

Table S1. A nucleotide sequence alignment of each forward and reverse hgcA-targeted PCR primers to select genomic sequences. Mismatched base pairs are indicated in red.

Strain	Phylum	Taxonomic position	hgcA	F forward primer	hgcB	R reverse primer
			Gene Locus	GGNRTTAAATGTTGGTGYGC	Gene Locus	CADGCNCRCAYTCVATRCA
<i>Geobacter metallireducens</i> RCH3	Proteobacteria	<i>Deltaproteobacteria</i>	GeoDRRAFT_0749	GGGATCAATGTCCTGGTGGCG	GeoDRRAFT_T748	CAGGCCGCCGCAATTTCATGCA
<i>Geobacter metallireducens</i> GS-15	Proteobacteria	<i>Deltaproteobacteria</i>	Gbm_100	GGGATCAATGTCCTGGTGGCG	Gbm_140	CAGGCCGCCGCAATTTCATGCA
<i>Geobacter sulfurreducens</i> PCA	Proteobacteria	<i>Deltaproteobacteria</i>	GSU1440	GGCATATACTGTCGTGCGCG	GSU1441	CAGGCCGCCGCAATTTCATGCA
<i>Geobacter sulfurreducens</i> KW400	Proteobacteria	<i>Deltaproteobacteria</i>	KN400_1466	GGCATATACTGTCGTGCGCG	KN400_1468	CAGGCCGCCGCAATTTCATGCA
<i>Geobacter sp.</i> FRC-32	Proteobacteria	<i>Deltaproteobacteria</i>	Geob_2483	GGGATCAATGTCCTGGTGGCG	Geob_2482	CAGGCCGCCGCAATTTCATGCA
<i>Geobacter uranireducens</i> R4	Proteobacteria	<i>Deltaproteobacteria</i>	Gura_0480	GGGATTAACCGTCCTGGTGGCG	Gura_0481	CAGGCCGCCGCAATTTCATGCA
<i>Geobacter bermensis</i> Bem	Proteobacteria	<i>Deltaproteobacteria</i>	Gbm_1183	GGGATCAACCGTCCTGGTGGCG	Gbm_1184	CAGGCCGCCGCAATTTCATGCA
<i>Geobacter sp.</i> M18	Proteobacteria	<i>Deltaproteobacteria</i>	GM18_1031	GGGATCAACCGTCCTGGTGGCG	GM18_1032	CAGGCCGCCGCAATTTCATGCA
<i>Geobacter sp.</i> M21	Proteobacteria	<i>Deltaproteobacteria</i>	GM21_3091	GGGATCAACCGTCCTGGTGGCG	GM21_3090	CAGGCCGCCGCAATTTCATGCA
<i>Desulfovibrio desulfuricans</i> ND132	Proteobacteria	<i>Deltaproteobacteria</i>	Dnd132_1056	GGGATCAACCGTCCTGGTGGCG	Dnd132_1057	CAGGCCGCCGCAATTTCATGCA
<i>Desulfovibrio aespoeensis</i> Asp-3	Proteobacteria	<i>Deltaproteobacteria</i>	Daes_2662	GGGATCAACCGTCCTGGTGGCG	Daes_2663	CAGGCCGCCGCAATTTCATGCA
<i>Desulfovibrio vulgaris</i> Hilden Bay	Proteobacteria	<i>Deltaproteobacteria</i>	Desv_1117	GGGATCAACCGTCCTGGTGGCG	Desv_1115	CAGGCCGCCGCAATTTCATGCA
<i>Desulfovibrio oxydans</i> DSM 11468	Proteobacteria	<i>Deltaproteobacteria</i>	B140CRRAFT_02526	GGCATTACATGTCGTGCGCG	B140CRRAFT_02527	CAGGCCGCCGCAATTTCATGCA
<i>Desulfovibulus propionicus</i> DSM 2032	Proteobacteria	<i>Deltaproteobacteria</i>	Desp_0439	GGGATCAATGTCCTGGTGGCG	Desp_0438	CAGGCCGCCGCAATTTCATGCA
<i>Desulfomicrobium baculum</i> DSM 4028	Proteobacteria	<i>Deltaproteobacteria</i>	Dbac_0376	GGGATCAACACATCTGGTGGCG	Dbac_0375	CAGGCCGCCGCAATTTCATGCA
<i>Desulfovotrophe spiri thiodismutans</i> ASO3-1	Proteobacteria	<i>Deltaproteobacteria</i>	Dthio_P01043	GGGATTAATGTCCTGGTGGCG	Dthio_P01042	CAGGCCGCCGCAATTTCATGCA
Uncultured <i>Desulfovibrio</i> sp.	Proteobacteria	<i>Deltaproteobacteria</i>	N47_A07900	GGTATCACATGTAATGGTGGCG	N47_A07910	CAGGCCGCCGCAATTTCATGCA
<i>Desulfovotrophe lacustre</i> T-7651	Proteobacteria	<i>Deltaproteobacteria</i>	DeslaDRRAFT_0127	GGGATCAACATGTCGTGCGCG	DeslaDRRAFT_0126	CAGGCCGCCGCAATTTCATGCA
<i>Desfonsoma camini</i> S3R1	Proteobacteria	<i>Deltaproteobacteria</i>	DefcaDRRAFT_2106	GGGATCAACCGTCCTGGTGGCG	DefcaDRRAFT_2107	CAGGCCGCCGCAATTTCATGCA
<i>Syntrophobacter</i> sp. <i>advenovorans</i> UI	Proteobacteria	<i>Deltaproteobacteria</i>	SyntroDRRAFT_0655	GGGATCAATGTCCTGGTGGCG	SyntroDRRAFT_0656	CAGGCCGCCGCAATTTCATGCA
<i>Desulfovibrio</i> sp. D2CB-1	Proteobacteria	<i>Deltaproteobacteria</i>	Desv_1022	GGGATTAATGTCCTGGTGGCG	Desv_1023	CAGGCCGCCGCAATTTCATGCA
<i>Syntrophobacter</i> sp. SB	Proteobacteria	<i>Deltaproteobacteria</i>	SYN_00351	GGGATCAACATGTCGTGCGCG	SYN_00352	CAGGCCGCCGCAATTTCATGCA
<i>Delta proteobacterium</i> NanS2	Proteobacteria	<i>Deltaproteobacteria</i>	NPH_5533	GGGATCAACATGTCGTGCGCG	NPH_5534	CAGGCCGCCGCAATTTCATGCA
