

Supplementary Information for

Network-directed efficient isolation of previously uncultivated *Chloroflexi* and related bacteria in hot spring microbial mats

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Supplementary Table 1. Physicochemical parameters of the hot spring samples used in the study.

Sample	Location	°N	°E	Elevation	Temperature (°C)	pH	Sampling time
S51	Tibet (QZM)	28.24646	91.79549	4388	63.0	6.8	2015.8
S52	Tibet (QZM)	28.24860	91.80365	4450	62.0	6.5	2015.8
S56	Tibet (QZM)	28.24816	91.80855	4505	67.0	7.0	2015.8
S57	Tibet (QZM)	28.24816	91.80855	4505	65.0	7.0	2015.8
S58	Tibet (QZM)	28.24816	91.80855	4505	64.0	6.8	2015.8
S59	Tibet (QZM)	28.24816	91.80855	4505	62.0	6.8	2015.8
S60	Tibet (QZM)	28.24851	91.80342	4438	65.7	6.7	2015.8
S61	Tibet (QZM)	28.24722	91.80970	4502	67.5	6.5	2015.8
S81	Tibet (QC)	30.66632	91.59135	4497	61.4	6.9	2016.8
S93	Tibet (DGJ)	29.60516	85.74628	5079	66.7	7.4	2016.8
S94	Tibet (DGJ)	29.60516	85.74628	5079	62.3	7.3	2016.8
Y1	Yunnan (Rehai)	24.94670	98.43709	1439	66.0	7.5	2017.5
Y2	Yunnan (Rehai)	24.94664	98.43703	1439	63.0	7.5	2017.5
Y3	Yunnan (Rehai)	24.94647	98.43682	1352	55.0	7.0	2017.5
A6	Tibet (DGQ)	82.10560	30.70526	4861	57.0	7.0	2018.8
A8	Tibet (DGQ)	82.10560	30.70526	4861	65.0	7.0	2018.8
A9	Tibet (DGQ)	82.10560	30.70526	4861	55.0	7.0	2018.8
A47	Tibet (MS)	80.75408	31.12466	4355	71.7	7.9	2018.8
A62	Tibet (MLJ)	80.49134	31.36898	4865	55.0	7.0	2018.8
A66	Tibet (BAR)	80.40778	31.44331	4807	55.0	6.5	2018.8
A75	Tibet (LJ)	80.36404	32.35644	4495	52.0	7.0	2018.8
A93	Tibet (DGJ)	29.59870	85.75069	5057	60.0	8.0	2018.8
A94	Tibet (DGJ)	29.59872	85.75070	5057	54.0	8.0	2018.8
A95	Tibet (DGJ)	29.59875	85.75074	5057	52.0	8.0	2018.8
A96	Tibet (DGJ)	29.59877	85.75076	5057	45.0	8.0	2018.8
A99	Tibet (DGJ)	29.60607	85.74900	5076	68.0	8.0	2018.8

Note: The samples Y1, Y2, Y3 and A96 were used for isolation.

Supplementary Table 2. Statistical parameters of the high-throughput sequencing.

Sample ID	Raw reads count	Filtered reads count	OTU count
S51	166889	140817	379
S52	100172	75934	310
S56	129194	101748	612
S57	113332	90315	633
S58	104825	83742	650
S59	118868	91745	722
S60	122801	99326	655
S61	149358	112642	537
S81	64946	46773	597
S93	114633	102512	316
S94	76605	69993	238
Y1	80448	74969	596
Y2	66516	62275	416
Y3	76393	70332	177
A6	105460	81111	511
A8	91599	74289	670
A9	118359	102334	518
A47	95561	71279	359
A62	96497	79830	340
A66	95559	74829	913
A75	113624	98565	199
A93	83907	67820	361
A94	99329	77926	342
A95	84620	70335	465
A96	91067	76169	385
A99	96662	76262	494

Supplementary Table 3. Conventional isolation media used in the current study.

Media	Composition (g/L)
Reasoner's 2A (R2A) agar [DSM 830 medium]	Yeast extract 0.5, peptone 0.5, casamino acids 0.5, glucose 0.5, starch 0.5, K ₂ HPO ₄ 0.3, MgSO ₄ 0.05, sodium pyruvate 0.3, agar 20.0, pH 7.2
CC agar	Microcrystalline cellulose 1.0, casamino acids 1.0, KNO ₃ 0.2, Na ₂ HPO ₄ 0.5, MgSO ₄ ·7H ₂ O 0.05, FeSO ₄ ·7H ₂ O 0.01, agar 20.0, pH 7.5 *Cellulose is one of the important carbon source in hot spring microbial mats.
<i>Thermus</i> 162 agar medium (DSM 878 medium)	Yeast extract 1.0, tryptone 1.0, nitrilotriacetic acid 100.0 mg, CaSO ₄ ·2H ₂ O 40.0 mg, MgCl ₂ ·6H ₂ O 200.0 mg, 0.01 M ferric citrate 0.5 mL, trace element solution 0.5 mL, phosphate buffer 100.0 mL, agar 20.0, pH 7.2. 1. Phosphate buffer (g/L) [KH ₂ PO ₄ 5.44, Na ₂ HPO ₄ ·12H ₂ O 43.0, pH 7.2]. 2. Trace element solution (g/L) [MnSO ₄ ·H ₂ O 2.28, ZnSO ₄ ·7H ₂ O 0.5, H ₃ BO ₃ 0.5, CuSO ₄ ·5H ₂ O Na ₂ MoO ₄ ·2H ₂ O 25.0 mg, CoCl ₂ ·6H ₂ O 45.0 mg]
T5 agar	Tryptone 0.5, yeast extract 2.0, glucose 1.0, lotus root starch 1.0, agar 20.0, pH 7.2

***Reference:**

Romling, U., and M. Y. Galperin (2015). Bacterial cellulose biosynthesis: diversity of operons, subunits, products, and functions. *Trends Microbiol* **23**: 545-557.

Supplementary Table 4. Taxonomic affiliation of the strains isolated in this study.

Strain ID	Sample	Isolation media	Group	Top-hit taxon	Top-hit strain	Similarity (%)
SYSU GT96-39	A96	SCM-R2A	Group 21	FJ529921	NBDTU1	89.23
SYSU GT96-1	A96	SCM-R2A	Group 18	<i>Schleiferia thermophila</i>	TU-20(T)	91.34
SYSU GT96-37	A96	SCM-R2A	Group 18	<i>Schleiferia thermophila</i>	TU-20(T)	91.34
SYSU GT96-40-1	A96	SCM-R2A	Group 20	AF445665	SM1C08	94.07
SYSU GT96-46	A96	SCM-R2A	Group 37	<i>Sandaracinobacter sibiricus</i>	RB16-17(T)	95.46
SYSU GT96-18	A96	R2A	Group 37	<i>Sandaracinobacter sibiricus</i>	RB16-17(T)	95.47
SYSU GT96-61	A96	R2A	Group 37	<i>Sandaracinobacter sibiricus</i>	RB16-17(T)	95.47
SYSU GT96-4	A96	SCM-R2A	Group 37	<i>Sandaracinobacter sibiricus</i>	RB16-17(T)	95.47
SYSU GT96-72	A96	R2A	Group 37	<i>Sandaracinobacter sibiricus</i>	RB16-17(T)	95.48
SYSU GT96-53	A96	SCM-R2A	Group 37	<i>Sandaracinobacter sibiricus</i>	RB16-17(T)	95.49
SYSU GT96-54	A96	SCM-R2A	Group 37	<i>Sandaracinobacter sibiricus</i>	RB16-17(T)	95.5
SYSU GT96-34	A96	SCM-R2A	Group 37	<i>Sandaracinobacter sibiricus</i>	RB16-17(T)	95.52
SYSU GT96-47	A96	SCM-R2A	Group 37	<i>Sandaracinobacter sibiricus</i>	RB16-17(T)	95.52
SYSU GT96-57	A96	SCM-R2A	Group 37	<i>Sandaracinobacter sibiricus</i>	RB16-17(T)	95.53
SYSU GT96-56	A96	SCM-R2A	Group 37	<i>Sandaracinobacter sibiricus</i>	RB16-17(T)	95.54
SYSU GT96-71	A96	R2A	Group 37	<i>Sandaracinobacter sibiricus</i>	RB16-17(T)	95.55
SYSU GT96-34-1	A96	SCM-R2A	Group 25	AF407720	B35	96.96
SYSU GT96-19	A96	R2A	Group 15	<i>Chloroflexus islandicus</i>	isl-2(T)	98.06
SYSU GT96-45	A96	SCM-R2A	Group 15	<i>Chloroflexus islandicus</i>	isl-2(T)	98.08
SYSU GT96-3	A96	SCM-R2A	Group 15	<i>Chloroflexus islandicus</i>	isl-2(T)	98.19
SYSU GT96-40	A96	SCM-R2A	Group 15	<i>Chloroflexus islandicus</i>	isl-2(T)	98.19
SYSU GT96-52	A96	SCM-R2A	Group 15	<i>Chloroflexus islandicus</i>	isl-2(T)	98.19
SYSU GT96-20	A96	R2A	Group 15	<i>Chloroflexus islandicus</i>	isl-2(T)	98.21
SYSU GT96-17	A96	R2A	Group 41	AM777983	CVClOAm2Ph106	98.74

