

Microscale distributions of freshwater planktonic viruses and prokaryotes are patchy and taxonomically distinct

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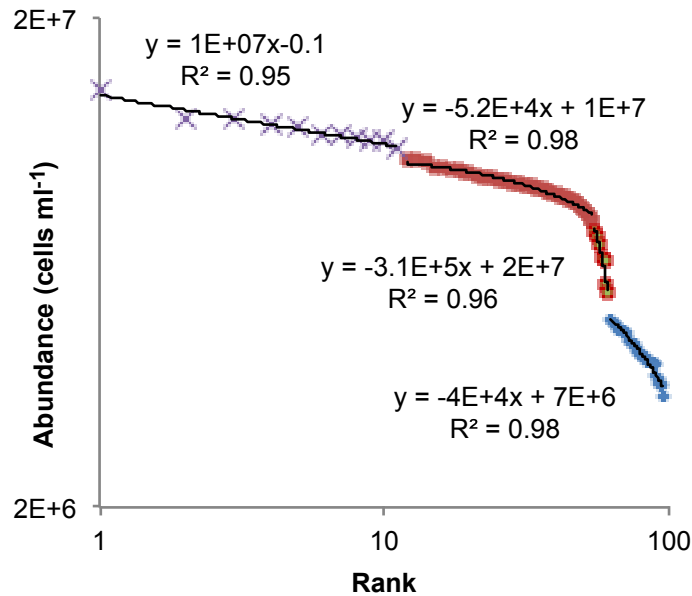


Fig. S1. Representative rank abundance graph used for hotspot, background and coldspot determination. Hotspot, background and coldspot samples are indicated by crosses, squares and diamonds.

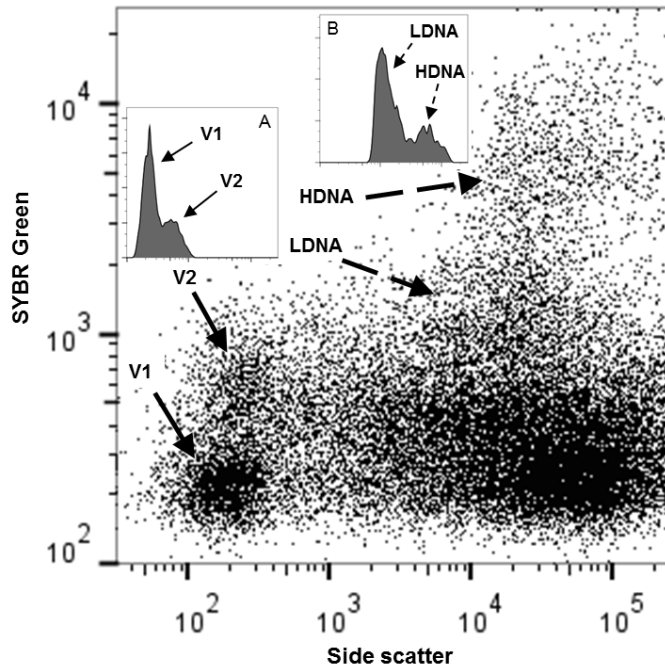


Fig. S2. Flow cytometric determination of bacterial and viral subpopulations in biparametric cytogram of SYBR Green fluorescence vs. side scatter (size) showing the presence of prokaryotic (LDNA and HDNA) and viral (V1 and V2) subpopulations. Inset are the corresponding histograms showing the **A** viral and **B** bacterial subpopulations via discrete peaks.