<i>Dehalococcoides incertae</i> DSM285	Clostridia	<i>Dehalococcoidetes</i>	dcmB_330	GGGATCAACATGTCGTGCGCG	dcmB_329	CAGGCCGCCGCAATTTCATGCA
<i>Desulfovopionaceus</i> scaphilplus SJ4	Firmicutes	<i>Clostridia</i>	Desaci_1621	GGGATTAACCGTCCTGGTGGCG	Desaci_1622	CAGGCCGCCGCAATTTCATGCA
<i>Desulfovibacter</i> dehalogenans DSM9161	Firmicutes	<i>Clostridia</i>	Desde_2772	GGGATTAACATGTCGTGCGCG	Desde_2771	CAGGCCGCCGCAATTTCATGCA
<i>Dehalobacter</i> sp. CF	Firmicutes	<i>Clostridia</i>	DCF50_p1170	GGGATTAATGTCCTGGTGGCG	DCF50_p1169	CAGGCCGCCGCAATTTCATGCA
<i>Dehalobacter</i> sp. 11DCA	Firmicutes	<i>Clostridia</i>	DHBDC4_p1092	GGGATCAACATGTCGTGCGCG	DHBDC4_p1091	CAGGCCGCCGCAATTTCATGCA
<i>Desulfovopionaceus</i> orientis DSM 765	Firmicutes	<i>Clostridia</i>	Desor_2652	GGGATCAACATGTCGTGCGCG	Desor_2653	CAGGCCGCCGCAATTTCATGCA
<i>Desulfovibrio</i> sp. dichlorleminans LMG P-21439	Firmicutes	<i>Clostridia</i>	Desv_1040	GGGATCAACATGTCGTGCGCG	Desv_1041	CAGGCCGCCGCAATTTCATGCA
<i>Desulfovopionaceus</i> sp. OT	Firmicutes	<i>Clostridia</i>	DOT_5805	GGGATCAACATGTCGTGCGCG	DOT_5807	CAGGCCGCCGCAATTTCATGCA
<i>Desulfovopionaceus</i> youngiae DSM 17734	Firmicutes	<i>Clostridia</i>	DesyodDRRAFT_4238	GGGGCTCAACATGTCGTGCGCG	DesyodDRRAFT_4237	CAGGCCGCCGCAATTTCATGCA
<i>Acetinema longum</i> DSM 8540	Firmicutes	<i>Clostridia</i>	ALO_18015	GGGATCAACATGTCGTGCGCG	ALO_18015	CAGGCCGCCGCAATTTCATGCA
<i>Dehalobacter alkaliphilus</i> AHT 1	Firmicutes	<i>Clostridia</i>	DealDRRAFT_3158	GGGATTAATGTCCTGGTGGCG	DealDRRAFT_3157	CAGGCCGCCGCAATTTCATGCA
<i>Dehalobacter</i> sp. DSM 9455	Firmicutes	<i>Clostridia</i>	Delve_1982	GGGATTAATGTCCTGGTGGCG	Delve_1981	CAGGCCGCCGCAATTTCATGCA
<i>Dehalobacter</i> sp. FTH1	Firmicutes	<i>Clostridia</i>	A37GDRAFT_03566	GGGATTAATGTCCTGGTGGCG	A37GDRAFT_03565	CAGGCCGCCGCAATTTCATGCA
<i>Desulfovibacter</i> metallireducens 853-15A	Firmicutes	<i>Clostridia</i>	Desme_1742	GGGATCAATGTCGTGCGCG	Desme_1741	CATGCCGCCAACATTCATGCA
<i>Desulfovibacter</i> sp. PCE1	Firmicutes	<i>Clostridia</i>	DesPCE1DRRAFT_2748	GGGATCAATGTCGTGCGCG	DesPCE1DRRAFT_2747	CAGGCCGCCGCAATTTCATGCA
<i>Ethanoligenen</i> harbinense JUAN-3	Firmicutes	<i>Clostridia</i>	Desv_1075	GGGATCAACATGTCGTGCGCG	Desv_1076	CAGGCCGCCGCAATTTCATGCA
<i>Syntrophobacter</i> sp. DSM 9271	Firmicutes	<i>Clostridia</i>	Spd_102	GGGATCAACATGTCGTGCGCG	Spd_101	CAGGCCGCCGCAATTTCATGCA
<i>Methanofollis</i> limnatis DSM 4140	Euryarcheota	<i>Methanomicrobia</i>	Meli_1885	GGGATCAACATGTCGTGCGCG	Meli_1884	CAGGCCGCCGCAATTTCATGCA
<i>Methanoregula</i> boonei 648	Euryarcheota	<i>Methanomicrobia</i>	Mbo_0422	GGGATTAACATGTCGTGCGCG	Mbo_0421	CATGCCGCCAACATTCATGCA
<i>Methanoregula</i> formica S3MP	Euryarcheota	<i>Methanomicrobia</i>	Mefor_0951	GGGATCAACATGTCGTGCGCG	Mefor_0952	CAGGCCGCCGCAATTTCATGCA
<i>Methanospirillum</i> palustris E1-9c	Euryarcheota	<i>Methanomicrobia</i>	Mpal_1034	GGGATCAACATGTCGTGCGCG	Mpal_1035	CAGGCCGCCGCAATTTCATGCA
<i>Methanospirillum</i> hungatei JF-1	Euryarcheota	<i>Methanomicrobia</i>	Mfun_0876	GGGATCAACATGTCGTGCGCG	Mfun_0875	CATGCCGCCAACATTCATGCA
<i>Methanomethylbacter</i> hollandica DSM 15978	Euryarcheota	<i>Methanomicrobia</i>	Metho_0631	GGGATTAATGTCGTGCGCG	Metho_0630	CATGCCGCCAACATTCATGCA
<i>Methanobolus</i> psychrophilus MRE50	Euryarcheota	<i>Methanomicrobia</i>	Mpsv_0567	GGGATTAATGTCGTGCGCG	Mpsv_0566	CATGCCGCCAACATTCATGCA
<i>Methanocella</i> arvoryzae MRE50	Euryarcheota	<i>Methanomicrobia</i>	RCX2342	GGGATCAACATGTCGTGCGCG	RCX2341	CAGGCCGCCGCAATTTCATGCA
<i>Methanocella</i> paludicola SANAE	Euryarcheota	<i>Methanomicrobia</i>	MCP_0718	GGGATCAACATGTCGTGCGCG	MCP_0717	CAGGCCGCCGCAATTTCATGCA
<i>Methanobius</i> tridentus DSM 2278	Euryarcheota	<i>Methanomicrobia</i>	MettDRRAFT_2866	GGGATTAATGTCGTGCGCG	MettDRRAFT_2865	CATGCCGCCAACATTCATGCA

