

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	Taxonomic position		hgcA_F forward primer		hgcB_R reverse primer	
	Phylum	Class	Gene Locus	GCNRTYAAVRTNIGGTGGCG	Gene Locus	CAGGCCCGCAATCCATGCA
<i>Geobacter metallireducens</i> RCH3	Proteobacteria	Deltaproteobacteria	GeomsDRAFT_0749	GGATCAATGCTGGTGGCG	GeomsDRAFT_0748	CAGGCCCGCAATCCATGCA
<i>Geobacter metallireducens</i> GS-15	Proteobacteria	Deltaproteobacteria	Gmet_1240	GGATCAATGCTGGTGGCG	Gmet_1241	CAGGCCCGCAATCCATGCA
<i>Geobacter sulfurreducens</i> PCA	Proteobacteria	Deltaproteobacteria	GSU1440	GGATTAATGCTGGTGGCG	GSU1441	CAGGCCCGCAATCCATGCA
<i>Geobacter sulfurreducens</i> KM400	Proteobacteria	Deltaproteobacteria	KM400_1466	GGATTAATGCTGGTGGCG	KM400_1468	CAGGCCCGCAATCCATGCA
<i>Geobacter</i> sp. FRC-32	Proteobacteria	Deltaproteobacteria	Geob_2483	GGATCAATGCTGGTGGCG	Geob_2482	CAGGCCCGCAATCCATGCA
<i>Geobacter uranireducens</i> Rf4	Proteobacteria	Deltaproteobacteria	Gura_0480	GGATTAACGCTGGTGGCG	Gura_0481	CAGGCCCGCAATCCATGCA
<i>Geobacter bemidjensis</i> Bem	Proteobacteria	Deltaproteobacteria	Gbem_1163	GGATCAACGCTGGTGGCG	Gbem_1164	CAGGCCCGCAATCCATGCA
<i>Geobacter</i> sp. M18	Proteobacteria	Deltaproteobacteria	GM18_1031	GGATCAACGCTGGTGGCG	GM18_1032	CAGGCCCGCAATCCATGCA
<i>Geobacter</i> sp. M21	Proteobacteria	Deltaproteobacteria	GM21_3091	GGATCAACGCTGGTGGCG	GM21_3090	CAGGCCCGCAATCCATGCA
<i>Desulfovibrio desulfuricans</i> ND132	Proteobacteria	Deltaproteobacteria	Dnd132_1056	GGATCAACGCTGGTGGCG	Dnd132_1057	CAGGCCCGCAATCCATGCA
<i>Desulfovibrio aespeensis</i> Aspo-2	Proteobacteria	Deltaproteobacteria	Daes_2682	GGATCAACGCTGGTGGCG	Daes_2683	CAGGCCCGCAATCCATGCA
<i>Desulfovibrio africanus</i> Welis Bay	Proteobacteria	Deltaproteobacteria	Desaf_0117	GGATCAACGCTGGTGGCG	Desaf_0115	CAGGCCCGCAATCCATGCA
<i>Desulfovibrio oxydinae</i> DSM 11498	Proteobacteria	Deltaproteobacteria	B149DRRAFT_02526	GGATCAATGCTGGTGGCG	B149DRRAFT_02527	CAGGCCCGCAATCCATGCA
<i>Desulfobulbus propionicus</i> DSM 2032	Proteobacteria	Deltaproteobacteria	Despr_0439	GGATCAATGCTGGTGGCG	Despr_0438	CAGGCCCGCAATCCATGCA
<i>Desulfomicrobium baculatum</i> DSM 4028	Proteobacteria	Deltaproteobacteria	Dbac_0376	GGATCAACGCTGGTGGCG	Dbac_0375	CAGGCCCGCAATCCATGCA
<i>Desulfonatronospira thiodismutans</i> ASO3-1	Proteobacteria	Deltaproteobacteria	Dtho_PD1043	GGAA ^T AAATGCTGGTGGCG	Dtho_PD1042	CAGGCCCGCAATCCATGCA
Uncultured <i>Desulfobacterium</i> sp.	Proteobacteria	Deltaproteobacteria	NAT_A07900	GGATCAATGCTGGTGGCG	NAT_A07910	CAGGCCCGCAATCCATGCA
<i>Desulfonatronum lacustris</i> Z-7951	Proteobacteria	Deltaproteobacteria	DeslaDRAFT_0127	GGATCAATGCTGGTGGCG	DeslaDRAFT_0126	CAGGCCCGCAATCCATGCA
<i>Deferriusoma camini</i> S3R1	Proteobacteria	Deltaproteobacteria	DefcaDRAFT_2106	GGATCAACGCTGGTGGCG	DefcaDRAFT_2107	CAGGCCCGCAATCCATGCA
<i>Syntrophorhabdus aromalicovorans</i> UI	Proteobacteria	Deltaproteobacteria	SynarDRAFT_0655	GGATTAACGCTGGTGGCG	SynarDRAFT_0656	CAGGCCCGCAATCCATGCA
<i>Desulfomonile bedjei</i> DCB-1	Proteobacteria	Deltaproteobacteria	Desb_1022	GGAA ^T AAATGCTGGTGGCG	Desb_1023	CATGTCGGCAATCCATGCA
<i>Syntrophus aciditrophicus</i> SB	Proteobacteria	Deltaproteobacteria	SYN_00351	GGATCAATGCTGGTGGCG	SYN_00352	CAGGCCCGCAATCCATGCA
<i>Deitis proteobacterium</i> NaphS2	Proteobacteria	Deltaproteobacteria	NPH_5533	GGATCAACGCTGGTGGCG	NPH_5534	CAGGCCCGCAATCCATGCA