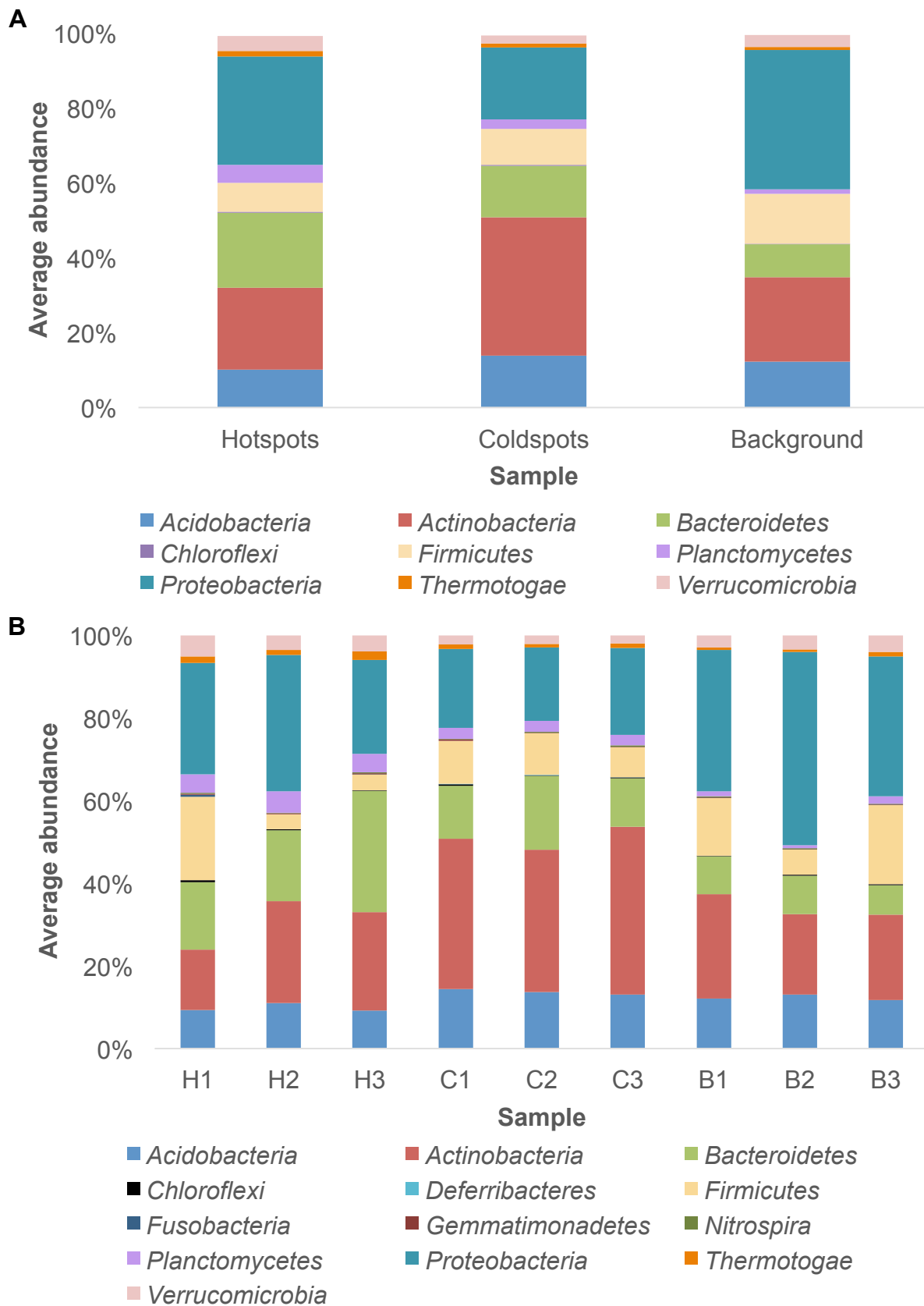


Fig. S3. A Averaged phylogenetic profiles of hotspot (n = 20), coldspot (n = 20) and background (n = 20) samples. **B** Phylogenetic profiles of individual background, coldspot and hotspot samples. For clarity, phyla representing < 0.1% average abundance were omitted.

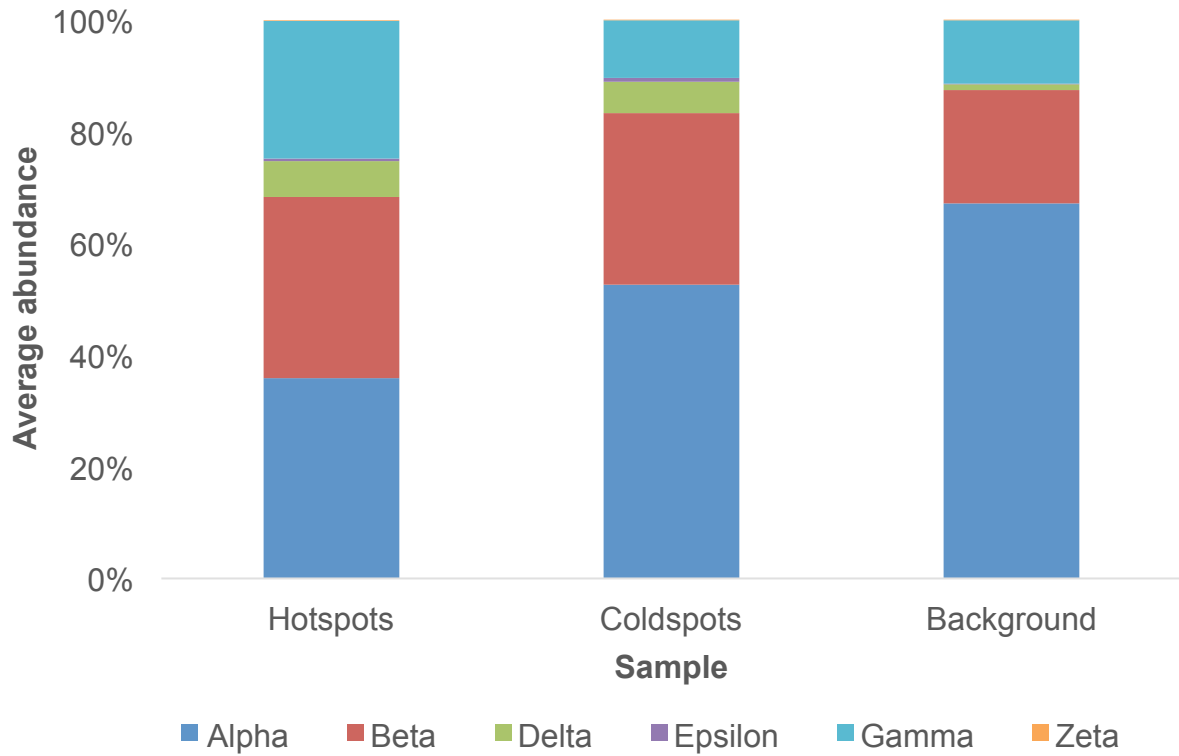


Fig. S4. Average abundance of *Proteobacteria* at the class level in averaged hotspot (n = 20), coldspot (n = 20) and background (n = 20) samples.

Table S1. Pearson correlation results and corresponding r^2 and p-values for the significantly correlated single vertical profiles of prokaryotic and viral subpopulations.

Subpopulations	Vertical profile	r^2	p-value
V1 and V2	1	0.98	< 0.0001
	2	0.99	< 0.0001
	3	0.94	< 0.0001
	4	0.97	< 0.0001
	5	0.99	< 0.0001
	6	0.96	< 0.0001
	7	0.99	< 0.0001
	8	0.97	< 0.0001
LDNA and HDNA	1	0.72	0.01
	2	0.89	< 0.0001
	6	0.73	0.01
	8	0.91	< 0.0001
V1 and LDNA	All 8 vertical profiles were not significantly correlated		
V1 and HDNA			
V2 and LDNA			
V2 and HDNA			
Total virus and prokaryotes			

Table S2. Average abundances at the phyla and genus level within the averaged hotspot, coldspot and background samples. n = 20. 95% confidence intervals provided for each abundance. Empty cells indicate an absence of that genus for those particular samples.