Mixed base definitions: R=A/G, Y=C/T, V=A/C/G, D=A/T/G, N=A/C/G/T

Table S2. Mean concentrations in the surface waters, porewaters, and soils for ortho-phosphate, total phosphorus, sulfate, methylmercury, dissolved iron, dissolved organic carbon, and dissolved oxygen at the study sites. The oxidation-reduction potential (SHE) of the soils are also provided.

Geochemical factors	Sample collection number	WCA-2A		WCA-3A
		F1	U3	W3
Ortho-Phosphate	Surface water ($\mu\text{g/L}$)	7	9	2
	Pore water ($\mu\text{g/L}$)	21	640	3
Total Phosphorus	Surface water ($\mu\text{g/L}$)	7	66	8
	Soil (mg/kg)	4	842	311
Sulfate	Surface (mg/L)	7	19.2	16.9
	Pore water (mg/L)	21	5.4	3.7
Methylmercury	Surface water (ng/L)	7	0.088	0.438
	Pore water (ng/L)	21	0.028	0.087
	Soil (ng/g)	4	0.229	0.591
Dissolved Iron	Surface water ($\mu\text{g/L}$)	7	48	49
	Pore water ($\mu\text{g/L}$)	21	120	78
	Soil (mg/kg)	4	2115	2580
Dissolved Organic Carbon	Surface water ($\mu\text{g/L}$)	7	40.6	34.6
	Pore water ($\mu\text{g/L}$)	21	123.9	41.3
Oxidation-Reduction Potential (SHE)*	Soil (mV)	U3: 4 F1 and W3: 10		-151 -50 144
Dissolved Oxygen	Surface water (mg/L)	6	2.8	2.8

Notes: The surface and pore waters (6-10 cm soil interval) were collected at study sites from August and September in 2010, October 2011, February, June and November in 2012, and March 2013, with the exception of dissolved oxygen which was measured on all dates except for March 2013.

The soils (0-10 cm interval) were collected on August 2010, February and June in 2012, and in March 2013. Methylmercury analyses were performed on unfiltered surface waters and on filtered pore water samples (except for Nov. 2012, when pore waters were unfiltered). All solids data reported on a dry wt. basis.

Source of data: South Florida Water Management District. SHE = Standard Hydrogen Electrode.

N= number of samples collected during the entire sampling period (single sample for surface waters and soils, and triplicate pore water samples per sampling date).

*oxidation-reduction potential was measured at F1 on 12/13/06 at a soil depth of 6-10 cm, at U3 on 1/15/09 at a soil depth of 3-7 cm, and at W3 on 1/19/09 and 12/8/10 at a soil depth of 4-8 cm.

Table S3. Composition of *hgcA* and phylogenetic affiliation of OTUs with known sequences

