

Electronic Supplementary Information for

When chicken manure compost meets iron nanoparticles: an implication for the remediation of chlorophenothane-polluted riverine sediment

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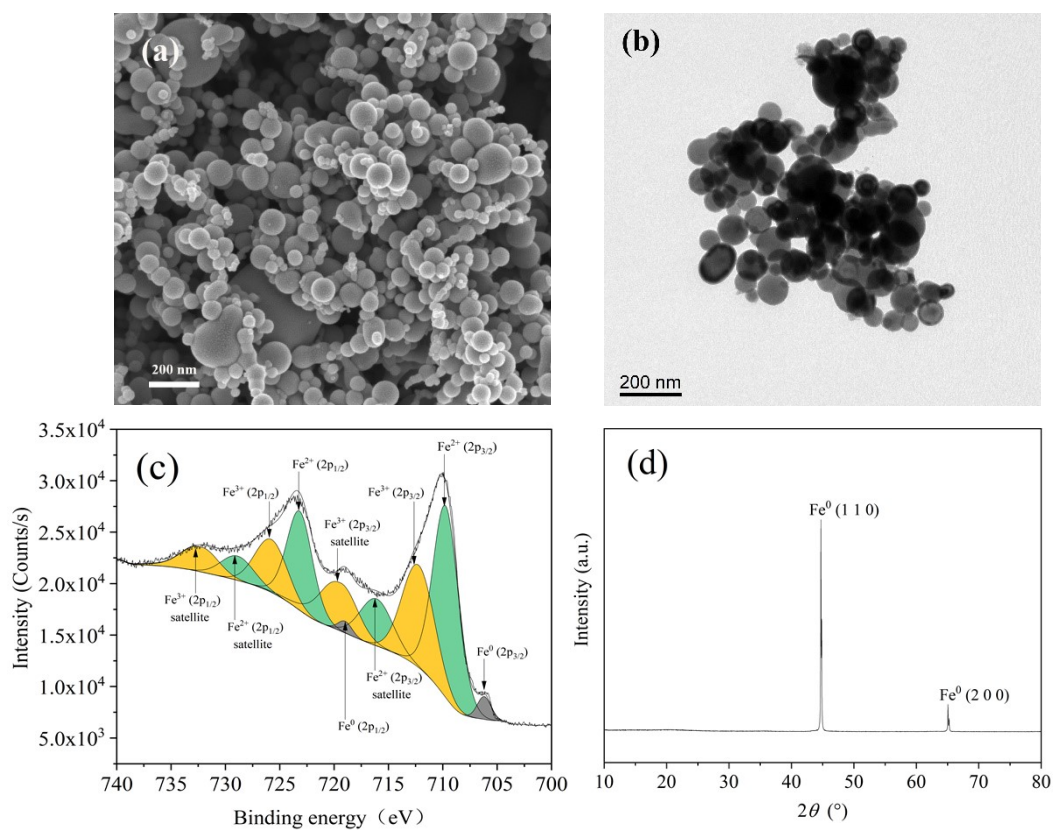


Fig. S1. Scanning (a) and transmission (b) electron microscope images, Fe 2p XPS spectrum (c), and X-ray diffraction spectrum (d) of the used nZVI in this study.

