

1 **Supplemental Material**

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3 **Colonization habitat controls biomass, composition, and metabolic activity of attached**  
4 **microbial communities in the Columbia River hyporheic corridor**

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15 Supplemental Text 1-2

16 Supplemental Figures S1-S11

17 Supplemental Tables S1-S6

### **Supplemental Text 1 – Analytical Methods**

**DOC measurement.** Dissolved organic carbon (DOC) was determined with a Shimadzu combustion carbon analyzer TOC-Vcsh with ASI-V auto sampler. DIC was removed in the instrument by acidification of the sample with 2M HCl (Fisher) with a 5 minute sparging time. The sample was then injected into the furnace set to 680 °C. Organic carbon standards were made from potassium hydrogen phthalate solid, (Acros Organics). The calibration range for the DOC determinations was from 0.10 to 10 mg C L<sup>-1</sup>.

**ATP biomass assay.** ATP content was used as a measure of microbial biomass in the reactors. The methods employed were adapted from those reported in Graham et al. (11), using the Promega Glomax 20/20 Luminator with Bactiter-Glo Microbial Cell Viability Assay (Promega). Approximately 0.5 g of wet sand sample was mixed with 0.5 mL of sterile (autoclaved) 20 mM EDTA (Fluka) in 2 mL Nalgene Cryogenic Vials (Thermoscientific) and stored at -20°C. Samples were returned to room temperature prior to analysis and measured after 5 min incubation with Bactiter-Glo reagent and 25 µL of 0.4M MgCl<sub>2</sub>. Standard curves were prepared with Adenosine 5'-triphosphate magnesium salt (Sigma) in 20 mM EDTA and ranged from 0 – 10 nM.

**Resazurin reduction assay.** Resazurin reduction assays were conducted with samples from the microcosms as a measure of aerobic respiratory activity (12). The methods employed were adapted from those reported in Graham et al. (11). Assays were started by adding approximately 2.5 g of wet sand to 100 µl of 30 µM resazurin and 2.5 mL of feed stock solution to vials, gently mixing and then incubating at room temperature in the dark on an angle at 50 rpm. After 48 hr the vials were weighed and 3 mL of acetonitrile (ACN) (HPLC Grade, Fischer Chemical) was added. After ACN addition, vials were sealed, vortexed, and reweighed before being placed in a

sonicator bath for 10 min. After sonication, vials were put back on the 50 rpm shaker. After a 1 hr extraction time, vials were vortexed and the sand was allowed to settle. The screw cap was removed and 5 mL of extract was passed through a 17 mm, 0.22  $\mu\text{m}$  Teflon syringe filter (Thermoscientific) into pre-labeled 12 mL glass amber vials and stored at 4°C. The extraction vial with the remaining sand was dried at 75 °C for 72 hr then weighed to obtain dry sand weight. Fluorescence emission maxima for resazurin (630 nm) and resorufin (585 nm) were measured on resazurin sample extracts using a Horiba Fluorolog 3 fluorimeter. Resazurin reduction extracts were analyzed in quartz cuvettes and diluted 1:1 with ACN:ARW when above the calibration range. Fluorescence intensity was quantified by comparison to standards of resazurin ranging from 0 to 1.0  $\mu\text{M}$  (Sigma) and resorufin ranging from 0 to 0.2  $\mu\text{M}$  (Sigma) prepared in ACN:ARW (1:1).

**Linear mixed modeling.** Linear mixed model (LMM) analysis was used to determine the influence of sand type, feed stock solution, and time on biomass and respiration values in the reactors. The LMM analysis was implemented using packages lme4 and lmerTest in the R statistical package (30). Additional R packages ggplot, tidyr, dplyr, and viridis were also used (1, 5, 8, 10, 31, 32). Implementation included an adaptation of the original linear fit equation to use the final time point from each experiment to calculate the modeled intercepts; this allowed for comparison of the final status of the reactors based on the fitted model intercept. For the cross feed biomass LMM, both three-way and four-way interactions were significant. In all other cases three-way and four way-factor interactions were not significant and were therefore removed from the models. Biomass data for the two replicate cross feeding experiments (CF1 and CF2) were consistent and were modeled together. Due to the presence of a handful of CF1 respiration data points that were close to the detection limit, separate models were required for the CF1 and CF2

respiration data. Pair wise comparisons were performed using standard t-test on the difference between the log of the final time point for the two reactors being compared.

**DNA extraction, sequencing and processing.** Samples from replicate reactor types at each time point were pooled for DNA extraction. This approach was required to obtain sufficient DNA for 16S rRNA gene sequencing. DNA was extracted from the pooled materials as described in Graham et al. (11). DNA extracts were amplified using the universal 16S rRNA gene primers (515F-806R) described in Caporaso et al. (4), adapted for the Illumina MiSeq platform by adding nine extra bases in the adapter region of the forward amplification primer that support paired-end sequencing. The reverse amplification primer contained a twelve base barcode sequence. Each 25  $\mu$ L PCR reaction contained 12  $\mu$ L of MoBio PCR Water (Certified DNA472 Free), 10  $\mu$ L of 5 Prime HotMasterMix (1x), 1  $\mu$ L of forward primer (5  $\mu$ M concentration, 200 pM final), 1  $\mu$ L Golay Barcode Tagged Reverse Primer (5  $\mu$ M concentration, 200 pM final), and 1  $\mu$ L of template DNA. The conditions for PCR were: 94°C for 3 min to denature DNA, with 35 cycles at 94°C for 45 s, 50°C for 60 s, and 72°C for 90 s; with a final extension of 10 min at 72°. Amplicons were quantified using PicoGreen (Invitrogen) and a plate reader. Appropriate volumes of PCR product from each sample were then pooled so that each sample was represented with an equal amount of product. This pool was cleaned using the UltraClean® PCR Clean-Up Kit (MoBIO), and quantified using the Qubit (Invitrogen). After quantification, the molarity of the pool was determined and diluted to 2 nM, denatured, and then diluted to a final concentration of 6.7 5pM with a 10% PhiX spike for sequencing on the Illumina MiSeq.

The 16S rRNA gene amplicon sequences were processed in QIIME 1.8.0. (3). First, the function `split_libraries_fastq.py` was used to demultiplex the fastq-formatted sequences, with a Phred quality cutoff of 20. To identify chimeras the function `identify_chimeric_seqs.py` was used

to call USEARCH v6.1 with 'non\_chimera\_retention' set to 'intersection.' After removing identified chimeras (with function filter\_fasta.py) the function pick\_open\_reference\_otus.py was used to call USEARCH v6.1, pick operational taxonomic units (OTUs), and generate the associated phylogeny (97% similarity) using the SILVA (Release 111) database. The number of reads per library (107 total) ranged from ca. 13,000 to 125,000, with a mean of  $51,726 \pm 28,079$ . The software package Primer (version 7.0) was used for non-metric dimensional scaling (NMDS) analysis of microbial community composition, and for analysis of similarity (ANOSIM) comparisons of community composition among different reactor treatments.

## Supplemental Text 2 – Comparative analysis of Proteobacterial and non-Proteobacterial taxa in the colonized sand reactors

*Proteobacteria*. Several basic patterns were evident within the dominant Proteobacterial classes. For the *Alphaproteobacteria* (ca. 9 to 28 % of all Proteobacteria), there was considerable variation among sand types across the three experiments, but in general the dominant taxa were heterotrophs (15) from the *Hyphomicrobiaceae*, *Hyphomonadaceae*, *Rhodospirillaceae*, *Rhodobacteraceae*, and *Sphingomonadaceae*. Similarly, for all sand types the *Betaproteobacteria* (ca. 27 to 65 % of all Proteobacteria) were dominated by the heterotrophic families *Comamonadaceae*, *Methylophilaceae*, *Oxalobacteraceae*, and *Rhodocyclaceae*. Likewise, the *Gammaproteobacteria* (ca. 12 to 34 % of all Proteobacteria) were dominated by a common group of heterotrophic taxa from the *Alteromonadaceae*, *Coxiellaceae*, *Moraxellaceae*, *Piscirickettsiaceae*, *Pseudomonadaceae*, *Sinobacteraceae*, and *Xanthomonadaceae*.

By far the largest distinction among Proteobacteria across sand type was the much higher abundance of *Deltaproteobacteria* in RBS and PZS, both initially and throughout the incubation experiments (Figure 8). Across all sand types and time points, *Deltaproteobacteria* accounted for 2-3 % of total *Proteobacteria* in GWS, 14-17 % for RBS, and 7-11 % for PZS (Table 3). For GWS, the dominant families were *Bdellovibrionaceae* (and the related family OM27, 24) and *Haliangiaceae*, which represent gram-negative, obligate predators of other gram-negative bacteria (26); and bacteriolytic- and non-cellulolytic-type myxobacteria (9), respectively. Although these families (along with other myxobacteria and predatory families such as *Myxococcaceae* and *Bacteriovoracaceae*; Tables S2-S4) were present in RBS and PZS, *Deltaproteobacteria* in these two sand types also contained significant numbers of anaerobic fermentative and respiratory taxa such as *Syntrophobacteraceae* (16) and *Geobacteraceae* (25).

*Syntrophobacteraceae* accounted for 1-2 % of total Proteobacteria in RBS and PZS, whereas *Geobacteraceae* were ca. 10-fold more abundant in RBS (1-2 %) compared to PZS (ca. 0.1 %). It is also significant that the majority (60-70 %) of the unclassified *Delatproteobacterial* families in RBS and PZS (3-8 % of total Proteobacteria) were from in the order *Myxococcales*, which includes a wide variety of heterotrophic taxa, including the well-known anaerobic respiratory family *Anaeromyxobacteraceae* (28, 33).

*Non-Proteobacteria*. Several broad trends in the dominant non-Proteobacterial taxa were also evident (Table 3). The abundance of *Bacteroidetes* and *Nitrospirae* was consistent across all three sand types. Although there were differences in the distribution of families within the *Bacteroidetes* (Tables S4-S6), in general the dominant ones (e.g. *Chitinophagaceae*, *Flavobacteriaceae*, *Saprospiraceae*, as well as unassigned (at the family level) organisms from class *Sphingobacteria*, order *Sphingobacteriales*, which includes the genus *Sphingobacterium*) are all metabolically versatile heterotrophs known to occupy soil, aquatic, sewage sludge, and compost habitats (2, 17, 19). For the phylum *Nitrospirae*, organisms from the nitrite-oxidizing genus *Nitrospira* (6) accounted for 1-2 % of total reads and for more than 80% of all reads in the phylum. Similarly, *Crenarchaeota* from the families *Cenarchaeaceae* or *Nitrososphaeraceae* (class *Thaumarchaeota*), both of which include aerobic ammonium-oxidizing organisms (21) were detected in each of the sand types at ca. 2-4 % of all reads.

In contrast to *Bacteroidetes*, *Nitrospirae*, and the *Crenarchaeota*, organisms from the *Acidobacteria*, *Planctomycetes*, and *Verruimicrobia* phyla were several-fold more abundant in RBS and PZS compared to GWS (Table 3). The *Acidobacteria* were dominated by families within classes *Chloracidobacteria* and *Acidobacteria*, which have been identified in soil habitats and are known for their ability to degrade plant and microbial polysaccharides (2, 23, 27). The

*Planctomycetes* taxa were affiliated with the *Gemmataceae*, *Isosphaeraceae*, *Pirellulaceae*, and *Planctomycetaceae* families, all of which are aerobic heterotrophic budding bacteria with unique intracellular compartmental (organelle) structures (18, 22). The *Verrucomicrobia* were dominated by taxa related to cultivated and uncultivated organisms from classes *Opitutae*, *Pedosphaerae*, *Spartobacteria*, and *Verrucomicrobiae*. Organisms within these families are mainly aerobes common in soils or other organic-rich environments (e.g. 7, 13, 14, 20, 29, 34).