Sequence no. included in OTUs	Cluster ID	Inferred phylogeny											
		Zt	U2	W3	Sum	OTU ID	Clusters	Subclustering	Reference strains included in clade (accession no.)	Phylum	Class	Order	Family
3	2	0	0	5	5	UH012	DP-DP-I	Unidentified Deltaproteobacteria I	No included reference organism	Proteobacteria	Deltaproteobacteria	Syntrophobacterales	Unknown
0	0	0	4	4	4	WC43A09							
2	0	0	4	4	4	F1028							
0	0	2	2	3	3	F1014							
2	0	0	0	3	3	F1020							
1	2	0	0	3	3	F1027							
0	3	0	0	3	3	U3C02							
0	0	0	0	3	3	F1024							
2	0	0	0	2	2	F1028							
2	0	0	0	2	2	F1059							
0	0	2	2	2	2	U3H01							
2	0	0	0	2	2	F1059							
0	0	2	2	2	2	U3C08							
0	0	2	2	2	2	WC43G07							
0	0	2	0	2	2	U3A08							
0	0	2	0	2	2	U3A10							
1	0	0	1	1	1	U3B05							
0	1	0	0	1	1	U3B02							
1	0	0	0	1	1	F1055							
1	0	0	0	1	1	F1022							
1	0	0	0	1	1	F1C12							
0	1	0	1	1	1	U3C12							
0	1	0	0	1	1	F1055							
1	0	0	0	1	1	F1022							
0	1	0	0	1	1	U3C12							
0	1	0	0	1	1	U3D09							
0	1	0	0	1	1	F1004							
0	0	0	1	1	1	WC43F08							
1	0	0	0	1	1	F1059							
0	0	0	1	1	1	WC43G09							
1	0	0	0	1	1	F1C11							
1	0	0	0	1	1	F1C12							
0	1	0	0	1	1	U3B04							
0	0	0	1	1	1	WC43H08							
0	0	0	1	1	1	F1004							
1	0	0	0	1	1	F1022							
0	0	0	0	1	1	U3D09							
0	0	0	0	1	1	F1004							
0	0	0	0	1	1	WC43H04							
1	0	0	0	1	1	U3B11							
0	0	0	0	1	1	F1011							
0	0	0	1	1	1	WC43H06							
0	0	0	0	1	1	WC43A07							
0	0	0	0	1	1	F1C11							
0	0	0	0	1	1	U3B12							
0	1	0	0	1	1	U3B04							
1	0	0	0	1	1	F1009							
1	0	0	0	1	1	U3B09							
0	0	0	0	1	1	F1009							
0	0	0	0	1	1	U3D09							
0	0	0	0	1	1	WC43F11							
0	0	0	1	1	1	WC43G05	DP-DP-I	Unidentified Deltaproteobacterium Naph52	Delta proteobacterium Naph52 (EF405849)	Proteobacteria	Deltaproteobacteria	Syntrophobacterales	unknown
0	0	0	1	1	1	WC43G01	DP-DP-I	Syntrophobacteraceae	Desulfovomilus tiedjei DCB-1 (AFM23739)	Proteobacteria	Deltaproteobacteria	Syntrophobacterales	Syntrophobacteraceae
0	0	0	1	1	1	WC43G02							
0	0	0	1	1	1	WC43G03							
0	0	0	1	1	1	WC43G11	DP-DP-I	Unidentified Deltaproteobacteria II	No included reference organism	Proteobacteria	Deltaproteobacteria	Syntrophobacterales	unknown
1	0	0	0	1	1	F1028	DP-DP-I	Unidentified Deltaproteobacteria III	No included reference organism	Proteobacteria	Deltaproteobacteria	Syntrophobacterales	unknown
2	0	0	0	2	2	F1F12	DP-DP-I	Unidentified Deltaproteobacteria III	No included reference organism	Proteobacteria	Deltaproteobacteria	Syntrophobacterales	unknown
2	0	0	0	2	2	F1H12	DP-DP-I	Unidentified Deltaproteobacteria III	No included reference organism	Proteobacteria	Deltaproteobacteria	Syntrophobacterales	unknown
0	0	0	1	1	1	F1H10							
0	0	0	1	1	1	U3C04							
0	0	0	1	1	1	WC43C06	DP-DP-I	Syntrophobabaceae	Syntrophobabus aromaticivorans UI-1	Proteobacteria	Deltaproteobacteria	Syntrophobacterales	Syntrophobabaceae
0	0	0	1	1	1	WC43C03							
0	0	0	1	1	1	WC43C06							
1	0	0	0	1	1	F1C10	DP-DP-II	Desulfobivorales	Desulfovibrio africanus Walvis Bay (EG48477)	Proteobacteria	Desulfobacteriales	Desulfobacteraceae	Desulfobacteraceae
0	0	0	0	1	1	WC43G10	DP-DP-II	Desulfobivorales	Desulfovibrio armeniacus DSM 53-1 (EF513704)	Proteobacteria	Desulfobacteriales	Desulfobacteraceae	Desulfobacteraceae
0	0	0	0	1	1	WC43H10	DP-DP-II	Desulfobivorales	Desulfovibrio desulfuricans sp. 10-1 (DSM 2426)	Proteobacteria	Desulfobacteriales	Desulfobacteraceae	Desulfobacteraceae
0	0	0	0	1	1	U3C03	DP-DP-II	Desulfobivorales	Desulfovibrio desulfuricans Np132 (EG484269)	Proteobacteria	Desulfobacteriales	Desulfobacteraceae	Desulfobacteraceae
0	0	0	0	1	1	WC43C06	DP-DP-II	Desulfobivorales	Desulfovibrio baculum DSM 654 (ACU8503)	Proteobacteria	Desulfobacteriales	Desulfobacteraceae	Desulfobacteraceae
0	0	0	0	1	1	U3C01	DP-DP-II	Desulfobivorales	Desulfovibrio propionicus DSM 2032 (ADW16620)	Proteobacteria	Desulfobacteriales	Desulfobacteraceae	Desulfobacteraceae
0	0	0	1	1	1	WC43B01	DP-DP-II	Geobacter	Geobacter benzenalis Item (ACH3822)	Proteobacteria	Desulfobacteriales	Geobacteraceae	Geobacteraceae
0	0	0	1	1	1	WC43A06	DP-DP-II	Geobacter	Geobacter sp. M13 (ADW12506)	Proteobacteria	Desulfobacteriales	Geobacteraceae	Geobacteraceae
0	0	0	1	1	1	WC43J05	DP-DP-II	Geobacter	Geobacter benzenalis Item (ACH3822)	Proteobacteria	Desulfobacteriales	Geobacteraceae	Geobacteraceae
0	0	0	1	1	1	F1C09	DP-DP-II	Geobacter	Geobacter sp. M13 (ADW12506)	Proteobacteria	Desulfobacteriales	Geobacteraceae	Geobacteraceae
0	0	1	0	1	1	U3E12	DP-DP-II	Geobacter	Geobacter sp. F1C3 (ACM20383)	Proteobacteria	Desulfobacteriales	Geobacteraceae	Geobacteraceae
0	1	0	0	1	1	U3H10	DP-DP-II	Geobacter	Geobacter sp. F1C3 (ACM20383)	Proteobacteria	Desulfobacteriales	Geobacteraceae	Geobacteraceae