Phyla	Average Abundance (%)		
	Hotspots	Coldspots	Background
<i>Proteobacteria</i>	28.9 (0.02)	19.3 (0.02)	37.2 (0.03)
<i>Actinobacteria</i> ,	21.9 (0.04)	37.0 (0.02)	22.6 (0.02)
<i>Bacteroidetes</i>	20.0 (0.04)	13.8 (0.02)	8.7 (0.01)
<i>Acidobacteria</i>	10.1 (0.02)	13.8 (0.02)	12.2 (0.01)
<i>Firmicutes</i>	7.8 (0.05),	9.6 (0.03)	13.3 (0.04)
<i>Planctomycetes</i>	4.8 (0.01),	2.6 (0.01)	1.2 (0.004)
<i>Verrucomicrobia</i>	4.0 (0.01)	2.1 (0.003)	3.3 (0.005)
<i>Thermotogae</i>	1.5 (0.003)	1.0 (0.002)	
Genus			
<i>Geothrix</i>	12.7 (0.02)	15.7 (0.02)	13.2 (0.01)
<i>Nocardioides</i>	9.1 (0.02)	14.7 (0.01)	8.7 (0.01)
<i>Flexibacter</i>	7.8 (0.01),	7.0 (0.01)	4.1 (0.01)
<i>Chryseoglobus</i>	5.6 (0.005)	8.3 (0.01)	4.9 (0.005)
<i>Thiobacillus</i>	4.9 (0.01)		
<i>Bacteroides</i>	4.8 (0.04)		
<i>Pseudomonas</i>	4.3 (0.07)		
<i>Planctomyces</i>	4.1 (0.01)		
<i>Austwickia</i>		6.7 (0.01)	
<i>Kaistia</i>		6.3 (0.01)	19.9 (0.03)
<i>Parasporobacterium</i>		5.1 (0.03)	6.4 (0.03)
<i>Lachnospiraceae incertae sedis</i>			5.4 (0.03)

Table S3. Average abundances of phyla and genera showing heightened abundance in individual hotspot samples. For H2, n = 10. For H1 and H3, n = 5. 95% confidence intervals provided for each abundance. Blank cells indicate an absence of that genera for that specific sample.

	Average Abundance (%)		
	H2	H1	H3
Phyla	<i>Proteobacteria</i> 33.0 (0.13)	<i>Firmicutes</i> 20.2 (0.15)	<i>Bacteroidetes</i> 29.2 (0.10)
Genus	<i>Pseudomonas</i> 9.4 (0.15)	<i>Parasporobacterium</i> 10.2 (0.06)	<i>Bacteroides</i> 14.2 (0.14)
		<i>Lachnospiraceae incertae sedis</i> 9.4 (0.002)	

Table S4. Sample dissimilarity and genera exclusivity between averaged and individual hotspot, coldspot and background samples as determined via SIMPER analysis and presence vs. absence data.

Samples	Dissimilarity		# genera exclusive
	Average abundance	Presence vs. absence	
Hotspots	55.4	56.5	-
Coldspots	69.8	75.2	-
Background	74.3	77.3	-
Hotspots and coldspots	47.2	55.4	52 (48 in coldspots)
Hotspots and background	51.0	56.9	61 (54 in background)
Coldspots and background	39.6	36.7	74 (39 in coldspots)
H1 and H2	46.5	-	24 (16 in H1)
H2 and H3	43.4	-	15 (9 in H3)
H3 and H1	42.9	-	35 (25 in H1)
C1 and C2	29.2	-	-
C2 and C3	31.7	-	-
C3 and C1	31.4	-	-
B1 and B2	27.2	-	-
B2 and B3	26.6	-	-
B3 and B1	25.5	-	-
C2 and H1	47.2	54.3	103 (98 in C2)
C1 and H1	46.1	53.3	94 (90 in C1)
C1 and C2	29.2	24.4	17 (10 in C1)
H3 and B2	50.0	53.7	81 (72 in B2)
H3 and B3	50.9	56.2	115 (106 in B3)
B1 and B2	27.2	24.9	18 (all in B1)

Table S5. Genera exclusive between individual hotspot (H1, H2 and H3), coldspot (C1, C2 and C3) and background (B1, B2 and B3) samples, as determined via SIMPER presence vs. absence data analysis. X indicates presence of genera and – indicates absence of genera.