<i>Dehalococcoides mccartyi</i> DCMB5	Chloroflexi	Dehalococcoidetes	dcmB_330	GGATCAATGCTGGTGGCG	dcmB_329	CAGGCCCGCAATCCATGCA
<i>Desulfosporosinus acidiphilus</i> S14	Firmicutes	Clostridia	Desaa_1621	GGAA ^T TAACGCTGGTGGCG	Desaa_1622	CATGTCGGCAATCCATGCA
<i>Desulfobacterium dehalogenans</i> DSM9161	Firmicutes	Clostridia	Desde_2772	GGAA ^T AAATGCTGGTGGCG	Desde_2771	CAGGCCCGCAATCCATGCA
<i>Dehalobacter</i> sp. CF	Firmicutes	Clostridia	DCF50_p1170	GGATTAATGCTGGTGGCG	DCF50_p1169	CAGGCCCGCAATCCATGCA
<i>Dehalobacter</i> sp. 11DCA	Firmicutes	Clostridia	DHBDCA_p1092	GGTATTAATGCTGGTGGCG	DHBDCA_p1091	CAGGCCCGCAATCCATGCA
<i>Desulfosporosinus orientis</i> DSM 765	Firmicutes	Clostridia	Desor_2652	GGATCAATGCTGGTGGCG	Desor_2653	CAGGCCCGCAATCCATGCA
<i>Desulfobacterium dichrocolimminans</i> LMG P-21439	Firmicutes	Clostridia	Desd_0780	GGATCAATGCTGGTGGCG	Desd_0781	CAGGCCCGCAATCCATGCA
<i>Desulfosporosinus</i> sp. OT	Firmicutes	Clostridia	DOT_5805	GGATCAATGCTGGTGGCG	DOT_5807	CAGGCCCGCAATCCATGCA
<i>Desulfosporosinus youngiae</i> DSM 17734	Firmicutes	Clostridia	DesyDRAFT_4238	GGGTCAATGCTGGTGGCG	DesyDRAFT_4237	CAGGCCCGCAATCCATGCA
<i>Acetoneama longum</i> DSM 6540	Firmicutes	Clostridia	ALO_18015	GGATCAACGCTGGTGGCG	ALO_18015	CAGGCCCGCAATCCATGCA
<i>Dehalobacter alkaliphilus</i> AHT 1	Firmicutes	Clostridia	DealDRAFT_3158	GGATTAATGCTGGTGGCG	DealDRAFT_3157	CAGGCCCGCAATCCATGCA
<i>Dehalobacter restrictus</i> DSM 9455	Firmicutes	Clostridia	Dehre_1982	GGATTAATGCTGGTGGCG	Dehre_1981	CAGGCCCGCAATCCATGCA
<i>Dehalobacter</i> sp. FTH1	Firmicutes	Clostridia	A37GDRAFT_03566	GGTATTAATGCTGGTGGCG	A37GDRAFT_03565	CAGGCCCGCAATCCATGCA
<i>Desulfobacterium metallireducens</i> 853-15A	Firmicutes	Clostridia	Desme_1742	GGATCAATGCTGGTGGCG	Desme_1741	CATGTCGGCAATCCATGCA
<i>Desulfobacterium</i> sp. PCE1	Firmicutes	Clostridia	DesPCE1DRAFT_2748	GGAA ^T AAATGCTGGTGGCG	DesPCE1DRAFT_2747	CAGGCCCGCAATCCATGCA
<i>Ethanoligenens harbinensis</i> YJIAN-3	Firmicutes	Clostridia	Ethna_0975	GGTGTAAATGCTGGTGGCG	Ethna_0976	CAGGCCCGCAATCCATGCA
<i>Syntrophobactilus glycolicus</i> DSM 8271	Firmicutes	Clostridia	Sgly_2362	GGGTAAATGCTGGTGGCG	Sgly_2361	CAGGCCCGCAATCCATGCA
<i>Methanofollis limnatis</i> DSM 4140	Euryarchaeota	Methanomicrobia	Meth_1685	GGATCAATGCTGGTGGCG	Meth_1684	CAGGCCCGCAATCCATGCA
<i>Methanoregula boonei</i> 6A8	Euryarchaeota	Methanomicrobia	Mboo_0422	GGGCTAAATGCTGGTGGCG	Mboo_0421	CATGTCGGCAATCCATGCA
<i>Methanoregula formica</i> SMSP	Euryarchaeota	Methanomicrobia	Mefor_0951	GGATCAATGCTGGTGGCG	Mefor_0952	CAGGCCCGCAATCCATGCA
<i>Methanospirillum hungatei</i> E1-9c	Euryarchaeota	Methanomicrobia	Mhu_1034	GGATCAATGCTGGTGGCG	Mhu_1035	CAGGCCCGCAATCCATGCA
<i>Methanospirillum hungatei</i> F-1	Euryarchaeota	Methanomicrobia	Mhun_0876	GGATTAATGCTGGTGGCG	Mhun_0875	CATGTCGGCAATCCATGCA
<i>Methanomethylovorus hollandicus</i> DSM 15978	Euryarchaeota	Methanomicrobia	Metho_0631	GGATTAATGCTGGTGGCG	Metho_0630	CATGTCGGCAATCCATGCA
<i>Methanobolbus psychrophilus</i> R15	Euryarchaeota	Methanomicrobia	Mpsy_0587	GGATTAATGCTGGTGGCG	Mpsy_0586	CATGTCGGCAATCCATGCA
<i>Methanocella arvoryzae</i> MRE50	Euryarchaeota	Methanomicrobia	RCIX2342	GGATCAACGCTGGTGGCG	RCIX2341	CAGGCCCGCAATCCATGCA
<i>Methanocella paludicola</i> SA1AE	Euryarchaeota	Methanomicrobia	MCP_0718	GGATCAACGCTGGTGGCG	MCP_0717	CAGGCCCGCAATCCATGCA
<i>Methanobolbus indarius</i> DSM 2278	Euryarchaeota	Methanomicrobia	MethDRAFT_2866	GGATTAACGCTGGTGGCG	MethDRAFT_2865	CATGTCGGCAATCCATGCA

