Article

Insights on Microbial Communities Inhabiting Non-Volcanic Hot Springs

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Supplementary Materials: The following supporting information can be downloaded at: www.mdpi.com/xxx/s1, Figure S1: Schematic representation of Muiño da Veiga hot springs and sampling site. Figure S2: Rarefaction plot. Figure S3: CheckM plot. Table S1: Statistics for the metagenome from Muiño da Veiga hot spring. Table S2. CheckM report.
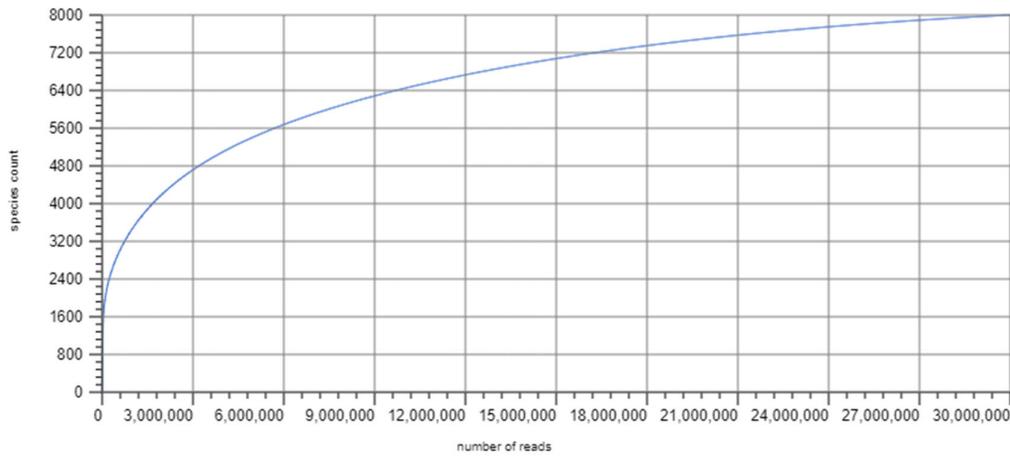
Supplementary Figure S1. Rarefaction plot. Assessment of the sequencing depth by plotting species annotation counts against the number of reads analyzed.
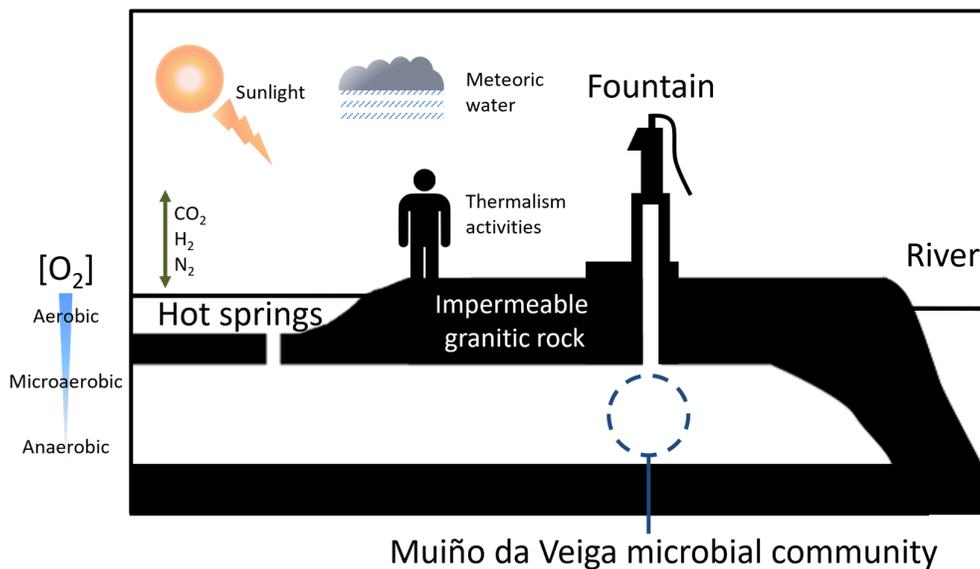
Supplementary Figure S2. Schematic representation of Muiño da Veiga hot springs and sampling site. The impermeable granitic rock prevents water with meteoric origins (rain, Miño river) from mixing