Supplemental Material for

Bacterial communities associated with subsurface geochemical processes in continental serpentinite springs

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Supplemental Material includes:

Figure S1

Figure S2

Table S1

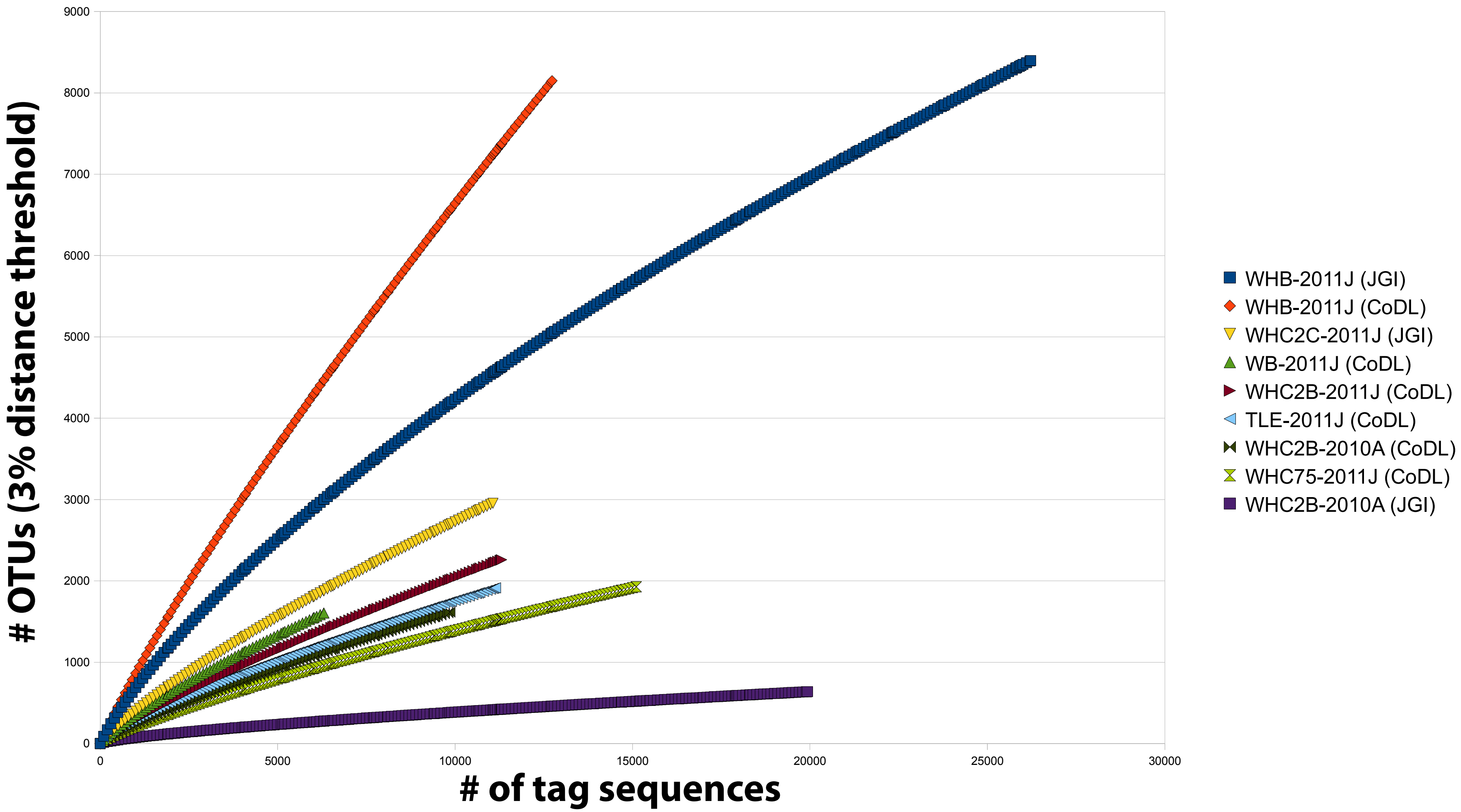

Figure S1. Rarefaction curves of OTU (operational taxonomic unit) discovery as a function of sequencing coverage (represented as number of tag sequences). For OTU counts reported in the manuscript, each dataset was subsampled down to the same level of sequencing coverage (6277 sequences for CoDL datasets and 6305 tag sequences for JGI datasets).