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

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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 (µg/L)	7	9	2	3
	Pore water (µg/L)	21	640	3	2
Total Phosphorus	Surface water (µg/L)	7	66	8	5
	Soil (mg/kg)	4	842	311	448
Sulfate	Surface (mg/L)	7	19.2	16.9	0.4
	Pore water (mg/L)	21	5.4	3.7	0.4
Methylmercury	Surface water (ng/L)	7	0.088	0.438	0.083
	Pore water (ng/L)	21	0.028	0.087	0.121
	Soil (ng/g)	4	0.229	0.591	1.4
Dissolved Iron	Surface water (µg/L)	7	48	49	108
	Pore water (µg/L)	21	120	78	1556
	Soil (mg/kg)	4	2115	2580	5275
Dissolved Organic Carbon	Surface water (µg/L)	7	40.6	34.6	17.4
	Pore water (µg/L)	21	123.9	41.3	26.1
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	2.7

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

Table with columns: Sequence no. included in OTUs (F1, U3, W3, Sum), Cluster I.D., Cluster, Subcluster, Reference strains included in clade (accession no.), Phylum, Class, Order, Family. Rows include various OTUs like OTU12, WCAB309, U3F08, etc., categorized by phylum such as Proteobacteria, Firmicutes, and Euryarchaeota.