with the subterranean hot water. Sunlight exposition is limited to the surface of the hot spring's pools, where the exchange of gaseous elements takes place. Oxygen concentration decreases with water depth. As the pools are open for thermalism activities, some degree of cross contamination may take place too.
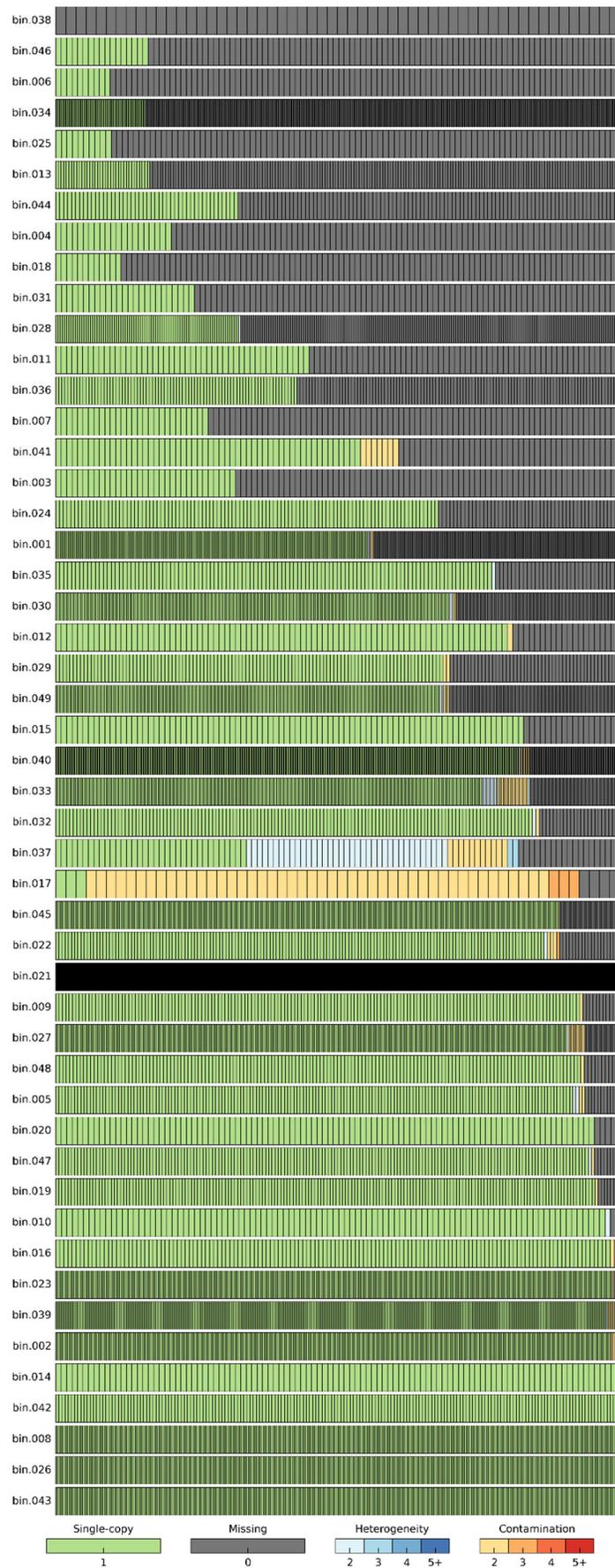
Supplementary Figure S3. CheckM plot of the bins obtained from Muiño da Veiga metagenomic read processing. Single copy phylogenetic markers are used to evaluate the bin's completeness and contamination: green color indicates one copy present for the marker gene in the bin; gray indicates an absence; the various shades of orange indicate multiple copies of the marker gene, suggesting a contamination of the bin; various shades of blue indicate multiple copies of the marker gene from closely related strains, suggesting strain heterogeneity in the sample.