0	0	1	0	1	1	WC43H02	DP-DP-II	Geobacter	Geobacter metallireducens RCH3 cgb103 (EF988456)	Proteobacteria	Desulfobacteriales	Geobacteraceae	Geobacteraceae
0	0	0	1	1	1	WC43H07	DP-DP-II	Geobacter	Geobacter sulfurreducens PCA (AB517180)	Proteobacteria	Desulfobacteriales	Geobacteraceae	Geobacteraceae
0	0	0	1	1	1	U3C03	DP-DP-II	Geobacter	Geobacter sulfurreducens PCA (AB517180)	Proteobacteria	Desulfobacteriales	Geobacteraceae	Geobacteraceae
0	0	0	1	1	1	F1A04	DP-DP-II	Geobacter	Geobacter sulfurreducens PCA (AB517180)	Proteobacteria	Desulfobacteriales	Geobacteraceae	Geobacteraceae
0	0	0	3	3	3	WC43C05	FIRM	Unidentified Firmicutes I	No included reference organism	Firmicutes	Oscillospora	Oscillibrachia	Unknown
2	0	0	2	2	2	U3E10	FIRM	Unidentified Firmicutes I	No included reference organism	Firmicutes	Oscillospora	Oscillibrachia	Unknown
0	1	0	1	1	1	F1F03	FIRM	Unidentified Firmicutes I	No included reference organism	Firmicutes	Oscillospora	Oscillibrachia	Unknown
0	0	1	0	1	1	F1G07	FIRM	Unidentified Firmicutes I	No included reference organism	Firmicutes	Oscillospora	Oscillibrachia	Unknown
1	0	0	0	1	1	F1E12	FIRM	Unidentified Firmicutes I	No included reference organism	Firmicutes	Oscillospora	Oscillibrachia	Unknown
0	0	1	0	1	1	WC43G09	FIRM	Unidentified Firmicutes I	No included reference organism	Firmicutes	Oscillospora	Oscillibrachia	Unknown
0	0	0	0	1	1	F1C09	FIRM	Unidentified Firmicutes I	No included reference organism	Firmicutes	Oscillospora	Oscillibrachia	Unknown
0	0	1	0	1	1	U3E12	FIRM	Unidentified Firmicutes I	No included reference organism	Firmicutes	Oscillospora	Oscillibrachia	Unknown
0	1	0	0	1	1	U3H10	FIRM	Unidentified Firmicutes I	No included reference organism	Firmicutes	Oscillospora	Oscillibrachia	Unknown
0	0	1	0	1	1	WC43H02	FIRM	Unidentified Firmicutes I	No included reference organism	Firmicutes	Oscillospora	Oscillibrachia	Unknown
0	0	0	1	1	1	WC43H07	FIRM	Unidentified Firmicutes I	No included reference organism	Firmicutes	Oscillospora	Oscillibrachia	Unknown
0	0	0	1	1	1	U3C03	FIRM	Unidentified Firmicutes I	No included reference organism	Firmicutes	Oscillospora	Oscillibrachia	Unknown
0	0	0	1	1	1	F1A04	FIRM	Unidentified Firmicutes I	No included reference organism	Firmicutes	Oscillospora	Oscillibrachia	Unknown
1	0	0	0	1	1	WC43G05	FIRM	Unidentified Firmicutes II	No included reference organism	Firmicutes	Oscillospora	Oscillibrachia	Unknown
0	0	0	1	1	1	WC43E11	FIRM	Unidentified Firmicutes II	No included reference organism	Firmicutes	Oscillospora	Oscillibrachia	Unknown
0	0	1	0	1	1	U3C03	FIRM	Unidentified Firmicutes II	No included reference organism	Firmicutes	Oscillospora	Oscillibrachia	Unknown
0	0	0	1	1	1	WC43B02	FIRM	Unidentified Firmicutes II	No included reference organism	Firmicutes	Oscillospora	Oscillibrachia	Unknown
0	0	0	0	1	1	F1C09	FIRM	Unidentified Firmicutes II	No included reference organism	Firmicutes	Oscillospora	Oscillibrachia	Unknown
0	0	0	1	1	1	WC43H07	FIRM	Unidentified Firmicutes II	No included reference organism	Firmicutes	Oscillospora	Oscillibrachia	Unknown
0	0	0	1	1	1	U3C03	FIRM	Unidentified Firmicutes II	No included reference organism	Firmicutes	Oscillospora	Oscillibrachia	Unknown
0	0	0	1	1	1	F1E12	FIRM	Unidentified Firmicutes II	No included reference organism	Firmicutes	Oscillospora	Oscillibrachia	Unknown
0	0	0	1	1	1	WC43G09	FIRM	Unidentified Firmicutes II	No included reference organism	Firmicutes	Oscillospora	Oscillibrachia	Unknown
0	0	0	1	1	1	F1C09	FIRM	Unidentified Firmicutes II	No included reference organism	Firmicutes	Oscillospora	Oscillibrachia	Unknown
0	0	0	1	1	1	U3C03	FIRM	Unidentified Firmicutes II	No included reference organism	Firmicutes	Oscillospora	Oscillibrachia	Unknown
0	0	0	1	1	1	WC43H07	FIRM	Unidentified Firmicutes II	No included reference organism	Firmicutes	Oscillospora	Oscillibrachia	Unknown
0	0	0	1	1	1	U3C03	FIRM	Unidentified Firmicutes II	No included reference organism	Firmicutes	Oscillospora	Oscillibrachia	Unknown
0	0	0	1	1	1	F1C09	FIRM	Unidentified Firmicutes II	No included reference organism	Firmicutes	Oscillospora	Oscillibrachia	Unknown
0	0	0	1	1	1	WC43G09	FIRM	Unidentified Firmicutes II	No included reference organism	Firmicutes	Oscillospora	Oscillibrachia	Unknown
0	0	0	1	1	1	F1C09	FIRM	Unidentified Firmicutes II	No included reference organism	Firmicutes	Oscillospora	Oscillibrachia	Unknown
0	0	0	1	1	1	WC43E11	FIRM	Unidentified Firmicutes II	No included reference organism	Firmicutes	Oscillospora	Oscillibrachia	Unknown
0	0	0	1	1	1	U3C03	FIRM	Unidentified Firmicutes II	No included reference organism	Firmicutes	Oscillospora	Oscillibrachia	Unknown
0	0	0	1	1	1	WC43B02	FIRM	Unidentified Firmicutes II	No included reference organism	Firmicutes	Oscillospora	Oscillibrachia	Unknown
0</													

