

**Headd and Engel**  
**“Geographic distribution of sulfur oxidation genes in a terrestrial sulfidic spring reveals evidence for niche partitioning”**

**Supplemental Table 1.** Number of 16S rRNA pyrosequences (pyrotags) and taxonomic affiliations (class or phylum) along the Rattlesnake Spring flowpath, differentiated by genera, when possible. Operational taxonomic units (OTUs) defined at the 96% sequence identity level.

	0 m Orifice	1.6 m Drop	5.5 m 1st Tran	9.5 m 2nd Tran	14 m End	Total Pyrotags	OTUs*
<b><i>Alphaproteobacteria</i></b>	<b>86</b>	<b>66</b>	<b>207</b>	<b>802</b>	<b>1401</b>	<b>2562</b>	<b>460</b>
<i>Hyphomonas</i>	1	0	1	29	25	56	8
<i>Parvularcula</i>	0	0	2	22	92	116	10
<i>Rhodobacter</i>	7	2	5	12	13	39	6
<i>Rhodovulum</i>	4	0	9	1	0	14	1*
Other	10	3	7	80	90	190	42
Unidentified	64	61	183	658	1181	2147	393
<b><i>Betaproteobacteria</i></b>	<b>8</b>	<b>12</b>	<b>68</b>	<b>924</b>	<b>249</b>	<b>1261</b>	<b>126</b>
<i>Hydrogenophaga</i>	0	0	5	23	23	51	5
<i>Thiobacillus</i>	0	0	9	226	77	312	33
<i>Thiomonas</i>	4	3	7	1	0	15	2
Other	0	0	1	7	4	12	8
Unidentified	4	9	46	667	145	871	78
<b><i>Deltaproteobacteria</i></b>	<b>487</b>	<b>24</b>	<b>122</b>	<b>66</b>	<b>9</b>	<b>708</b>	<b>97</b>
<i>Desulfocapsa</i>	247	10	55	0	0	312	14
<i>Desulfuromusa</i>	38	0	14	0	0	52	9
Other	12	3	2	10	0	27	9
Unidentified	190	11	51	56	9	317	65
<b><i>Epsilonproteobacteria</i></b>	<b>1385</b>	<b>64</b>	<b>27</b>	<b>15</b>	<b>46</b>	<b>1537</b>	<b>51</b>
<i>Arcobacter</i>	0	0	0	0	43	43	6
<i>Sulfurimonas</i>	8	0	0	0	0	8	*
<i>Sulfurospirillum</i>	1	2	2	0	0	5	1
<i>Sulfurovum</i>	25	2	3	2	0	32	3
<i>Wolinella</i>	0	0	1	0	0	1	1
Unidentified	1351	60	21	13	3	1448	40
<b><i>Gammaproteobacteria</i></b>	<b>153</b>	<b>11148</b>	<b>9090</b>	<b>516</b>	<b>3108</b>	<b>24015</b>	<b>425</b>
<i>Aeromonas</i>	0	0	0	15	2486	2501	57
<i>Thiofaba</i>	59	37	268	54	11	429	19
<i>Thiothrix</i>	43	6745	3273	143	12	10216	58
<i>Thiovirga</i>	0	70	0	0	0	70	2
<i>Vibrio</i>	0	0	0	0	30	30	1
	0 m	1.6 m	5.5 m	9.5 m	14 m	Total	OTUs

	Orifice	Drop	1st Tran	2nd Tran	End	Pyrotags	
Other	7	0	10	13	113	143	19
Unidentified	44	4296	5539	291	456	10626	269
<b>Unidentified <i>Proteobacteria</i></b>	<b>302</b>	<b>643</b>	<b>996</b>	<b>838</b>	<b>216</b>	<b>2995</b>	<b>**</b>
<b><i>Acidobacteria</i></b>	<b>0</b>	<b>0</b>	<b>1</b>	<b>9</b>	<b>9</b>	<b>19</b>	<b>5</b>
Group 3	0	0	0	1	0	1	1
Group 4	0	0	0	5	8	13	1
Group 9	0	0	0	0	1	1	1
Group 17	0	0	0	1	0	1	1
Unidentified	0	0	1	2	0	3	1
<b><i>Actinobacteria</i></b>	<b>1</b>	<b>0</b>	<b>0</b>	<b>2</b>	<b>9</b>	<b>12</b>	<b>7</b>
<i>Ilumatobacter</i>	0	0	0	1	0	1	1
<i>Microbacterium</i>	0	0	0	0	1	1	1
<i>Propionibacterium</i>	0	0	0	0	1	1	1
Unidentified	1	0	0	1	7	9	4
<b><i>Bacteroidetes</i></b>	<b>312</b>	<b>499</b>	<b>305</b>	<b>87</b>	<b>97</b>	<b>1300</b>	<b>179</b>
<i>Cloacibacterium</i>	0	0	0	1	0	1	1
<i>Dysgonomonas</i>	0	0	0	0	1	1	1
<i>Flavobacterium</i>	1	12	4	1	5	23	6
Unidentified	311	487	301	85	91	1275	171
<b><i>Chlorobi</i></b>	<b>347</b>	<b>0</b>	<b>4</b>	<b>1</b>	<b>0</b>	<b>352</b>	<b>18</b>
<i>Chlorobium</i>	322	0	4	1	0	327	14
Unidentified	25	0	0	0	0	25	4
<b><i>Chloroflexi</i></b>	<b>541</b>	<b>24</b>	<b>9</b>	<b>1</b>	<b>1</b>	<b>576</b>	<b>39</b>
<i>Chloroflexus</i>	126	0	0	0	0	126	12
Unidentified	415	24	9	1	1	450	27
<b><i>Cyanobacteria</i></b>	<b>9236</b>	<b>47</b>	<b>302</b>	<b>314</b>	<b>782</b>	<b>10681</b>	<b>261</b>
<i>Gpl</i>	686	3	15	135	63	902	30
Other	99	0	0	0	11	110	5
Unidentified	8451	44	287	179	708	9669	226
<b><i>Firmicutes</i></b>	<b>0</b>	<b>3</b>	<b>7</b>	<b>8</b>	<b>15</b>	<b>33</b>	<b>21</b>
<i>Clostridium</i>	0	0	0	0	2	2	1
<i>Faecalibacterium</i>	0	1	0	0	1	2	1
<i>Gemella</i>	0	0	2	0	0	2	1
<i>Halobacillus</i>	0	0	0	0	1	1	1
<i>Lactococcus</i>	0	0	2	0	1	3	1
<i>Oscillibacter</i>	0	0	0	1	0	1	2
Unidentified	0	2	3	7	10	22	14
<b><i>Fusobacteria</i></b>	<b>0</b>	<b>0</b>	<b>3</b>	<b>15</b>	<b>12</b>	<b>30</b>	<b>13</b>
Unidentified	0	0	3	15	12	30	13

