



### Supplemental Figure S1:

Multidimensional scaling plot of Jinata samples. Each point represents the recovered microbial community from a given sample, with sites identified by color and sample type by shape. Samples plotting close to each other are relatively more similar in community composition. Abundance data are transformed by the 4<sup>th</sup> root to down-weight the effect of abundant taxa. Stress value is 0.0658.

### Supplemental Figure S2:

Microscopy images of sediment (Source Pool and Pool 1) or mat (Pool 2, Pool 3, and Out Flow). Left are light microscopy images. Center and right are fluorescence images. At center, blue signal is DAPI-stained (Excitation: 365nm, Emission: BP445~50nm). At right, red is autofluorescence signal of Cyanobacteria (BP395~440nm, LP470nm). Scale bars 50  $\mu\text{m}$ .

**Supplemental Table S1:** Geochemistry and brief description at sampling sites along the flow path of Jinata Onsen as discussed in the text.

	pH	T ( $^{\circ}\text{C}$ )	Fe(II) ( $\mu\text{M}$ )	DO ( $\mu\text{M}$ )	DIC (mM)	DOC (mM)	Descriptions
Source Pool	5.4	60-63	260	4.7 (source) 39	Not measured	Not measured	Fluffy red iron oxide precipitate

				(surface)			
<b>Pool 1</b>	<b>5.8</b>	<b>59-59.5</b>	<b>265</b>	<b>58</b>	<b>5.51 ± 0.28</b>	<b>1.31 ± 0.18</b>	<b>Reddish precipitate and streamers in shallower regions, more yellowish deeper</b>
<b>Pool 2</b>	<b>6.5</b>	<b>44.5-54</b>	<b>151</b>	<b>134</b>	<b>2.09 ± 0.11</b>	<b>0.76 ± 0.10</b>	<b>Iron oxide-coated microbial mats. Orange to orange-green.</b>
<b>Pool 3</b>	<b>6.7</b>	<b>37.3-46</b>	<b>100</b>	<b>175</b>	<b>1.79 ± 0.09</b>	<b>0.70 ± 0.10</b>	<b>Green or mottled orange-green microbial mats, commonly with 1-5cm finger-like morphology.</b>
<b>Outflow</b>	<b>6.5</b>	<b>27-32</b>	<b>45</b>	<b>234</b>	<b>Not measured</b>	<b>Not measured</b>	<b>Ocean water within mixing zone at high tide, with constant flow of spring water from Pool 2. Thin green microbial mats.</b>

**Supplemental Table S2:** Gas composition of bubbles collected from the Source Pool at Jinata Onsen.

	Average of gas compositions (percent composition)								
Sampling dates (mm/dd/yyyy)	Measurement number	N <sub>2</sub>	SE	O <sub>2</sub>	SE	CH <sub>4</sub>	SE	CO <sub>2</sub>	SE

10/03/2017	2	30.5	4.6	0.10	0.01	0.04	0.01	69.3	4.6
04/13/2018	4	55.5	5.5	0.07	0.04	0.05	0.01	44.4	5.0

**Supplemental Table S3:**

Diversity metrics of Jinata sequencing. Diversity metrics calculated for both 99% and 97% sequence identity cutoffs for assigning OTUs.

Sample:	Reads:	OTUs (99%):	Good's Coverage (99%):	Shannon Index (99%):	Inverse Simpson (99%):	OTUs (97%):	Good's Coverage (97%):	Shannon Index (97%):	Inverse Simpson (97%):
Source Pool A	48680	1883 2	0.665	10.443	35.146	6951	0.907	7.996	17.361
Source Pool B	18235	7772	0.646	10.388	68.018	4139	0.844	8.651	31.822
Pool 1 A	96268	2530 5	0.788	10.172	53.546	11734	0.920	8.403	28.691
Pool 1 B	56672	1383 5	0.797	8.813	26.975	5598	0.933	6.818	13.827
Pool 2 A	35690	1248 9	0.713	9.625	22.248	7352	0.855	8.271	16.600
Pool 2 B	4454	2274	0.560	9.066	49.599	1729	0.689	8.104	27.390
Pool 3 A	28273	1133 4	0.665	10.046	35.705	6766	0.824	8.403	20.034
Pool 3 B	2076	1166	0.522	8.832	75.900	786	0.699	7.489	35.312
Outflow A	31980	1848 6	0.497	11.989	64.318	11994	0.712	10.538	34.881
Outflow B	32465	1089 6	0.713	9.281	25.691	5918	0.857	7.133	11.585

**Supplemental Table S4:**

16S rRNA gene amplicon data as OTU table with sequences.

**Supplemental Table S5:**

16S rRNA gene amplicon data as relative abundance binned at the class level.

**Supplemental Table S6:**

1. High- and medium-quality metagenome-assembled genomes (MAGs) (>50% completeness and <10% contamination) recovered from Jinata Onsen. Predicted taxonomy based on placement in reference phylogeny as presented in Figure 4 and by GTDB-Tk (87). Optimal growth temperatures predicted following methods from (Li, G., Rabe, K.S., Nielsen, J. and Engqvist, M.K., 2019. Machine learning applied to predicting microorganism growth temperatures and enzyme catalytic optima. *BioRxiv*, p.522342).

**Supplemental Table S7:**

Presence of genes involved in aerobic respiration, hydrogen- and iron-oxidation, and carbon fixation in MAGs discussed in the text, with NCBI accession numbers provided.