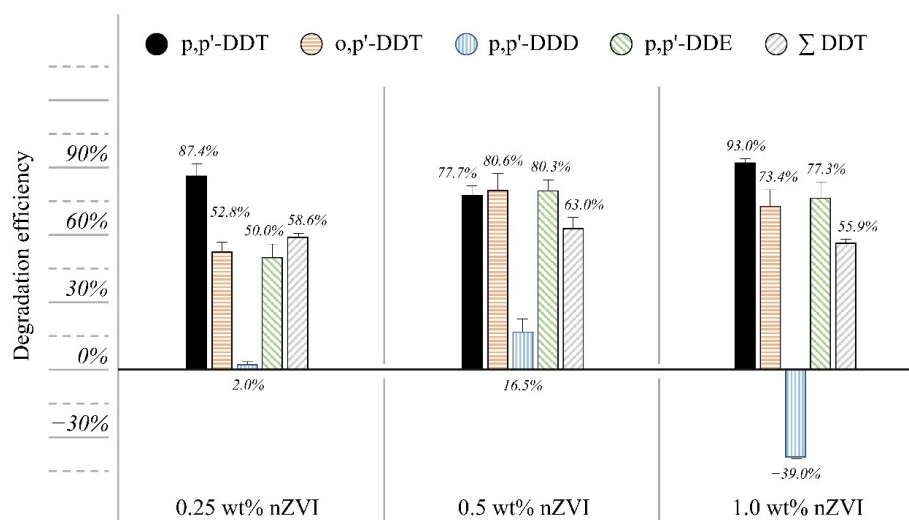


Fig. S2. Degradation of chlorophenothane in sediments by adding different amount of nZVI. Experimental conditions: adding 0.25 wt%, 0.5 wt%, or 1.0 wt% of nZVI at the beginning of remediation, treatment time = 30 days.

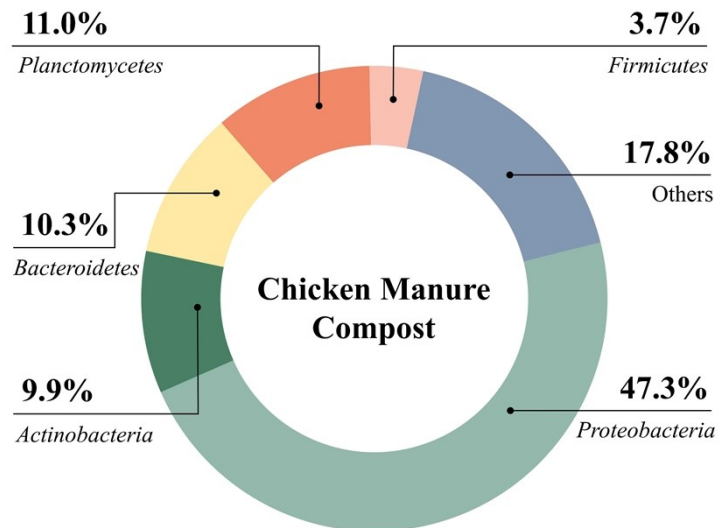


Fig. S3. Relative abundance of bacterial species at phylum level in the used chicken manure compost.

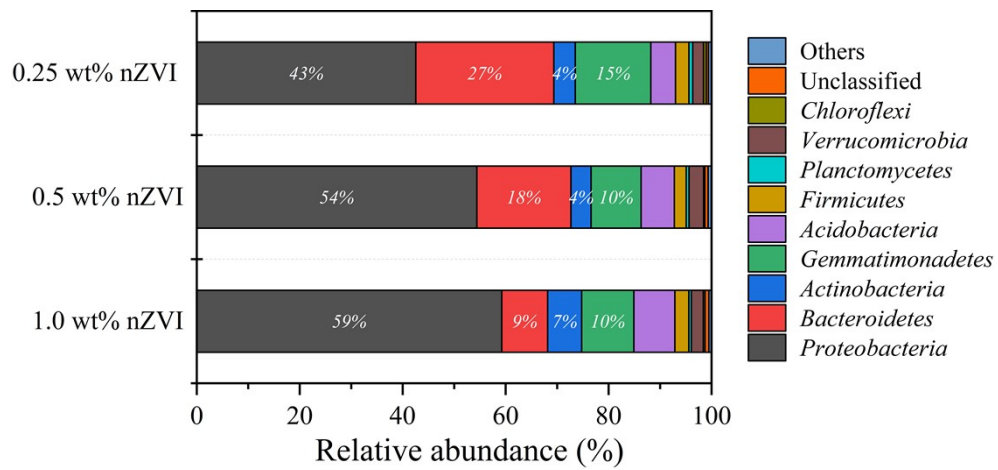


Fig. S4. Relative abundance of bacterial species at phylum level in sediments treated with different amount of nZVI.