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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.

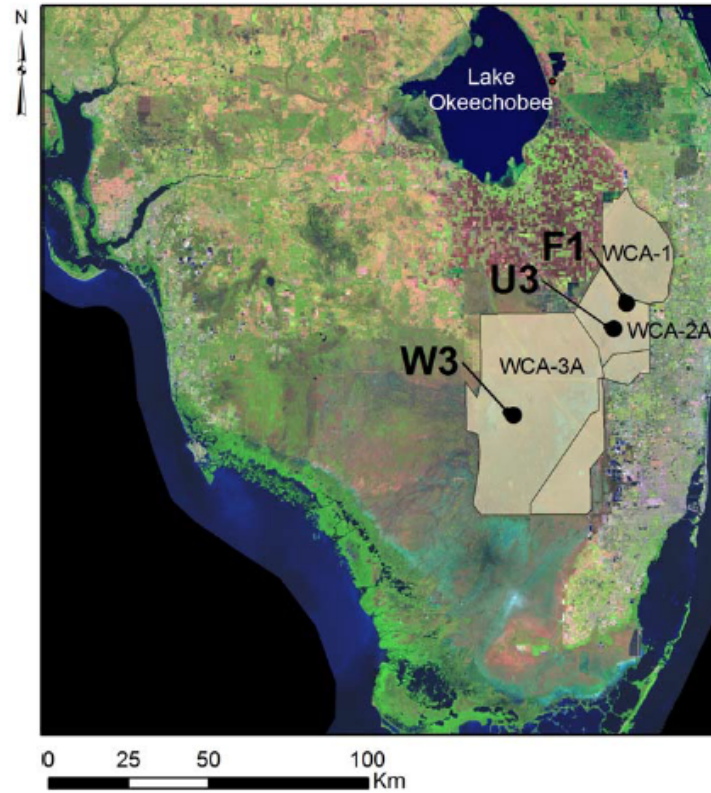


Fig. S1. Location of sampling sites F1 and U3 in WCA-2A and W3 in WCA-3A of the Everglades.