SYSU GT96-60	A96	R2A	Group 39	<i>Elioraea tepidiphila</i>	DSM 17972(T)	99.74
SYSU GT96-24	A96	R2A	Group 39	<i>Elioraea tepidiphila</i>	DSM 17972(T)	99.75
SYSU GT96-14	A96	SCM-R2A	Group 19	<i>Roseomonas alkaliterrae</i>	YIM 78007(T)	99.87
SYSU GT96-26	A96	R2A	Group 38	LJIY	FJAT-21963	100
SYSU GT96-12	A96	SCM-R2A	Group 38	LJIY	FJAT-21963	100
SYSU GY1-61	Y1	SCM- <i>Thermus</i> 162 medium	Group 8	JN825371	Alchichica_AI52_2_1B_100	89.81
SYSU GY1-62	Y1	SCM- <i>Thermus</i> 162 medium	Group 8	JN825371	Alchichica_AI52_2_1B_100	89.81
SYSU GY1-30	Y1	SCM-R2A	Group 18	<i>Schleiferia thermophila</i>	TU-20(T)	92.99
SYSU GY1-233	Y1	<i>Thermus</i> 162 medium	Group 36	DQ129304	AKIW813	93.42
SYSU GY1-259	Y1	SCM- <i>Thermus</i> 162 medium	Group 36	DQ129304	AKIW813	93.42
SYSU GY1-P12	Y1	SCM-R2A	Group 36	EF516779	FCPP721	93.87
SYSU GY1-29	Y1	SCM-R2A	Group 14	<i>Chloroflexus islandicus</i>	isl-2(T)	94.74
SYSU GY1-23	Y1	SCM-R2A	Group 36	EF205457	YCB86	94.99
SYSU GY1-75	Y1	R2A	Group 37	<i>Sandaracinobacter sibiricus</i>	RB16-17(T)	95.47
SYSU GY1-100	Y1	R2A	Group 27	JQ426256	AN0C1AD06	95.53
SYSU GY1-247	Y1	<i>Thermus</i> 162 medium	Group 26	<i>Meiothermus cateniformans</i>	LY1(T)	95.57
SYSU GY1-96	Y1	R2A	Group 27	JN038861	P-R74	95.71
SYSU GY1-59	Y1	SCM- <i>Thermus</i> 162 medium	Group 29	<i>Thermus tengchongensis</i>	YIM 77924(T)	96.3
SYSU GY1-65	Y1	SCM- <i>Thermus</i> 162 medium	Group 13	<i>Roseiflexus castenholzii</i>	DSM 13941(T)	96.52
SYSU GY1-4	Y1	SCM-R2A	Group 12	<i>Tepidimonas ignava</i>	SPS-1037(T)	96.68
SYSU GY1-28	Y1	SCM-R2A	Group 12	<i>Tepidimonas ignava</i>	SPS-1037(T)	96.92
SYSU GY1-58	Y1	SCM- <i>Thermus</i> 162 medium	Group 12	<i>Tepidimonas ignava</i>	SPS-1037(T)	96.92
SYSU GY1-64	Y1	SCM- <i>Thermus</i> 162 medium	Group 12	<i>Tepidimonas ignava</i>	SPS-1037(T)	97
SYSU GY1-60	Y1	SCM- <i>Thermus</i> 162 medium	Group 12	<i>Tepidimonas ignava</i>	SPS-1037(T)	97.04
SYSU GY1-63	Y1	SCM- <i>Thermus</i> 162 medium	Group 12	<i>Tepidimonas ignava</i>	SPS-1037(T)	97.08
SYSU GY1-278	Y1	SCM- <i>Thermus</i> 162 medium	Group 25	AF407725	B63	97.23
SYSU GY1-272	Y1	SCM- <i>Thermus</i> 162 medium	Group 25	AF407725	B63	97.27
SYSU GY1-174	Y1	SCM-R2A	Group 26	<i>Meiothermus hypogaeus</i>	AZM34c11(T)	97.38

SYSU GY1-105	Y1	R2A	Group 25	AF407720	B35	97.76
SYSU GY1-82	Y1	R2A	Group 25	AF407720	B35	97.77
SYSU GY1-241	Y1	<i>Thermus</i> 162 medium	Group 25	AF407720	B35	97.78
SYSU GY1-224	Y1	<i>Thermus</i> 162 medium	Group 25	AF407720	B35	97.79
SYSU GY1-66	Y1	SCM- <i>Thermus</i> 162 medium	Group 12	<i>Tepidimonas ignava</i>	SPS-1037(T)	97.81
SYSU GY1-56	Y1	SCM- <i>Thermus</i> 162 medium	Group 12	<i>Tepidimonas ignava</i>	SPS-1037(T)	97.83
SYSU GY1-67	Y1	SCM- <i>Thermus</i> 162 medium	Group 12	<i>Tepidimonas ignava</i>	SPS-1037(T)	97.84
SYSU GY1-57	Y1	SCM- <i>Thermus</i> 162 medium	Group 12	<i>Tepidimonas ignava</i>	SPS-1037(T)	97.92
SYSU GY1-239	Y1	<i>Thermus</i> 162 medium	Group 33	AF407714	B11	98.17
SYSU GY1-242	Y1	<i>Thermus</i> 162 medium	Group 33	AF407714	B11	98.17
SYSU GY1-67P	Y1	SCM- <i>Thermus</i> 162 medium	Group 12	<i>Tepidimonas ignava</i>	SPS-1037(T)	98.17
SYSU GY1-38P	Y1	SCM-R2A	Group 23	<i>Thermus caliditerrae</i>	YIM 77925(T)	98.18
SYSU GY1-99	Y1	R2A	Group 23	<i>Thermus caliditerrae</i>	YIM 77925(T)	98.2
SYSU GY1-170	Y1	SCM-R2A	Group 26	<i>Meiothermus cerbereus</i>	DSM 11376(T)	98.23
SYSU GY1-122	Y1	SCM-R2A	Group 23	<i>Thermus caliditerrae</i>	YIM 77925(T)	98.28
SYSU GY1-284	Y1	SCM- <i>Thermus</i> 162 medium	Group 26	<i>Meiothermus cerbereus</i>	DSM 11376(T)	98.3
SYSU GY1-252	Y1	SCM- <i>Thermus</i> 162 medium	Group 23	<i>Thermus caliditerrae</i>	YIM 77925(T)	98.3
SYSU GY1-283	Y1	SCM- <i>Thermus</i> 162 medium	Group 23	<i>Thermus caliditerrae</i>	YIM 77925(T)	98.3
SYSU GY1-222	Y1	<i>Thermus</i> 162 medium	Group 26	<i>Meiothermus cerbereus</i>	DSM 11376(T)	98.31
SYSU GY1-182	Y1	SCM-R2A	Group 26	<i>Meiothermus cerbereus</i>	DSM 11376(T)	98.31
SYSU GY1-253	Y1	SCM- <i>Thermus</i> 162 medium	Group 26	<i>Meiothermus cerbereus</i>	DSM 11376(T)	98.31
SYSU GY1-254	Y1	SCM- <i>Thermus</i> 162 medium	Group 26	<i>Meiothermus cerbereus</i>	DSM 11376(T)	98.31
SYSU GY1-277	Y1	SCM- <i>Thermus</i> 162 medium	Group 23	<i>Thermus caliditerrae</i>	YIM 77925(T)	98.31
SYSU GY1-257	Y1	SCM- <i>Thermus</i> 162 medium	Group 26	<i>Meiothermus cerbereus</i>	DSM 11376(T)	98.32
SYSU GY1-258	Y1	SCM- <i>Thermus</i> 162 medium	Group 26	<i>Meiothermus cerbereus</i>	DSM 11376(T)	98.32
SYSU GY1-164	Y1	SCM-R2A	Group 26	<i>Meiothermus cerbereus</i>	DSM 11376(T)	98.35
SYSU GY1-5	Y1	SCM-R2A	Group 40	<i>Chloroflexus islandicus</i>	isl-2(T)	98.67
SYSU GY1-P29	Y1	SCM-R2A	Group 2	<i>Thermoleophilum album</i>	ATCC 35263(T)	98.7