Genera	Sample								
	H1	H2	H3	C1	C2	C3	B1	B2	B3
<i>Phascolarctobacterium</i>	-	-	X	X	-	-	-	-	-
<i>Faecalibacterium</i>	-	-	X	X	-	-	-	-	-
<i>Mucilaginibacter</i>	-	X	X	-	-	-	-	-	-
<i>Psychrobacter</i>	-	-	X	-	-	-	-	-	-
<i>Levilinea</i>	-	-	X	-	-	-	-	-	-
<i>Rothia</i>	-	-	X	X	X	-	-	-	-
<i>Sutterella</i>	-	-	X	-	-	-	-	-	-
<i>Dyadobacter</i>	-	-	X	X	-	-	-	-	-
<i>Joostella</i>	-	-	X	-	X	X	-	-	-
<i>Butyricoccus</i>	-	-	X	X	X	-	-	-	-
<i>Neisseria</i>	-	-	X	-	-	-	-	-	-
<i>Parvibaculum</i>	-	-	X	-	-	-	-	-	-
<i>Rivibacter</i>	-	-	X	-	-	-	-	-	-
<i>Sphingobacterium</i>	-	-	X	-	-	-	-	-	-
<i>Thermodesulfobium</i>	-	-	X	-	-	-	-	-	-
<i>Corynebacterium</i>	-	-	X	X	X	-	-	-	-
<i>Dictyoglomus</i>	-	-	X	-	-	-	-	-	-
<i>Mycoplasma</i>	-	-	X	-	-	-	-	-	-
<i>Tetrasphaera</i>	-	-	X	-	-	-	-	-	-
<i>Brevundimonas</i>	X	-	X	-	-	-	-	-	-
<i>Sediminobacterium</i>	-	-	X	-	-	-	-	-	-
<i>Thermovenabulum</i>	-	-	X	-	-	-	-	-	-
<i>Bauldia</i>	-	-	X	-	-	-	-	-	-
<i>Janthinobacterium</i>	-	-	X	-	-	-	-	-	-
<i>Rhodobacteraceae</i>	X	-	X	-	-	-	-	-	-
<i>Xanthomonas</i>	-	-	X	-	-	-	-	-	-
<i>Vibrio</i>	-	-	X	-	-	-	-	-	-
<i>Geobacter</i>	X	X	-	-	-	-	-	X	X
<i>Devosia</i>	X	-	-	-	-	-	-	X	X
<i>Solirubrobacter</i>	X	-	-	-	-	-	-	X	X
<i>Anaplasma</i>	X	-	-	-	-	-	-	-	X
<i>Aeromonas</i>	X	-	-	-	-	-	-	-	X
<i>Geosporobacter</i>	X	-	-	-	-	-	-	-	X
<i>Bellilinea</i>	X	-	-	-	-	-	-	X	X
<i>Cytophaga</i>	X	-	-	-	-	-	-	-	-
<i>Laribacter</i>	X	-	-	-	-	-	-	-	-
<i>Gluconacetobacter</i>	X	-	-	-	-	-	-	X	X
<i>Hyphomicrobiaceae</i>	X	-	-	-	-	-	-	-	-
<i>Kineococcus</i>	X	-	-	-	-	-	-	-	-
<i>Pandora</i>	X	-	-	-	-	-	-	X	X
<i>Lechevalieria</i>	X	X	-	-	-	-	-	X	X
<i>Enterococcus</i>	X	-	-	-	-	-	-	-	-
<i>Nitrobacter</i>	X	X	-	-	-	-	-	X	X
<i>Desulfobulbus</i>	X	-	-	-	-	-	-	-	-
<i>Actinoplanes</i>	X	-	-	-	-	-	-	X	X
<i>Altererythrobacter</i>	X	-	-	-	-	-	-	-	-
<i>Campylobacter</i>	X	-	-	-	-	-	-	-	-
<i>Hydrogenoanaerobacterium</i>	X	-	-	-	-	-	-	-	-

Genera	Sample								
	H1	H2	H3	C1	C2	C3	B1	B2	B3
<i>Kytococcus</i>	X	-	-	-	-	-	-	-	-
<i>Leptolinea</i>	X	-	-	-	-	-	-	X	X
<i>Leptospira</i>	X	-	-	-	-	-	-	-	-
<i>Microlunatus</i>	X	-	-	-	-	-	-	X	X
<i>Fusobacterium</i>	X	-	-	-	-	-	-	-	-
<i>Cyclobacterium</i>	X	-	-	-	-	-	-	-	-
<i>Thiorhodospira</i>	X	-	-	-	-	-	-	-	-
<i>Niabella</i>	X	-	-	-	-	-	-	-	-
<i>Singulisphaera</i>	-	X	-	X	-	-	-	-	-
<i>Paludibacter</i>	-	X	-	X	X	-	-	-	-
<i>Rhodobacter</i>	-	X	-	-	-	-	-	-	-
<i>Zoogloea</i>	-	X	-	-	-	-	-	-	X
<i>Kerstersia</i>	-	X	-	-	-	-	-	X	X
<i>Sulfurimonas</i>	-	X	-	-	-	-	-	X	-
<i>Zooamonas</i>	-	X	-	-	-	-	-	-	-
<i>Desulfonema</i>	-	-	-	-	X	-	-	-	-
<i>Rhodocista</i>	-	-	-	-	X	-	-	-	-
<i>Marinobacterium</i>	-	-	-	-	X	-	-	-	-
<i>Lysobacter</i>	-	-	-	-	X	-	-	-	X
<i>Syntrophus</i>	-	-	-	-	X	-	-	-	-
<i>Anaerococcus</i>	-	-	-	-	X	-	-	-	-
<i>Desulfococcus</i>	-	-	-	-	X	-	-	-	-
<i>Chthonomonas/Armatimonadetes_gp3</i>	-	-	-	X	-	-	-	-	-
<i>Odoribacter</i>	-	-	-	X	-	-	X	-	-
<i>Agrococcus</i>	-	-	-	X	-	-	-	-	-
<i>Beggiatoa</i>	-	-	-	X	-	-	-	-	-
<i>Bilophila</i>	-	-	-	X	-	-	-	-	-
<i>Geoalkalibacter</i>	-	-	-	X	-	-	-	-	-
<i>Pleomorphomonas</i>	-	-	-	X	-	-	-	-	-
<i>Robiginitalea</i>	-	-	-	X	-	-	-	-	-
<i>Gaetbulibacter</i>	-	-	-	X	-	-	-	-	X
<i>Rhizobium</i>	-	-	-	X	-	-	-	X	-
<i>Desulfobacterium</i>	-	-	-	X	X	-	-	X	X
<i>Frateuria</i>	-	-	-	X	X	-	-	X	X
<i>Herbaspirillum</i>	-	-	-	X	X	-	-	X	X
<i>Ilumatobacter</i>	-	-	-	X	X	-	-	-	-
<i>Inhella</i>	-	-	-	X	-	X	-	X	X
<i>Methylomicrobium</i>	-	-	-	X	X	-	-	-	-
<i>Niastella</i>	-	-	-	X	X	-	-	-	-
<i>Opitutus</i>	-	-	-	X	X	-	-	-	-
<i>Parabacteroides</i>	-	-	-	X	X	-	-	-	-
<i>Paracraurococcus</i>	-	-	-	X	X	-	-	-	-
<i>Beijerinckia</i>	-	-	-	X	X	-	-	-	-
<i>Naxibacter</i>	-	-	-	X	X	-	-	-	X
<i>Agaricicola</i>	-	-	-	X	X	-	-	X	X
<i>Staphylococcus</i>	-	-	-	X	X	-	-	X	X
<i>Rhodopirellula</i>	-	-	-	X	X	-	-	-	-
<i>Acidiphilium</i>	-	-	-	X	X	-	-	-	-
<i>Anaerofilum</i>	-	-	-	X	X	-	-	-	-
<i>Capnocytophaga</i>	-	-	-	X	X	-	-	-	-
<i>Catenulispora</i>	-	-	-	X	X	-	-	-	-