Table S4. Distribution of *dsrB* and phylogenetic affiliation of OTUs with known sequences

Table S5. Richness and diversity of *hgcA*- and *dsrB*-OTUs in the clone libraries.

All parameters were estimated in Mothur (see Materials and Methods of text of manuscript)

Gene	Site	Clone no. screened	Cutoff	No. of OUT	Chao1 richness (CI) ^a	Shannon diversity (CI)	Coverage (%)
<i>hgcA</i>	F1	66	5%	51	125 (83, 225)	3.9 (3.7, 4.0)	41
			10%	51	125 (82, 225)	3.9 (3.7, 4.0)	41
			15%	50	110 (76, 193)	3.8 (3.6, 4.0)	44
			20%	46	120 (75, 231)	3.6 (3.4, 3.9)	47
	U3	76	5%	57	139 (93, 242)	3.9 (3.8, 4.1)	43
			10%	53	112 (78, 189)	3.8 (3.7, 4.0)	50
			15%	49	87 (65, 141)	3.7 (3.6, 3.9)	59
			20%	45	87 (62, 156)	3.6 (3.5, 3.8)	63
	W3	64	5%	64	250 (146, 483)	4.1 (3.9, 4.2)	29
			13%	63	216 (132, 404)	4.0 (3.8, 4.2)	32
			17%	59	255 (139, 535)	3.9 (3.7, 4.1)	37
			24%	58	212 (123, 425)	3.9 (3.7, 4.1)	40
<i>dsrB</i>	F1	79	5%	29	36 (31, 57)	3.0 (2.8, 3.2)	85
			10%	19	26 (20, 53)	2.5 (2.3, 2.7)	90
			15%	14	17 (14, 36)	2.1 (1.9, 2.3)	94
			20%	11	14 (11, 34)	1.9 (1.7, 2.1)	95
	U3	80	5%	38	88 (56, 180)	3.2 (3.0, 3.5)	69
			10%	27	50 (33, 109)	2.7 (2.5, 3.0)	83
			15%	22	40 (27, 98)	2.5 (2.3, 2.8)	87
			20%	20	43 (25, 116)	2.2 (1.9, 2.5)	88
	W3	78	5%	35	70 (47, 140)	3.2 (3.0, 3.4)	73
			10%	19	58 (29, 169)	2.1 (1.9, 2.4)	83
			15%	17	83 (39, 213)	1.9 (1.7, 2.2)	86
			20%	16	71 (33, 187)	1.8 (1.6, 2.1)	86

^a95% confidence interval.

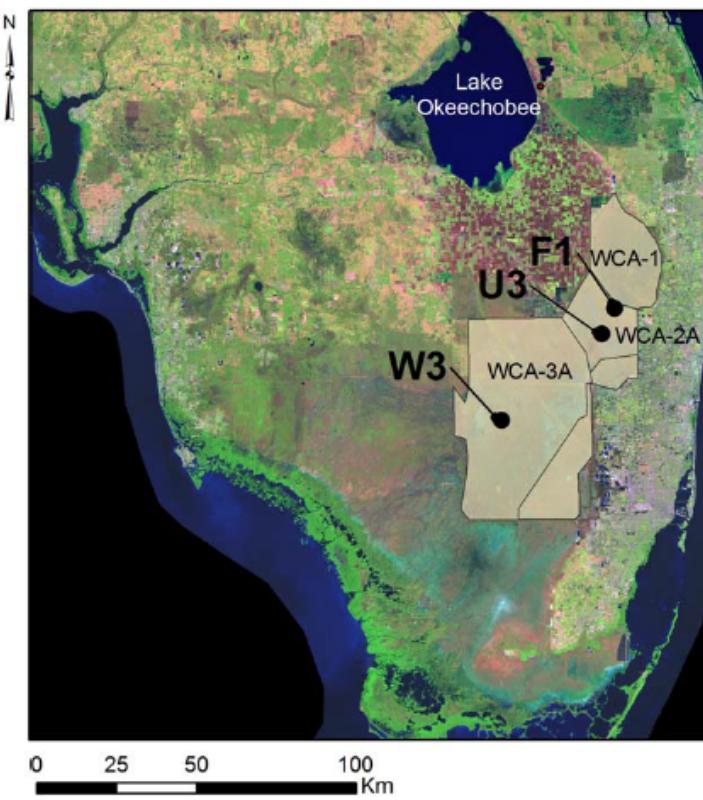


Fig. S1. Location of sampling sites F1 and U3 in WCA-2A and W3 in WCA-3A of the Everglades.

HgcA

HgcB

Proteobacteria

Chloroflexi

Euryarchaeota

<i>Geobacter metallireducens RCH3</i>
<i>Geobacter metallireducens GS-15</i>
<i>Geobacter sulfurreducens PCA</i>
<i>Geobacter sulfurreducens KN400</i>
<i>Geobacter sp. FRC-32</i>
<i>Geobacter uranireducens Rf4</i>
<i>Geobacter bermidjensis Bem</i>
<i>Geobacter sp. M18</i>
<i>Geobacter sp. M21</i>
<i>Desulfovibrio desulfuricans ND132</i>
<i>Desulfovibrio aespoeensis Aspo-2</i>
<i>Desulfovibrio africanus Walvis Bay</i>
<i>Desulfovibrio oxydclineae DSM 11498</i>
<i>Desulfovobulus propionicus DSM 2032</i>
<i>Desulfomicrobium baculumatum DSM 4028</i>
<i>Desulfonatronospira thiodismutans ASO3-1</i>
Uncultured Desulfovobacterium sp.
<i>Desulfonatronum lacustre Z-7951</i>
<i>Deferimosa camini S3R1</i>
<i>Syntrophorhabdus aromaticivorans UI</i>
<i>Desulfomonile tiedjei DCB-1</i>
<i>Syntrophus aciditrophicus SB</i>
<i>Delta proteobacterium NaphS2</i>
Dehalococcoides mccartyi DCB5
<i>Desulfosporosinus acidiphilus SJ4</i>
<i>Desulfobacterium dehalogenans DSM9161</i>
<i>Dehalobacter sp. CF</i>
<i>Dehalobacter sp. DCA</i>
<i>Desulfosporosinus orientis DSM 765</i>
<i>Desulfobacterium dichloroeliminans LMG P-21439</i>
<i>Desulfosporosinus sp. OT</i>
<i>Desulfosporosinus youngiae DSM 17734</i>
<i>Acetonema longum DSM 6540</i>
<i>Dethiobacter alkaliphilus AHT 1</i>
<i>Dehalobacter restrictus DSM 9455</i>
<i>Dehalobacter sp. FTH1</i>
<i>Desulfobacterium metallireducens 853-15A</i>
<i>Desulfobacterium sp. PCE1</i>
<i>Ethanoligenes harbinense YUAN-3</i>
<i>Syntrophobutulus glycolicus DSM 8271</i>
<i>Methanofollis limnatinans DSM 4140</i>
<i>Methanoregula boonei 6A8</i>
<i>Methanoregula formicica SMSP</i>
<i>Methanospaeraula palustris E1-9c</i>
<i>Methanospirillum hungatei JF-1</i>
<i>Methanomethyllovoran hollandica DSM 15978</i>
<i>Methanolobus psychrophilus R15</i>
<i>Methanocella arvoryzae MRE50</i>
<i>Methanocella paludicola SANAE</i>
<i>Methanolobus tindarius DSM 2278</i>