Supplementary Table S1. Statistics for the metagenome from Muiño da Veiga hot spring.

FEATURE	NUMBER	UNITS
Sequences (uploaded)	27,113,937	sequences
Basepairs (uploaded)	3,968,584,153	bp
Mean sequence length (uploaded)	146 ± 24	bp
Mean GC content (uploaded)	44 ± 13	%
QC failed	9,290,572	Sequences
	34.265	% of total
Artificial duplicate reads	4,807,111	Sequences
	17.729	% of total
Sequences (post QC)	17,823,365	Sequences
	65.735	% of total
Basepairs (post QC)	2,658,836,275	bp
	66.997	% of total
Mean sequence length (post QC)	149 ± 24	bp
Mean GC content (post QC)	46 ± 14	%
Predicted features	16,639,799	sequences
	93.359	% of total post QC
rRNA genes	72,722	sequences
	0.408	% of total post QC
Predicted protein with known function	13,052,391	sequences
	73.232	% of total post QC
	78.441	% of predicted features
Predicted protein with unknown function	3,514,686	sequences
	19.720	% of total post QC
	21.122	% of predicted features
Unknown features	1,183,566	sequences
	6.641	% of total post QC

Supplementary Table S2. CheckM report for Muiño da Veiga hot spring bins.

BIN	# Genomes	# Markers	# Marker Sets	0	1	2	3	Completeness	Contamination
001	193	427	214	188	234	5	0	58.19	1.67
002	138	335	243	5	327	3	0	97.94	1.23
003	5449	104	58	71	33	0	0	48.28	0.0
004	5449	103	57	82	21	0	0	18.66	0.0
005	2258	181	110	12	165	4	0	92.67	1.82
006	5449	104	58	94	10	0	0	13.79	0.0
007	5449	104	58	76	28	0	0	41.38	0.0
008	138	336	246	2	333	1	0	99.19	0.1
009	901	171	117	12	158	1	0	91.03	0.85
010	5443	102	57	2	99	1	0	96.49	1.75
011	5443	105	59	58	47	0	0	32.9	0.0
012	5449	104	58	20	83	1	0	68.39	1.72
013	54	217	168	181	36	0	0	17.26	0.0
014	5449	104	58	1	103	0	0	98.28	0.0
015	5449	104	58	18	86	0	0	73.41	0.0
016	2993	140	85	2	137	1	0	97.65	1.18
017	5656	56	24	4	3	46	3	86.11	78.7
018	5449	104	58	92	12	0	0	18.97	0.0
019	2258	184	114	8	175	1	0	95.95	0.88
020	5449	104	58	5	99	0	0	92.95	0.0
021	134	1169	335	146	1012	11	0	87.87	0.72
022	2258	180	109	20	155	4	1	87.36	3.26
023	138	338	246	6	331	1	0	97.76	0.2
024	924	151	101	49	102	0	0	57.72	0.0
025	5449	102	57	92	10	0	0	15.79	0.0

026	138	336	246	2	334	0	0	99.19	0.0
027	138	338	246	23	304	11	0	91.4	3.05
028	1495	261	164	176	84	1	0	29.19	0.61
029	924	161	108	49	110	2	0	70.58	1.23
030	169	313	233	92	217	4	0	68.31	1.07
031	5449	102	57	77	25	0	0	27.19	0.0
032	924	163	110	24	137	2	0	83.18	1.82
033	169	316	236	52	237	26	1	82.51	7.55
034	32	488	209	411	77	0	0	15.03	0.0
035	2993	143	89	32	110	1	0	66.56	0.1
036	2258	188	117	108	80	0	0	35.16	0.0
037	5449	104	58	19	35	48	2	84.97	49.06
038	5656	56	24	56	0	0	0	0.0	0.0
039	323	386	233	6	374	6	0	97.85	2.15
040	30	540	241	90	439	11	0	80.03	1.28
041	5449	104	58	41	56	7	0	43.97	4.23
042	2258	181	110	1	180	0	0	99.09	0.0
043	138	336	246	1	335	0	0	99.59	0.0
044	2993	143	89	97	46	0	0	17.59	0.0
045	138	338	246	38	299	1	0	86.59	0.2
046	5449	104	58	87	17	0	0	13.17	0.0
047	2258	181	110	9	170	2	0	93.18	1.82
048	924	163	110	11	151	1	0	91.82	0.91
049	169	316	236	97	214	5	0	72.23	1.91