Genera	Sample								
	H1	H2	H3	C1	C2	C3	B1	B2	B3
<i>Propionibacterium</i>	-	-	-	X	X	-	-	-	-
<i>Filimonas</i>	-	-	-	X	X	-	-	-	-
<i>Paucimonas</i>	-	-	-	X	X	-	-	-	-
<i>Variovorax</i>	-	-	-	X	X	-	-	X	X
<i>Bosea</i>	-	-	-	X	-	-	-	-	X
<i>Citrobacter</i>	-	-	-	X	X	-	-	-	-
<i>Burkholderia</i>	-	-	-	X	X	-	-	X	X
<i>Perlucidibaca</i>	-	-	-	X	X	-	-	X	X
<i>Veillonella</i>	-	-	-	X	X	-	-	-	-
<i>Runella</i>	-	-	-	X	-	-	-	-	-
<i>Dysgonomonas</i>	-	-	-	X	X	-	-	-	X
<i>Halochromatium</i>	-	-	-	X	-	-	-	-	-
<i>Tepidimonas</i>	-	-	-	X	X	-	-	-	-
<i>Nitrosococcus</i>	-	-	-	X	X	-	-	-	-
<i>Thiomicrospira</i>	-	-	-	X	X	-	-	X	X
<i>Ahrensia</i>	-	-	-	X	X	-	-	X	X
<i>Rubrobacter</i>	-	-	-	X	X	-	-	-	-
<i>Desulforhabdus</i>	-	-	-	X	X	-	-	X	X
<i>Heliobacterium</i>	-	-	-	X	x	-	x	-	-
<i>Bowmanella</i>	-	-	-	X	X	-	-	-	X
<i>Arenibacter</i>	-	-	-	X	-	-	-	-	-
<i>Natronincola</i>	-	-	-	X	X	-	-	X	X
<i>Roseibacillus</i>	-	-	-	X	X	-	-	-	-
<i>Caldanaerobacter</i>	-	-	-	X	X	-	-	X	X
<i>Zunongwangia</i>	-	-	-	X	X	-	-	-	-
<i>Sediminibacterium</i>	-	-	-	X	X	-	-	X	X
<i>Sphaerotilus</i>	-	-	-	X	X	-	-	-	-
<i>Sporomusa</i>	-	-	-	X	X	-	-	-	-
<i>Zavarzinella</i>	-	-	-	X	X	-	-	-	-
<i>Thermocrispum</i>	-	-	-	X	-	-	-	-	-
<i>Ideonella</i>	-	-	-	X	X	-	-	X	X
<i>Microvirgula</i>	-	-	-	X	X	-	-	X	X
<i>Pedomicrobium</i>	-	-	-	X	X	-	-	-	X
<i>Eubacterium</i>	-	-	-	X	X	-	-	-	-
<i>Erysipelothrix</i>	-	-	-	X	-	-	-	-	-
<i>Sporobacter</i>	-	-	-	X	X	-	-	-	-
<i>Rhizobacter</i>	-	-	-	X	X	-	-	X	-
<i>Thermotoga</i>	-	-	-	X	X	-	-	X	X
<i>Saprospira</i>	-	-	-	X	X	-	-	-	-
<i>Cupriavidus</i>	-	-	-	X	X	-	-	X	X
<i>Comamonas</i>	-	-	-	X	X	-	-	-	-
<i>Acidocella</i>	-	-	-	X	X	-	-	X	X
<i>Novosphingobium</i>	-	-	-	X	X	-	-	-	-
<i>Rugamonas</i>	-	-	-	X	X	-	-	X	X
<i>Thioalkalivibrio</i>	-	-	-	X	X	-	-	-	-
<i>Sedimnicola</i>	-	-	-	X	X	-	-	-	-
<i>Lactobacillus</i>	-	-	-	X	X	-	-	-	-
<i>Rhodiferax</i>	-	-	-	X	-	-	X	-	X
<i>Meniscus</i>	-	-	-	X	X	-	-	-	X
<i>Cellvibrio</i>	-	-	-	X	X	-	-	X	X
<i>Phaeospirillum</i>	-	-	-	X	-	-	-	-	X