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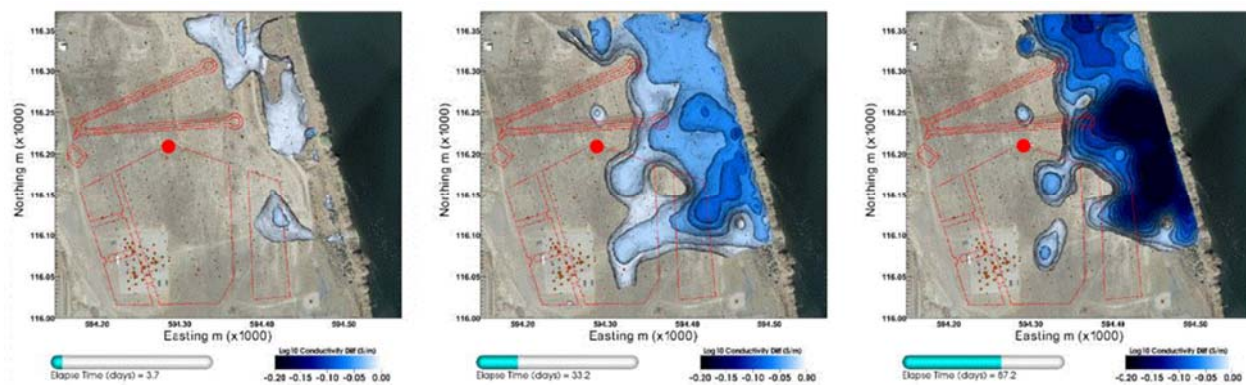


Figure S1. The varying stages of river water intrusion at the Hanford Area 300 site (modified from Figs. 11 and 12 in Johnson et al., 2015, *Water Resour. Res.*, 51, doi:10.1002/2014WR016129; used by permission). Darker blue coloration shows decrease in conductivity associated with higher DOC in river water. Elapsed time shown for a period of approximately 54 days. The red dot shows the location of groundwater well 2-32, from which water was obtained for the experiments reported in this paper.

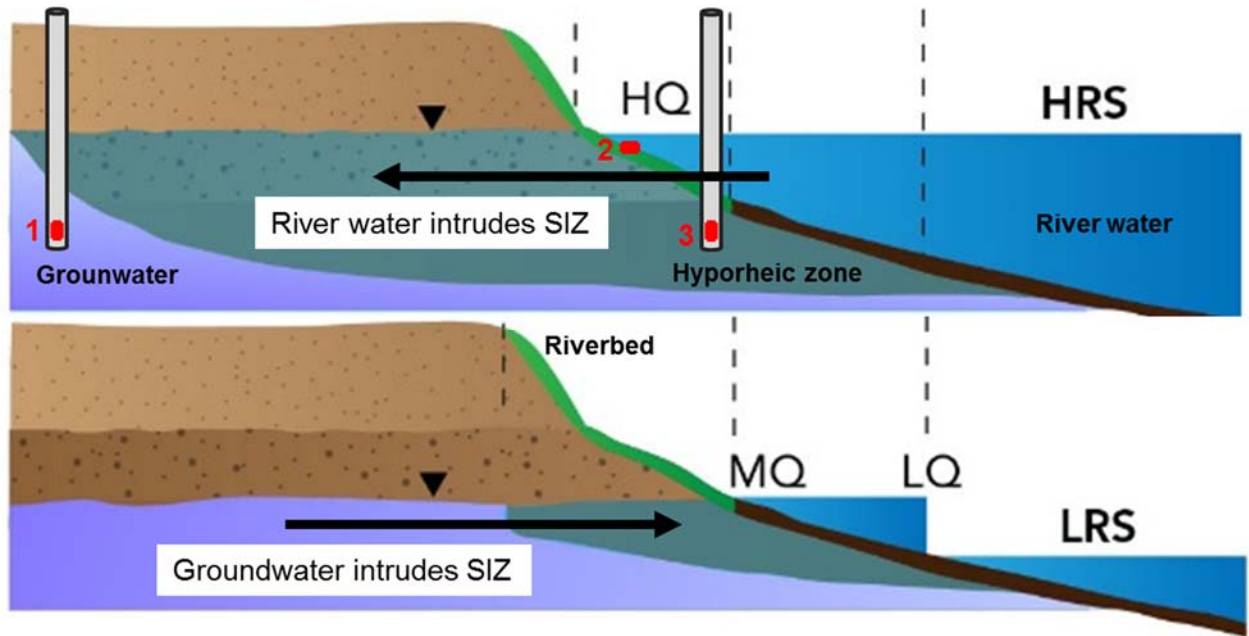
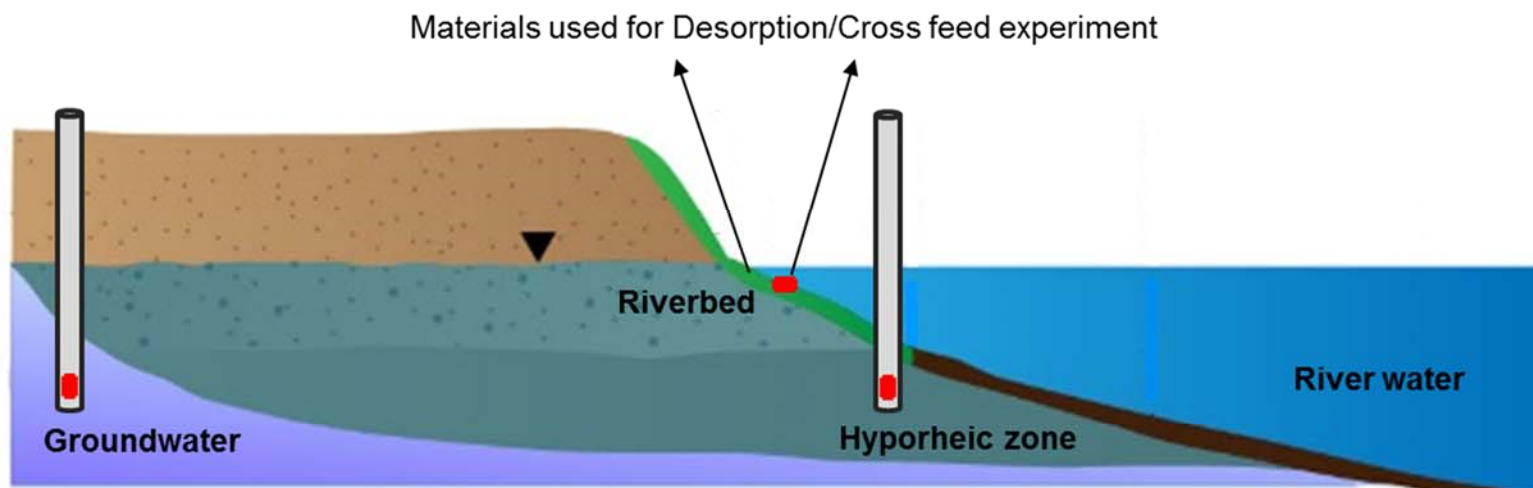


Figure S2. Diagrammatic representation of river stage driven hydrological dynamics within the Hanford 300 Area SIZ. During high river stage (HRS), large river water-groundwater exchange (HQ) takes place during river water intrusion into the SIZ, whereas during low river stage (LRS), medium (MQ) or low (LQ) river water-groundwater exchange takes place and net groundwater release into the SIZ may take place. The red dots correspond to the three habitats examined in this study (1 = groundwater; 2 = riverbed; 3 = hyporheic zone piezometer).



### Cross feed experiments 1 and 2:

Step 1: Incubate sand packs (red ovals) *in situ* within groundwater, riverbed, and hyporheic zone environments for 6 weeks to allow for microbial colonization.

Step 2: Expose the different colonized sand materials to either (1) filter-sterilized groundwater, (2) filter-sterilized river water, or (3) autoclaved (DOC-free) artificial groundwater and/or artificial river water.

### Desorption/Cross feed experiment:

Step 1: Incubate sand packs (red ovals) *in situ* within groundwater, riverbed, and hyporheic zone environments for 6 weeks to allow for microbial colonization.

Step 2: Collect “desorbed” DOC from either riverbed sediment or riverbed colonized sand packs.

Step 2: Expose the different colonized sand materials to either (1) filter-sterilized river water, (2) filtered-sterilized “desorbed” DOC from riverbed sediment, (3) filtered-sterilized “desorbed” DOC from riverbed colonized sand packs, or (4) autoclaved (DOC-free) artificial river water.

Figure S3. Conceptual explanation of the cross feeding and desorption/cross feeding experiments. See Materials and Methods for details.

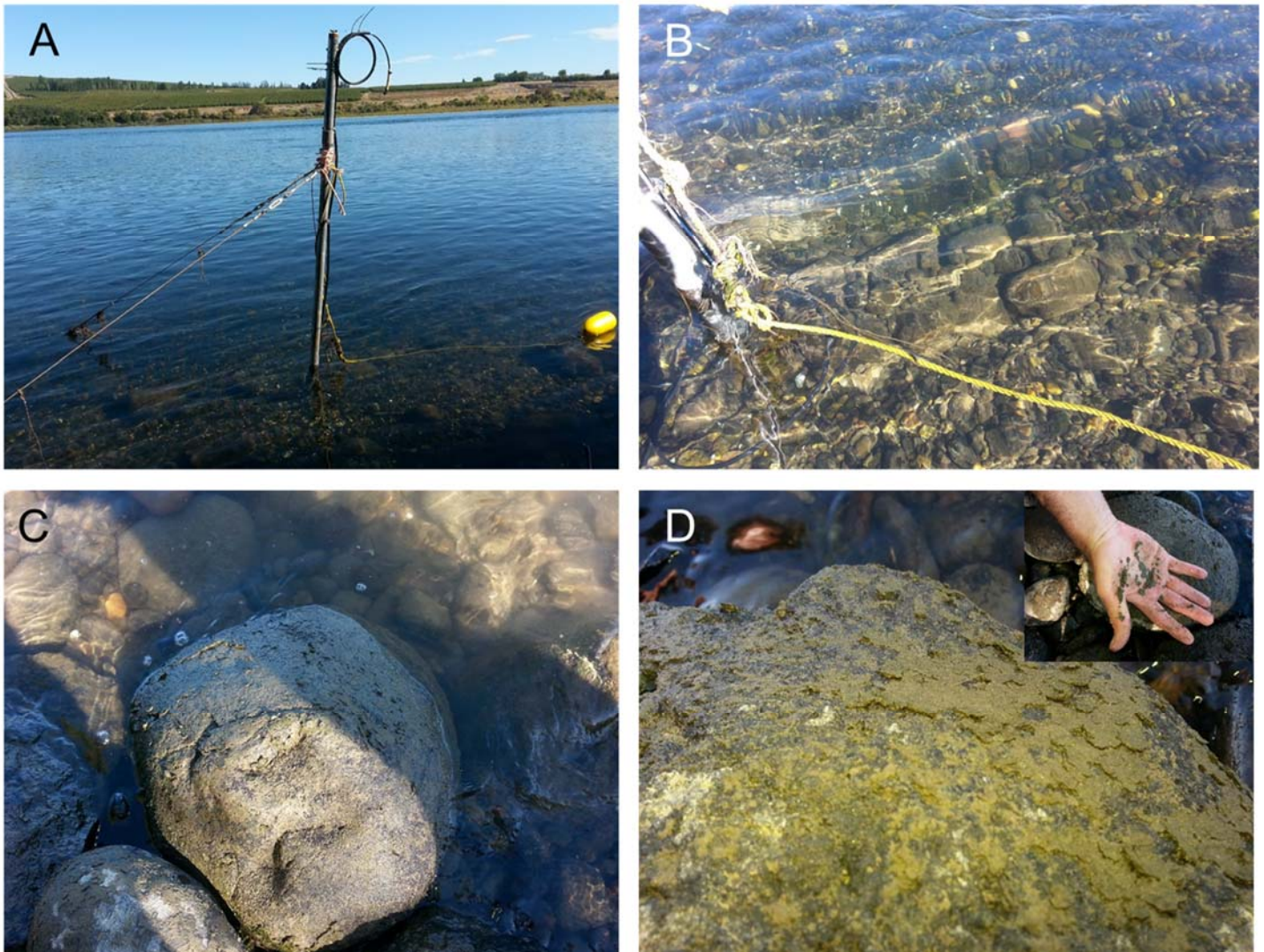


Figure S4. Photos of near-shore riverbed environment at the Hanford 300 Area. (A) View from the north side of the Columbia River, illustrating the location of piezometer T3. (B) Close up of the riverbed gravel layer. (C) A large, periphyton-coated gravel stone. (D) Close up of the periphyton-coated gravel stone, illustrating the presence of abundant photosynthetic biomass. The inset in (D) shows periphyton material loosely-associated with the gravel stone.

