

Supplementary Materia

Supplementary Tables

Table S1. Quality score and GTDB taxonomy of 34 MAGs retrieved from the Tangyin hydrothermal vent and 17 reference genomes.

Genome	Completeness	Contamination	Taxonomy
MAG16	94.20529801	0.220750552	d__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__PS1; f__Thioglobaceae; g__s__
MAG29	89.73160796	2.803738318	d__Bacteria; p__Thermoproteota; c__Bathyarchaea; o__TCS64; f__TCS64; g__GCA-2726865; s__
MAG19	88.85304659	1.612903226	d__Bacteria; p__Desulfobacterota; c__Desulfobacteria; o__Desulfobacterales; f__SURF-7; g__s__
MAG32	87.06896552	3.761755486	d__Bacteria; p__Chloroflexota; c__Anaerolineae; o__Anaerolineales; f__UBA11858; g__UBA11858; s__
MAG4	83.82838284	0	d__Bacteria; p__Chloroflexota; c__Dehalococcoidia; o__SZUA-161; f__SZUA-161; g__s__
MAG23	81.25448029	0.896057348	d__Bacteria; p__Desulfobacterota; c__Desulfobacteria; o__Desulfatiglandales; f__s__g__s__
MAG15	81.17913832	1.636904762	d__Bacteria; p__Desulfobacterota; c__Desulfobulbia; o__Desulfobulbales; f__BM004; g__BM004; s__
MAG12	78.48358357	2.248941319	d__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Thiohalobacterales; f__DSM-19610; g__Thiogranum; s__
MAG6	76.79723502	1.290322581	d__Bacteria; p__Desulfobacterota; c__Desulfobacteria; o__Desulfobacterales; f__SURF-7; g__s__
MAG24	73.87096774	1.612903226	d__Bacteria; p__Desulfobacterota; c__Desulfobacteria; o__Desulfobacterales; f__BuS5; g__s__
MAG30	73.34833527	0.571041425	d__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Chromatiales; f__Sedimenticolaceae; g__s__
MAG9	70.90919701	1.680672269	d__Bacteria; p__Desulfobacterota; c__s__o__f__g__s__
MAG13	67.81003584	1.095750128	d__Bacteria; p__Desulfobacterota; c__Desulfobacteria; o__C00003060; f__C00003060; g__s__
MAG18	66.65566557	2.090209021	d__Bacteria; p__Chloroflexota; c__Dehalococcoidia; o__f__g__s__
MAG10	66.25759459	1.232394366	d__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__UBA4486; f__UBA4486; g__SMWN01; s__
MAG27	66.06024289	1.681048258	d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Flavobacteriales; f__Flavobacteriaceae; g__QNYL01; s__
MAG17	65.86844528	2.697302697	d__Bacteria; p__Fermentibacterota; c__Fermentibacteria; o__Fermentibacterales; f__Fermentibacteraceae; g__Aegiribacteria; s__
MAG33	65.37137114	4.651080827	d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Cytophagales; f__Cyclobacteriaceae; g__s__
MAG21	63.31738437	0	d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Flavobacteriales; f__Flavobacteriaceae; g__QNYL01; s__
MAG22	63.05948953	1.648351648	d__Bacteria; p__Eisenbacteria; c__s__o__f__g__s__
MAG31	62.53779289	1.785714286	d__Bacteria; p__Desulfobacterota; c__Desulfobulbia; o__Desulfobulbales; f__Desulfobulbaceae; g__Electrothrix; s__
MAG8	61.57706093	0	d__Bacteria; p__Desulfobacterota; c__Desulfobacteria; o__Desulfobacterales; f__UBA5852; g__s__
MAG25	60.47654596	1.32387462	d__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Woeseiales; f__Woeseiaceae; g__UBA1847; s__
MAG14	60.00921659	0.921658986	d__Bacteria; p__Desulfobacterota; c__Desulfobacteria; o__Desulfobacterales; f__BuS5; g__UBA11574; s__
MAG28	58.62068966	0	d__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__UBA10353; f__LS-SOB; g__s__
MAG3	57.24471607	5.238878768	d__Bacteria; p__Gemmatimonadota; c__Gemmatimonadetes; o__Gemmatimonadales; f__GWC2-71-9; g__s__
MAG1	55.85909418	2.803738318	d__Bacteria; p__Thermoproteota; c__Bathyarchaea; o__TCS64; f__TCS64; g__RBG-16-57-9; s__
MAG20	54.9489726	1.098901099	d__Bacteria; p__Zixibacteria; c__MSB-5A5; o__f__g__s__
MAG2	54.4488656	4.000603865	d__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Xanthomonadales; f__SZUA-36; g__s__
MAG7	52.9109063	2.580645161	d__Bacteria; p__Desulfobacterota; c__Desulfobacteria; o__Desulfobacterales; f__BuS5; g__S5133MH16; s__
MAG34	52.87114846	2.315592904	d__Bacteria; p__Proteobacteria; c__Zetaproteobacteria; o__Mariprofundales; f__Mariprofundaceae; g__s__
MAG11	52.50332821	2.424475166	d__Bacteria; p__Desulfobacterota; c__Desulfobacteria; o__Desulfobacterales; f__BuS5; g__s__
MAG26	52.36303123	0.537634409	d__Bacteria; p__Desulfobacterota; c__Desulfobacteria;