Genera	Sample								
	H1	H2	H3	C1	C2	C3	B1	B2	B3
<i>Pseudoflavonifractor</i>	-	-	-	X	X	-	-	-	-
<i>Dehalobacter</i>	-	-	-	X	-	-	-	-	-
<i>Zhangella</i>	-	-	-	X	-	-	-	-	-
<i>Succiniclasticum</i>	-	-	-	X	X	-	-	-	X
<i>Gemmobacter</i>	-	-	-	X	X	-	-	X	X
<i>Sulfurovum</i>	-	-	-	X	X	-	X	-	X
<i>Leptothrix</i>	-	-	-	X	X	-	-	-	-
<i>Sphingosinicella</i>	-	-	-	X	X	-	-	-	X
<i>Prevotella</i>	-	-	-	X	X	-	-	-	-
<i>Azospirillum</i>	-	-	-	-	X	-	-	-	-
<i>Rikenella</i>	-	-	-	-	X	-	-	-	-
<i>Schwartzia</i>	-	-	-	-	X	-	-	-	-
<i>Acidaminococcus</i>	-	-	-	-	X	-	-	-	-
<i>Anaeromyxobacter</i>	-	-	-	-	X	-	-	-	-
<i>Desulfonauticus</i>	-	-	-	-	X	-	-	-	-
<i>Labrys</i>	-	-	-	-	X	-	-	X	X
<i>Paracoccus</i>	-	-	-	-	X	-	-	X	X
<i>Segetibacter</i>	-	-	-	-	X	-	-	-	-
<i>Sulfuricella</i>	-	-	-	-	X	-	-	-	-
<i>Thermodesulfatator</i>	-	-	-	-	X	-	-	-	-
<i>Salinhabitans</i>	-	-	-	-	X	-	-	-	-
<i>Larkinella</i>	-	-	-	-	X	-	-	-	-
<i>Sandarakinotalea</i>	-	-	-	-	X	-	-	-	-
<i>Coenonia</i>	-	-	-	-	X	-	-	-	-
<i>Caedibacter</i>	-	-	-	-	X	-	-	X	-
<i>Cellulomonas</i>	-	-	-	-	X	-	-	X	X
<i>Longilinea</i>	-	-	-	-	X	-	-	-	-
<i>Thermosediminibacter</i>	-	-	-	-	X	-	-	X	X
<i>Magnetospirillum</i>	-	-	-	-	X	-	-	-	-
<i>Anaeroplasm</i>	-	-	-	-	X	-	-	-	-
<i>Mucispirillum</i>	-	-	-	-	X	-	-	-	-
<i>Papillibacter</i>	-	-	-	-	X	-	-	-	-
<i>Spirochaeta</i>	-	-	-	-	X	-	-	-	X
<i>Bradyrhizobium</i>	-	-	-	-	-	-	-	X	X
<i>Cerasicoccus</i>	-	-	-	-	-	-	-	X	X
<i>Dechloromonas</i>	-	-	-	-	-	-	-	X	X
<i>Ectothiorhodospinus</i>	-	-	-	-	-	-	-	X	X
<i>Lutispora</i>	-	-	-	-	-	-	-	X	X
<i>Spirillum</i>	-	-	-	-	-	-	-	X	-
<i>Porphyrobacter</i>	-	-	-	-	-	-	-	X	-
<i>Caldanaerobius</i>	-	-	-	-	-	-	-	X	-
<i>Pseudoxanthobacter</i>	-	-	-	-	-	-	-	X	X
<i>Ralstonia</i>	-	-	-	-	-	-	-	X	X
<i>Roseiflexus</i>	-	-	-	-	-	-	-	X	X
<i>Megamonas</i>	-	-	-	-	-	-	-	X	X
<i>Derxia</i>	-	-	-	-	-	-	-	X	-
<i>Alkaliphilus</i>	-	-	-	-	-	-	-	X	X
<i>Wautersia</i>	-	-	-	-	-	-	-	X	-
<i>Tistlia</i>	-	-	-	-	-	-	-	X	X
<i>Hahella</i>	-	-	-	-	-	-	-	X	X
<i>Patulibacter</i>	-	-	-	-	-	-	-	X	-

