
	515F/806R	95°C 300s	30	94°C 60s	58°C 60s	72°C 60s	72°C 600s				
qPCR	564F/840R	94°C 240s	45	94°C 30s	Touchdown 65°C, 0 Cyc -> 55°C (-0.5°C)	72°C 30s		95°C 20s, 55°C 15s, 72°C 20s	10^{0}, 10^{-2}, 10^{-4}, 10^{-6}, 10^{-8}	1.00	82.0%
	A189F/mb661R	95°C 30s	45	95°C 30s	56°C 30s	72°C 30s		95°C 20s, 55°C 15s, 72°C 20s	10^{0}, 10^{-2}, 10^{-4}, 10^{-6}, 10^{-8}	1.00	83.0%
	515F/806R	95°C 300s	45	95°C 20s	55°C 15s	72°C 20s		95°C 20s, 55°C 15s, 72°C 20s	10^{0}, 10^{-2}, 10^{-4}, 10^{-6}, 10^{-8}	0.960	99.0%

Table S3. Oxygen diffusion across cathode

Terms			Units	Notes
Diffusion coefficient	D	0.000322	cm^2/s	$k=D/\varepsilon$
Mass transfer coefficient	k	0.0023	cm/s	0.6 to $3.9*10^{-3}$ [Chen et al. 2006]
Membrane thickness	ε	0.14	cm	[Chen et al. 2006]
Outside oxygen gradient/concentration (Saturated)	C_s	7.8	mg/L	[Chen et al. 2006]
Inside oxygen gradient/concentration	C	0	mg/L	
Membrane area	A	60	cm^2	
Oxygen diffusion/wastewater	Δm	0.258	mg O_2/mL	16 h HRT, 0.25 mL/min
		0.129		8 h HRT, 0.5 mL/min
		0.0646		4 h HRT, 1 mL/min

Table S4. Proportion of electrons diverted to electron acceptor and to cell maintenance based on overall energy balance

Term	Formula/value	Notes
Formate	$1/2HCO_3^- + H^+ + e^- = 1/2HCOO^- + 1/2H_2O$	$\Delta G^{0'} = 39.19$ kJ/e^- eq
Acetate	$1/8CO_2 + 1/8HCO_3^- + H^+ + e^- = 1/8CH_3COO^- + 3/8H_2O$	$\Delta G^{0'} = 27.4$ kJ/e^- eq
Oxygen	$1/4O_2 + H^+ + e^- = 1/2H_2O$	$\Delta G^{0'} = -78.72$ kJ/e^- eq
Pyruvate		$\Delta G^{0'} = 35.09$ kJ/e^- eq
$\Delta G_{donor}^{0'}/\Delta G_c$	Formate or Acetate	Electron donor or carbon source
ΔG_p	$\Delta G_p = \Delta G_{pyr}^{0'} - \Delta G_c^{0'}$	Energy to synthesis pyruvate from carbon source
ΔG_{pc}	18.8 kJ/e^- eq when ammonia is nitrogen source	Energy to make cells from intermediates, based on empirically derived number of 3.33kJ/g cells, $C_5H_7O_2N$ for cells, and 20 e^- transferred/ more cells yields
ΔG_r	$\Delta G_p = \Delta G_{acceptor}^{0'} - \Delta G_{donor}^{0'}$	Energy available from electron donor to electron acceptor
ε	0.6	Energy loss including energy transfer efficiency, ranges from 0.4 to 0.8
A	$A = -\left[\dfrac{\dfrac{\Delta G_P}{\varepsilon^n} + \dfrac{\Delta G_{PC}}{\varepsilon}}{\varepsilon \Delta G_r}\right] = \dfrac{f_e^o}{f_s^o}$	Energy consumption for cell synthesis/ energy produced from donor to acceptor
f_e^0	$f_e^o = \dfrac{A}{1+A}$	Proportion of electrons flow from electron donor to electron acceptor

Table S5. Addition volume of methanol, formaldehyde, and formate and corresponding Coulombic efficiency.