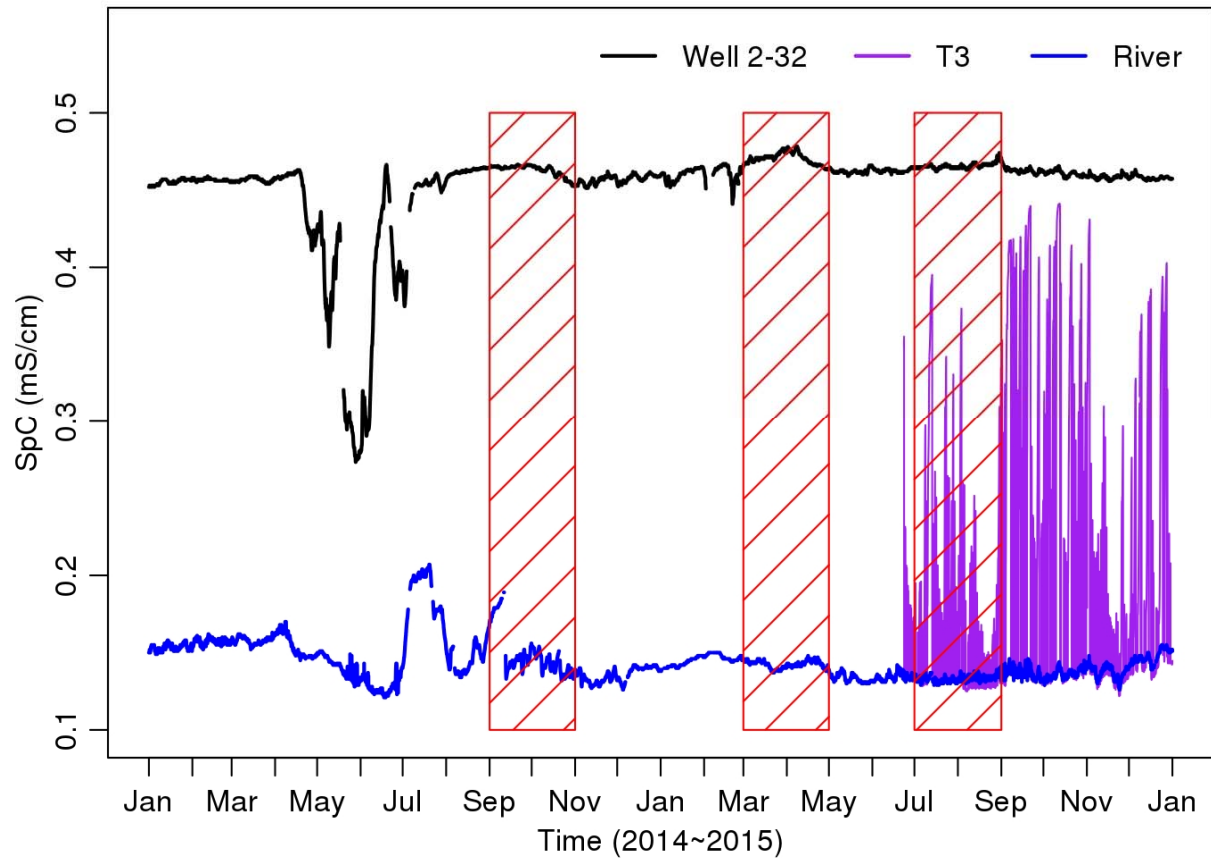


Figure S5. Specific conductivity (SpC) of groundwater well 2-32, piezometer T3, and river water during 2014-2015 (data for piezometer T3 are available only the second half of 2015). Results are hourly measurements from a data logger connected to an *in situ* conductivity probe. The hatched orange rectangles indicate the times of *in situ* sand pack deployment. The frequent variation in piezometer fluid SpC indicates extensive river water-groundwater mixing.

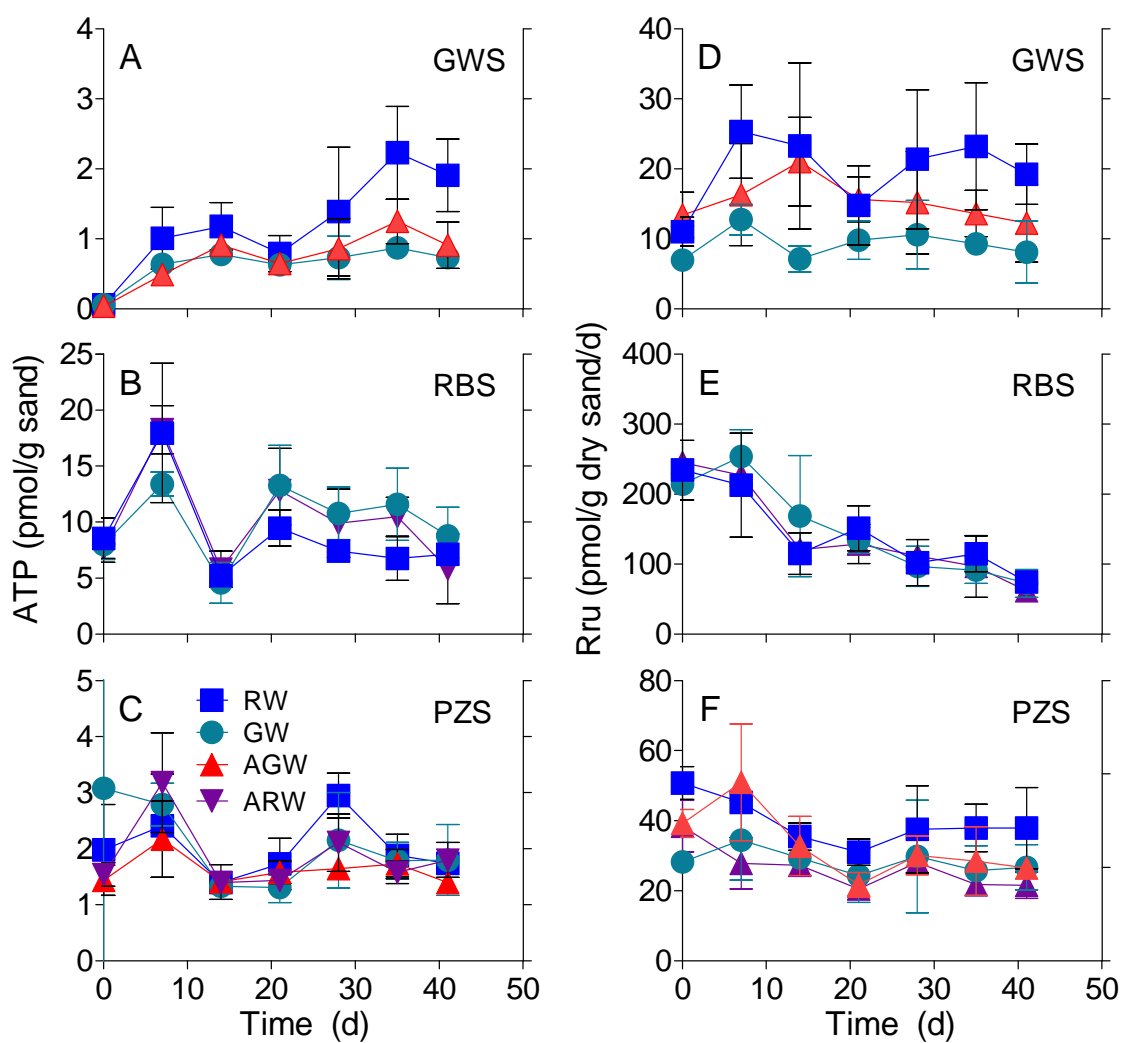


Figure S6. ATP content and rates of resazurin transformation to resorufin for the groundwater (A, D), riverbed (B, E), and piezometer (C, F) sand colonized reactors for Cross feed experiment 2. Each data point shows the mean  $\pm$  SD or range of triplicate or duplicate



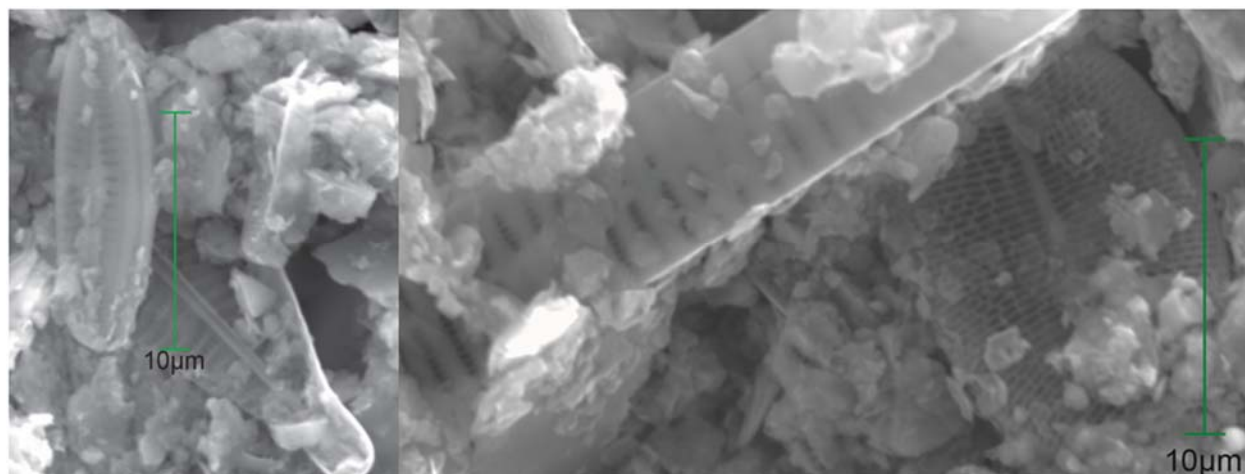


Figure S7. SEM images of diatom frustules in RBS material.

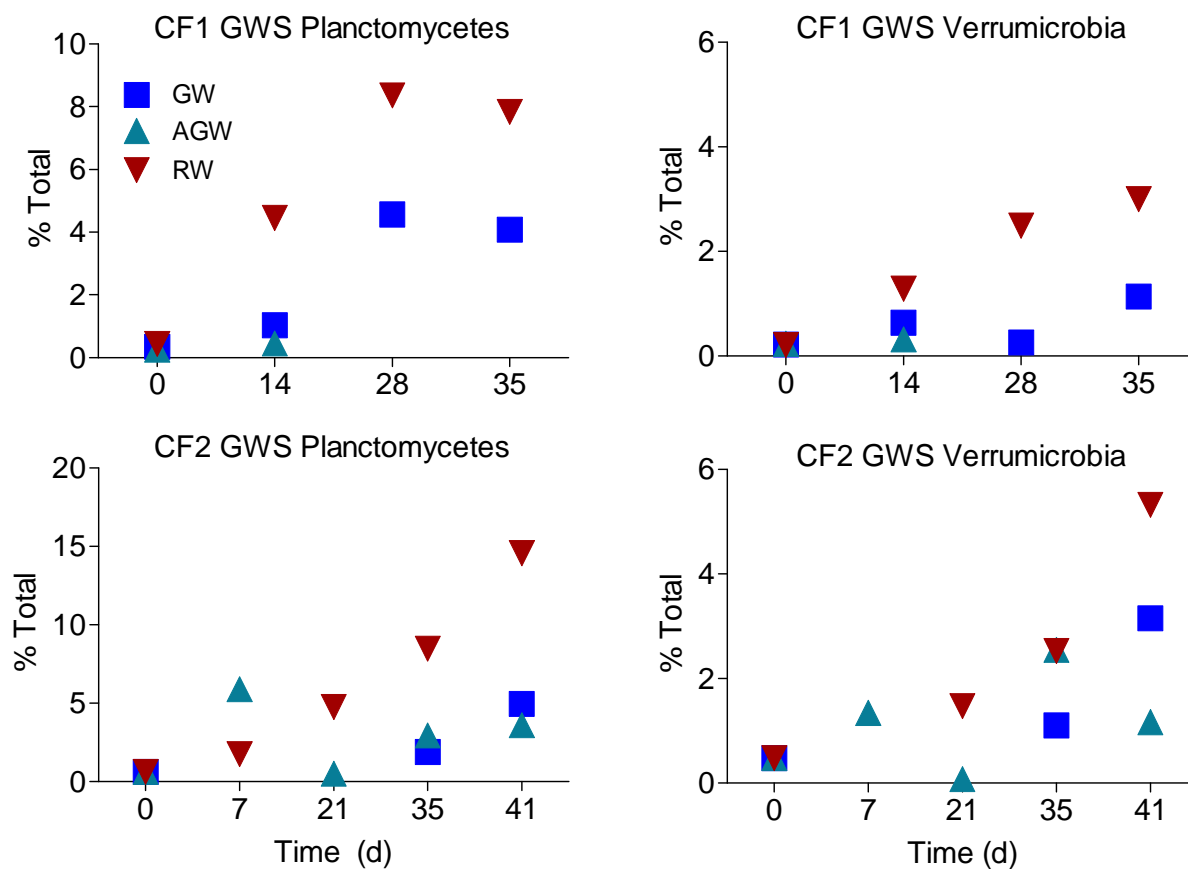


Figure S8. Relative abundance of *Planctomycetes* and *Verrumicrobia* in the CF1 and CF2 GWS reactors exposed to different fluid types (GW, AGW, or RW). Each symbol represents results from a single 16S rRNA gene amplicon library.