Cap helix

[4Fe-4S]

[4Fe-4S]

Forward primer binding site

Reverse primer binding site

Fig. S2. Binding sites for primers hgcA_F (forward) and hgcB-R (reverse) targeting a Cap-helix consensus sequence motif and upper neighbor sequences G(V/I) N(V/I)WCA(A/G)GK: underlined sequences are exact binding seqs] of *hgcA*, and [4Fe-4S] motifs region (CX₂CX₂CX₃C) of *hgcB*, respectively. The blue arrow denotes the single Chloroflexi sequence.

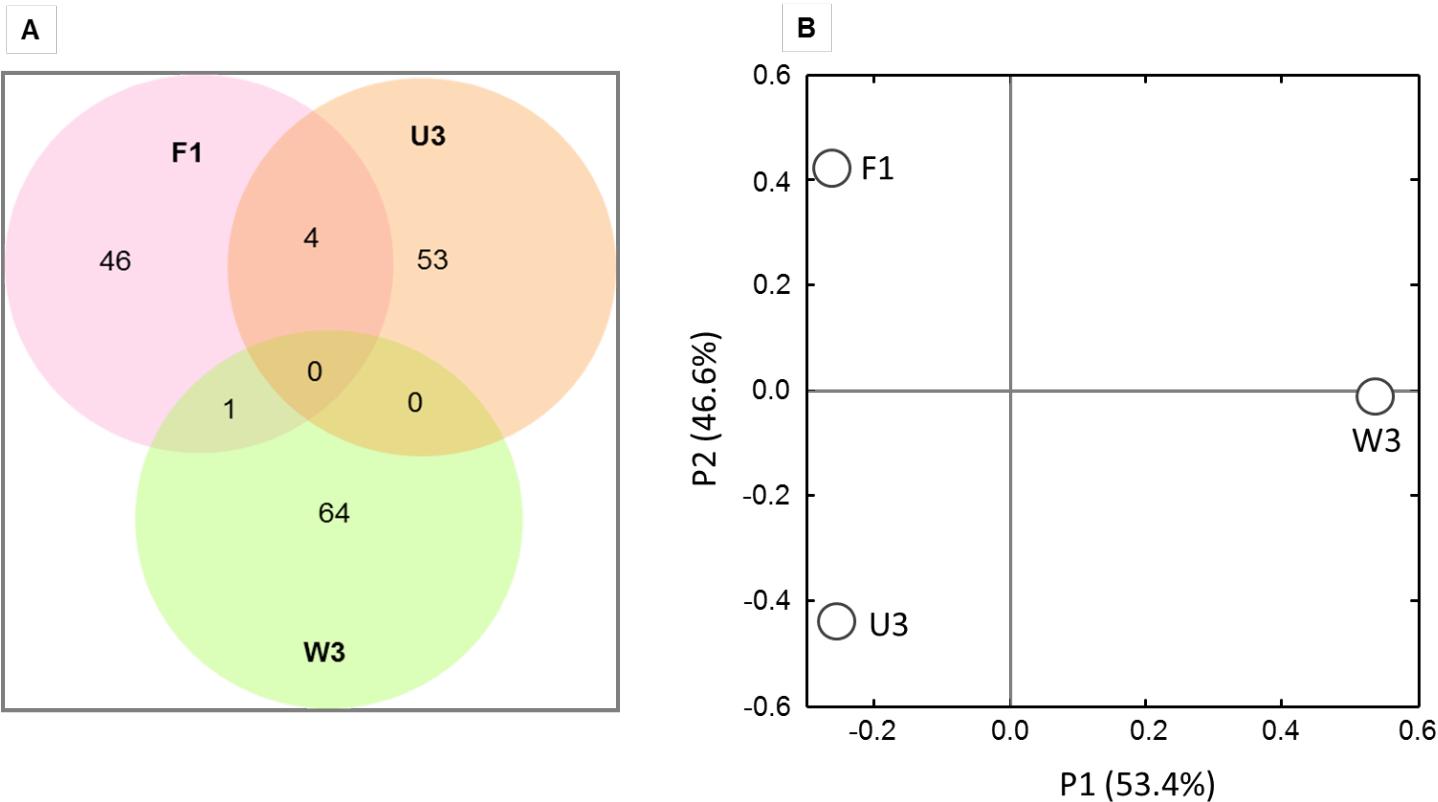


Fig. S3. Venn diagram representing the number of OTUs of *hgcA* shared between sampling sites (A), and PCoA plot showing the distribution *hgcA* community occurred from each study site (B).