Substrate	**Volume added µL (per 240 mL)**	**Theoretical current from full substrate conversion (C)**	**Total electrons production (C)**		**Coulombic efficiency**	
			Reactor A	Reactor B	Reactor A	Reactor B
Methanol	12.1	173.67	1.97	3.91	1.14%	2.25%
Formaldehyde	11.0	115.78	8.33	15.25	7.20%	13.17%
Formate	11.3	57.89	29.66	44.06	51.24%	76.10%

Table S6. Primer coverage of *Archaea* and *Bacteria* for 16S rRNA gene primers F515 (GTGCCAGCMGCCGCGGTAA) and R806 (GGACTACHVGGGTWTCTAAT) targeting the V4 region (Kozich et al. 2013) according to TestPrime 1.0. TestPrime 1.0 evaluates the coverage of primer pairs by running an *in silico* PCR using the SILVA databases. Zero primer mismatches were allowed.

Domain	**Phylum**	**Coverage (%)**	**Domain**	**Phylum**	**Coverage (%)**
Archaea					52.6
Archaea	Aenigmarchaeota	21.5	Archaea	Lokiarchaeota	85.1
Archaea	Aigarchaeota	1.2	Archaea	MSBL1	84.8
Archaea	AK8	86.7	Archaea	Nanoarchaeota	0
Archaea	Altiarchaeales	0	Archaea	Nanohaloarchaeota	0
Archaea	Bathyarchaeota	0.2	Archaea	Parvarchaeota	68.8
Archaea	Crenarchaeota	0.2	Archaea	pCIRA-13	0
Archaea	Diapherotrites	5	Archaea	pMC2A209	20
Archaea	Euryarchaeota	87.7	Archaea	Thaumarchaeota	0.7
Archaea	Hadesarchaea	83.4	Archaea	TVG8AR30	0
Archaea	Korarchaeota	46.3	Archaea	WSA2	77
Bacteria					**86.5**
Bacteria	AC1	67.6	Bacteria	Gemmatimonadetes	88
Bacteria	Acetothermia	26.1	Bacteria	GN01	72.4
Bacteria	Acidobacteria	91.8	Bacteria	Gracilibacteria	74.8
Bacteria	Actinobacteria	81.1	Bacteria	Hydrogenedentes	88.8
Bacteria	Aerophobetes	3.2	Bacteria	Ignavibacteriae	89.6
Bacteria	Aminicenantes	88.6	Bacteria	Latescibacteria	91.1
Bacteria	Aquificae	86.9	Bacteria	LCP-89	100
Bacteria	Armatimonadetes	86.4	Bacteria	Lentisphaerae	82.5
Bacteria	Atribacteria	93.5	Bacteria	MD2896-B216	33.3

Bacteria	Bacteroidetes	88.5	Bacteria	Microgenomates		1.3
Bacteria	BJ-169	83.3	Bacteria	Nitrospinae		70.4
Bacteria	BP4	100	Bacteria	Nitrospirae		89.8
Bacteria	BRC1	85.6	Bacteria	Omnitrophica		62.1
Bacteria	Caldiserica	5.3	Bacteria	Parcubacteria		4.3
Bacteria	Calescamantes	0	Bacteria	PAUC34f		60.1
Bacteria	Chlamydiae	18.8	Bacteria	Peregrinibacteria		57.2
Bacteria	Chlorobi	55.8	Bacteria	Planctomycetes		80.9
Bacteria	Chloroflexi	52.4	Bacteria	Poribacteria		11.8
Bacteria	Chrysiogenetes	100	Bacteria	RsaHF231		85.7
Bacteria	Cloacimonetes	82.9	Bacteria	Saccharibacteria		3.9
Bacteria	CPR2	72.2	Bacteria	SBR1093		88.3
Bacteria	Cyanobacteria	80.7	Bacteria	Spirochaetae		71.9
Bacteria	Deferribacteres	87.8	Bacteria	Synergistetes		89.2
Bacteria	Deinococcus-Thermus	92.1	Bacteria	TA06		75
Bacteria	Dictyoglomi	88.9	Bacteria	Tectomicrobia		89
Bacteria	Elusimicrobia	88.8	Bacteria	Tenericutes		84.2
Bacteria	FBP	15	Bacteria	Thermodesulfobacteria		93.2
Bacteria	FCPU426	75.8	Bacteria	Thermotogae		88.5
Bacteria	Fervidibacteria	100	Bacteria	Verrucomicrobia		84.1
Bacteria	Fibrobacteres	85.4	Bacteria	WA-aaa01f12		75
Bacteria	Firmicutes	88.5	Bacteria	WS1		82.2
Bacteria	FL0428B-PF49	73.3	Bacteria	WS2		84.6
Bacteria	Fusobacteria	88.3	Bacteria	WS6		0
Bacteria	GAL15	88.6	Bacteria	WWE3		0
Domain	**Phylum**	**Class**	**Order**	**Family**	**Genus**	**Coverage (%)**
Bacteria	Proteobacteria					89.8