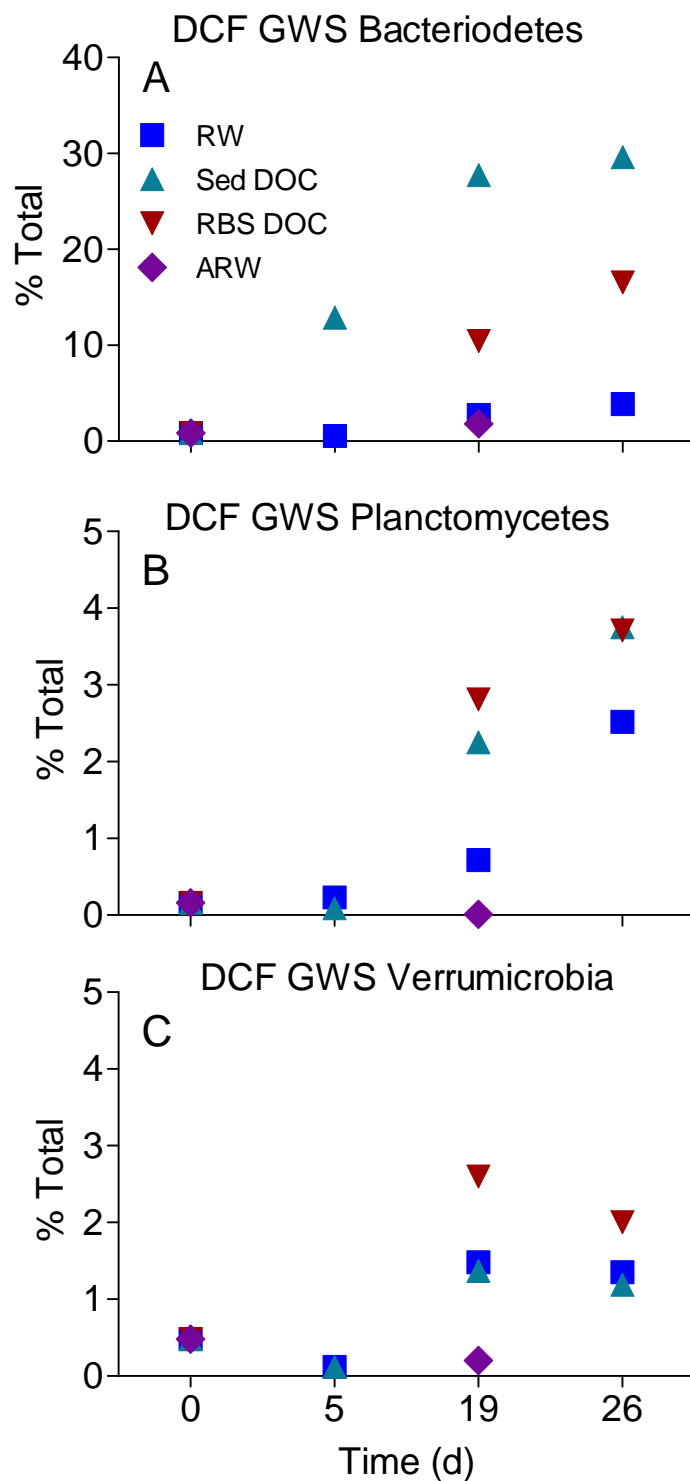


Figure S9. Relative abundance of *Bacteroidetes* (A), *Planctomycetes* (B), and *Verrumicrobia* (C) in the DCF GWS reactors exposed to different fluid types (RW, Sed DOC, RBS DOC, or ARW). Each symbol represents results from a single 16S rRNA gene amplicon library.

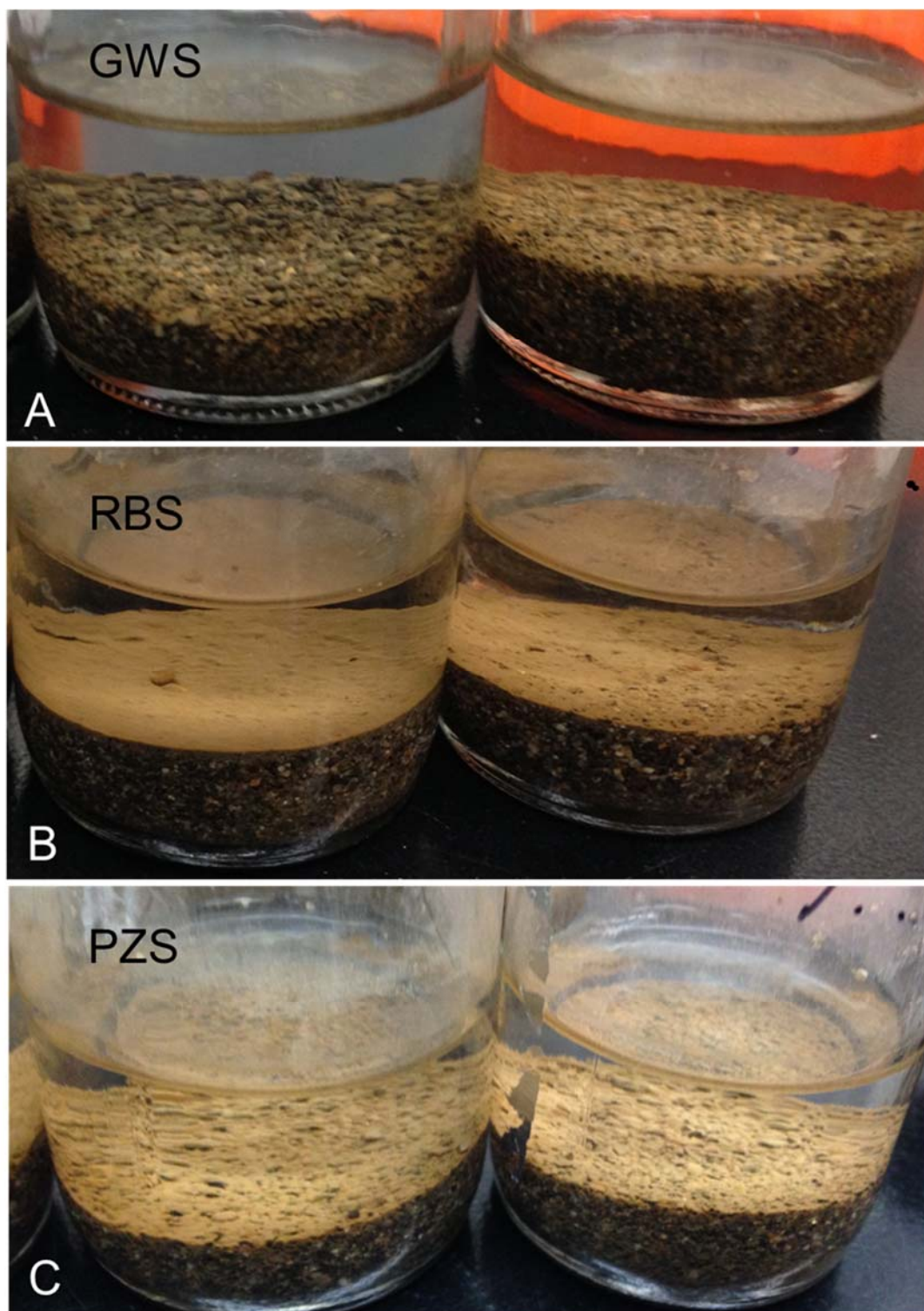


Figure S10. Photos of GWS, RBS, and PZS reactors at the start of CF1. Note the presence of fine-grained materials on the surface the RBS, which are less abundant in the PZS and absent from the GWS.

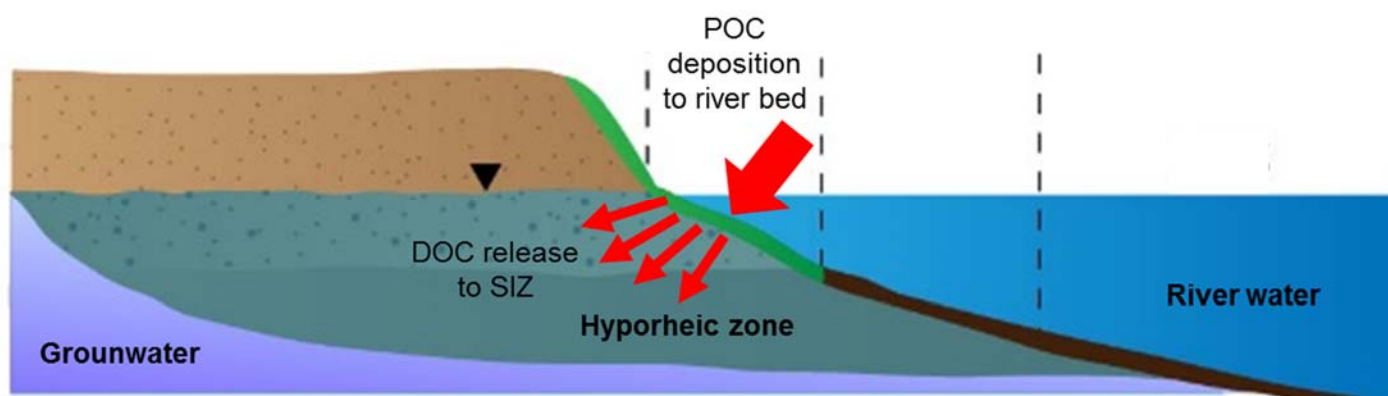


Figure S11. Conceptual illustration of a key biogeochemical implication of this study, i.e. the potential for hydrologically-driven input of labile POC in the form of river water and/or periphyton photosynthetic biomass into the riverbed, and for subsequent flux of DOC derived from that biomass into the HC.

Table S1. Pairwise reactor comparison for the cross feeding experiments. Only comparisons that were significant at  $P < 0.05$  are shown (all other comparisons were not significant).

Treatment Comparison	Parameter	Value	Difference	p
CF1 GWS+AGW	Biomass <sup>a</sup>	0.53	0.20	0.0409
CF1 GWS+GW		0.33		
CF2 RWS+GW	Biomass	9.75	2.88	0.0307
CF2 RWS+RW		6.87		
CF2 GWS+RW	Biomass	1.62	0.87	2.99E-06
CF2 GWS+GW		0.75		
CF2 GWS+RW	Biomass	1.62	0.68	0.0009
CF2 GWS+AGW		0.94		
CF1 RWS+ARW	Respiration <sup>b</sup>	316.23	130.02	0.0374
CF1 RWS+RW		186.21		
CF2 GWS+RW	Respiration	38.02	21.04	5.36E-06
CF2 GWS+GW		16.98		
CF2 GWS+AGW	Respiration	26.30	9.32	0.0133
CF2 GWS+GW		16.98		
CF2 GWS+RW	Respiration	38.02	11.72	0.0326
CF2 GWS+AGW		26.30		
CF2 PZS+RW	Respiration	70.79	25.09	0.0127
CF2 PZS+ARW		45.71		

<sup>a</sup> Units = pmol/g sand

<sup>b</sup> Units = pmol/g sand/48 hr

Table S2. Pairwise comparisons for the desorption/cross feeding experiment. Only comparisons that were significant at  $P < \sim 0.05$  are shown (all other comparisons were not significant).