SYSU GY1-83	Y1	R2A	Group 41	AM777983	CVCloAm2Ph106	98.7
SYSU GY1-86	Y1	R2A	Group 41	AM777983	CVCloAm2Ph106	98.7
SYSU GY1-106	Y1	R2A	Group 41	AM777983	CVCloAm2Ph106	98.7
SYSU GY1-236	Y1	<i>Thermus</i> 162 medium	Group 41	AM777983	CVCloAm2Ph106	98.7
SYSU GY1-141	Y1	SCM-R2A	Group 41	AM777983	CVCloAm2Ph106	98.7
SYSU GY1-87	Y1	R2A	Group 41	AM777983	CVCloAm2Ph106	98.71
SYSU GY1-149	Y1	SCM-R2A	Group 41	AM777983	CVCloAm2Ph106	98.71
SYSU GY1-1	Y1	SCM-R2A	Group 41	AM777983	CVCloAm2Ph106	98.72
SYSU GY1-251	Y1	SCM- <i>Thermus</i> 162 medium	Group 23	<i>Thermus caliditerrae</i>	YIM 77925(T)	98.95
SYSU GY1-184	Y1	SCM-R2A	Group 40	<i>Chloroflexus islandicus</i>	isl-2(T)	99.04
SYSU GY1-21	Y1	SCM-R2A	Group 40	<i>Chloroflexus islandicus</i>	isl-2(T)	99.08
SYSU GY1-140	Y1	SCM-R2A	Group 40	<i>Chloroflexus islandicus</i>	isl-2(T)	99.08
SYSU GY1-159	Y1	SCM-R2A	Group 40	<i>Chloroflexus islandicus</i>	isl-2(T)	99.08
SYSU GY1-212	Y1	SCM-R2A	Group 40	<i>Chloroflexus islandicus</i>	isl-2(T)	99.08
SYSU GY1-183	Y1	SCM-R2A	Group 40	<i>Chloroflexus islandicus</i>	isl-2(T)	99.09
SYSU GY1-77	Y1	R2A	Group 40	<i>Chloroflexus islandicus</i>	isl-2(T)	99.1
SYSU GY1-160	Y1	SCM-R2A	Group 40	<i>Chloroflexus islandicus</i>	isl-2(T)	99.14
SYSU GY1-158	Y1	SCM-R2A	Group 40	<i>Chloroflexus islandicus</i>	isl-2(T)	99.21
SYSU GY1-195	Y1	SCM-R2A	Group 40	<i>Chloroflexus islandicus</i>	isl-2(T)	99.22
SYSU GY1-272-2	Y1	SCM- <i>Thermus</i> 162 medium	Group 40	<i>Chloroflexus islandicus</i>	isl-2(T)	99.22
SYSU GY1-71	Y1	SCM- <i>Thermus</i> 162 medium	Group 35	AY753393	SK47	99.23
SYSU GY1-179	Y1	SCM-R2A	Group 6	<i>Francisella piscicida</i>	GM2212(T)	99.25
SYSU GY1-103	Y1	SCM-R2A	Group 35	AY753393	SK47	99.32
SYSU GY1-84	Y1	SCM-R2A	Group 35	AY753393	SK47	99.33
SYSU GY1-11	Y1	SCM-R2A	Group 40	<i>Chloroflexus islandicus</i>	isl-2(T)	99.35
SYSU GY1-12	Y1	SCM-R2A	Group 40	<i>Chloroflexus islandicus</i>	isl-2(T)	99.35
SYSU GY1-121	Y1	SCM-R2A	Group 40	<i>Chloroflexus islandicus</i>	isl-2(T)	99.35
SYSU GY1-146	Y1	SCM-R2A	Group 40	<i>Chloroflexus islandicus</i>	isl-2(T)	99.35

SYSU GY1-22	Y1	SCM-R2A	Group 35	AY753393	SK47	99.35
SYSU GY1-68	Y1	SCM- <i>Thermus</i> 162 medium	Group 35	AY753393	SK47	99.35
SYSU GY1-69	Y1	SCM- <i>Thermus</i> 162 medium	Group 35	AY753393	SK47	99.35
SYSU GY1-228	Y1	<i>Thermus</i> 162 medium	Group 30	<i>Thermus caliditerrae</i>	YIM 77925(T)	99.35
SYSU GY1-55	Y1	SCM- <i>Thermus</i> 162 medium	Group 30	<i>Thermus caliditerrae</i>	YIM 77925(T)	99.35
SYSU GY1-57-2	Y1	SCM- <i>Thermus</i> 162 medium	Group 30	<i>Thermus caliditerrae</i>	YIM 77925(T)	99.35
SYSU GY1-19	Y1	SCM-R2A	Group 35	AY753393	SK47	99.36
SYSU GY1-156	Y1	SCM-R2A	Group 40	<i>Chloroflexus islandicus</i>	isl-2(T)	99.37
SYSU GY1-157	Y1	SCM-R2A	Group 40	<i>Chloroflexus islandicus</i>	isl-2(T)	99.37
SYSU GY1-109	Y1	SCM-R2A	Group 35	AY753393	SK47	99.37
SYSU GY1-80	Y1	R2A	Group 28	AY555804	PK324	99.38
SYSU GY1-89	Y1	R2A	Group 40	<i>Chloroflexus islandicus</i>	isl-2(T)	99.48
SYSU GY1-178	Y1	SCM-R2A	Group 40	<i>Chloroflexus islandicus</i>	isl-2(T)	99.49
SYSU GY1-74	Y1	R2A	Group 39	<i>Eliaorea tepidiphila</i>	DSM 17972(T)	99.74
SYSU GY1-238-2	Y1	<i>Thermus</i> 162 medium	Group 22	<i>Thiobacter subterraneus</i>	NCTC9001(T)	99.74
SYSU GY1-173	Y1	SCM-R2A	Group 29	<i>Thermus tengchongensis</i>	YIM 77924(T)	99.87
SYSU GY1-136	Y1	SCM-R2A	Group 9	<i>Bacillus siamensis</i>	KCTC 13613(T)	99.87
SYSU GY1-139	Y1	SCM-R2A	Group 9	<i>Bacillus siamensis</i>	KCTC 13613(T)	99.87
SYSU GY1-176	Y1	SCM-R2A	Group 9	<i>Bacillus siamensis</i>	KCTC 13613(T)	99.87
SYSU GY1-273	Y1	SCM- <i>Thermus</i> 162 medium	Group 9	<i>Bacillus siamensis</i>	KCTC 13613(T)	99.87
SYSU GY1-35-1	Y1	SCM-R2A	Group 7	<i>Caldimonas taiwanensis</i>	NBRC 104434(T)	99.87
SYSU GY1-36	Y1	SCM-R2A	Group 7	<i>Caldimonas taiwanensis</i>	NBRC 104434(T)	99.87
SYSU GY1-37	Y1	SCM-R2A	Group 7	<i>Caldimonas taiwanensis</i>	NBRC 104434(T)	99.87
SYSU GY1-211	Y1	SCM-R2A	Group 4	<i>Tepidimonas fonticaldi</i>	AT-A2(T)	99.87
SYSU GY1-73	Y1	SCM- <i>Thermus</i> 162 medium	Group 7	<i>Tepidimonas taiwanensis</i>	l1-1(T)	99.87
SYSU GY1-226	Y1	<i>Thermus</i> 162 medium	Group 29	<i>Thermus tengchongensis</i>	YIM 77924(T)	100
SYSU GY1-243	Y1	<i>Thermus</i> 162 medium	Group 29	<i>Thermus tengchongensis</i>	YIM 77924(T)	100
SYSU GY1-128	Y1	SCM-R2A	Group 29	<i>Thermus tengchongensis</i>	YIM 77924(T)	100

SYSU GY1-175	Y1	SCM-R2A	Group 29	<i>Thermus tengchongensis</i>	YIM 77924(T)	100
SYSU GY1-181	Y1	SCM-R2A	Group 29	<i>Thermus tengchongensis</i>	YIM 77924(T)	100
SYSU GY1-78	Y1	R2A	Group 24	<i>Thermus brockianus</i>	YS038(T)	100
SYSU GY1-90	Y1	R2A	Group 24	<i>Thermus brockianus</i>	YS038(T)	100
SYSU GY1-91	Y1	R2A	Group 24	<i>Thermus brockianus</i>	YS038(T)	100
SYSU GY1-54	Y1	SCM- <i>Thermus</i> 162 medium	Group 24	<i>Thermus brockianus</i>	YS038(T)	100
SYSU GY1-276	Y1	SCM- <i>Thermus</i> 162 medium	Group 24	<i>Thermus brockianus</i>	YS038(T)	100
SYSU GY1-232	Y1	<i>Thermus</i> 162 medium	Group 22	<i>Thiobacter subterraneus</i>	C55(T)	100
SYSU GY1-234	Y1	<i>Thermus</i> 162 medium	Group 22	<i>Thiobacter subterraneus</i>	C55(T)	100
SYSU GY2-132	Y2	SCM-R2A	Group 36	DQ129304	AKIW813	93.48
SYSU GY2-90	Y2	SCM-R2A	Group 13	<i>Roseiflexus castenholzii</i>	DSM 13941(T)	96.07
SYSU GY2-8	Y2	SCM-R2A	Group 13	<i>Roseiflexus castenholzii</i>	DSM 13941(T)	96.09
SYSU GY2-10	Y2	SCM-R2A	Group 13	<i>Roseiflexus castenholzii</i>	DSM 13941(T)	96.09
SYSU GY2-99	Y2	SCM-R2A	Group 13	<i>Roseiflexus castenholzii</i>	DSM 13941(T)	96.17
SYSU GY2-6	Y2	SCM-R2A	Group 13	<i>Roseiflexus castenholzii</i>	DSM 13941(T)	96.24
SYSU GY2-106	Y2	SCM-R2A	Group 10	AF521186	RH-914	96.35
SYSU GY2-123	Y2	SCM-R2A	Group 10	AF521186	RH-914	96.39
SYSU GY2-124	Y2	SCM-R2A	Group 10	AF521186	RH-914	96.39
SYSU GY2-136	Y2	SCM-R2A	Group 10	AF521186	RH-914	96.39
SYSU GY2-110	Y2	SCM-R2A	Group 10	AF521186	RH-914	96.46
SYSU GY2-121	Y2	SCM-R2A	Group 10	AF521186	RH-914	96.48
SYSU GY2-86	Y2	SCM-R2A	Group 10	AF521186	RH-914	96.49
SYSU GY2-115	Y2	SCM-R2A	Group 10	AF521186	RH-914	96.57
SYSU GY2-32	Y2	SCM- <i>Thermus</i> 162 medium	Group 12	<i>Tepidimonas ignava</i>	SPS-1037(T)	96.7
SYSU GY2-128	Y2	SCM-R2A	Group 25	AF407725	B63	96.95
SYSU GY2-12	Y2	SCM-R2A	Group 26	<i>Meiothermus hypogaeus</i>	AZM34c11(T)	97.43
SYSU GY2-45	Y2	SCM- <i>Thermus</i> 162 medium	Group 12	<i>Tepidimonas ignava</i>	SPS-1037(T)	98.18
SYSU GY2-68	Y2	SCM- <i>Thermus</i> 162 medium	Group 24	<i>Thermus brockianus</i>	YS038(T)	98.83