			o Desulfobacterales; f SG8-13; g ; s
			(Continued)
MAG5	51.96523054	0	d_Bacteria; p_Desulfobacterota; c_Desulfobulbia;
GCA_00030	100	0	o_Desulfobulbales; f_Desulfobulbaceae; g_QNYF01; s__
7955.1			d_Bacteria; p_Desulfobacterota; c_Desulfovibrionia;
GCA_00179	94.96	1.68	o_Desulfovibrionales; f_Desulfovibrionaceae;
7445.1			g_Solidesulfobulbia; s_Solidesulfobulbia magneticus A
GCA_00179	94.84	2.26	d_Bacteria; p_Desulfobacterota E; c_Deferrimicrobia;
7465.1			o_Deferrimicrobiales; f_Deferrimicrobiaceae;
GCA_00203	95.05	2.2	g_Deferrimicrobium; s_Deferrimicrobium sp001797445
0045.1			d_Bacteria; p_Desulfobacterota F; c_GWC2-55-46; o_GWC2-
GCA_01472	96.15	1.28	55-46; f_GWC2-55-46; g_GWB2-55-19; s_GWB2-55-19
8175.1			sp001797465
GCA_00589	92.66	1.1	d_Bacteria; p_Fermentibacterota; c_Fermentibacteria;
3265.1			o_Fermentibacterales; f_Fermentibacteraceae; g_Aegiribacteria;
GCA_00178	98.9	0	s_Aegiribacteria sp002030045
0165.1			d_Bacteria; p_Fermentibacterota; c_Fermentibacteria;
GCA_01692	91.16	3.3	o_Fermentibacterales; f_Fermentibacteraceae; g_WJMA01;
8395.1			s_WJMA01 sp014728175
GCA_01693	92.31	2.2	d_Bacteria; p_Eisenbacteria; c_RBG-16-71-46; o_SZUA-252;
GCA_00364	93.1	2.5	f_SZUA-252; g_WS-7; s_WS-7 sp005893265
1425.1			d_Bacteria; p_Eisenbacteria; c_RBG-16-71-46; o_RBG-16-71-
GCA_00359	91.21	1.1	46; f_RBG-16-71-46; g_RBG-16-71-46; s_RBG-16-71-46
9535.1			sp001780165
GCA_00156	97.27	0	d_Bacteria; p_Fermentibacterota; c_JAFGKV01;
7485.1			o_JAFGKV01; f_JAFGKV01; g_JAFGKV01; s_JAFGKV01
GCF_00052	97.58	0	sp016928395
6415.1			d_Bacteria; p_Fermentibacterota; c_Fermentibacteria;
GCF_00019	99.7	0	o_Fermentibacterales; f_Fermentibacteraceae; g_Aegiribacteria;
3795.1			s_Aegiribacteria sp016936235
GCA_00001	99.7	0.1	d_Bacteria; p_Zixibacteria; c_MSB-5A5; o_GN15;
6325.1			f_PGXB01; g_PGXB01; s_PGXB01 sp003641425
GCA_00026	100	0.3	d_Bacteria; p_AABM5-125-24; c_B3-LCP; o_B3-LCP; f_B3-
GCA_00043	98.1	0.96	LCP; g_SURF-9; s_SURF-9 sp003599535
GCA_01839	94.86	0	d_Bacteria; p_Chloroflexota; c_Anaerolineae;
GCA_00014	100	0	o_Aggregatilineales; f_Phototrophicaceae; g_OLB13;
5985.1			s_OLB13 sp001567485
			d_Bacteria; p_Chloroflexota; c_Chloroflexia;
			o_Chloroflexales; f_Herpetosiphonaceae; g_JKG1; s_JKG1
			sp000526415
			d_Bacteria; p_Pseudomonadota; c_Gammaproteobacteria;
			o_Burkholderiales; f_Neisseriaceae; g_Neisseria; s_Neisseria
			lactamica A
			d_Bacteria; p_Pseudomonadota; c_Gammaproteobacteria;
			o_Enterobacterales; f_Enterobacteriaceae; g_Lelliottia;
			s_Lelliottia sp000016325
			d_Bacteria; p_Bacteroidota; c_Bacteroidia; o_Cytophagales;
			f_Spirosomaceae; g_Emticicia; s_Emticicia oligotrophica
			d_Bacteria; p_Bacteroidota; c_Bacteroidia; o_Bacteroidales;
			f_Rikenellaceae; g_Alistipes; s_Alistipes avistercoris
			d_Archaea; p_Thermoproteota; c_Bathyarchaea; o_TCS64;
			f_TCS64; g_JAGTRB01; s_JAGTRB01 sp018396865
			d_Archaea; p_Thermoproteota; c_Thermoprotei A;
			o_Sulfolobales; f_Ignisphaeraceae; g_Ignisphaera;
			s_Ignisphaera aggregans