Treatment Comparison	Parameter	Value	Difference	p
GWS+RW	Biomass <sup>a</sup>	0.66	0.37	0.0064
GWS+ARW		0.29		
GWS+Sed DOC	Biomass	0.60	0.32	0.0138
GWS+ARW		0.29		
GWS+RBS DOC	Biomass	0.51	0.22	0.0571
GWS+ARW		0.29		
GWS+ Sed DOC	Respiration <sup>b</sup>	89.13	51.97	0.0021
GWS+RW		37.15		
GWS+RBS DOC	Respiration	91.20	54.05	0.0015
GWS+RW		37.15		
PZS+ARW	Respiration	97.72	45.24	0.0253
PZS+RW		52.48		
PZS+Sed DOC	Respiration	109.65	57.17	0.0098
PZS+RW		52.48		
PZS+RBS DOC	Respiration	120.23	67.75	0.0038
PZS+RW		52.48		

<sup>a</sup> Units = pmol/g sand

<sup>b</sup> Units = pmol/g sand/48 hr

Table S3. Shannon and Simpson diversity indices for GWS, RBS, and PZS in the cross feeding experiments.

Experiment	Shannon Index			Simpson Index		
	GWS	RBS	PZS	GWS	RBS	PZS
CF1	4.44	7.34	6.80	0.0407	0.0027	0.0076
CF2	4.97	7.47	6.83	0.0237	0.0024	0.0067
DCF	4.21	7.17	6.73	0.0545	0.033	0.0064



Table S4. Relative abundance of families within the major Proteobacterial classes and select non-Proteobacterial phyla in CF1. For a given sand type, the number of OTU hits for each family was summed across all water types and divided by the total number of hits for the corresponding phylum. Only families that comprised  $\geq 0.1\%$  of the phylum are shown. The notations p\_, c\_, o\_, and f\_ refer to phylum, class, order, and family, respectively.

Taxa	GWS % of Phylum	Taxa	RBS % of Phylum	Taxa	PZS % of Phylum
<b>p__Proteobacteria</b>		<b>p__Proteobacteria</b>		<b>p__Proteobacteria</b>	
c__Alphaproteobacteria	17.407	c__Alphaproteobacteria	28.080	c__Alphaproteobacteria	32.021
f__Unclassified	3.155	f__Unclassified	8.941	f__Unclassified	12.211
f__Acetobacteraceae	2.993	f__Rhodobacteraceae	5.373	f__Sphingomonadaceae	4.265
f__Aurantimonadaceae	1.870	f__Sphingomonadaceae	4.819	f__Hyphomicrobiaceae	3.614
f__Beijerinckiaceae	1.661	f__Hyphomicrobiaceae	4.142	f__Rhodobacteraceae	3.492
f__Bradyrhizobiaceae	1.555	f__Rhodospirillaceae	1.717	f__Rhodospirillaceae	2.458
f__Brucellaceae	1.488	f__Hyphomonadaceae	0.717	f__Phyllobacteriaceae	2.144
f__Caulobacteraceae	1.484	f__Phyllobacteriaceae	0.695	f__Bradyrhizobiaceae	0.961
f__Erythrobacteraceae	1.034	f__Caulobacteraceae	0.455	f__Hyphomonadaceae	0.951
f__Holosporaceae	0.654	f__Methylocystaceae	0.275	f__Caulobacteraceae	0.642
f__Hyphomicrobiaceae	0.579	f__Bradyrhizobiaceae	0.231	f__Rhizobiaceae	0.626
f__Hyphomonadaceae	0.298	f__Acetobacteraceae	0.199	f__Acetobacteraceae	0.219
f__Methylobacteriaceae	0.249	f__Rhizobiaceae	0.129	f__Pelagibacteraceae	0.132
f__Methylocystaceae	0.225			f__Methylocystaceae	0.107
c__Betaproteobacteria	46.058	c__Betaproteobacteria	24.176	c__Betaproteobacteria	30.194
f__Comamonadaceae	22.621	f__Unclassified	12.340	f__Methylophilaceae	11.837
f__Methylophilaceae	18.323	f__Comamonadaceae	4.631	f__Comamonadaceae	7.552
f__Rhodocyclaceae	2.753	f__Methylophilaceae	2.518	f__Unclassified	7.416
f__Unclassified	1.051	f__Alcaligenaceae	1.636	f__Rhodocyclaceae	2.109
f__Oxalobacteraceae	0.651	f__Rhodocyclaceae	1.620	f__Oxalobacteraceae	0.464
f__Nitrosomonadaceae	0.268	f__Oxalobacteraceae	0.594	f__Alcaligenaceae	0.395
f__Hydrogenophilaceae	0.179	f__Neisseriaceae	0.282	f__Neisseriaceae	0.170
f__Gallionellaceae	0.105				
c__Deltaproteobacteria	2.157	c__Deltaproteobacteria	13.804	c__Deltaproteobacteria	6.960
f__Unclassified	0.909	f__Unclassified	5.921	f__Unclassified	2.653
f__OM27	0.772	f__Syntrophobacteraceae	2.373	f__Syntrophobacteraceae	1.240
f__Bdellovibrionaceae	0.228	f__Geobacteraceae	0.986	f__Haliangiaceae	0.790
f__Haliangiaceae	0.113	f__Haliangiaceae	0.668	f__Bdellovibrionaceae	0.496

		f__Myxococcaceae	0.583	f__OM27	0.462
		f__JTB38	0.566	f__JTB38	0.380
		f__Bdellovibrionaceae	0.426	f__Cystobacterineae	0.264
		f__Desulfuromonadaceae	0.296	f__Nannocystaceae	0.113
		f__Desulfobulbaceae	0.260		
		f__OM27	0.250		
		f__Polyangiaceae	0.246		
		f__MND4	0.243		
		f__NB1-i	0.200		
		f__Cystobacterineae	0.180		
		f__Bacteriovoracaceae	0.158		
		f__Desulfobacteraceae	0.112		
c__Gammaproteobacteria	34.331	c__Gammaproteobacteria	32.945	c__Gammaproteobacteria	30.456
f__Pseudomonadaceae	27.772	f__Sinobacteraceae	7.775	f__Pseudomonadaceae	10.695
f__Sinobacteraceae	2.499	f__Xanthomonadaceae	7.408	f__Unclassified	2.982
f__Unclassified	1.007	f__Unclassified	4.248	f__Sinobacteraceae	2.641
f__Alteromonadaceae	0.471	f__Piscirickettsiaceae	3.574	f__Xanthomonadaceae	2.310
f__Moraxellaceae	0.278	f__Coxiellaceae	2.673	f__Ectothiorhodospiraceae	2.030
f__Legionellaceae	0.259	f__Pseudomonadaceae	2.032	f__Moraxellaceae	1.715
f__Coxiellaceae	0.255	f__Marinicellaceae	1.235	f__Alteromonadaceae	1.332
f__Chromatiaceae	0.253	f__OM60	1.000	f__Piscirickettsiaceae	1.143
f__Oleiphilaceae	0.213	f__Legionellaceae	0.699	f__Coxiellaceae	1.023
f__Xanthomonadaceae	0.121	f__125ds10	0.518	f__125ds10	0.920
		f__Moraxellaceae	0.504	f__Marinicellaceae	0.785
		f__Crenotrichaceae	0.390	f__Legionellaceae	0.380
		f__HTCC2089	0.248	f__OM60	0.341
				f__HTCC2188	0.229
				f__HTCC2089	0.103
<b>p_Acidobacteria</b>	GWS % of Phylum	<b>p_Acidobacteria</b>	RBS % of Phylum	<b>p_Acidobacteria</b>	PZS % of Phylum
c__Chloracidobacteria	46.481	c__Chloracidobacteria	39.80261	c__Chloracidobacteria	29.080
f__Ellin6075	42.640	f__Ellin6075	33.66153	f__Ellin6075	25.325
f__Unclassified	3.828	f__Unclassified	6.12575	f__Unclassified	3.748
c__Acidobacteria-6	44.881	c__Acidobacteria-6	40.29668	c__Acidobacteria-6	46.767

f__mb2424	30.869	f__Unclassified	25.13737	f__Unclassified	31.242
f__Unclassified	13.527	f__mb2424	7.94873	f__mb2424	8.656
f__RB40	0.485	f__RB40	7.20822	f__RB40	6.869
c__Holophagae	5.204	c__Holophagae	2.66255	c__Holophagae	1.173
f__Holophagaceae	5.204	f__Holophagaceae	2.65665	f__Holophagaceae	1.096
c__Sva0725	0.459	c__Sva0725	3.98439	c__Sva0725	4.347
f__Unclassified	0.459	f__Unclassified	3.98439	f__Unclassified	4.347
c__RB25	0.406	c__RB25	2.94201	c__RB25	4.308
f__Unclassified	0.406	f__Unclassified	2.94201	f__Unclassified	4.308
c__iii1-8	0.223	c__iii1-8	4.16598	c__iii1-8	3.140
f__Unclassified	0.223	f__Unclassified	4.13414	f__Unclassified	3.134
<b>p__Bacteroidetes</b>	GWS % of Phylum	<b>p__Bacteroidetes</b>	RBS % of Phylum	<b>p__Bacteroidetes</b>	PZS % of Phylum
c__Saprospirae	19.111	c__Saprospirae	49.964	c__Saprospirae	32.061
f__Unclassified	0.000	f__Saprospiraceae	36.402	f__Chitinophagaceae	21.943
f__Saprospiraceae	1.829	f__Saprospiraceae	12.597	f__Saprospiraceae	9.656
f__Chitinophagaceae	17.282	f__Unclassified	0.965	f__Unclassified	0.463
c__Flavobacteriia	45.843	c__Flavobacteriia	20.249	c__Flavobacteriia	25.117
f__Flavobacteriaceae	26.054	f__Flavobacteriaceae	18.139	f__Flavobacteriaceae	17.745
f__Cryomorphaceae	19.781	f__Cryomorphaceae	2.096	f__Cryomorphaceae	7.354
c__Sphingobacteriia	15.951	c__Sphingobacteriia	15.139	c__Sphingobacteriia	22.377
f__Unclassified	15.934	f__Unclassified	15.044	f__Unclassified	22.284
c__Cytophagia	3.855	c__Cytophagia	11.823	c__Cytophagia	18.890
f__Cytophagaceae	3.839	f__Cytophagaceae	11.539	f__Cytophagaceae	18.726
		f__Amoebophilaceae	0.263		
c__Bacteroidia	7.612	c__Bacteroidia	1.780	c__Bacteroidia	0.402
f__Marinilabiaceae	4.574	f__Unclassified	1.392	f__Unclassified	0.174
f__Unclassified	1.870	f__SB-1	0.193		

f__Rikenellaceae	0.931				
f__S24-7	0.237				
<b>p__Cyanobacteria</b>	GWS % of Phylum	<b>p__Cyanobacteria</b>	RBS % of Phylum	<b>p__Cyanobacteria</b>	PZS % of Phylum
c__Chloroplast	7.419	c__Chloroplast	94.049	c__Chloroplast	71.560
o__Streptophyta	5.906	o__Stramenopiles	93.168	o__Stramenopiles	69.791
o__Stramenopiles	1.513	o__Chlorophyta	0.634	o__Chlorophyta	1.084
		o__Streptophyta	0.232	o__Streptophyta	0.561
f__Unclassified	7.419	f__Unclassified	93.499	f__Unclassified	70.700
		f__Chlamydomonadaceae	0.537	f__Chlamydomonadaceae	0.785
c__ML635J-21	88.335	c__ML635J-21	2.142	c__ML635J-21	19.039
f__Unclassified	88.335	f__Unclassified	2.142	f__Unclassified	19.039
c__4C0d-2	4.237	c__4C0d-2	2.103	c__4C0d-2	5.729
f__Unclassified	4.237	f__Unclassified	2.103	f__Unclassified	5.729
		c__Synechococcophycideae	1.325	c__Synechococcophycideae	3.469
		f__Synechococcaceae	1.141	f__Synechococcaceae	3.411
<b>p__Nitrospiraea</b>	GWS % of Phylum	<b>p__Nitrospiraea</b>	RBS % of Phylum	<b>p__Nitrospiraea</b>	PZS % of Phylum
c__Nitrospira	100.000	c__Nitrospira	100.000	c__Nitrospira	100.000
f__Nitrospiraceae	98.408	f__Nitrospiraceae	89.446	f__Nitrospiraceae	92.481
f__0319-6A21	0.628	f__0319-6A21	7.919	f__0319-6A21	6.713
f__Thermodesulfovibrionaceae	0.597	f__Thermodesulfovibrionaceae	2.287	f__Leptospirillaceae	0.327
f__Unclassified	0.322	f__FW	0.323	f__Unclassified	0.265
				f__Thermodesulfovibrionaceae	0.214
<b>p__Planctomycetes</b>	GWS % of Phylum	<b>p__Planctomycetes</b>	RBS % of Phylum	<b>p__Planctomycetes</b>	PZS % of Phylum
c__Planctomycetia	92.642	c__Planctomycetia	89.916	c__Planctomycetia	78.868
f__Planctomycetaceae	67.862	f__Gemmataceae	34.411	f__Gemmataceae	31.293
f__Gemmataceae	18.651	f__Pirellulaceae	33.514	f__Pirellulaceae	26.308
f__Pirellulaceae	5.609	f__Planctomycetaceae	16.059	f__Planctomycetaceae	16.834
f__Isosphaeraceae	0.415	f__Isosphaeraceae	5.143	f__Isosphaeraceae	3.870