HgcA

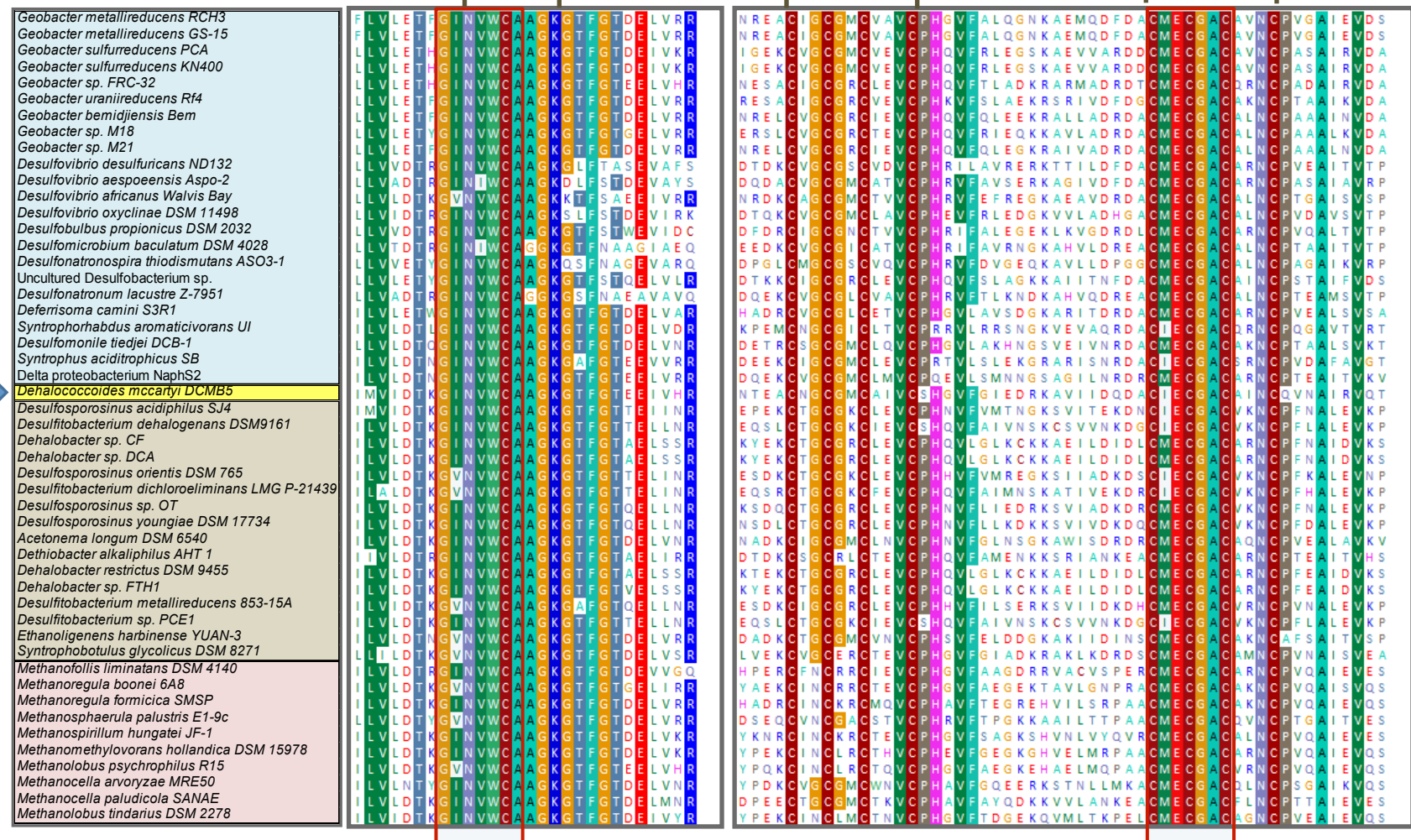
Cap helix

HgcB

[4Fe-4S]

[4Fe-4S]

Proteobacteria
 Chloroflexi
 Firmicutes
 Euryarchaeota



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.