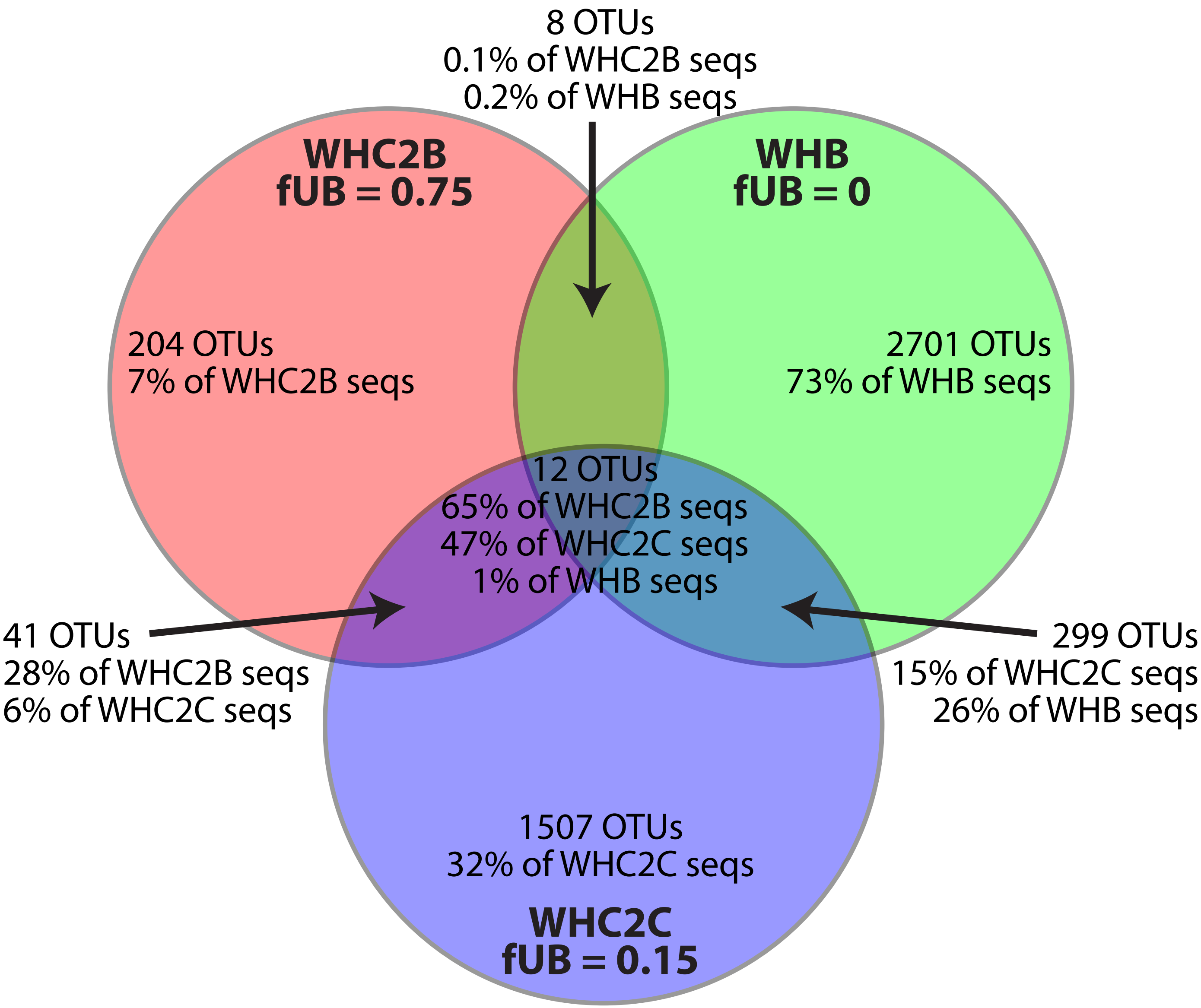

Figure S2. A Venn diagram illustrating JGI tag sequence OTUs shared by the most ultrabasic spring (WHC2B), a mixing site (WHC2C), and surface freshwater (WHB). The number of OTUs and the percentage of total tag sequences represented by those OTUs are indicated for each combination of samples.