f__Unclassified	0.104	f__Unclassified	0.788	f__Unclassified	0.563
c__Phycisphaerae	1.564	c__Phycisphaerae	4.352	c__Phycisphaerae	4.648
f__Unclassified	0.585	f__Unclassified	4.331	f__Unclassified	4.590
f__Phycisphaeraceae	0.978				
c__OM190	3.535	c__OM190	2.587	c__OM190	8.005
f__Unclassified	3.535	f__Unclassified	2.587	f__Unclassified	8.005
c__BD7-11	1.349	c__BD7-11	0.557	c__BD7-11	4.027
f__	1.349	f__	0.557	f__	4.027
c__vadinHA49	0.163	c__vadinHA49	0.929	c__vadinHA49	2.359
f__Unclassified	0.163	f__Unclassified	0.929	f__Unclassified	2.359
<b>p_Verrumicrobia</b>	GWS % of Phylum	<b>p_Verrumicrobia</b>	RBS % of Phylum	<b>p_Verrumicrobia</b>	PZS % of Phylum
c__Pedosphaerae	75.022	c__Pedosphaerae	34.924	c__Pedosphaerae	61.473
f__Ellin517	44.158	f__auto67_4W	15.616	f__Unclassified	24.152
f__Unclassified	19.356	f__Unclassified	12.522	f__auto67_4W	13.660
f__R4-41B	4.762	f__R4-41B	2.629	f__Ellin517	12.132
f__auto67_4W	3.219	f__Ellin515	2.209	f__R4-41B	6.592
f__Pedosphaeraceae	0.772	f__Ellin517	0.833	f__Ellin515	1.425
f__Ellin515	0.639	f__Pedosphaeraceae	0.168	f__Pedosphaeraceae	1.050
c__Spartobacteria	4.277	c__Spartobacteria	19.842	c__Spartobacteria	7.239
f__Chthoniobacteraceae	4.277	f__Chthoniobacteraceae	19.827	f__Chthoniobacteraceae	7.239
c__Verrucomicrobiae	5.732	c__Verrucomicrobiae	31.255	c__Verrucomicrobiae	10.073
f__Verrucomicrobiaceae	5.732	f__Verrucomicrobiaceae	31.255	f__Verrucomicrobiaceae	10.073
c__Opitutae	14.683	c__Opitutae	6.408	c__Opitutae	16.440
f__Opitutaceae	14.683	f__Opitutaceae	6.237	f__Opitutaceae	16.224
		f__Cerasiococcaceae	0.105	f__Cerasiococcaceae	0.182
c__Verruco-5	0.132	c__Verruco-5	3.042	c__Verruco-5	1.366

f__Unclassified	0.132	f__Unclassified	3.030	f__Unclassified	1.355
c__Methylacidiphilae	0.154	c__Methylacidiphilae	1.897	c__Methylacidiphilae	2.133
f__Unclassified	0.154	f__Unclassified	1.885	f__Unclassified	2.049
<b>p_Crenarchaeota</b>	GWS % of Phylum	<b>p_Crenarchaeota</b>	RBS % of Phylum	<b>p_Crenarchaeota</b>	PZS % of Phylum
c__Thaumarchaeota	100.000	c__Thaumarchaeota	99.975	c__Thaumarchaeota	99.984
f__Cenarchaeaceae	95.667	f__Cenarchaeaceae	86.344	f__Cenarchaeaceae	95.610
f__Nitrososphaeraceae	3.298	f__Nitrososphaeraceae	13.403	f__Nitrososphaeraceae	2.168
f__SAGMA-X	1.035	f__SAGMA-X	0.228	f__SAGMA-X	2.156

Table S5. Relative abundance of families within the major Proteobacterial classes and select non-Proteobacterial phyla in CF2. For a given sand type, the number of OTU hits for each family was summed across all water types and divided by the total number of hits for the corresponding phylum. Only families that comprised  $\geq 0.1\%$  of the phylum are shown. The notations p\_, c\_, o\_, and f\_ refer to phylum, class, order, and family, respectively.

Taxa	GWS % of Phylum	Taxa	RBS % of Phylum	Taxa	PZS % of Phylum
<b>p__Proteobacteria</b>		<b>p__Proteobacteria</b>		<b>p__Proteobacteria</b>	
c__Alphaproteobacteria	20.411	c__Alphaproteobacteria	22.694	c__Alphaproteobacteria	24.836
f__Unclassified	5.079	f__Unclassified	7.657	f__Unclassified	7.991
f__Sphingomonadaceae	2.196	f__Rhodobacteraceae	3.849	f__Hyphomicrobiaceae	3.382
f__Caulobacteraceae	2.115	f__Sphingomonadaceae	3.174	f__Rhodobacteraceae	2.976
f__Hyphomicrobiaceae	1.934	f__Hyphomicrobiaceae	2.574	f__Sphingomonadaceae	2.667
f__Rhodospirillaceae	1.901	f__Rhodospirillaceae	2.436	f__Rhodospirillaceae	2.492
f__Rhodobacteraceae	1.449	f__Hyphomonadaceae	1.531	f__Hyphomonadaceae	1.664
f__Bradyrhizobiaceae	1.412	f__Phyllobacteriaceae	0.334	f__Phyllobacteriaceae	0.913
f__Phyllobacteriaceae	1.362	f__Acetobacteraceae	0.255	f__Rhizobiaceae	0.763
f__Beijerinckiaceae	1.168	f__Caulobacteraceae	0.245	f__Bradyrhizobiaceae	0.704
f__Hyphomonadaceae	1.150	f__Methylocystaceae	0.132	f__Caulobacteraceae	0.456
f__Methylobacteriaceae	0.175	f__Bradyrhizobiaceae	0.114	f__Acetobacteraceae	0.221
f__Acetobacteraceae	0.132			f__Pelagibacteraceae	0.187
f__Rhizobiaceae	0.107			f__Methylocystaceae	0.115
c__Betaproteobacteria	64.742	c__Betaproteobacteria	32.082	c__Betaproteobacteria	48.173
f__Comamonadaceae	36.658	f__Comamonadaceae	11.035	f__Methylophilaceae	17.652
f__Rhodocyclaceae	12.638	f__Unclassified	7.746	f__Comamonadaceae	16.960
f__Methylophilaceae	11.723	f__Rhodocyclaceae	6.556	f__Unclassified	6.134
f__Unclassified	1.830	f__Methylophilaceae	3.832	f__Rhodocyclaceae	5.753
f__Hydrogenophilaceae	0.968	f__Oxalobacteraceae	0.884	f__Oxalobacteraceae	0.526
f__Oxalobacteraceae	0.659	f__Neisseriaceae	0.711	f__Neisseriaceae	0.348
		f__Alcaligenaceae	0.385	f__Alcaligenaceae	0.229
		f__Nitrosomonadaceae	0.141		
c__Deltaproteobacteria	3.018	c__Deltaproteobacteria	17.268	c__Deltaproteobacteria	10.948
f__Unclassified	1.780	f__Unclassified	7.726	f__Unclassified	5.084
f__OM27	0.695	f__Syntrophobacteraceae	1.937	f__Syntrophobacteraceae	1.859
f__Haliangiaceae	0.202	f__Geobacteraceae	1.260	f__Haliangiaceae	0.790
f__Bdellovibrionaceae	0.162	f__Haliangiaceae	0.933	f__Bdellovibrionaceae	0.716

		f__Myxococcaceae	0.757	f__OM27	0.411
		f__Bdellovibrionaceae	0.710	f__JTB38	0.368
		f__Polyangiaceae	0.692	f__Cystobacterineae	0.322
		f__OM27	0.620	f__Polyangiaceae	0.264
		f__JTB38	0.333	f__Myxococcaceae	0.217
		f__Bacteriovoracaceae	0.290	f__Nannocystaceae	0.204
		f__NB1-i	0.263	f__Bacteriovoracaceae	0.192
		f__MND4	0.227	f__Geobacteraceae	0.137
		f__Cystobacterineae	0.158	f__MND4	0.122
		f__Nannocystaceae	0.150		
		f__Desulfobulbaceae	0.125		
		f__Entotheonellaceae	0.114		
c__Gammaproteobacteria	11.746	c__Gammaproteobacteria	27.104	c__Gammaproteobacteria	15.743
f__Pseudomonadaceae	3.301	f__Pseudomonadaceae	5.911	f__Sinobacteraceae	2.906
f__Unclassified	2.485	f__Xanthomonadaceae	3.500	f__Unclassified	2.698
f__Alteromonadaceae	1.466	f__Sinobacteraceae	3.131	f__Coxiellaceae	1.578
f__Sinobacteraceae	1.253	f__Unclassified	2.800	f__Xanthomonadaceae	1.301
f__Moraxellaceae	1.052	f__OM60	2.112	f__OM60	1.196
f__Coxiellaceae	0.494	f__Piscirickettsiaceae	2.021	f__Piscirickettsiaceae	1.082
f__Oleiphilaceae	0.409	f__Coxiellaceae	1.914	f__Marinicellaceae	0.928
f__Chromatiaceae	0.381	f__Moraxellaceae	1.411	f__Pseudomonadaceae	0.894
f__Piscirickettsiaceae	0.334	f__Marinicellaceae	1.226	f__Moraxellaceae	0.654
f__211ds20	0.162	f__Alteromonadaceae	0.668	f__Alteromonadaceae	0.604
		f__125ds10	0.546	f__125ds10	0.502
		f__Aeromonadaceae	0.413	f__HTCC2089	0.274
		f__HTCC2089	0.399	f__Legionellaceae	0.248
		f__Legionellaceae	0.177	f__HTCC2188	0.239
		f__Crenotrichaceae	0.148	f__Crenotrichaceae	0.106
		f__Chromatiaceae	0.131		
<b>p_Acidobacteria</b>	<b>GWS % of Phylum</b>	<b>p_Acidobacteria</b>	<b>RBS % of Phylum</b>	<b>p_Acidobacteria</b>	<b>PZS % of Phylum</b>
c__Chloracidobacteria	28.734	c__Chloracidobacteria	34.223	c__Chloracidobacteria	33.659
f__Unclassified	16.795	f__Ellin6075	21.949	f__Ellin6075	23.417
f__Ellin6075	11.938	f__Unclassified	12.274	f__Unclassified	10.242



c__Acidobacteria-6	54.426	c__Acidobacteria-6	32.994	c__Acidobacteria-6	37.981
f__mb2424	41.943	f__Unclassified	20.427	f__Unclassified	23.648
f__Unclassified	10.168	f__mb2424	7.054	f__mb2424	7.278
f__RB40	2.315	f__RB40	5.507	f__RB40	7.056
c__Holophagae	1.316	c__Holophagae	10.919	c__Holophagae	1.561
f__Holophagaceae	1.316	f__Holophagaceae	10.669	f__Holophagaceae	1.471
		f__Unclassified	0.249		
c__Sva0725	0.272	c__Sva0725	3.267	c__Sva0725	3.992
f__Unclassified	0.272	f__Unclassified	3.267	f__Unclassified	3.992
c__RB25	0.318	c__RB25	4.724	c__RB25	6.784
f__Unclassified	0.318	f__Unclassified	4.724	f__Unclassified	6.784
c__iii1-8	1.226	c__iii1-8	2.717	c__iii1-8	1.430
f__Unclassified	1.226	f__Unclassified	2.717	f__Unclassified	1.430
c__AT-s54	1.226	c__AT-s54	1.008	c__AT-s54	1.774
f__Unclassified	1.226	f__Unclassified	1.008	f__Unclassified	1.774
<b>p__Bacteroidetes</b>	<b>GWS % of Phylum</b>	<b>p__Bacteroidetes</b>	<b>RBS % of Phylum</b>	<b>p__Bacteroidetes</b>	<b>PZS % of Phylum</b>
c__Saprospirae	54.813	c__Saprospirae	52.803	c__Saprospirae	41.912
f__Saprospiraceae	45.558	f__Chitinophagaceae	36.950	f__Chitinophagaceae	27.282
f__Chitinophagaceae	9.255	f__Saprospiraceae	14.805	f__Saprospiraceae	13.812
		f__Unclassified	1.048	f__Unclassified	0.818
c__Sphingobacteriia	8.249	c__Sphingobacteriia	14.876	c__Sphingobacteriia	25.613
f__Unclassified	8.018	f__Unclassified	14.698	f__Unclassified	25.327
f__Sphingobacteriaceae	0.231	f__Sphingobacteriaceae	0.126	f__Sphingobacteriaceae	0.169
c__Cytophagia	9.503	c__Cytophagia	14.775	c__Cytophagia	21.380
f__Cytophagaceae	9.486	f__Cytophagaceae	14.484	f__Cytophagaceae	20.926
f__Cyclobacteriaceae	0.008	f__Amoebophilaceae	0.123	f__Flammeovirgaceae	0.281
				f__Amoebophilaceae	0.101
c__Flavobacteriia	17.694	c__Flavobacteriia	14.344	c__Flavobacteriia	9.002
f__Cryomorphaceae	14.237	f__Flavobacteriaceae	12.012	f__Cryomorphaceae	6.296
f__Flavobacteriaceae	3.440	f__Cryomorphaceae	2.281	f__Flavobacteriaceae	2.653