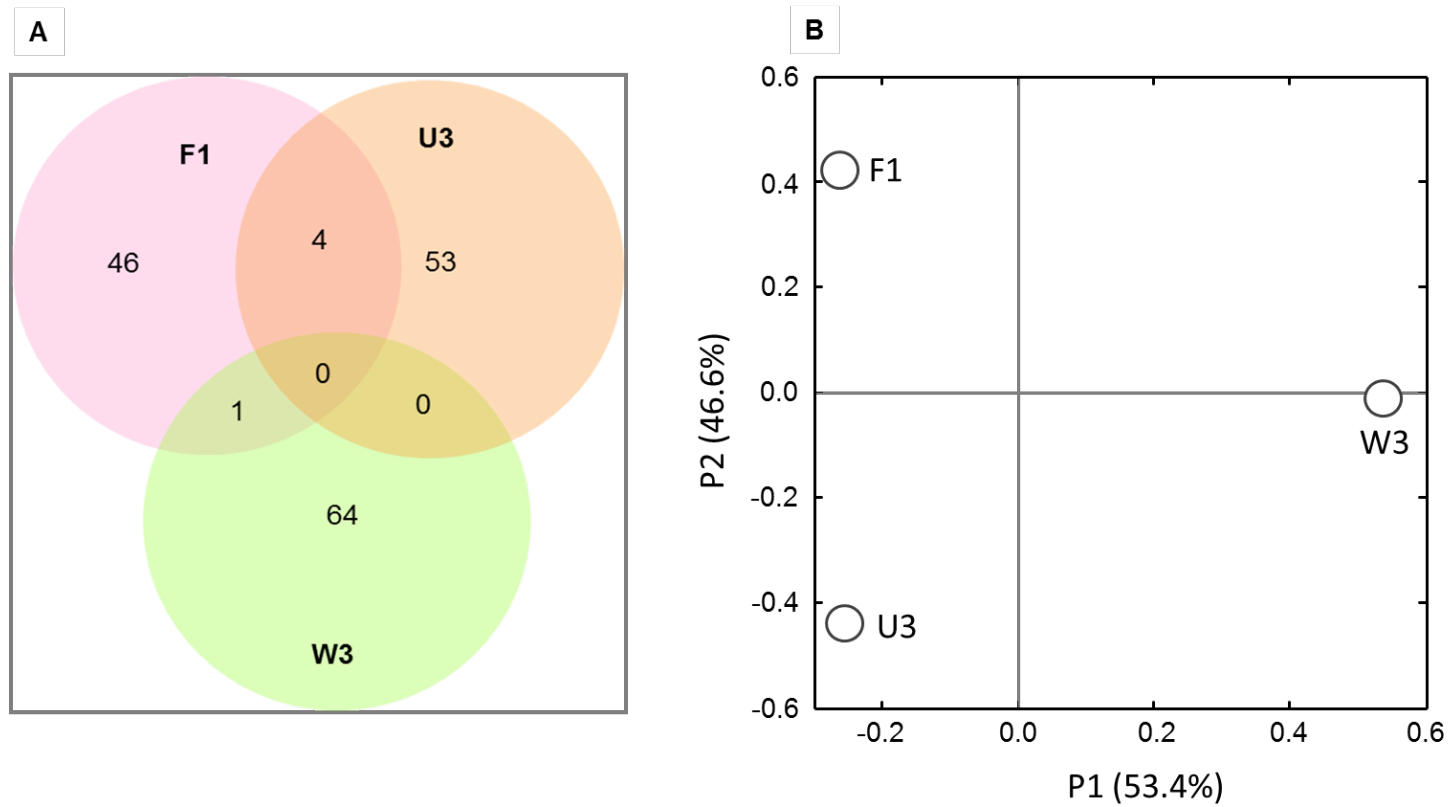


Fig. S3. Venn diagram representing the number of OTUs of *hgcA* shared between sampling sites (A), and PCoA plot showing the distribution *hgcA* community occurred from each study site (B).