Bacteria	Proteobacteria	Alphaproteobacteria				84.8
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales			92.9
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Beijerinckiaceae	Methylocapsa	100
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Beijerinckiaceae	Methylocella	100
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Beijerinckiaceae	Methyloferula	100
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Beijerinckiaceae	Methylorosula	88.9
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Beijerinckiaceae	Methylovirgula	94.4
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Hyphomicrobiaceae		92
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Hyphomicrobiaceae	Methylorhabdus	100
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Hyphomicrobiaceae	Methyloterrigena	100
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methylobacteriaceae		89.7
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methylobacteriaceae	Meganema	94.3
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methylobacteriaceae	Methylobacterium	89.2
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methylobacteriaceae	Microvirga	88.9
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methylobacteriaceae	Psychroglaciecola	89.5
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methylobacteriaceae	uncultured	92.3
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methylocystaceae		94.8
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methylocystaceae	Albibacter	100
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methylocystaceae	Hansschlegelia	100
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methylocystaceae	Hartmannibacter	100
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methylocystaceae	Methylocystis	94
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methylocystaceae	Methylopila	100
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methylocystaceae	Methylosinus	97.1
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methylocystaceae	Pleomorphomonas	96.4
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methylocystaceae	uncultured	85.2
Bacteria	Proteobacteria	Betaproteobacteria				91.4
Bacteria	Proteobacteria	Betaproteobacteria	Methylophilales			89.1
Bacteria	Proteobacteria	Betaproteobacteria	Methylophilales	Methylophilaceae		89.1

Bacteria	Proteobacteria	Betaproteobacteria	Methylophilales	Methylophilaceae	Candidatus Methylopumilus	95.2
Bacteria	Proteobacteria	Betaproteobacteria	Methylophilales	Methylophilaceae	Methylobacillus	90
Bacteria	Proteobacteria	Betaproteobacteria	Methylophilales	Methylophilaceae	Methylophilus	76.9
Bacteria	Proteobacteria	Betaproteobacteria	Methylophilales	Methylophilaceae	Methylotenera	93
Bacteria	Proteobacteria	Betaproteobacteria	Methylophilales	Methylophilaceae	Methylovorus	100
Bacteria	Proteobacteria	Betaproteobacteria	Methylophilales	Methylophilaceae	OM43 clade	91.4
Bacteria	Proteobacteria	Betaproteobacteria	Methylophilales	Methylophilaceae	PRD01a011B	96.7
Bacteria	Proteobacteria	Betaproteobacteria	Methylophilales	Methylophilaceae	uncultured	91.2
Bacteria	Proteobacteria	Betaproteobacteria	Rhodocyclales			91.7
Bacteria	Proteobacteria	Betaproteobacteria	Rhodocyclales	Rhodocyclaceae		91.7
Bacteria	Proteobacteria	Betaproteobacteria	Rhodocyclales	Rhodocyclaceae	Methyloversatilis	92.4
Bacteria	Proteobacteria	Deltaproteobacteria				89.3
Bacteria	Proteobacteria	Deltaproteobacteria	Desulfuromonadales			91.4
Bacteria	Proteobacteria	Deltaproteobacteria	Desulfuromonadales	Geobacteraceae		90.9
Bacteria	Proteobacteria	Deltaproteobacteria	Desulfuromonadales	Geobacteraceae	Geobacter	91.1
Bacteria	Proteobacteria	Gammaproteobacteria				91.9
Bacteria	Proteobacteria	Gammaproteobacteria	Methylococcales			92.6
Bacteria	Proteobacteria	Gammaproteobacteria	Methylococcales	Marine Methylotrophic Group 1		95.9
Bacteria	Proteobacteria	Gammaproteobacteria	Methylococcales	Marine Methylotrophic Group 1	Methyloprofundus	100
Bacteria	Proteobacteria	Gammaproteobacteria	Methylococcales	Marine Methylotrophic Group 2		92.1
Bacteria	Proteobacteria	Gammaproteobacteria	Methylococcales	Methylococcaceae		93.8
Bacteria	Proteobacteria	Gammaproteobacteria	Methylococcales	Methylococcaceae	Candidatus Methylospira	100
Bacteria	Proteobacteria	Gammaproteobacteria	Methylococcales	Methylococcaceae	Methylobacter	83.1
Bacteria	Proteobacteria	Gammaproteobacteria	Methylococcales	Methylococcaceae	Methylocaldum	90