c__Bacteroidia	6.599	c__Bacteroidia	2.660	c__Bacteroidia	0.961
f__Unclassified	5.642	f__Unclassified	1.667	f__Unclassified	0.428
f__S24-7	0.685	f__Rikenellaceae	0.273	f__S24-7	0.311
f__VC21_Bac22	0.107	f__S24-7	0.264		
		f__Porphyromonadaceae	0.187		
		f__SB-1	0.126		
<b>p__Cyanobacteria</b>	GWS % of Phylum	<b>p__Cyanobacteria</b>	RBS % of Phylum	<b>p__Cyanobacteria</b>	PZS % of Phylum
c__Chloroplast	16.614	c__Chloroplast	89.501	c__Chloroplast	80.722
o__Stramenopiles	11.378	o__Stramenopiles	88.365	o__Stramenopiles	77.300
o__Streptophyta	4.843	o__Chlorophyta	0.864	o__Chlorophyta	2.237
o__Chlorophyta	0.394	o__Streptophyta	0.172	o__Streptophyta	0.664
				o__Cryptophyta	0.255
				o__UA01	0.166
f__Unclassified	16.614	f__Unclassified	88.863	f__Unclassified	79.116
		f__Chlamydomonadaceae	0.604	f__Chlamydomonadaceae	1.384
			0.034	f__Trebouxiophyceae	0.221
c__ML635J-21	82.087	c__ML635J-21	4.460	c__ML635J-21	8.703
f__Unclassified	82.087	f__Unclassified	4.460	f__Unclassified	8.703
c__4C0d-2	0.394	c__4C0d-2	3.549	c__4C0d-2	6.677
f__Unclassified	0.394	f__Unclassified	3.549	f__Unclassified	6.677
c__Synechococcophycideae	0.394	c__Synechococcophycideae	1.232	c__Synechococcophycideae	3.410
f__Synechococcaceae	0.394	f__Synechococcaceae	0.753	f__Synechococcaceae	3.200
		f__Unclassified	0.218	f__Unclassified	0.111
		f__Pseudanabaenaceae	0.168		
<b>p__Nitrospiraea</b>	GWS % of Phylum	<b>p__Nitrospiraea</b>	RBS % of Phylum	<b>p__Nitrospiraea</b>	PZS % of Phylum
c__Nitrospira	100.000	c__Nitrospira	100.000	c__Nitrospira	100.000
f__Nitrospiraceae	95.983	f__Nitrospiraceae	95.802	f__Nitrospiraceae	94.855
f__0319-6A21	0.057	f__0319-6A21	3.349	f__0319-6A21	2.491
f__Unclassified	2.942	f__Unclassified	0.000	f__Unclassified	2.226
f__Thermodesulfovibrionaceae	0.820	f__Thermodesulfovibrionaceae	0.554	f__Thermodesulfovibrionaceae	0.277
f__Leptospirillaceae	0.198	f__Leptospirillaceae	0.047		
		f__FW	0.248		

<b>p_Planctomycetes</b>	GWS % of Phylum	<b>p_Planctomycetes</b>	RBS % of Phylum	<b>p_Planctomycetes</b>	PZS % of Phylum
c_Planctomycetia	77.789	c_Planctomycetia	72.329	c_Planctomycetia	74.614
f_Planctomycetaceae	59.399	f_Gemmataceae	28.807	f_Gemmataceae	28.560
f_Gemmataceae	15.045	f_Pirellulaceae	27.892	f_Pirellulaceae	27.072
f_Pirellulaceae	2.623	f_Planctomycetaceae	13.418	f_Planctomycetaceae	16.021
f_Unclassified	0.713	f_Isosphaeraceae	1.402	f_Isosphaeraceae	2.345
		f_Unclassified	0.810	f_Unclassified	0.617
c_Phycisphaerae	1.359	c_Phycisphaerae	8.292	c_Phycisphaerae	7.373
f_Phycisphaeraceae	0.409	f_Unclassified	8.178	f_Unclassified	7.231
		f_Phycisphaeraceae	0.114	f_Phycisphaeraceae	0.141
c_OM190	4.999	c_OM190	7.244	c_OM190	7.591
f_Unclassified	4.999	f_Unclassified	7.244	f_Unclassified	7.591
c_BD7-11	8.164	c_BD7-11	1.937	c_BD7-11	2.864
f_Unclassified	8.164	f_Unclassified	1.937	f_Unclassified	2.864
c_vadinHA49	7.204	c_vadinHA49	3.052	c_vadinHA49	3.722
f_Unclassified	7.204	f_Unclassified	3.052	f_Unclassified	3.722
<b>p_Verrumicrobia</b>	GWS % of Phylum	<b>p_Verrumicrobia</b>	RBS % of Phylum	<b>p_Verrumicrobia</b>	PZS % of Phylum
c_Pedosphaerae	55.756	c_Pedosphaerae	46.661	c_Pedosphaerae	55.233
f_Ellin517	17.455	f_Unclassified	17.181	f_Unclassified	21.533
f_Unclassified	15.524	f_auto67_4W	15.751	f_auto67_4W	17.364
f_R4-41B	10.968	f_R4-41B	4.210	f_R4-41B	6.342
f_Ellin515	7.749	f_Ellin517	3.374	f_Ellin517	3.924
f_auto67_4W	2.426	f_Ellin515	2.304	f_Ellin515	2.412
f_Pedosphaeraceae	0.545	f_Pedosphaeraceae	1.735	f_Pedosphaeraceae	1.985
c_Spartobacteria	7.081	c_Spartobacteria	13.830	c_Spartobacteria	12.223
f_Chthoniobacteraceae	7.081	f_Chthoniobacteraceae	13.830	f_Chthoniobacteraceae	12.211
c_Verrucomicrobiae	5.447	c_Verrucomicrobiae	15.806	c_Verrucomicrobiae	12.729
f_Verrucomicrobiaceae	5.447	f_Verrucomicrobiaceae	15.806	f_Verrucomicrobiaceae	12.729
c_Opitutae	30.775	c_Opitutae	16.358	c_Opitutae	17.976
f_Opitutaceae	30.255	f_Opitutaceae	15.487	f_Opitutaceae	17.657

f__Cerasiococcaceae	0.396	f__Cerasiococcaceae	0.774	f__Cerasiococcaceae	0.242
f__Unclassified	0.124				
		c__Verruco-5	3.634	c__Verruco-5	1.689
		f__Unclassified	3.615	f__Unclassified	1.684
c__Methylacidiphilae	0.891	c__Methylacidiphilae	2.014	c__Methylacidiphilae	1.729
f__Unclassified	0.891	f__Unclassified	1.914	f__Unclassified	1.627
<b>p_Crenarchaeota</b>	GWS % of Phylum	<b>p_Crenarchaeota</b>	RBS % of Phylum	<b>p_Crenarchaeota</b>	PZS % of Phylum
c__Thaumarchaeota	100.000	c__Thaumarchaeota	100.000	c__Thaumarchaeota	99.974
f__Cenarchaeaceae	99.328	f__Cenarchaeaceae	98.328	f__Cenarchaeaceae	97.745
f__Nitrososphaeraceae	0.493	f__Nitrososphaeraceae	1.532	f__Nitrososphaeraceae	1.206
f__SAGMA-X	0.179	f__SAGMA-X	0.140	f__SAGMA-X	1.023

Table S6. Relative abundance of families within the major Proteobacterial classes and select non-Proteobacterial phyla in DCF. For a given sand type, the number of OTU hits for each family was summed across all water types and divided by the total number of hits for the corresponding phylum. Only families that comprised  $\geq 0.1\%$  of the phylum are shown. The notations p\_, c\_, o\_, and f\_ refer to phylum, class, order, and family, respectively.

Taxa	GWS % of Phylum	Taxa	RBS % of Phylum	Taxa	PZS % of Phylum
<b>p_Proteobacteria</b>		<b>p_Proteobacteria</b>		<b>p_Proteobacteria</b>	
c__Alphaproteobacteria	8.777	c__Alphaproteobacteria	24.927	c__Alphaproteobacteria	31.361
f__Unclassified	1.868	f__Unclassified	6.983	f__Unclassified	12.153
f__Hyphomicrobiaceae	1.526	f__Rhodobacteraceae	6.023	f__Sphingomonadaceae	4.906
f__Sphingomonadaceae	1.099	f__Sphingomonadaceae	5.376	f__Rhodobacteraceae	4.543
f__Phyllobacteriaceae	0.731	f__Hyphomicrobiaceae	2.560	f__Hyphomicrobiaceae	3.527
f__Rhodospirillaceae	0.729	f__Rhodospirillaceae	1.010	f__Rhodospirillaceae	2.250
f__Rhodobacteraceae	0.702	f__Hyphomonadaceae	0.787	f__Phyllobacteriaceae	0.915
f__Bradyrhizobiaceae	0.575	f__Caulobacteraceae	0.648	f__Caulobacteraceae	0.880
f__Caulobacteraceae	0.491	f__Phyllobacteriaceae	0.428	f__Bradyrhizobiaceae	0.817
f__Beijerinckiaceae	0.377	f__Bradyrhizobiaceae	0.331	f__Rhizobiaceae	0.336
f__Methylobacteriaceae	0.167	f__Acetobacteraceae	0.211	f__Hyphomonadaceae	0.333
f__Hyphomonadaceae	0.141	f__Rickettsiaceae	0.111	f__Erythrobacteraceae	0.193
f__Rhizobiaceae	0.134			f__Acetobacteraceae	0.192
c__Betaproteobacteria	56.867	c__Betaproteobacteria	26.499	c__Betaproteobacteria	36.519
f__Comamonadaceae	27.178	f__Comamonadaceae	10.821	f__Comamonadaceae	12.791
f__Methylophilaceae	19.440	f__Unclassified	8.704	f__Methylophilaceae	11.614
f__Rhodocyclaceae	5.270	f__Rhodocyclaceae	2.288	f__Unclassified	6.287
f__Oxalobacteraceae	3.590	f__Methylophilaceae	1.716	f__Rhodocyclaceae	2.594
f__Unclassified	0.728	f__Oxalobacteraceae	1.392	f__Oxalobacteraceae	2.156
f__Hydrogenophilaceae	0.456	f__Alcaligenaceae	0.778	f__Alcaligenaceae	0.270
f__Neisseriaceae	0.109	f__Neisseriaceae	0.166	f__Nitrosomonadaceae	0.188
				f__Neisseriaceae	0.186
				f__Hydrogenophilaceae	0.142
c__Deltaproteobacteria	3.014	c__Deltaproteobacteria	14.104	c__Deltaproteobacteria	7.807
f__OM27	1.586	f__Unclassified	6.188	f__Unclassified	3.133
f__Bdellovibrionaceae	0.787	f__Geobacteraceae	1.556	f__Syntrophobacteraceae	1.249
f__Unclassified	0.558	f__Syntrophobacteraceae	1.472	f__Haliangiaceae	0.626
		f__OM27	0.750	f__Nannocystaceae	0.495