Table S2. Quality score and GTDB taxonomy of reference MAGs.

Genome	Completeness	Contamination	Taxonomy
GCA_001593855.1	74.3	1.32	d_Archaea; p_Thermoproteota; c_Bathyarchaea;
GCA_002255025.1	73.83	0.93	o_B25; f_B25; g_B25; s_B25 sp001593855
GCA_003661975.1	83.64	6.07	d_Archaea; p_Thermoproteota; c_Bathyarchaea;
GCA_001273345.1	50.34	9.22	o_ex4484-135; f_ex4484-135; g_ex4484-135;
GCA_002726865.1	92.99	3.31	s_ex4484-135 sp002255025
			d_Archaea; p_Thermoproteota; c_Bathyarchaea;
			o_B26-1; f_B26-1; g_B63; s_B63 sp003661975
			d_Archaea; p_Bathyarchaeota; s_SG8-32-1
			d_Archaea; p_Thermoproteota; c_Bathyarchaea;
			o_TCS64; f_TCS64; g_GCA-2726865; s_GCA-

(Continued)

GCA_002010925.1	77.28	1.25	d__Archaea; p__Thermoproteota; c__Bathyarchaea; o__B26-1; f__UBA233; g__UBA233; s__UBA233 sp002010925
GCA_004376295.1	97.82	1.87	d__Archaea; p__Thermoproteota; c__Bathyarchaea; o__B26-1; f__BA1; g__SOJZ01; s__SOJZ01 sp004376295
GCA_001768965.1	72.26	1.94	d__Archaea; p__Thermoproteota; c__Bathyarchaea; o__40CM-2-53-6; f__FEN-987; g__FEN-987; s__FEN- 987 sp001768965
GCA_003978185.1	60.21	0.7	d__Bacteria; p__Pseudomonadota; c__Gammaproteobacteria; o__PS1; f__Thioglobaceae; g__Thioglobus_C; s__Thioglobus_C sp003978185
GCA_012964205.1	90.02	4.25	d__Bacteria; p__Pseudomonadota; c__Gammaproteobacteria; o__PS1; f__Thioglobaceae; g__Thioglobus_A; s__Thioglobus_A sp012963715
GCA_008080915.1	82.42	0	d__Bacteria; p__Pseudomonadota; c__Gammaproteobacteria; o__PS1; f__Thioglobaceae; g__VMDI01; s__VMDI01 sp008080915
GCA_001628345.1	86.6	3.53	d__Bacteria; p__Pseudomonadota; c__Gammaproteobacteria; o__PS1; f__Thioglobaceae; g__Pseudothioglobus; s__Pseudothioglobus sp001628405
GCA_014384345.1	97.35	0	d__Bacteria; p__Pseudomonadota; c__Gammaproteobacteria; o__PS1; f__Thioglobaceae; g__Thioglobus_A; s__Thioglobus_A pontius
GCA_018645225.1	95.81	0	d__Bacteria; p__Pseudomonadota; c__Gammaproteobacteria; o__PS1; f__Thioglobaceae; g__SUP05; s__SUP05 sp000205985
GCA_018697175.1	78.57	5.68	d__Bacteria; p__Pseudomonadota; c__Gammaproteobacteria; o__PS1; f__Thioglobaceae; g__SUP05; s__SUP05 sp000205985