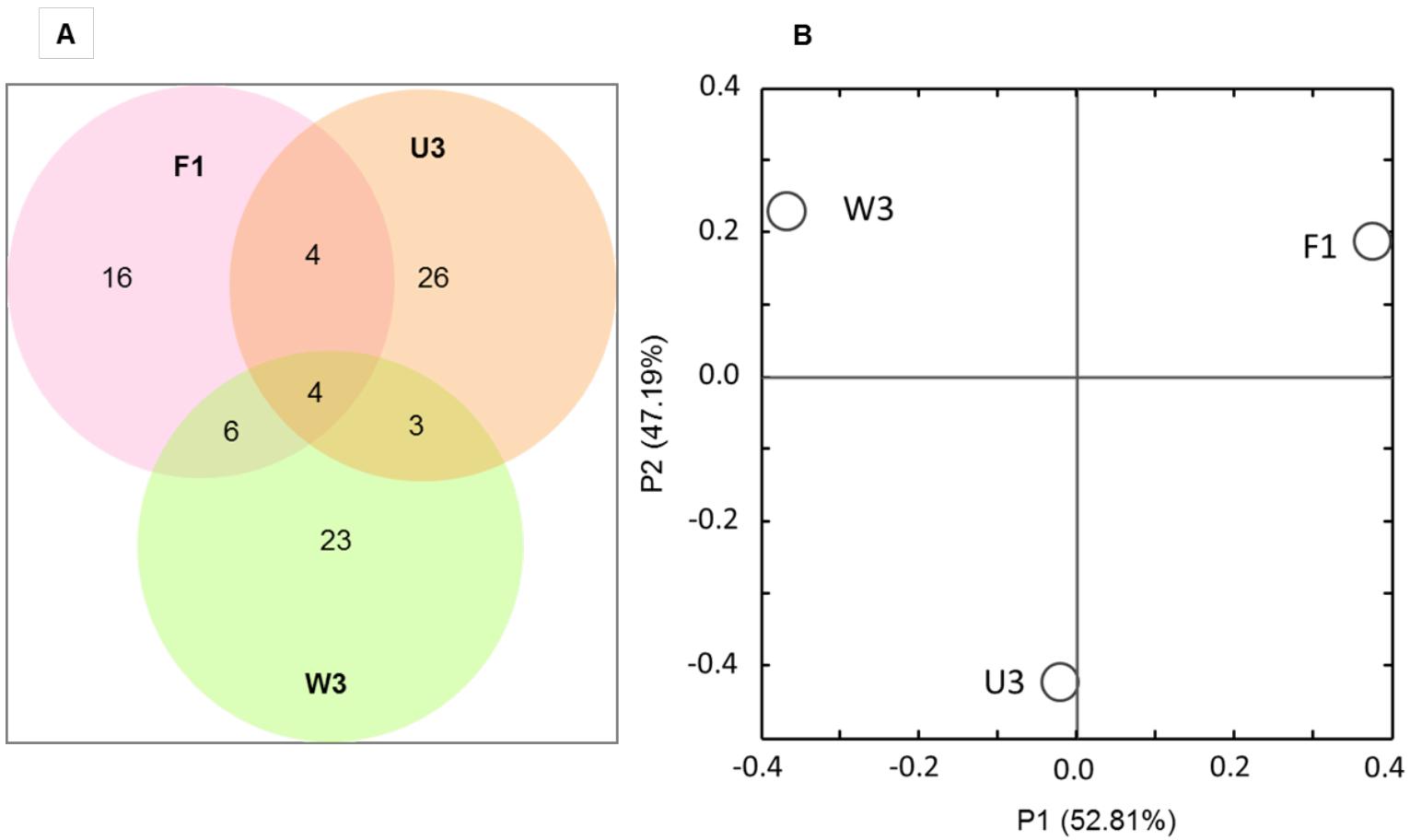


Fig. S4. Venn diagram representing the number of OTUs of *dsrB* shared between sampling sites (A), and PCoA plot showing the distribution *dsrB* community occurred from each study site (B).

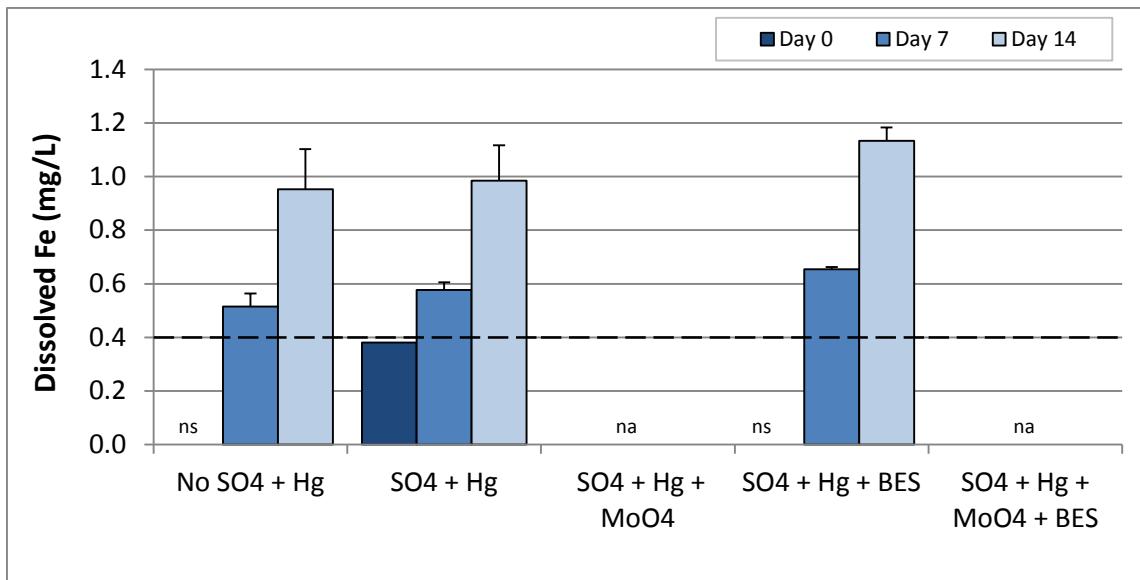


Fig. S5. Concentration of dissolved Fe concentration in the laboratory incubation with W3 soils under treatment of Mo (SuRP inhibitor) and BES (methanogen inhibitor).