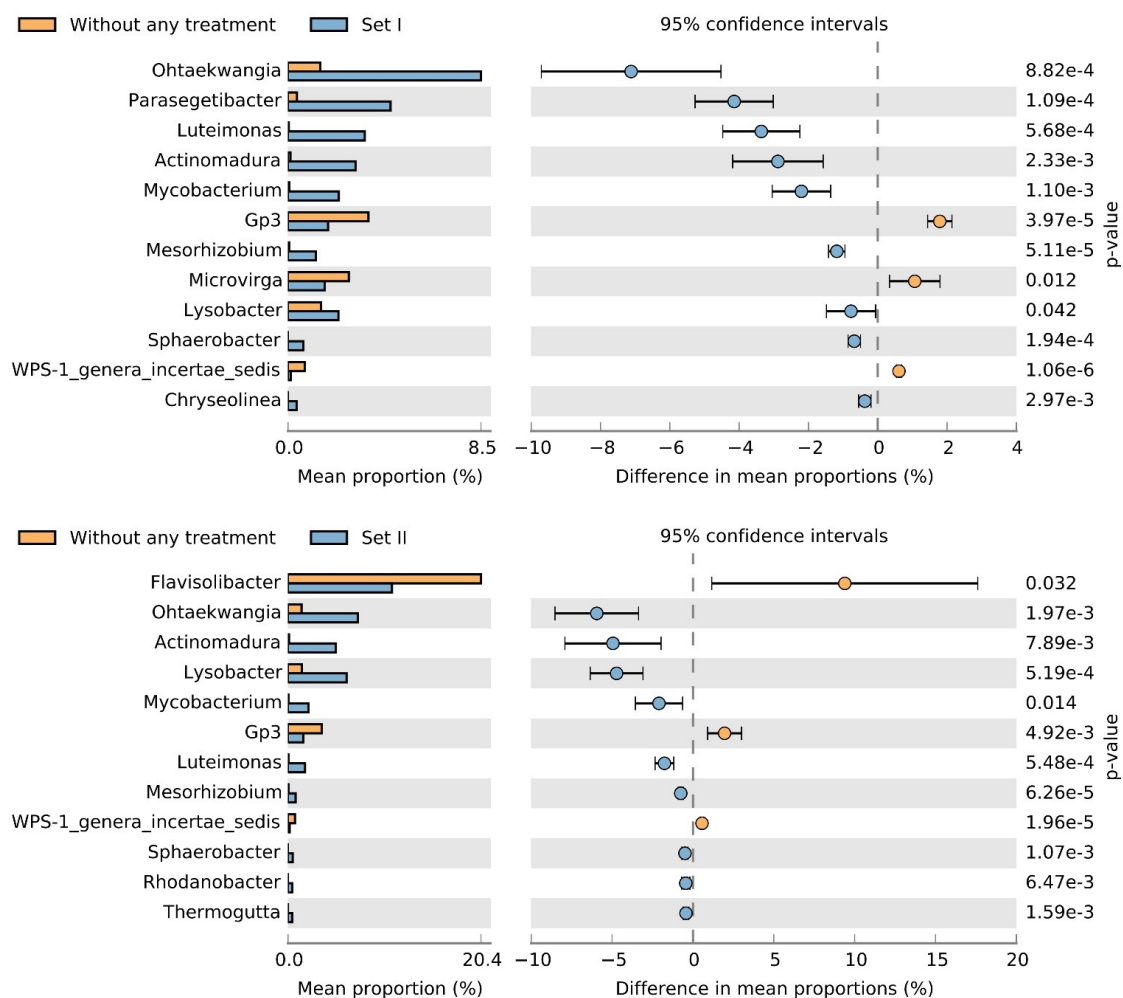


Fig. S5. The comparison of sediment bacterial genera with significant differences ($P < 0.05$) between the Set I or Set II group and the control group. In the analysis, the unclassified reads of the results were removed and only the top 12 bacterial genera based on the effect size were displayed for concise presentation.