Genera	Sample								
	H1	H2	H3	C1	C2	C3	B1	B2	B3
<i>Sarcina</i>	-	-	-	-	-	-	-	X	-
<i>Prostheco bacter</i>	-	-	-	-	-	-	-	X	X
<i>Methylibium</i>	-	-	-	-	-	-	-	X	X
<i>Verrucomicrobium</i>	-	-	-	-	-	-	-	X	X
<i>Wandonia</i>	-	-	-	-	-	-	-	X	X
<i>Methylosarcina</i>	-	-	-	-	-	-	-	X	X
<i>Melitea</i>	-	-	-	-	-	-	-	X	X
<i>Pelomonas</i>	-	-	-	-	-	-	-	X	X
<i>Pseudorhodofera x</i>	-	-	-	-	-	-	-	X	X
<i>Thioflavico coccus</i>	-	-	-	-	-	-	-	X	X
<i>Steroidobacter</i>	-	-	-	-	-	-	X	-	X
<i>Azonexus</i>	-	-	-	-	-	-	X	-	X
<i>Acinetobacter</i>	-	-	-	-	-	-	X	-	-
<i>Desulforhopalus</i>	-	-	-	-	-	-	X	-	X
<i>Lacibacter</i>	-	-	-	-	-	-	X	-	-
<i>Frigoribacterium</i>	-	-	-	-	-	-	X	-	-
<i>Pigmentiphaga</i>	-	-	-	-	-	-	X	-	-
<i>Thermomonas</i>	-	-	-	-	-	-	X	-	-
<i>Desulfobacca</i>	-	-	-	-	-	-	X	-	-
<i>Bacteriovorax</i>	-	-	-	-	-	-	X	-	-
<i>Yersinia</i>	-	-	-	-	-	-	X	-	-
<i>Dokdonella</i>	-	-	-	-	-	-	X	-	-
<i>Pectinatus</i>	-	-	-	-	-	-	X	-	-
<i>Parasutterella</i>	-	-	-	-	-	-	X	-	-
<i>Chitinimonas</i>	-	-	-	-	-	-	X	-	-
<i>Aquaspirillum</i>	-	-	-	-	-	-	-	-	X
<i>Luteimonas</i>	-	-	-	-	-	-	-	-	X
<i>Chondromyces</i>	-	-	-	-	-	-	-	-	X
<i>Duganella</i>	-	-	-	-	-	-	-	-	X
<i>Fontibacter</i>	-	-	-	-	-	-	-	-	X
<i>Thermolithobacter</i>	-	-	-	-	-	-	-	-	X
<i>Serpens</i>	-	-	-	-	-	-	-	-	X
<i>Porphyromonas</i>	-	-	-	-	-	-	-	-	X
<i>Psychrosinus</i>	-	-	-	-	-	-	-	-	X
<i>Rhodoblastus</i>	-	-	-	-	-	-	-	-	X
<i>Desulfomicrobium</i>	-	-	-	-	-	-	-	-	X
<i>Rhodospirillum</i>	-	-	-	-	-	-	-	-	X
<i>Nevskia</i>	-	-	-	-	-	-	-	-	X
<i>Mesorhizobium</i>	-	-	-	-	-	-	-	-	X
<i>Psychromonas</i>	-	-	-	-	-	-	-	-	X
<i>Undibacterium</i>	-	-	-	-	-	-	-	-	X
<i>Algibacter</i>	-	-	-	-	-	-	-	-	X
<i>Anaerovirgula</i>	-	-	-	-	-	-	-	-	X
<i>Spiroplasma</i>	-	-	-	-	-	-	-	-	X
<i>Corallococcus</i>	-	-	-	-	-	-	-	-	X
<i>Maricaulis</i>	-	-	-	-	-	-	-	-	X
<i>Marivirga</i>	-	-	-	-	-	-	-	-	X
<i>Chryseobacterium</i>	-	-	-	-	-	-	-	-	X
<i>Zimmermannella</i>	-	-	-	-	-	-	-	-	X
<i>Haliaea</i>	-	-	-	-	-	-	-	-	X

Table S6. Genera exclusive between averaged hotspot, coldspot and background samples as determined via SIMPER presence vs. absence data analysis.

Genera	Hotspots	Coldspots	Background
<i>Acidiphilium</i>	-	X	-
<i>Acidocella</i>	-	X	X
<i>Agaricola</i>	-	X	X
<i>Anaerofilum</i>	-	X	-
<i>Anaerovorax</i>	-	X	-
<i>Arenibacter</i>	-	X	-
<i>Azonexus</i>	-	-	X
<i>Bauldia</i>	X	-	-
<i>Bowmanella</i>	-	X	X
<i>Burkholderia</i>	-	X	X
<i>Caldanaerobacter</i>	-	X	X
<i>Caldanaerobius</i>	-	-	X
<i>Capnocytophaga</i>	-	X	-
<i>Catenulispora</i>	-	X	-
<i>Cellulomonas</i>	-	-	X
<i>Cellvibrio</i>	-	X	X
<i>Cerasicoccus</i>	-	-	X
<i>Cerasicoccus</i>	-	-	X
<i>Chitinibacter</i>	-	-	X
<i>Chryseobacterium</i>	-	-	X
<i>Citrobacter</i>	-	X	-
<i>Coenonia</i>	-	X	-
<i>Comamonas</i>	-	X	-
<i>Cupriavidus</i>	-	X	X
<i>Dechloromonas</i>	-	-	X
<i>Desulfobacterium</i>	-	X	X
<i>Desulfomicrobium</i>	-	-	X
<i>Devosia</i>	-	-	X
<i>Dyadobacter</i>	-	X	-
<i>Dysgonomonas</i>	-	X	X
<i>Ectothiorhodospinus</i>	-	-	X
<i>Enterococcus</i>	-	X	-
<i>Eubacterium</i>	-	X	-
<i>Fontibacter</i>	-	-	X
<i>Gemmobacter</i>	-	X	X
<i>Halochromatium</i>	-	X	-
<i>Heliorestis</i>	-	X	-
<i>Inhella</i>	-	X	X
<i>Janthinobacterium</i>	X	-	-
<i>Labrys</i>	-	-	X
<i>Lactobacillus</i>	-	X	-
<i>Laribacter</i>	-	X	-
<i>Larkinella</i>	-	X	-
<i>Limnobacter</i>	-	X	-
<i>Longilinea</i>	-	X	-
<i>Luteimonas</i>	-	-	X
<i>Lysobacter</i>	-	-	X
<i>Megamonas</i>	-	-	X
<i>Melitea</i>	-	-	X
<i>Melitea</i>	-	-	X