SYSU GY2-54	Y2	SCM- <i>Thermus</i> 162 medium	Group 35	AY753393	SK47	99.23
SYSU GY2-42	Y2	SCM- <i>Thermus</i> 162 medium	Group 29	<i>Thermus tengchongensis</i>	YIM 77924(T)	99.25
SYSU GY2-29?	Y2	SCM- <i>Thermus</i> 162 medium	Group 30	<i>Thermus caliditerrae</i>	YIM 77925(T)	99.35
SYSU GY2-104	Y2	SCM-R2A	Group 40	<i>Chloroflexus islandicus</i>	isl-2(T)	99.47
SYSU GY2-88	Y2	SCM-R2A	Group 40	<i>Chloroflexus islandicus</i>	isl-2(T)	99.48
SYSU GY2-135	Y2	SCM-R2A	Group 40	<i>Chloroflexus islandicus</i>	isl-2(T)	99.48
SYSU GY2-39	Y2	SCM- <i>Thermus</i> 162 medium	Group 29	<i>Thermus tengchongensis</i>	YIM 77924(T)	99.48
SYSU GY2-83	Y2	R2A	Group 40	<i>Chloroflexus islandicus</i>	isl-2(T)	99.51
SYSU GY2-66	Y2	SCM- <i>Thermus</i> 162 medium	Group 29	<i>Thermus tengchongensis</i>	YIM 77924(T)	99.61
SYSU GY2-76	Y2	<i>Thermus</i> 162 medium	Group 29	<i>Thermus tengchongensis</i>	YIM 77924(T)	99.74
SYSU GY2-3	Y2	SCM-R2A	Group 29	<i>Thermus tengchongensis</i>	YIM 77924(T)	99.74
SYSU GY2-67	Y2	SCM- <i>Thermus</i> 162 medium	Group 29	<i>Thermus tengchongensis</i>	YIM 77924(T)	99.74
SYSU GY2-27	Y2	SCM- <i>Thermus</i> 162 medium	Group 29	<i>Thermus tengchongensis</i>	YIM 77924(T)	99.76
SYSU GY2-33	Y2	SCM- <i>Thermus</i> 162 medium	Group 29	<i>Thermus tengchongensis</i>	YIM 77924(T)	99.85
SYSU GY2-44	Y2	SCM- <i>Thermus</i> 162 medium	Group 29	<i>Thermus tengchongensis</i>	YIM 77924(T)	99.86
SYSU GY2-9	Y2	SCM-R2A	Group 29	<i>Thermus tengchongensis</i>	YIM 77924(T)	99.87
SYSU GY2-93	Y2	SCM-R2A	Group 29	<i>Thermus tengchongensis</i>	YIM 77924(T)	99.87
SYSU GY2-120	Y2	SCM-R2A	Group 29	<i>Thermus tengchongensis</i>	YIM 77924(T)	99.87
SYSU GY2-129	Y2	SCM-R2A	Group 29	<i>Thermus tengchongensis</i>	YIM 77924(T)	99.87
SYSU GY2-141	Y2	SCM-R2A	Group 29	<i>Thermus tengchongensis</i>	YIM 77924(T)	99.87
SYSU GY2-20	Y2	SCM- <i>Thermus</i> 162 medium	Group 29	<i>Thermus tengchongensis</i>	YIM 77924(T)	99.87
SYSU GY2-31	Y2	SCM- <i>Thermus</i> 162 medium	Group 29	<i>Thermus tengchongensis</i>	YIM 77924(T)	99.87
SYSU GY2-35	Y2	SCM- <i>Thermus</i> 162 medium	Group 29	<i>Thermus tengchongensis</i>	YIM 77924(T)	99.87
SYSU GY2-40	Y2	SCM- <i>Thermus</i> 162 medium	Group 29	<i>Thermus tengchongensis</i>	YIM 77924(T)	99.87
SYSU GY2-46	Y2	SCM- <i>Thermus</i> 162 medium	Group 29	<i>Thermus tengchongensis</i>	YIM 77924(T)	99.87
SYSU GY2-60	Y2	SCM- <i>Thermus</i> 162 medium	Group 29	<i>Thermus tengchongensis</i>	YIM 77924(T)	99.87
SYSU GY2-62	Y2	SCM- <i>Thermus</i> 162 medium	Group 29	<i>Thermus tengchongensis</i>	YIM 77924(T)	99.87
SYSU GY2-69	Y2	SCM- <i>Thermus</i> 162 medium	Group 29	<i>Thermus tengchongensis</i>	YIM 77924(T)	99.87

SYSU GY2-98	Y2	SCM-R2A	Group 9	<i>Bacillus siamensis</i>	KCTC 13613(T)	99.87
SYSU GY2-155	Y2	SCM-R2A	Group 9	<i>Bacillus siamensis</i>	KCTC 13613(T)	99.87
SYSU GY2-148	Y2	SCM-R2A	Group 9	<i>Bacillus siamensis</i>	KCTC 13613(T)	99.88
SYSU GY2-14	Y2	<i>Thermus</i> 162 medium	Group 29	<i>Thermus tengchongensis</i>	YIM 77924(T)	100
SYSU GY2-75	Y2	<i>Thermus</i> 162 medium	Group 29	<i>Thermus tengchongensis</i>	YIM 77924(T)	100
SYSU GY2-48	Y2	SCM- <i>Thermus</i> 162 medium	Group 29	<i>Thermus tengchongensis</i>	YIM 77924(T)	100
SYSU GY2-89	Y2	SCM-R2A	Group 29	<i>Thermus tengchongensis</i>	YIM 77924(T)	100
SYSU GY2-97	Y2	SCM-R2A	Group 29	<i>Thermus tengchongensis</i>	YIM 77924(T)	100
SYSU GY2-105	Y2	SCM-R2A	Group 29	<i>Thermus tengchongensis</i>	YIM 77924(T)	100
SYSU GY2-140	Y2	SCM-R2A	Group 29	<i>Thermus tengchongensis</i>	YIM 77924(T)	100
SYSU GY2-34	Y2	SCM- <i>Thermus</i> 162 medium	Group 29	<i>Thermus tengchongensis</i>	YIM 77924(T)	100
SYSU GY2-47	Y2	SCM- <i>Thermus</i> 162 medium	Group 29	<i>Thermus tengchongensis</i>	YIM 77924(T)	100
SYSU GY2-58	Y2	SCM- <i>Thermus</i> 162 medium	Group 29	<i>Thermus tengchongensis</i>	YIM 77924(T)	100
SYSU GY3-13	Y3	SCM-R2A	Group 36	EF205457	YCB86	92.76
SYSU GY3-101	Y3	SCM- <i>Thermus</i> 162 medium	Group 15	<i>Chloroflexus islandicus</i>	isl-2(T)	93.39
SYSU GY3-23	Y3	SCM-R2A	Group 18	<i>Schleiferia thermophila</i>	TU-20(T)	93.43
SYSU GY3-42	Y3	R2A	Group 37	<i>Sandaracinobacter sibiricus</i>	RB16-17(T)	94.8
SYSU GY3-136	Y3	SCM-R2A	Group 37	<i>Sandaracinobacter sibiricus</i>	RB16-17(T)	94.93
SYSU GY3-35	Y3	SCM-R2A	Group 37	<i>Sandaracinobacter sibiricus</i>	RB16-17(T)	95.06
SYSU GY3-37	Y3	R2A	Group 37	<i>Sandaracinobacter sibiricus</i>	RB16-17(T)	95.07
SYSU GY-37	Y3	SCM-R2A	Group 37	<i>Sandaracinobacter sibiricus</i>	RB16-17(T)	95.19
SYSU GY3-P8	Y3	SCM- <i>Thermus</i> 162 medium	Group 13	<i>Roseiflexus castenholzii</i>	DSM 13941(T)	95.44
SYSU GY3-138	Y3	SCM-R2A	Group 13	<i>Roseiflexus castenholzii</i>	DSM 13941(T)	95.51
SYSU GY3-144	Y3	SCM-R2A	Group 36	EF205514	DTM38	95.69
SYSU GY3-41	Y3	R2A	Group 34	<i>Eliaorea tepidiphila</i>	DSM 17972(T)	95.82
SYSU GY3-147	Y3	SCM-R2A	Group 10	AF521186	RH-914	96.12
SYSU GY3-17	Y3	SCM-R2A	Group 14	<i>Chloroflexus islandicus</i>	isl-2(T)	96.22
SYSU GY3-112	Y3	SCM-R2A	Group 10	AF521186	RH-914	96.38