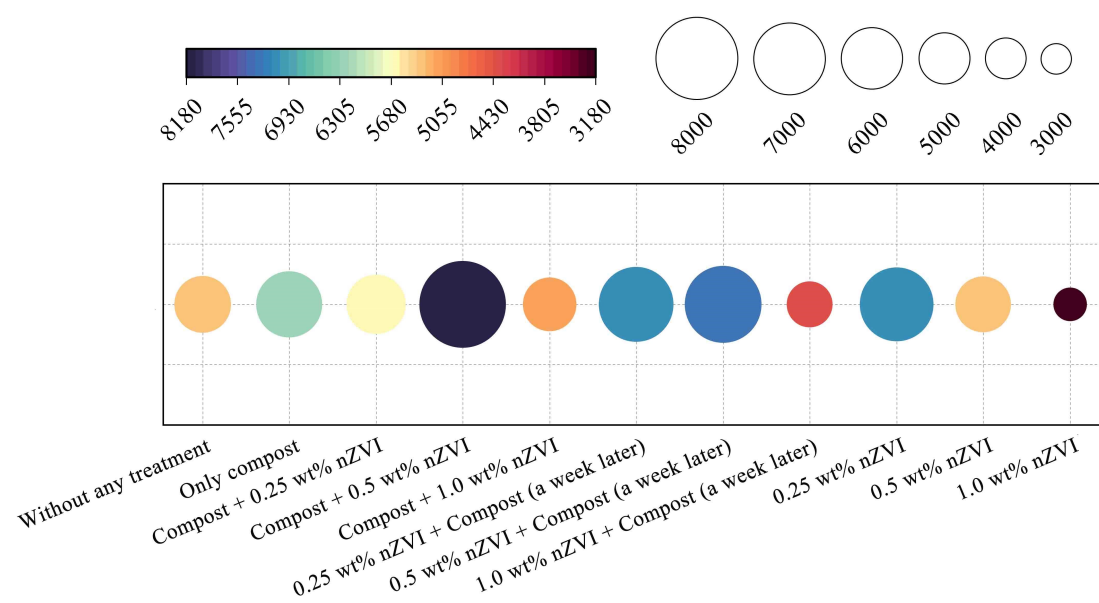


Fig. S6. The abundance differences in the function concerning DDT degradation between different treatment groups. Circle size and colors indicate the functional abundance according to the legends on the top.

Table S1

Significantly different bacterial taxa between the control without any treatment and the sediment remediated with only compost.

Phylum	Class	Order	Family	Genus	<i>P</i> -value	Difference in mean proportions (%)
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Actinomycetales</i>	<i>Thermomonosporaceae</i>	<i>Actinomadura</i>	0.039	−3.310
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Xanthomonadales</i>	<i>Xanthomonadaceae</i>	<i>Luteimonas</i>	0.024	−2.750
<i>Bacteroidetes</i>	<i>Sphingobacteriia</i>	<i>Sphingobacteriales</i>	<i>Chitinophagaceae</i>	<i>Parasegetibacter</i>	0.039	−2.496
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Rhizobiales</i>	<i>Methylobacteriaceae</i>	<i>Microvirga</i>	0.018	2.032
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Rhizobiales</i>	<i>Phyllobacteriaceae</i>	<i>Mesorhizobium</i>	0.018	−0.924
<i>Chloroflexi</i>	<i>Thermomicrobia</i>	<i>Sphaerobacterales</i>	<i>Sphaerobacteraceae</i>	<i>Sphaerobacter</i>	0.027	−0.738
<i>Acidobacteria</i>	<i>Acidobacteria_Gp7</i>	<i>norank_Acidobacteria_Gp7</i>	<i>norank_Acidobacteria_Gp7</i>	<i>Gp7</i>	0.048	−0.546
<i>Proteobacteria</i>	<i>Betaproteobacteria</i>	<i>Burkholderiales</i>	<i>Comamonadaceae</i>	<i>Ramlibacter</i>	0.020	−0.541
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Rhizobiales</i>	<i>Hyphomicrobiaceae</i>	<i>Hyphomicrobium</i>	0.026	−0.314
<i>Acidobacteria</i>	<i>Acidobacteria_Gp4</i>	<i>norank_Acidobacteria_Gp4</i>	<i>norank_Acidobacteria_Gp4</i>	<i>Aridibacter</i>	0.036	−0.246
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Acidimicrobiales</i>	<i>Acidimicrobiaceae</i>	<i>Ilumatobacter</i>	0.035	−0.160
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Rhizobiales</i>	<i>Hyphomicrobiaceae</i>	<i>Devosia</i>	0.012	−0.121

Table S2

Significantly different bacterial taxa between the control without any treatment and the sediment remediated with only nZVI.