	0 m Orifice	1.6 m Drop	5.5 m 1st Tran	9.5 m 2nd Tran	14 m End	Total Pyrotags	OTUs
<b><i>Gemmatimonadetes</i></b>	<b>1</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>1</b>	<b>2</b>	<b>2</b>
<i>Gemmatimonas</i>	1	0	0	0	0	1	1
Unidentified	0	0	0	0	1	1	1
<b><i>Nitrospira</i></b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>66</b>	<b>8</b>	<b>74</b>	<b>8</b>
<i>Nitrospira</i>	0	0	0	59	6	65	6
Unidentified	0	0	0	7	2	9	2
<b><i>Planctomycetes</i></b>	<b>1</b>	<b>0</b>	<b>1</b>	<b>21</b>	<b>30</b>	<b>53</b>	<b>28</b>
Gemmata	0	0	0	1	0	1	*
Planctomyces	0	0	0	1	7	8	2
Rhodopirellula	0	0	0	0	2	2	*
Unidentified	1	0	1	19	21	42	26
<b><i>Spirochaetes</i></b>	<b>104</b>	<b>27</b>	<b>37</b>	<b>3</b>	<b>3</b>	<b>174</b>	<b>21</b>
<i>Leptonema</i>	0	0	30	1	0	31	3
<i>Spirochaeta</i>	16	1	0	0	0	17	3
<i>Treponema</i>	0	1	0	0	0	1	*
<i>Turneriella</i>	65	19	2	0	0	86	4
Unidentified	23	6	5	2	3	39	11
<b><i>Verrucomicrobia</i></b>	<b>10</b>	<b>4</b>	<b>1</b>	<b>15</b>	<b>66</b>	<b>96</b>	<b>36</b>
<i>Cerasicoccus</i>	0	0	0	0	2	2	2
<i>Haloferula</i>	0	0	0	4	0	4	4
<i>Luteolibacter</i>	0	0	0	5	0	5	6
Opitutus	0	0	0	0	1	1	*
Subdivision3 genera	1	0	0	0	0	1	1
Unidentified	9	4	1	6	63	83	23
<b>Candidate Division OP10</b>	<b>5</b>	<b>0</b>	<b>2</b>	<b>0</b>	<b>1</b>	<b>8</b>	<b>3</b>
OP10 genera	5	0	1	0	0	6	1
Unidentified	0	0	1	0	1	2	2
<b>Candidate Division SR1</b>	<b>14</b>	<b>57</b>	<b>2</b>	<b>0</b>	<b>0</b>	<b>73</b>	<b>14</b>
SR1 genera	14	36	2	0	0	52	9
Unidentified	0	21	0	0	0	21	5
<b>Candidate Division TM7</b>	<b>1</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>1</b>	<b>1</b>
Unidentified	1	0	0	0	0	1	1
<b>Candidate Division WS3</b>	<b>1</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>1</b>	<b>1</b>
Unidentified	1	0	0	0	0	1	1
<b><i>Eukaryota</i></b>	<b>1</b>	<b>5</b>	<b>68</b>	<b>7916</b>	<b>2324</b>	<b>10314</b>	<b>239</b>
<i>Bacillariophyta</i>	1	4	64	3338	633	4040	199
<i>Streptophyta</i>	0	1	1	3860	1234	5096	38
<i>Chlorophyta</i>	0	0	0	0	3	3	2
Unidentified	0	0	3	718	454	1175	**

<b>Unidentified Bacteria</b>	<b>694</b>	<b>247</b>	<b>554</b>	<b>1086</b>	<b>821</b>	<b>3402</b>	<b>1037</b>
Total						60279	3092

\*Group affiliation with OTUs is based on the most abundant pyrosequences in the OTUs. Many OTUs at the genus level contain 16S rRNA sequences with identified genera and unidentified 16S rRNA sequences. As a result some lesser abundant genera reside in OTUs predominated by unidentified sequences and are accounted for in the unidentified bacteria OTUs.

\*\*Unidentified *Proteobacteria* and *Eukaryota* OTUs are accounted for in unidentified bacteria.

Other refers to those genera within a major group in which only a few 16S rRNA sequences were found in the entire spring.

Unidentified refers to those sequences that were less than 80% similar to a major group or less than 94% similar to a genus.