SYSU GY3-6-2	Y3	SCM-R2A	Group 13	<i>Roseiflexus castenholzii</i>	DSM 13941(T)	96.39
SYSU GY3-63	Y3	SCM- <i>Thermus</i> 162 medium	Group 25	AF407725	B63	96.88
SYSU GY3-141	Y3	SCM-R2A	Group 25	AF407725	B63	97.15
SYSU GY3-81	Y3	<i>Thermus</i> 162 medium	Group 32	JX298759	9B-25	97.58
SYSU GY3-83	Y3	<i>Thermus</i> 162 medium	Group 32	JX298759	9B-25	97.79
SYSU GY3-67	Y3	SCM- <i>Thermus</i> 162 medium	Group 32	JX298759	9B-25	97.8
SYSU GY3-146	Y3	SCM-R2A	Group 23	<i>Thermus caliditerrae</i>	YIM 77925(T)	98.05
SYSU GY3-201	Y3	SCM-R2A	Group 23	<i>Thermus caliditerrae</i>	YIM 77925(T)	98.05
SYSU GY3-61	Y3	SCM- <i>Thermus</i> 162 medium	Group 12	<i>Tepidimonas ignava</i>	SPS-1037(T)	98.06
SYSU GY3-77	Y3	<i>Thermus</i> 162 medium	Group 33	AF407714	B11	98.18
SYSU GY3-85	Y3	<i>Thermus</i> 162 medium	Group 33	AF407714	B11	98.18
SYSU GY3-193	Y3	SCM- <i>Thermus</i> 162 medium	Group 23	<i>Thermus caliditerrae</i>	YIM 77925(T)	98.18
SYSU GY3-150	Y3	SCM-R2A	Group 23	<i>Thermus caliditerrae</i>	YIM 77925(T)	98.19
SYSU GY3-89	Y3	R2A	Group 36	EF205457	YCB86	98.3
SYSU GY3-38	Y3	R2A	Group 23	<i>Thermus caliditerrae</i>	YIM 77925(T)	98.31
SYSU GY3-121	Y3	SCM-R2A	Group 23	<i>Thermus caliditerrae</i>	YIM 77925(T)	98.32
SYSU GY3-194	Y3	SCM- <i>Thermus</i> 162 medium	Group 23	<i>Thermus caliditerrae</i>	YIM 77925(T)	98.32
SYSU GY3-33	Y3	SCM-R2A	Group 23	<i>Thermus caliditerrae</i>	YIM 77925(T)	98.34
SYSU GY3-31	Y3	SCM-R2A	Group 23	<i>Thermus caliditerrae</i>	YIM 77925(T)	98.7
SYSU GY3-36	Y3	SCM-R2A	Group 23	<i>Thermus caliditerrae</i>	YIM 77925(T)	98.7
SYSU GY3-192	Y3	SCM- <i>Thermus</i> 162 medium	Group 23	<i>Thermus caliditerrae</i>	YIM 77925(T)	98.7
SYSU GY3-96	Y3	SCM- <i>Thermus</i> 162 medium	Group 23	<i>Thermus caliditerrae</i>	YIM 77925(T)	98.88
SYSU GY3-14	Y3	SCM-R2A	Group 23	<i>Thermus caliditerrae</i>	YIM 77925(T)	98.96
SYSU GY3-44	Y3	R2A	Group 40	<i>Chloroflexus islandicus</i>	isl-2(T)	99.09
SYSU GY3-188	Y3	<i>Thermus</i> 162 medium	Group 30	<i>Thermus caliditerrae</i>	YIM 77925(T)	99.09
SYSU GY3-196	Y3	SCM- <i>Thermus</i> 162 medium	Group 30	<i>Thermus caliditerrae</i>	YIM 77925(T)	99.09
SYSU GY3-197	Y3	SCM- <i>Thermus</i> 162 medium	Group 30	<i>Thermus caliditerrae</i>	YIM 77925(T)	99.09
SYSU GY3-199	Y3	SCM- <i>Thermus</i> 162 medium	Group 30	<i>Thermus caliditerrae</i>	YIM 77925(T)	99.09

SYSU GY3-19	Y3	SCM-R2A	Group 35	AY753393	SK47	99.22
SYSU GY3-20	Y3	SCM-R2A	Group 35	AY753393	SK47	99.22
SYSU GY3-116	Y3	SCM-R2A	Group 30	<i>Thermus caliditerrae</i>	YIM 77925(T)	99.22
SYSU GY3-59	Y3	SCM- <i>Thermus</i> 162 medium	Group 30	<i>Thermus caliditerrae</i>	YIM 77925(T)	99.22
SYSU GY3-191	Y3	SCM- <i>Thermus</i> 162 medium	Group 30	<i>Thermus caliditerrae</i>	YIM 77925(T)	99.22
SYSU GY3-195	Y3	SCM- <i>Thermus</i> 162 medium	Group 30	<i>Thermus caliditerrae</i>	YIM 77925(T)	99.22
SYSU GY3-102	Y3	SCM- <i>Thermus</i> 162 medium	Group 30	<i>Thermus caliditerrae</i>	YIM 77925(T)	99.24
SYSU GY3-142	Y3	SCM-R2A	Group 35	AY753393	SK47	99.25
SYSU GY3-15	Y3	SCM-R2A	Group 30	<i>Thermus caliditerrae</i>	YIM 77925(T)	99.32
SYSU GY3-49	Y3	SCM-R2A	Group 35	AY753393	SK47	99.34
SYSU GY3-52	Y3	SCM-R2A	Group 35	AY753393	SK47	99.34
SYSU GY3-53	Y3	SCM-R2A	Group 35	AY753393	SK47	99.35
SYSU GY3-24	Y3	SCM-R2A	Group 35	AY753393	SK47	99.35
SYSU GY3-143	Y3	SCM-R2A	Group 35	AY753393	SK47	99.35
SYSU GY3-97	Y3	SCM- <i>Thermus</i> 162 medium	Group 29	<i>Thermus tengchongensis</i>	YIM 77924(T)	99.35
SYSU GY3-39	Y3	R2A	Group 30	<i>Thermus caliditerrae</i>	YIM 77925(T)	99.35
SYSU GY3-40	Y3	R2A	Group 30	<i>Thermus caliditerrae</i>	YIM 77925(T)	99.35
SYSU GY3-41-2	Y3	R2A	Group 30	<i>Thermus caliditerrae</i>	YIM 77925(T)	99.35
SYSU GY3-46	Y3	R2A	Group 30	<i>Thermus caliditerrae</i>	YIM 77925(T)	99.35
SYSU GY3-47	Y3	R2A	Group 30	<i>Thermus caliditerrae</i>	YIM 77925(T)	99.35
SYSU GY3-50	Y3	R2A	Group 30	<i>Thermus caliditerrae</i>	YIM 77925(T)	99.35
SYSU GY3-51	Y3	R2A	Group 30	<i>Thermus caliditerrae</i>	YIM 77925(T)	99.35
SYSU GY3-54	Y3	R2A	Group 30	<i>Thermus caliditerrae</i>	YIM 77925(T)	99.35
SYSU GY3-55	Y3	R2A	Group 30	<i>Thermus caliditerrae</i>	YIM 77925(T)	99.35
SYSU GY3-56	Y3	R2A	Group 30	<i>Thermus caliditerrae</i>	YIM 77925(T)	99.35
SYSU GY3-86	Y3	<i>Thermus</i> 162 medium	Group 30	<i>Thermus caliditerrae</i>	YIM 77925(T)	99.35
SYSU GY3-18	Y3	SCM-R2A	Group 30	<i>Thermus caliditerrae</i>	YIM 77925(T)	99.35
SYSU GY3-30	Y3	SCM-R2A	Group 30	<i>Thermus caliditerrae</i>	YIM 77925(T)	99.35