Genera	Hotspots	Coldspots	Background
<i>Meniscus</i>	-	X	X
<i>Mesorhizobium</i>	-	-	X
<i>Methylibium</i>	-	X	X
<i>Methylocapsa</i>	-	X	-
<i>Methylophilus</i>	-	-	X
<i>Methylosarcina</i>	-	-	X
<i>Microvirga</i>	-	X	-
<i>Mucispirillum</i>	-	X	-
<i>Natronincola</i>	-	X	X
<i>Neisseria</i>	-	-	X
<i>Nevskia</i>	-	-	X
<i>Niabella</i>	X	-	X
<i>Niastella</i>	-	X	-
<i>Novosphingobium</i>	-	X	-
<i>Pandoraea</i>	-	-	X
<i>Papillibacter</i>	-	X	-
<i>Parvibaculum</i>	-	-	X
<i>Paucimonas</i>	-	X	-
<i>Pedomicrobium</i>	-	X	X
<i>Pelomonas</i>	-	-	X
<i>Perlucidibaca</i>	-	X	X
<i>Phascolarctobacterium</i>	-	X	-
<i>Porphyromonas</i>	-	-	X
<i>Prostheco bacter</i>	-	-	X
<i>Pseudaminobacter</i>	-	X	-
<i>Psychrobacter</i>	-	-	X
<i>Psychromonas</i>	-	-	X
<i>Psychrosinus</i>	-	-	X
<i>Rheinheimera</i>	-	-	X
<i>Rhizobium</i>	-	-	X
Rhodobacteraceae	X	-	X
<i>Rhodoferax</i>	-	X	-
<i>Rhodopirellula</i>	-	X	-
<i>Rhodospirillum</i>	-	-	X
<i>Roseibacillus</i>	-	X	-
<i>Rubro bacter</i>	-	X	X
<i>Rugamonas</i>	-	X	X
<i>Runella</i>	-	X	-
<i>Saprospira</i>	-	X	-
<i>Schwartzia</i>	-	X	-
<i>Sediminibacterium</i>	-	X	X
<i>Sediminitomix</i>	-	-	X
<i>Sediminobacterium</i>	X	-	-
<i>Segetibacter</i>	-	X	-
<i>Serpens</i>	-	-	X
<i>Shinella</i>	-	-	X
<i>Sphingosinicella</i>	-	X	X
<i>Spirillum</i>	-	-	X
<i>Spirochaeta</i>	-	X	-
<i>Sporobacter</i>	-	X	-
<i>Staphylococcus</i>	-	X	X
<i>Sulfuricella</i>	-	X	-

Genera	Hotspots	Coldspots	Background
<i>Terracoccus</i>	-	X	-
<i>Thermocrispum</i>	-	X	-
<i>Thermolithobacter</i>	-	-	X
<i>Thermosediminibacter</i>	-	X	X
<i>Thermotoga</i>	-	X	X
<i>Thioflavicoccus</i>	-	-	X
<i>Thiomicrospira</i>	-	X	X
<i>Thiorhodospira</i>	X	-	X
<i>Tistlia</i>	-	-	X
<i>Undibacterium</i>	-	-	X
<i>Variovorax</i>	-	X	X
<i>Verrucomicrobium</i>	-	-	X
<i>Vibrio</i>	X	X	-
<i>Wautersia</i>	-	-	X
<i>Zhangella</i>	-	X	-
<i>Zoogloea</i>	-	-	X
<i>Zunongwangia</i>	-	X	-

Additional taxonomic analysis results

For the hotspots, a total of 2,127,612 primer matched sequences were quality filtered to yield 1,795,425 (84.4%) passed reads, 4,845 short reads discarded (< 250 bp) and 327,342 low quality records discarded (expected errors > 0.5). Dereplication resulted in 442,770 unique reads and 371,806 singletons. OTU clustering using 97% identity produced 1,601 OTUs and 2,945 chimeras (4.1%). Out of the 1,601 OTUs, reference-based chimera detection identified 47 chimeric reads. Taxonomy assignment via the RDP Classifier produced a total of 1,527 OTUs which contained 1,637,388 total reads. Samples H2 contained between 38,357 and 115,285 reads (mean = 68,426, std. dev. = 20,971), H1 contained between 46,545 and 114,499 reads (mean = 87,493, std. dev. = 26,146.7) and H3 contained between 55,989 and 146,072 reads (mean = 103,492, std. dev. = 31,990.4).

For the coldspots, a total of 1,366,587 primer matched sequences were quality filtered to yield 969,705 (71%) passed reads, 468 short reads discarded (< 250 bp) and 396,414 low quality reads discarded (expected errors > 0.5). Dereplication resulted in 273,700 unique reads and 233,597 singletons. OTU clustering at 97% identity produced 1,322 OTUs and 1,121 chimeras (2.8%). Of the 1,322 OTUs, reference-based chimera detection revealed 46 were chimeric reads. Taxonomy assignment via the RDP Classifier produced a total of 1,264 OTUs which contained 879,823 total reads. Samples C1 contained between 18,612 and 52,884 reads (mean = 36,280, std. dev. = 10,679.7), C2 contained between 34,271 and 63,451 reads (mean = 46,071, std. dev. = 11,920.3) and C3 contained between (mean = 57,333, std. dev. = 41,730.9).

For the background, a total of 1,300,203 primer matched sequences were quality filtered producing 1,007,474 passed reads, 819 short reads discarded (< 250 bp) and 291,910 low quality reads discarded (expected errors > 0.5). Dereplication resulted in 305,310 unique reads and 264,902 singletons. OTU clustering at 97% identity produced 1,299 OTUs and 2,131 chimeras (5.3%). Of these 1,299 OTUs, reference-based chimera detection revealed 46 were chimeric reads. Taxonomy assignment via the RDP Classifier produced a total of 1,244 OTUs which contained 889,419 total reads. Samples B2 contained between 15,399 and 31,150 reads (mean = 23,849, std. dev. = 6,003.8), samples B3 contained between 27,283 and 65,631 reads (mean = 50,699, std. dev. = 15,027.6) and samples B1 contained between 18,344 and 99,216 reads (mean = 68,177, std. dev. = 46,734.9).