Bacteria	Proteobacteria	Gammaproteobacteria	Methylococcales	Methylococcaceae	Methylococcus	97
Bacteria	Proteobacteria	Gammaproteobacteria	Methylococcales	Methylococcaceae	Methylogaea	100
Bacteria	Proteobacteria	Gammaproteobacteria	Methylococcales	Methylococcaceae	Methyloglobulus	100
Bacteria	Proteobacteria	Gammaproteobacteria	Methylococcales	Methylococcaceae	Methylohalobius	100
Bacteria	Proteobacteria	Gammaproteobacteria	Methylococcales	Methylococcaceae	Methylomarinum	77.8
Bacteria	Proteobacteria	Gammaproteobacteria	Methylococcales	Methylococcaceae	Methylomicrobium	100
Bacteria	Proteobacteria	Gammaproteobacteria	Methylococcales	Methylococcaceae	Methylomonas	98.1
Bacteria	Proteobacteria	Gammaproteobacteria	Methylococcales	Methylococcaceae	Methyloparacoccus	95.6
Bacteria	Proteobacteria	Gammaproteobacteria	Methylococcales	Methylococcaceae	Methylosarcina	100
Bacteria	Proteobacteria	Gammaproteobacteria	Methylococcales	Methylococcaceae	Methylosoma	100
Bacteria	Proteobacteria	Gammaproteobacteria	Methylococcales	Methylococcaceae	Methylosphaera	100
Bacteria	Proteobacteria	Gammaproteobacteria	Methylococcales	Methylococcaceae	Methylothermus	90
Bacteria	Proteobacteria	Gammaproteobacteria	Methylococcales	Methylococcaceae	Methylovulum	100
Bacteria	Proteobacteria	Gammaproteobacteria	Methylococcales	Methylococcaceae	uncultured	91.5
Bacteria	Proteobacteria	Gammaproteobacteria	Methylococcales	Milano-WF1B-03		85
Bacteria	Proteobacteria	Gammaproteobacteria	Methylococcales	Milano-WF1B-42		100
Bacteria	Proteobacteria	Gammaproteobacteria	Methylococcales	pItb-vmat-59		100
Bacteria	Proteobacteria	Gammaproteobacteria	Methylococcales	pLW-20		71.4
Bacteria	Proteobacteria	Gammaproteobacteria	Thiotrichales			93.3
Bacteria	Proteobacteria	Gammaproteobacteria	Thiotrichales	Thiotrichaceae		93.7
Bacteria	Proteobacteria	Gammaproteobacteria	Thiotrichales	Thiotrichaceae	Methylohalomonas	82.9

Table S7. Primer coverage of *Geobacter* for 16S rRNA gene primer 564F (AAGCGTTGTTCGGAWTTAT) and 840R (GGCACTGCAGGGGTCAATA) targeting *Geobacter* (Cummings, D.E., et al. 2003) according to TestPrime 1.0. TestPrime 1.0 evaluates the coverage of primer pairs by running an *in silico* PCR using the SILVA databases. Zero primer mismatches were allowed.