SYSU GY3-32	Y3	SCM-R2A	Group 30	<i>Thermus caliditerrae</i>	YIM 77925(T)	99.35
SYSU GY3-118	Y3	SCM-R2A	Group 30	<i>Thermus caliditerrae</i>	YIM 77925(T)	99.35
SYSU GY3-120	Y3	SCM-R2A	Group 30	<i>Thermus caliditerrae</i>	YIM 77925(T)	99.35
SYSU GY3-126	Y3	SCM-R2A	Group 30	<i>Thermus caliditerrae</i>	YIM 77925(T)	99.35
SYSU GY3-129	Y3	SCM-R2A	Group 30	<i>Thermus caliditerrae</i>	YIM 77925(T)	99.35
SYSU GY3-57	Y3	SCM- <i>Thermus</i> 162 medium	Group 30	<i>Thermus caliditerrae</i>	YIM 77925(T)	99.35
SYSU GY3-60	Y3	SCM- <i>Thermus</i> 162 medium	Group 30	<i>Thermus caliditerrae</i>	YIM 77925(T)	99.35
SYSU GY3-62	Y3	SCM- <i>Thermus</i> 162 medium	Group 30	<i>Thermus caliditerrae</i>	YIM 77925(T)	99.35
SYSU GY3-64	Y3	SCM- <i>Thermus</i> 162 medium	Group 30	<i>Thermus caliditerrae</i>	YIM 77925(T)	99.35
SYSU GY3-68	Y3	SCM- <i>Thermus</i> 162 medium	Group 30	<i>Thermus caliditerrae</i>	YIM 77925(T)	99.35
SYSU GY3-69	Y3	SCM- <i>Thermus</i> 162 medium	Group 30	<i>Thermus caliditerrae</i>	YIM 77925(T)	99.35
SYSU GY3-71	Y3	SCM- <i>Thermus</i> 162 medium	Group 30	<i>Thermus caliditerrae</i>	YIM 77925(T)	99.35
SYSU GY3-74	Y3	SCM- <i>Thermus</i> 162 medium	Group 30	<i>Thermus caliditerrae</i>	YIM 77925(T)	99.35
SYSU GY3-94	Y3	SCM- <i>Thermus</i> 162 medium	Group 30	<i>Thermus caliditerrae</i>	YIM 77925(T)	99.35
SYSU GY3-189	Y3	<i>Thermus</i> 162 medium	Group 30	<i>Thermus caliditerrae</i>	YIM 77925(T)	99.35
SYSU GY3-190	Y3	<i>Thermus</i> 162 medium	Group 30	<i>Thermus caliditerrae</i>	YIM 77925(T)	99.35
SYSU GY3-153	Y3	SCM-R2A	Group 30	<i>Thermus caliditerrae</i>	YIM 77925(T)	99.35
SYSU GY3-P5	Y3	SCM- <i>Thermus</i> 162 medium	Group 11	<i>Thermaerobacter subterraneus</i>	DSM 13965(T)	99.35
SYSU GY3-48	Y3	R2A	Group 30	<i>Thermus caliditerrae</i>	YIM 77925(T)	99.36
SYSU GY3-108	Y3	<i>Thermus</i> 162 medium	Group 30	<i>Thermus caliditerrae</i>	YIM 77925(T)	99.36
SYSU GY3-65	Y3	SCM- <i>Thermus</i> 162 medium	Group 30	<i>Thermus caliditerrae</i>	YIM 77925(T)	99.36
SYSU GY3-78	Y3	<i>Thermus</i> 162 medium	Group 30	<i>Thermus caliditerrae</i>	YIM 77925(T)	99.37
SYSU GY3-93	Y3	SCM- <i>Thermus</i> 162 medium	Group 30	<i>Thermus caliditerrae</i>	YIM 77925(T)	99.37
SYSU GY3-95	Y3	SCM- <i>Thermus</i> 162 medium	Group 30	<i>Thermus caliditerrae</i>	YIM 77925(T)	99.37
SYSU GY3-113	Y3	SCM-R2A	Group 30	<i>Thermus caliditerrae</i>	YIM 77925(T)	99.42
SYSU GY3-2	Y3	SCM-R2A	Group 40	<i>Chloroflexus islandicus</i>	isl-2(T)	99.48
SYSU GY3-34	Y3	SCM-R2A	Group 40	<i>Chloroflexus islandicus</i>	isl-2(T)	99.48
SYSU GY3-127	Y3	SCM-R2A	Group 40	<i>Chloroflexus islandicus</i>	isl-2(T)	99.48

SYSU GY3-104-2	Y3	SCM- <i>Thermus</i> 162 medium	Group 16	<i>Caldilinea tarbellica</i>	D1-25-10-4(T)	99.49
SYSU GY3-87	Y3	<i>Thermus</i> 162 medium	Group 30	<i>Thermus caliditerrae</i>	YIM 77925(T)	99.6
SYSU GY3-6	Y3	SCM-R2A	Group 16	<i>Caldilinea tarbellica</i>	D1-25-10-4(T)	99.61
SYSU GY3-103	Y3	SCM- <i>Thermus</i> 162 medium	Group 17	<i>Anoxybacillus mongoliensis</i>	T4(T)	99.61
SYSU GY3-99	Y3	SCM- <i>Thermus</i> 162 medium	Group 30	<i>Thermus caliditerrae</i>	YIM 77925(T)	99.73
SYSU GY3-11	Y3	SCM-R2A	Group 16	<i>Caldilinea tarbellica</i>	D1-25-10-4(T)	99.74
SYSU GY3-12	Y3	SCM-R2A	Group 16	<i>Caldilinea tarbellica</i>	D1-25-10-4(T)	99.74
SYSU GY3-181	Y3	SCM-R2A	Group 16	<i>Caldilinea tarbellica</i>	D1-25-10-4(T)	99.74
SYSU GY3-21	Y3	SCM-R2A	Group 29	<i>Thermus tengchongensis</i>	YIM 77924(T)	99.74
SYSU GY3-104-3	Y3	SCM- <i>Thermus</i> 162 medium	Group 17	<i>Anoxybacillus mongoliensis</i>	T4(T)	99.74
SYSU GY3-105	Y3	SCM- <i>Thermus</i> 162 medium	Group 17	<i>Anoxybacillus mongoliensis</i>	T4(T)	99.74
SYSU GY3-124	Y3	SCM-R2A	Group 29	<i>Thermus tengchongensis</i>	YIM 77924(T)	99.87
SYSU GY3-128	Y3	SCM-R2A	Group 29	<i>Thermus tengchongensis</i>	YIM 77924(T)	99.87
SYSU GY3-79	Y3	<i>Thermus</i> 162 medium	Group 31	<i>Tepidicella xavieri</i>	TU-16(T)	99.87
SYSU GY3-25	Y3	SCM-R2A	Group 29	<i>Thermus tengchongensis</i>	YIM 77924(T)	100

continued Supplementary Table 4:

Strain ID	Top-hit taxonomy	Relative abundance in community (%)
SYSU GT96-39	Bacteria;Bacteroidetes;Sphingobacteriia;CP012155;CP012155;FJ529921	ND
SYSU GT96-1	Bacteria;Bacteroidetes;Flavobacteria;Flavobacteriales;Schleiferiaceae;Schleiferia	0.776593981
SYSU GT96-37	Bacteria;Bacteroidetes;Flavobacteria;Flavobacteriales;Schleiferiaceae;Schleiferia	0.776593981
SYSU GT96-40-1	Bacteria;Bacteroidetes;Cytophagia;Cytophagales;Cytophagaceae;AF445665	ND
SYSU GT96-46	Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;Sandaracinobacter	0.773976248
SYSU GT96-18	Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;Sandaracinobacter	0.773976248
SYSU GT96-61	Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;Sandaracinobacter	0.773976248
SYSU GT96-4	Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;Sandaracinobacter	0.773976248
SYSU GT96-72	Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;Sandaracinobacter	0.773976248