Phylum	Class	Order	Family	Genus	P-value	Difference in mean proportions (%)
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Xanthomonadales</i>	<i>Xanthomonadaceae</i>	<i>Lysobacter</i>	0.001	−5.257
<i>Proteobacteria</i>	<i>Betaproteobacteria</i>	<i>Burkholderiales</i>	<i>Comamonadaceae</i>	<i>Ramlibacter</i>	0.015	−2.708
<i>Verrucomicrobia</i>	<i>Subdivision3</i>	<i>norank_Subdivision3</i>	<i>norank_Subdivision3</i>	<i>Subdivision3_gen era_incertae_sedi s</i>	0.009	−2.189
<i>Acidobacteria</i>	<i>Acidobacteria_Gp3</i>	<i>norank_Acidobacteria_Gp3</i>	<i>norank_Acidobacteria_Gp3</i>	<i>Gp3</i>	0.010	−1.601
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Rhizobiales</i>	<i>Methylobacteriaceae</i>	<i>Microvirga</i>	0.004	1.166
<i>Proteobacteria</i>	<i>Betaproteobacteria</i>	<i>Burkholderiales</i>	<i>Burkholderiaceae</i>	<i>Ralstonia</i>	0.035	−1.098
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Caulobacterales</i>	<i>Caulobacteraceae</i>	<i>Phenylobacterium</i>	0.037	−0.979
<i>Acidobacteria</i>	<i>Acidobacteria_Gp6</i>	<i>norank_Acidobacteria_Gp6</i>	<i>norank_Acidobacteria_Gp6</i>	<i>Gp6</i>	0.005	−0.902
<i>Bacteroidetes</i>	<i>Cytophagia</i>	<i>Cytophagales</i>	<i>norank_Cytophagales</i>	<i>Ohtaekwangia</i>	0.009	−0.768
<i>Acidobacteria</i>	<i>Acidobacteria_Gp4</i>	<i>norank_Acidobacteria_Gp4</i>	<i>norank_Acidobacteria_Gp4</i>	<i>Aridibacter</i>	0.003	−0.608
<i>candidate_division_WPS-1</i>	<i>norank_candidate_division_WPS-1</i>	<i>norank_candidate_division_WPS-1</i>	<i>norank_candidate_division_WPS-1</i>	<i>WPS- I_genera_incertae_sedis</i>	< 0.001	0.512
<i>Bacteroidetes</i>	<i>Sphingobacteriia</i>	<i>Sphingobacteriales</i>	<i>Chitinophagaceae</i>	<i>Flaviumibacter</i>	0.034	−0.413

Table S3

Significantly different bacterial taxa between the control without any treatment and the sediments of Set I.

Phylum	Class	Order	Family	Genus	<i>P</i> -value	Difference in mean proportions (%)
<i>Bacteroidetes</i>	<i>Cytophagia</i>	<i>Cytophagales</i>	<i>norank_Cytophagales</i>	<i>Ohtaekwangia</i>	0.001	−7.117
<i>Bacteroidetes</i>	<i>Sphingobacteriia</i>	<i>Sphingobacteriales</i>	<i>Chitinophagaceae</i>	<i>Parasegetibacter</i>	< 0.001	−4.143
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Xanthomonadales</i>	<i>Xanthomonadaceae</i>	<i>Luteimonas</i>	0.001	−3.361
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Actinomycetales</i>	<i>Thermomonosporaceae</i>	<i>Actinomadura</i>	0.002	−2.882
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Actinomycetales</i>	<i>Mycobacteriaceae</i>	<i>Mycobacterium</i>	0.001	−2.203
<i>Acidobacteria</i>	<i>Acidobacteria_Gp3</i>	<i>norank_Acidobacteria_Gp3</i>	<i>norank_Acidobacteria_Gp3</i>	<i>Gp3</i>	< 0.001	1.790
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Rhizobiales</i>	<i>Phyllobacteriaceae</i>	<i>Mesorhizobium</i>	< 0.001	−1.183
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Rhizobiales</i>	<i>Methylobacteriaceae</i>	<i>Microvirga</i>	0.012	1.067
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Xanthomonadales</i>	<i>Xanthomonadaceae</i>	<i>Lysobacter</i>	0.042	−0.771
<i>Chloroflexi</i>	<i>Thermomicrobia</i>	<i>Sphaerobacterales</i>	<i>Sphaerobacteraceae</i>	<i>Sphaerobacter</i>	< 0.001	−0.678
<i>candidate_division_WPS-1</i>	<i>norank_candidate_division_WPS-1</i>	<i>norank_candidate_division_WPS-1</i>	<i>norank_candidate_division_WPS-1</i>	<i>WPS-1_genera_incertae_sedis</i>	< 0.001	0.612
<i>Bacteroidetes</i>	<i>Cytophagia</i>	<i>Cytophagales</i>	<i>norank_Cytophagales</i>	<i>Chryseolinea</i>	0.003	−0.374

Table S4

Significantly different bacterial taxa between the control without any treatment and the sediments of Set II.