	WHC2B-2010A	**WHC2B-2011J**	**WHC75-2011J**	**WB-2011J**	**TLE-2011J**	**WHB-2011J**	**WHC2B-2010A**	**WHC2C-2011J**	**WHB-2011J**
	CoDL	**CoDL**	**CoDL**	**CoDL**	**CoDL**	**CoDL**	**JGI**	**JGI**	**JGI**
Total sequences	**9854**	**11311**	**15107**	**6305**	**11138**	**12733**	**19930**	**11068**	**26222**
Hydrogenophaga	18.0%	19.5%	21.7%	6.2%	11.2%	0.4%	54.0%	39.8%	0.1%
Erysipelothrix	36.3%	17.7%	2.8%	0.0%	0.0%	0.1%	17.3%	0.2%	0.0%
Malikia	12.8%	15.7%	2.1%	1.6%	1.5%	0.2%	1.3%	1.6%	0.0%
Propionispora	1.5%	2.3%	14.1%	0.0%	0.0%	0.0%	5.1%	0.3%	0.0%
uncultured Xanthomonadales	0.0%	0.4%	4.0%	14.0%	3.6%	0.0%	0.1%	0.2%	0.0%
Aquiflexum	0.0%	0.1%	0.2%	11.7%	1.3%	0.0%	0.0%	0.1%	0.0%
Dethiobacter	1.6%	2.9%	10.0%	0.1%	0.3%	0.0%	4.5%	0.4%	0.0%
Pseudoanabaena	0.0%	0.0%	0.0%	0.3%	7.9%	0.2%	0.0%	0.3%	0.1%
Rivularia	0.0%	0.0%	0.0%	0.0%	6.9%	0.0%	0.0%	0.0%	0.0%
Desulfonatronum	0.1%	2.6%	6.5%	0.4%	0.1%	0.0%	0.3%	0.1%	0.0%
Brumimimicrobium	0.5%	0.1%	6.3%	0.1%	0.5%	0.0%	1.4%	0.0%	0.0%
Roseibacillus	0.0%	0.0%	0.0%	0.0%	0.0%	2.3%	0.0%	0.1%	6.2%
Tepidimonas	5.4%	6.2%	0.7%	0.2%	0.1%	0.1%	0.1%	0.2%	0.0%
Oscillatoria	0.0%	0.0%	0.0%	0.0%	6.0%	0.0%	0.0%	0.0%	0.0%
Acidimicrobineae	0.0%	0.0%	0.2%	5.9%	1.3%	0.2%	0.0%	0.0%	0.1%
uncultured Acetobacteraceae	0.0%	0.1%	0.2%	5.9%	1.5%	0.0%	0.0%	0.2%	0.0%
Aspromonas	0.1%	0.6%	0.7%	5.6%	2.4%	0.1%	1.3%	2.2%	0.0%
unclassified Myxococcales	0.0%	0.1%	0.2%	0.1%	0.1%	5.3%	0.0%	0.8%	4.8%
Rhodovarius	0.1%	0.9%	0.9%	5.1%	0.9%	0.0%	0.0%	0.0%	0.0%
Anaerospora	5.1%	5.0%	2.2%	0.0%	0.1%	0.1%	4.5%	0.1%	0.0%
Desulfonauticus	0.0%	0.3%	5.0%	0.1%	0.2%	0.3%	0.0%	0.1%	0.2%
Bulleidia	5.0%	2.8%	0.1%	0.0%	0.0%	0.0%	0.5%	0.0%	0.0%
Phormidium	0.0%	0.0%	0.1%	0.1%	4.7%	0.1%	0.0%	0.1%	0.0%
Methylobacter	0.0%	0.0%	0.0%	4.7%	0.0%	0.0%	0.0%	0.0%	0.0%
unclassified OP3	0.0%	0.0%	0.2%	0.1%	0.0%	4.3%	0.0%	0.1%	3.3%
Allofustis	0.0%	0.0%	0.1%	0.0%	0.0%	1.9%	0.0%	0.0%	4.0%
Rhodoferax	0.0%	0.1%	0.0%	0.1%	0.1%	0.1%	0.0%	3.9%	0.2%
unclassified NPL-UPA2	0.0%	0.0%	0.1%	0.1%	0.1%	2.2%	0.0%	0.2%	3.7%
unclassified Verrucomicrobia	0.0%	0.0%	0.0%	0.0%	0.0%	1.7%	0.0%	0.2%	3.7%
Micrococcineae	0.0%	0.0%	0.1%	0.2%	3.4%	0.2%	0.0%	0.1%	0.2%
uncultured Clostridiales	1.9%	3.2%	2.1%	0.0%	0.0%	0.1%	3.4%	0.3%	0.0%
Chamaesiphon	0.0%	0.0%	0.1%	0.2%	0.1%	3.3%	0.0%	0.0%	1.0%
Turneriella	0.0%	0.0%	0.1%	0.1%	0.1%	1.7%	0.0%	0.2%	3.1%
Flexibacter	0.0%	0.0%	0.1%	0.1%	3.0%	0.1%	0.0%	0.1%	0.1%

Table S1. Taxonomic assignments for all 16S rRNA tag sequences recovered from Tablelands ultra-basic springs and the freshwater end-member (WHB), including the Joint Genome Institute and Census of Deep Life datasets. All taxa that comprise at least 3% of total sequences in one sample are shown.