SYSU GT96-53	Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;Sandaracinobacter	0.773976248
SYSU GT96-54	Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;Sandaracinobacter	0.773976248
SYSU GT96-34	Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;Sandaracinobacter	0.773976248
SYSU GT96-47	Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;Sandaracinobacter	0.773976248
SYSU GT96-57	Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;Sandaracinobacter	0.773976248
SYSU GT96-56	Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;Sandaracinobacter	0.773976248
SYSU GT96-71	Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;Sandaracinobacter	0.773976248
SYSU GT96-34-1	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Acetobacteraceae;Roseomonas	ND
SYSU GT96-19	Bacteria;Chloroflexi;Chloroflexia;Chloroflexales;Chloroflexaceae;Chloroflexus	28.16505676
SYSU GT96-45	Bacteria;Chloroflexi;Chloroflexia;Chloroflexales;Chloroflexaceae;Chloroflexus	28.16505676
SYSU GT96-3	Bacteria;Chloroflexi;Chloroflexia;Chloroflexales;Chloroflexaceae;Chloroflexus	28.16505676
SYSU GT96-40	Bacteria;Chloroflexi;Chloroflexia;Chloroflexales;Chloroflexaceae;Chloroflexus	28.16505676
SYSU GT96-52	Bacteria;Chloroflexi;Chloroflexia;Chloroflexales;Chloroflexaceae;Chloroflexus	28.16505676
SYSU GT96-20	Bacteria;Chloroflexi;Chloroflexia;Chloroflexales;Chloroflexaceae;Chloroflexus	28.16505676
SYSU GT96-17	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;AM777983	ND
SYSU GT96-60	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Acetobacteraceae;Eliaera	1.166636126
SYSU GT96-24	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Acetobacteraceae;Eliaera	1.166636126
SYSU GT96-14	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Acetobacteraceae;Roseomonas	0.027049903
SYSU GT96-26	Bacteria;Firmicutes;Bacilli;Bacillales;Bacillaceae;Bacillus	ND
SYSU GT96-12	Bacteria;Firmicutes;Bacilli;Bacillales;Bacillaceae;Bacillus	ND
SYSU GY1-61	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Alysiosphaera;FM242433	ND
SYSU GY1-62	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Alysiosphaera;FM242433	ND
SYSU GY1-30	Bacteria;Bacteroidetes;Flavobacteria;Flavobacteriales;Schleiferiaceae;Schleiferia	0.776593981
SYSU GY1-233	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Acetobacteraceae;Craurococcus	ND
SYSU GY1-259	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Acetobacteraceae;Craurococcus	ND
SYSU GY1-P12	Bacteria;Actinobacteria;Acidimicrobiia;Acidimicrobiales;Iamiaceae;EF516779	ND
SYSU GY1-29	Bacteria;Chloroflexi;Chloroflexia;Chloroflexales;Chloroflexaceae;Chloroflexus	28.16505676
SYSU GY1-23	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Acetobacteraceae;Eliaera	ND

SYSU GY1-75	Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;Sandaracinobacter	0.773976248
SYSU GY1-100	Bacteria;Actinobacteria;Acidimicrobiia;Acidimicrobiales;lamiaceae;EF632905	ND
SYSU GY1-247	Bacteria;Deinococcus-Thermus;Deinococci;Thermates;Thermaceae;Meiothermus	0.596843015
SYSU GY1-96	Bacteria;Actinobacteria;Acidimicrobiia;Acidimicrobiales;lamiaceae;EF632905	ND
SYSU GY1-59	Bacteria;Deinococcus-Thermus;Deinococci;Thermates;Thermaceae;Thermus	8.070469359
SYSU GY1-65	Bacteria;Chloroflexi;Chloroflexia;Chloroflexales;Roseiflexaceae;Roseiflexus	7.817421882
SYSU GY1-4	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Tepidimonas	0.724239331
SYSU GY1-28	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Tepidimonas	0.724239331
SYSU GY1-58	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Tepidimonas	0.724239331
SYSU GY1-64	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Tepidimonas	0.724239331
SYSU GY1-60	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Tepidimonas	0.724239331
SYSU GY1-63	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Tepidimonas	0.724239331
SYSU GY1-278	Bacteria;Proteobacteria;Gammaproteobacteria;Xanthomonadales;Xanthomonadaceae;AF407725	ND
SYSU GY1-272	Bacteria;Proteobacteria;Gammaproteobacteria;Xanthomonadales;Xanthomonadaceae;AF407725	ND
SYSU GY1-174	Bacteria;Deinococcus-Thermus;Deinococci;Thermates;Thermaceae;Meiothermus	0.596843015
SYSU GY1-105	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Acetobacteraceae;Roseomonas	ND
SYSU GY1-82	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Acetobacteraceae;Roseomonas	ND
SYSU GY1-241	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Acetobacteraceae;Roseomonas	ND
SYSU GY1-224	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Acetobacteraceae;Roseomonas	ND
SYSU GY1-66	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Tepidimonas	0.724239331
SYSU GY1-56	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Tepidimonas	0.724239331
SYSU GY1-67	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Tepidimonas	0.724239331
SYSU GY1-57	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Tepidimonas	0.724239331
SYSU GY1-239	Bacteria;Acidobacteria;Solibacteres;Solibacterales;Bryobacteraceae;Paludibaculum	ND
SYSU GY1-242	Bacteria;Acidobacteria;Solibacteres;Solibacterales;Bryobacteraceae;Paludibaculum	ND
SYSU GY1-67P	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Tepidimonas	0.724239331
SYSU GY1-38P	Bacteria;Deinococcus-Thermus;Deinococci;Thermates;Thermaceae;Thermus	8.070469359
SYSU GY1-99	Bacteria;Deinococcus-Thermus;Deinococci;Thermates;Thermaceae;Thermus	8.070469359

SYSU GY1-170	Bacteria;Deinococcus-Thermus;Deinococci;Thermates;Thermaceae;Meiothermus	0.596843015
SYSU GY1-122	Bacteria;Deinococcus-Thermus;Deinococci;Thermates;Thermaceae;Thermus	8.070469359
SYSU GY1-284	Bacteria;Deinococcus-Thermus;Deinococci;Thermates;Thermaceae;Meiothermus	0.596843015
SYSU GY1-252	Bacteria;Deinococcus-Thermus;Deinococci;Thermates;Thermaceae;Thermus	8.070469359
SYSU GY1-283	Bacteria;Deinococcus-Thermus;Deinococci;Thermates;Thermaceae;Thermus	8.070469359
SYSU GY1-222	Bacteria;Deinococcus-Thermus;Deinococci;Thermates;Thermaceae;Meiothermus	0.596843015
SYSU GY1-182	Bacteria;Deinococcus-Thermus;Deinococci;Thermates;Thermaceae;Meiothermus	0.596843015
SYSU GY1-253	Bacteria;Deinococcus-Thermus;Deinococci;Thermates;Thermaceae;Meiothermus	0.596843015
SYSU GY1-254	Bacteria;Deinococcus-Thermus;Deinococci;Thermates;Thermaceae;Meiothermus	0.596843015
SYSU GY1-277	Bacteria;Deinococcus-Thermus;Deinococci;Thermates;Thermaceae;Thermus	8.070469359
SYSU GY1-257	Bacteria;Deinococcus-Thermus;Deinococci;Thermates;Thermaceae;Meiothermus	0.596843015
SYSU GY1-258	Bacteria;Deinococcus-Thermus;Deinococci;Thermates;Thermaceae;Meiothermus	0.596843015
SYSU GY1-164	Bacteria;Deinococcus-Thermus;Deinococci;Thermates;Thermaceae;Meiothermus	0.596843015
SYSU GY1-5	Bacteria;Chloroflexi;Chloroflexia;Chloroflexales;Chloroflexaceae;Chloroflexus	28.16505676
SYSU GY1-P29	Bacteria;Actinobacteria;Thermoleophilia;Thermoleophilales;Thermoleophilaceae;Thermoleophilum	0.015706395
SYSU GY1-83	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;AM777983	ND
SYSU GY1-86	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;AM777983	ND
SYSU GY1-106	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;AM777983	ND
SYSU GY1-236	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;AM777983	ND
SYSU GY1-141	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;AM777983	ND
SYSU GY1-87	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;AM777983	ND
SYSU GY1-149	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;AM777983	ND
SYSU GY1-1	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;AM777983	ND
SYSU GY1-251	Bacteria;Deinococcus-Thermus;Deinococci;Thermates;Thermaceae;Thermus	8.070469359
SYSU GY1-184	Bacteria;Chloroflexi;Chloroflexia;Chloroflexales;Chloroflexaceae;Chloroflexus	28.16505676
SYSU GY1-21	Bacteria;Chloroflexi;Chloroflexia;Chloroflexales;Chloroflexaceae;Chloroflexus	28.16505676
SYSU GY1-140	Bacteria;Chloroflexi;Chloroflexia;Chloroflexales;Chloroflexaceae;Chloroflexus	28.16505676
SYSU GY1-159	Bacteria;Chloroflexi;Chloroflexia;Chloroflexales;Chloroflexaceae;Chloroflexus	28.16505676