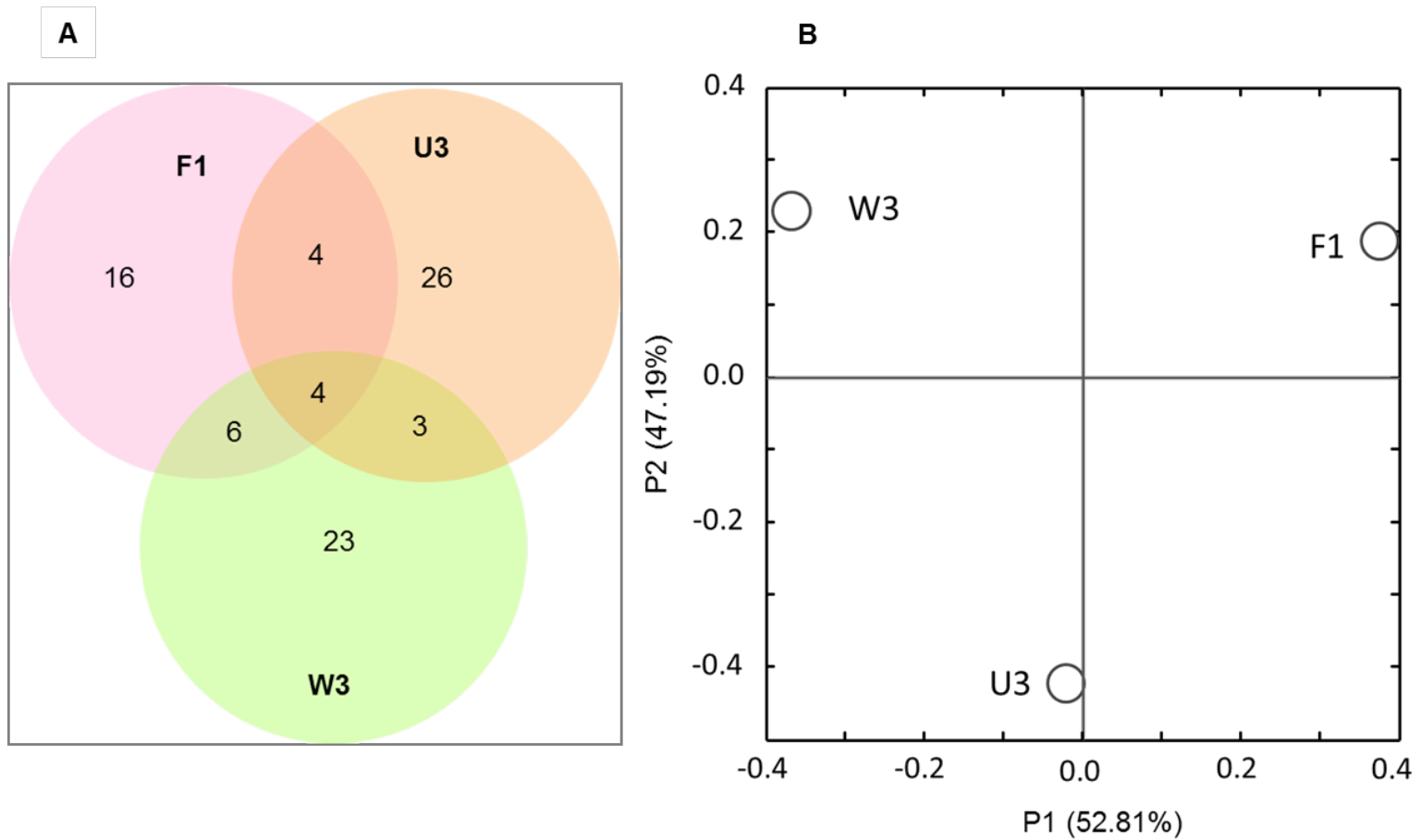


Fig. S4. Venn diagram representing the number of OTUs of *dsrB* shared between sampling sites (A), and PCoA plot showing the distribution *dsrB* community occurred from each study site (B).

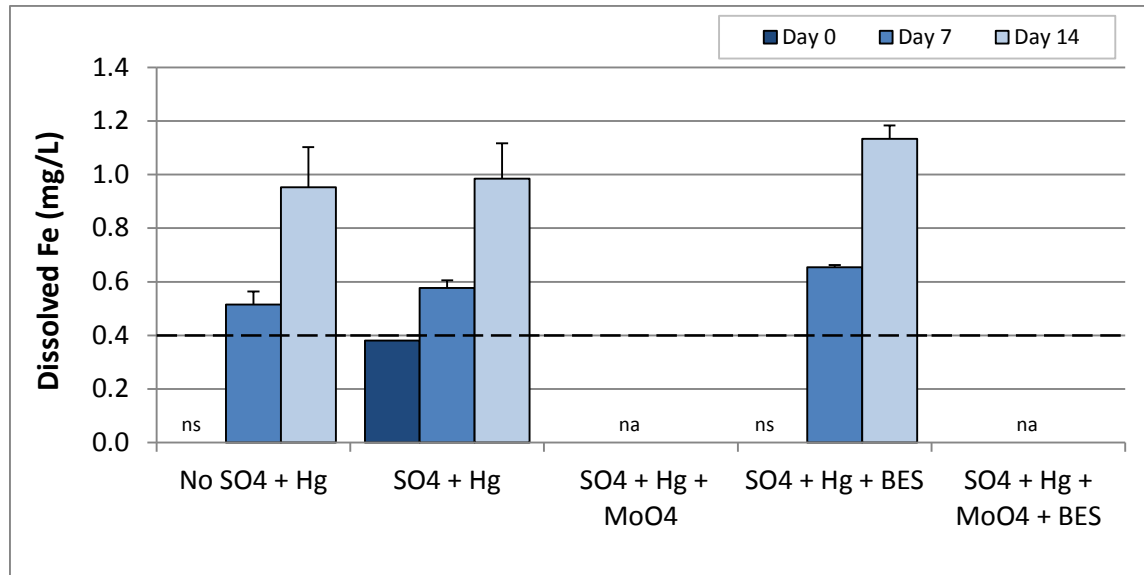


Fig. S5. Concentration of dissolved Fe concentration in the laboratory incubation with W3 soils under treatment of Mo (SuRP inhibitor) and BES (methanogen inhibitor).