		f__Polyangiaceae	0.633	f__OM27	0.470
		f__Myxococcaceae	0.561	f__Bdellovibrionaceae	0.408
		f__Haliangiaceae	0.552	f__JTB38	0.274
		f__JTB38	0.416	f__Bacteriovoracaceae	0.184
		f__Nannocystaceae	0.311	f__Myxococcaceae	0.176
		f__Bdellovibrionaceae	0.305	f__Geobacteraceae	0.140
		f__Desulfobulbaceae	0.250	f__Polyangiaceae	0.136
		f__Desulfuromonadaceae	0.211	f__MND4	0.122
		f__Bacteriovoracaceae	0.186		
		f__Desulfobacteraceae	0.178		
		f__MND4	0.147		
		f__Syntrophaceae	0.144		
c__Gammaproteobacteria	31.310	c__Gammaproteobacteria	33.941	c__Gammaproteobacteria	24.021
f__Pseudomonadaceae	26.094	f__Xanthomonadaceae	13.810	f__Pseudomonadaceae	3.857
f__Legionellaceae	1.561	f__Sinobacteraceae	5.302	f__Unclassified	2.985
f__Coxiellaceae	0.824	f__Unclassified	4.253	f__Sinobacteraceae	2.898
f__Sinobacteraceae	0.683	f__Coxiellaceae	3.184	f__Xanthomonadaceae	2.724
f__Unclassified	0.659	f__Piscirickettsiaceae	2.000	f__Moraxellaceae	2.318
f__Moraxellaceae	0.554	f__OM60	1.135	f__Coxiellaceae	1.905
f__Alteromonadaceae	0.355	f__Marinicellaceae	1.055	f__Alteromonadaceae	1.264
f__Oleiphilaceae	0.228	f__Pseudomonadaceae	0.937	f__Piscirickettsiaceae	1.074
f__Chromatiaceae	0.162	f__HTCC2089	0.479	f__Legionellaceae	0.833
		f__Legionellaceae	0.412	f__Marinicellaceae	0.766
		f__Crenotrichaceae	0.315	f__HTCC2188	0.568
		f__125ds10	0.310	f__Colwelliaceae	0.504
		f__Moraxellaceae	0.205	f__Crenotrichaceae	0.424
		f__Chromatiaceae	0.134	f__125ds10	0.415
		f__Alteromonadaceae	0.116	f__Ectothiorhodospiraceae	0.399
				f__OM60	0.296
				f__HTCC2089	0.199
				f__Methylococcaceae	0.177
<b>p_Acidobacteria</b>	GWS % of Phylum	<b>p_Acidobacteria</b>	RBS % of Phylum	<b>p_Acidobacteria</b>	PZS % of Phylum
c__Chloracidobacteria	19.055	c__Chloracidobacteria	38.590	c__Chloracidobacteria	26.250
f__Ellin6075	15.773	f__Ellin6075	33.469	f__Ellin6075	22.928
f__Unclassified	3.283	f__Unclassified	5.115	f__Unclassified	3.315

c__Acidobacteria-6	75.661	c__Acidobacteria-6	39.903	c__Acidobacteria-6	51.451
f__mb2424	62.503	f__Unclassified	23.386	f__Unclassified	31.995
f__Unclassified	12.597	f__mb2424	9.061	f__mb2424	11.779
f__RB40	0.560	f__RB40	7.456	f__RB40	7.677
c__Holophagae	0.587	c__Holophagae	5.004	c__Holophagae	1.811
f__Holophagaceae	0.587	f__Holophagaceae	4.907	f__Holophagaceae	1.803
c__Sva0725	0.107	c__Sva0725	2.445	c__Sva0725	3.538
f__Unclassified	0.107	f__Unclassified	2.445	f__Unclassified	3.538
c__RB25	0.347	c__RB25	2.703	c__RB25	5.548
f__Unclassified	0.347	f__Unclassified	2.703	f__Unclassified	5.548
c__iii1-8	0.107	c__iii1-8	4.328	c__iii1-8	2.008
f__Unclassified	0.107	f__Unclassified	4.328	f__Unclassified	2.008
c__AT-s54	0.187	c__AT-s54	3.013	c__AT-s54	2.135
f__Unclassified	0.187	f__Unclassified	3.013	f__Unclassified	2.135
<b>p__Bacteroidetes</b>	GWS % of Phylum	<b>p__Bacteroidetes</b>	RBS % of Phylum	<b>p__Bacteroidetes</b>	PZS % of Phylum
c__Saprospirae	3.259	c__Saprospirae	38.642	c__Saprospirae	25.135
f__Chitinophagaceae	2.392	f__Chitinophagaceae	25.800	f__Chitinophagaceae	19.740
f__Saprospiraceae	0.867	f__Saprospiraceae	11.929	f__Saprospiraceae	4.833
		f__Unclassified	0.912	f__Unclassified	0.562
c__Bacteroidia	0.186	c__Bacteroidia	2.034	c__Bacteroidia	0.560
f__S24-7	0.110	f__Unclassified	1.641	f__Unclassified	0.483
		f__SB-1	0.165		
c__BME43		c__BME43	0.336	c__BME43	
		f__Unclassified	0.336		
c__Cytophagia	0.905	c__Cytophagia	15.801	c__Cytophagia	14.494
f__Cytophagaceae	0.905	f__Cytophagaceae	15.354	f__Cytophagaceae	14.337
		f__Flammeovirgaceae	0.252		
		f__Amoebophilaceae	0.103		

c__Flavobacteriia	91.760	c__Flavobacteriia	30.164	c__Flavobacteriia	49.247
f__Flavobacteriaceae	88.526	f__Flavobacteriaceae	28.085	f__Flavobacteriaceae	45.549
f__Cryomorphaceae	3.235	f__Cryomorphaceae	2.060	f__Cryomorphaceae	3.693
c__Sphingobacteriia	2.821	c__Sphingobacteriia	12.702	c__Sphingobacteriia	10.044
f__Unclassified	2.684	f__Unclassified	12.597	f__Unclassified	9.914
f__Sphingobacteriaceae	0.137	f__Sphingobacteriaceae	0.105	f__Sphingobacteriaceae	0.130
		c__VC2_1_Bac22	0.129		
		f__Unclassified	0.129		
<b>p_Cyanobacteria</b>	GWS % of Phylum	<b>p_Cyanobacteria</b>	RBS % of Phylum	<b>p_Cyanobacteria</b>	PZS % of Phylum
c__Chloroplast	6.150	c__Chloroplast	94.874	c__Chloroplast	83.913
o__Stramenopiles	4.513	o__Stramenopiles	93.952	o__Stramenopiles	81.304
o__Streptophyta	1.548	o__Chlorophyta	0.509	o__Chlorophyta	1.901
		o__Streptophyta	0.342	o__Streptophyta	0.397
f__Unclassified	6.061	f__Unclassified	94.442	f__Unclassified	82.264
f__Chlamydomonadaceae	0.088	f__Chlamydomonadaceae	0.301	f__Chlamydomonadaceae	0.896
		f__Trebouxiophyceae	0.129	f__Trebouxiophyceae	0.751
c__ML635J-21	93.584	c__ML635J-21	2.640	c__ML635J-21	3.713
f__Unclassified	93.584	f__Unclassified	2.640	f__Unclassified	3.713
c__4C0d-2	0.176	c__4C0d-2	0.509	c__4C0d-2	8.071
f__Unclassified	0.176	f__Unclassified	0.509	f__Unclassified	8.071
		c__Synechococcophycideae	1.133	c__Synechococcophycideae	3.833
		f__Synechococcaceae	0.765	f__Synechococcaceae	3.593
		f__Chamaesiphonaceae	0.200	f__Pseudanabaenaceae	0.157
		f__Pseudanabaenaceae	0.115		
<b>p_Nitrospiraea</b>	GWS % of Phylum	<b>p_Nitrospiraea</b>	RBS % of Phylum	<b>p_Nitrospiraea</b>	PZS % of Phylum
c__Nitrospira	100.000	c__Nitrospira	100.000	c__Nitrospira	100.000
f__Nitrospiraceae	98.972	f__Nitrospiraceae	92.435	f__Nitrospiraceae	94.491
f__Unclassified	0.673	f__Thermodesulfovibrionaceae	3.603	f__0319-6A21	4.503
f__0319-6A21	0.337	f__0319-6A21	3.430	f__Thermodesulfovibrionaceae	0.711
		f__FW	0.519	f__Leptospirillaceae	0.134



<b>p_Planctomycetes</b>	GWS % of Phylum	<b>p_Planctomycetes</b>	RBS % of Phylum	<b>p_Planctomycetes</b>	PZS % of Phylum
c__Planctomycetia	87.615	c__Planctomycetia	86.321	c__Planctomycetia	81.278
f__Planctomycetaceae	62.160	f__Gemmataceae	32.375	f__Gemmataceae	32.886
f__Gemmataceae	23.707	f__Pirellulaceae	30.186	f__Pirellulaceae	24.020
f__Pirellulaceae	1.277	f__Planctomycetaceae	19.411	f__Planctomycetaceae	19.787
f__Unclassified	0.296	f__Isosphaeraceae	3.806	f__Isosphaeraceae	4.191
f__Isosphaeraceae	0.174	f__Unclassified	0.543	f__Unclassified	0.394
c__Phycisphaerae	1.696	c__Phycisphaerae	4.520	c__Phycisphaerae	4.015
f__Phycisphaeraceae	1.594	f__Unclassified	4.480	f__Unclassified	3.977
f__Unclassified	0.102				
c__OM190	9.575	c__OM190	4.275	c__OM190	8.080
f__Unclassified	9.575	f__Unclassified	4.275	f__Unclassified	8.080
c__BD7-11	0.674	c__BD7-11	0.443	c__BD7-11	1.943
f__Unclassified	0.674	f__Unclassified	0.443	f__Unclassified	1.943
c__vadinHA49	0.102	c__vadinHA49	2.220	c__vadinHA49	2.655
f__Unclassified	0.102	f__Unclassified	2.220	f__Unclassified	2.655
<b>p_Verrumicrobia</b>	GWS % of Phylum	<b>p_Verrumicrobia</b>	RBS % of Phylum	<b>p_Verrumicrobia</b>	PZS % of Phylum
c__Pedosphaerae	84.460	c__Pedosphaerae	28.738	c__Pedosphaerae	56.901
f__Ellin517	60.278	f__auto67_4W	13.156	f__Unclassified	18.968
f__R4-41B	14.969	f__Unclassified	6.912	f__auto67_4W	18.620
f__Unclassified	5.710	f__R4-41B	5.389	f__R4-41B	6.868
f__Pedosphaeraceae	0.802	f__Ellin515	1.805	f__Ellin517	6.269
f__auto67_4W	0.432	f__Ellin517	0.501	f__Ellin515	1.725
		f__Pedosphaeraceae	0.216	f__Pedosphaeraceae	0.483
c__Spartobacteria	2.114	c__Spartobacteria	12.169	c__Spartobacteria	8.017
f__Chthoniobacteraceae	2.114	f__Chthoniobacteraceae	12.162	f__Chthoniobacteraceae	8.017
c__Verrucomicrobiae	2.407	c__Verrucomicrobiae	50.963	c__Verrucomicrobiae	21.837
f__Verrucomicrobiaceae	2.407	f__Verrucomicrobiaceae	50.963	f__Verrucomicrobiaceae	21.837
c__Opitutae	10.988	c__Opitutae	5.495	c__Opitutae	8.750
f__Cerasiococcaceae	6.049	f__Opitutaceae	5.398	f__Opitutaceae	7.671
f__Opitutaceae	4.877			f__Cerasiococcaceae	1.032

		c__Verruco-5	1.427	c__Verruco-5	1.535
		f__Unclassified	1.423	f__Unclassified	1.522
		c__Methylacidiphilae	0.529	c__Methylacidiphilae	1.505
		f__Unclassified	0.525	f__Unclassified	1.462
<b>p_Crenarchaeota</b>	GWS % of Phylum	<b>p_Crenarchaeota</b>	RBS % of Phylum	<b>p_Crenarchaeota</b>	PZS % of Phylum
c__Thaumarchaeota	100.000	c__Thaumarchaeota	99.693	c__Thaumarchaeota	99.974
f__Cenarchaeaceae	82.768	f__Cenarchaeaceae	54.506	f__Cenarchaeaceae	91.898
f__Nitrososphaeraceae	14.883	f__Nitrososphaeraceae	45.126	f__Nitrososphaeraceae	4.102
f__SAGMA-X	2.350			f__SAGMA-X	3.859
				f__Unclassified	0.115