Phylum	Class	Order	Family	Genus	P-value	Difference in mean proportions (%)
<i>Bacteroidetes</i>	<i>Sphingobacteriia</i>	<i>Sphingobacteriales</i>	<i>Chitinophagaceae</i>	<i>Flavisolibacter</i>	0.032	9.388
<i>Bacteroidetes</i>	<i>Cytophagia</i>	<i>Cytophagales</i>	<i>norank_Cytophagales</i>	<i>Ohtaekwangia</i>	0.002	-5.945
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Actinomycetales</i>	<i>Thermomonosporaceae</i>	<i>Actinomadura</i>	0.008	-4.944
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Xanthomonadales</i>	<i>Xanthomonadaceae</i>	<i>Lysobacter</i>	0.001	-4.720
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Actinomycetales</i>	<i>Mycobacteriaceae</i>	<i>Mycobacterium</i>	0.014	-2.101
<i>Acidobacteria</i>	<i>Acidobacteria_Gp3</i>	<i>norank_Acidobacteria_Gp3</i>	<i>norank_Acidobacteria_Gp3</i>	<i>Gp3</i>	0.005	1.956
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Xanthomonadales</i>	<i>Xanthomonadaceae</i>	<i>Luteimonas</i>	0.001	-1.761
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Rhizobiales</i>	<i>Phyllobacteriaceae</i>	<i>Mesorhizobium</i>	< 0.001	-0.752
<i>candidate_division_WPS-1</i>	<i>norank_candidate_division_WPS-1</i>	<i>norank_candidate_division_WPS-1</i>	<i>norank_candidate_division_WPS-1</i>	<i>WPS-1_genera_incertae_sedis</i>	< 0.001	0.562
<i>Chloroflexi</i>	<i>Thermomicrobia</i>	<i>Sphaerobacterales</i>	<i>Sphaerobacteraceae</i>	<i>Sphaerobacter</i>	0.001	-0.493
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Xanthomonadales</i>	<i>Xanthomonadaceae</i>	<i>Rhodanobacter</i>	0.006	-0.442
<i>Planctomycetes</i>	<i>Planctomycetia</i>	<i>Planctomycetales</i>	<i>Planctomycetaceae</i>	<i>Thermogutta</i>	0.002	-0.428

Table S5

Significantly different bacterial taxa between the sediments of Set I and Set II.

Phylum	Class	Order	Family	Genus	<i>P</i> -value	Difference in mean proportions (%)
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Sphingomonadales</i>	<i>Sphingomonadaceae</i>	<i>Sphingomonas</i>	0.030	−4.910
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Xanthomonadales</i>	<i>Xanthomonadaceae</i>	<i>Lysobacter</i>	0.001	−3.948
<i>Bacteroidetes</i>	<i>Sphingobacteriia</i>	<i>Sphingobacteriales</i>	<i>Chitinophagaceae</i>	<i>Parasegetibacter</i>	< 0.001	3.526
<i>Proteobacteria</i>	<i>Betaproteobacteria</i>	<i>Burkholderiales</i>	<i>Burkholderiaceae</i>	<i>Cupriavidus</i>	0.009	2.831
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Xanthomonadales</i>	<i>Xanthomonadaceae</i>	<i>Luteimonas</i>	0.012	1.600
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Rhizobiales</i>	<i>Methylobacteriaceae</i>	<i>Microvirga</i>	0.037	−0.872
<i>Bacteroidetes</i>	<i>Sphingobacteriia</i>	<i>Sphingobacteriales</i>	<i>Chitinophagaceae</i>	<i>Flaviumibacter</i>	0.003	−0.587
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Actinomycetales</i>	<i>Micromonosporaceae</i>	<i>Micromonospora</i>	0.036	−0.561
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Rhizobiales</i>	<i>Phyllobacteriaceae</i>	<i>Mesorhizobium</i>	0.004	0.431
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Actinomycetales</i>	<i>Microbacteriaceae</i>	<i>Agromyces</i>	0.048	−0.298
<i>Bacteroidetes</i>	<i>Cytophagia</i>	<i>Cytophagales</i>	<i>norank_Cytophagales</i>	<i>Chryseolinea</i>	0.013	0.254
<i>Proteobacteria</i>	<i>Betaproteobacteria</i>	<i>Nitrosomonadales</i>	<i>Nitrosomonadaceae</i>	<i>Nitrosospira</i>	0.001	0.196