Domain	**Phylum**	**Coverage (%)**	**Domain**	**Phylum**	**Coverage (%)**
Archaea		0			**0**
Archaea	Aenigmarchaeota	0	Archaea	Lokiarchaeota	0
Archaea	Aigarchaeota	0	Archaea	MSBL1	0
Archaea	AK8	0	Archaea	Nanoarchaeota	0
Archaea	Altiarchaeales	0	Archaea	Nanohaloarchaeota	0
Archaea	Bathyarchaeota	0	Archaea	Parvarchaeota	0
Archaea	Crenarchaeota	0	Archaea	pCIRA-13	0
Archaea	Diapherotrites	0	Archaea	pMC2A209	0
Archaea	Euryarchaeota	0	Archaea	Thaumarchaeota	0
Archaea	Hadesarchaea	0	Archaea	TVG8AR30	0
Archaea	Korarchaeota	0	Archaea	WSA2	0
Bacteria					**0.1**
Bacteria	AC1	0	Bacteria	Gemmatimonadetes	0
Bacteria	Acetothermia	0	Bacteria	GN01	0
Bacteria	Acidobacteria	0	Bacteria	Gracilibacteria	0
Bacteria	Actinobacteria	0	Bacteria	Hydrogenedentes	0
Bacteria	Aerophobetes	0	Bacteria	Ignavibacteriae	0
Bacteria	Aminicenantes	0	Bacteria	Latescibacteria	0
Bacteria	Aquificae	0	Bacteria	LCP-89	0
Bacteria	Armatimonadetes	0	Bacteria	Lentisphaerae	0
Bacteria	Atribacteria	0	Bacteria	MD2896-B216	0
Bacteria	Bacteroidetes	0	Bacteria	Microgenomates	0
Bacteria	BJ-169	0	Bacteria	Nitrospinae	0

Bacteria	BP4	0	Bacteria	Nitrospirae	0
Bacteria	BRC1	0	Bacteria	Omnitrophica	0
Bacteria	Caldiserica	0	Bacteria	Parcubacteria	0
Bacteria	Calescamantes	0	Bacteria	PAUC34f	0
Bacteria	Chlamydiae	0	Bacteria	Peregrinibacteria	0
Bacteria	Chlorobi	0	Bacteria	Planctomycetes	0
Bacteria	Chloroflexi	0	Bacteria	Poribacteria	0
Bacteria	Chrysiogenetes	0	Bacteria	RsaHF231	0
Bacteria	Cloacimonetes	0	Bacteria	Saccharibacteria	0
Bacteria	CPR2	0	Bacteria	SBR1093	0
Bacteria	Cyanobacteria	0	Bacteria	Spirochaetae	0
Bacteria	Deferribacteres	0	Bacteria	Synergistetes	0
Bacteria	Deinococcus-Thermus	0	Bacteria	TA06	0
Bacteria	Dictyoglomi	0	Bacteria	Tectomicrobia	0
Bacteria	Elusimicrobia	0	Bacteria	Tenericutes	0
Bacteria	FBP	0	Bacteria	Thermodesulfobacteria	0
Bacteria	FCPU426	0	Bacteria	Thermotogae	0
Bacteria	Fervidibacteria	0	Bacteria	Verrucomicrobia	0
Bacteria	Fibrobacteres	0	Bacteria	WA-aaa01f12	0
Bacteria	Firmicutes	0	Bacteria	WS1	0
Bacteria	FL0428B-PF49	0	Bacteria	WS2	0
Bacteria	Fusobacteria	0	Bacteria	WS6	0
Bacteria	GAL15	0	Bacteria	WWE3	0

Domain	**Phylum**	**Class**	**Order**	**Family**	**Genus**	**Coverage (%)**
Bacteria	Proteobacteria					0.3
Bacteria	Proteobacteria	Deltaproteobacteria	Desulfuromonadales	Geobacteraceae		56.3
Bacteria	Proteobacteria	Deltaproteobacteria	Desulfuromonadales	Geobacteraceae	Geobacter	63.1