SYSU GY1-212	Bacteria;Chloroflexi;Chloroflexia;Chloroflexales;Chloroflexaceae;Chloroflexus	28.16505676
SYSU GY1-183	Bacteria;Chloroflexi;Chloroflexia;Chloroflexales;Chloroflexaceae;Chloroflexus	28.16505676
SYSU GY1-77	Bacteria;Chloroflexi;Chloroflexia;Chloroflexales;Chloroflexaceae;Chloroflexus	28.16505676
SYSU GY1-160	Bacteria;Chloroflexi;Chloroflexia;Chloroflexales;Chloroflexaceae;Chloroflexus	28.16505676
SYSU GY1-158	Bacteria;Chloroflexi;Chloroflexia;Chloroflexales;Chloroflexaceae;Chloroflexus	28.16505676
SYSU GY1-195	Bacteria;Chloroflexi;Chloroflexia;Chloroflexales;Chloroflexaceae;Chloroflexus	28.16505676
SYSU GY1-272-2	Bacteria;Chloroflexi;Chloroflexia;Chloroflexales;Chloroflexaceae;Chloroflexus	28.16505676
SYSU GY1-71	Bacteria;Chloroflexi;EU335161;AB186887;AB186887;AB186887	ND
SYSU GY1-179	Bacteria;Proteobacteria;Gammaproteobacteria;Thiotrichales;Francisellaceae;Francisella	ND
SYSU GY1-103	Bacteria;Chloroflexi;EU335161;AB186887;AB186887;AB186887	ND
SYSU GY1-84	Bacteria;Chloroflexi;EU335161;AB186887;AB186887;AB186887	ND
SYSU GY1-11	Bacteria;Chloroflexi;Chloroflexia;Chloroflexales;Chloroflexaceae;Chloroflexus	28.16505676
SYSU GY1-12	Bacteria;Chloroflexi;Chloroflexia;Chloroflexales;Chloroflexaceae;Chloroflexus	28.16505676
SYSU GY1-121	Bacteria;Chloroflexi;Chloroflexia;Chloroflexales;Chloroflexaceae;Chloroflexus	28.16505676
SYSU GY1-146	Bacteria;Chloroflexi;Chloroflexia;Chloroflexales;Chloroflexaceae;Chloroflexus	28.16505676
SYSU GY1-22	Bacteria;Chloroflexi;EU335161;AB186887;AB186887;AB186887	ND
SYSU GY1-68	Bacteria;Chloroflexi;EU335161;AB186887;AB186887;AB186887	ND
SYSU GY1-69	Bacteria;Chloroflexi;EU335161;AB186887;AB186887;AB186887	ND
SYSU GY1-228	Bacteria;Deinococcus-Thermus;Deinococci;Thermales;Thermaceae;Thermus	8.070469359
SYSU GY1-55	Bacteria;Deinococcus-Thermus;Deinococci;Thermales;Thermaceae;Thermus	8.070469359
SYSU GY1-57-2	Bacteria;Deinococcus-Thermus;Deinococci;Thermales;Thermaceae;Thermus	8.070469359
SYSU GY1-19	Bacteria;Chloroflexi;EU335161;AB186887;AB186887;AB186887	ND
SYSU GY1-156	Bacteria;Chloroflexi;Chloroflexia;Chloroflexales;Chloroflexaceae;Chloroflexus	28.16505676
SYSU GY1-157	Bacteria;Chloroflexi;Chloroflexia;Chloroflexales;Chloroflexaceae;Chloroflexus	28.16505676
SYSU GY1-109	Bacteria;Chloroflexi;EU335161;AB186887;AB186887;AB186887	ND
SYSU GY1-80	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Alysiosphaera;AP011749	ND
SYSU GY1-89	Bacteria;Chloroflexi;Chloroflexia;Chloroflexales;Chloroflexaceae;Chloroflexus	28.16505676
SYSU GY1-178	Bacteria;Chloroflexi;Chloroflexia;Chloroflexales;Chloroflexaceae;Chloroflexus	28.16505676

SYSU GY1-74	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Acetobacteraceae;Eliaeraea	1.166636126
SYSU GY1-238-2	Bacteria;Proteobacteria;Betaproteobacteria;Hydrogenophilales;Thiobacter;Thiobacter	0.116925386
SYSU GY1-173	Bacteria;Deinococcus-Thermus;Deinococci;Thermales;Thermaceae;Thermus	8.070469359
SYSU GY1-136	Bacteria;Firmicutes;Bacilli;Bacillales;Bacillaceae;Bacillus	0.066315891
SYSU GY1-139	Bacteria;Firmicutes;Bacilli;Bacillales;Bacillaceae;Bacillus	0.066315891
SYSU GY1-176	Bacteria;Firmicutes;Bacilli;Bacillales;Bacillaceae;Bacillus	0.066315891
SYSU GY1-273	Bacteria;Firmicutes;Bacilli;Bacillales;Bacillaceae;Bacillus	0.066315891
SYSU GY1-35-1	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Caldimonas	ND
SYSU GY1-36	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Caldimonas	ND
SYSU GY1-37	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Caldimonas	ND
SYSU GY1-211	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Tepidimonas	0.724239331
SYSU GY1-73	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Tepidimonas	0.724239331
SYSU GY1-226	Bacteria;Deinococcus-Thermus;Deinococci;Thermales;Thermaceae;Thermus	8.070469359
SYSU GY1-243	Bacteria;Deinococcus-Thermus;Deinococci;Thermales;Thermaceae;Thermus	8.070469359
SYSU GY1-128	Bacteria;Deinococcus-Thermus;Deinococci;Thermales;Thermaceae;Thermus	8.070469359
SYSU GY1-175	Bacteria;Deinococcus-Thermus;Deinococci;Thermales;Thermaceae;Thermus	8.070469359
SYSU GY1-181	Bacteria;Deinococcus-Thermus;Deinococci;Thermales;Thermaceae;Thermus	8.070469359
SYSU GY1-78	Bacteria;Deinococcus-Thermus;Deinococci;Thermales;Thermaceae;Thermus	8.070469359
SYSU GY1-90	Bacteria;Deinococcus-Thermus;Deinococci;Thermales;Thermaceae;Thermus	8.070469359
SYSU GY1-91	Bacteria;Deinococcus-Thermus;Deinococci;Thermales;Thermaceae;Thermus	8.070469359
SYSU GY1-54	Bacteria;Deinococcus-Thermus;Deinococci;Thermales;Thermaceae;Thermus	8.070469359
SYSU GY1-276	Bacteria;Deinococcus-Thermus;Deinococci;Thermales;Thermaceae;Thermus	8.070469359
SYSU GY1-232	Bacteria;Proteobacteria;Betaproteobacteria;Hydrogenophilales;Thiobacter;Thiobacter	0.116925386
SYSU GY1-234	Bacteria;Proteobacteria;Betaproteobacteria;Hydrogenophilales;Thiobacter;Thiobacter	0.116925386
SYSU GY2-132	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Acetobacteraceae;Craurococcus	ND
SYSU GY2-90	Bacteria;Chloroflexi;Chloroflexia;Chloroflexales;Roseiflexaceae;Roseiflexus	7.817421882
SYSU GY2-8	Bacteria;Chloroflexi;Chloroflexia;Chloroflexales;Roseiflexaceae;Roseiflexus	7.817421882
SYSU GY2-10	Bacteria;Chloroflexi;Chloroflexia;Chloroflexales;Roseiflexaceae;Roseiflexus	7.817421882

SYSU GY2-99	Bacteria;Chloroflexi;Chloroflexia;Chloroflexales;Roseiflexaceae;Roseiflexus	7.817421882
SYSU GY2-6	Bacteria;Chloroflexi;Chloroflexia;Chloroflexales;Roseiflexaceae;Roseiflexus	7.817421882
SYSU GY2-106	Bacteria;Deinococcus-Thermus;Deinococci;Thermates;Thermaceae;Thermus	ND
SYSU GY2-123	Bacteria;Deinococcus-Thermus;Deinococci;Thermates;Thermaceae;Thermus	ND
SYSU GY2-124	Bacteria;Deinococcus-Thermus;Deinococci;Thermates;Thermaceae;Thermus	ND
SYSU GY2-136	Bacteria;Deinococcus-Thermus;Deinococci;Thermates;Thermaceae;Thermus	ND
SYSU GY2-110	Bacteria;Deinococcus-Thermus;Deinococci;Thermates;Thermaceae;Thermus	ND
SYSU GY2-121	Bacteria;Deinococcus-Thermus;Deinococci;Thermates;Thermaceae;Thermus	ND
SYSU GY2-86	Bacteria;Deinococcus-Thermus;Deinococci;Thermates;Thermaceae;Thermus	ND
SYSU GY2-115	Bacteria;Deinococcus-Thermus;Deinococci;Thermates;Thermaceae;Thermus	ND
SYSU GY2-32	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Tepidimonas	0.724239331
SYSU GY2-128	Bacteria;Proteobacteria;Gammaproteobacteria;Xanthomonadales;Xanthomonadaceae;AF407725	ND
SYSU GY2-12	Bacteria;Deinococcus-Thermus;Deinococci;Thermates;Thermaceae;Meiothermus	0.596843015
SYSU GY2-45	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Tepidimonas	0.724239331
SYSU GY2-68	Bacteria;Deinococcus-Thermus;Deinococci;Thermates;Thermaceae;Thermus	8.070469359
SYSU GY2-54	Bacteria;Chloroflexi;EU335161;AB186887;AB186887;AB186887	ND
SYSU GY2-42	Bacteria;Deinococcus-Thermus;Deinococci;Thermates;Thermaceae;Thermus	8.070469359
SYSU GY2-29?	Bacteria;Deinococcus-Thermus;Deinococci;Thermates;Thermaceae;Thermus	8.070469359
SYSU GY2-104	Bacteria;Chloroflexi;Chloroflexia;Chloroflexales;Chloroflexaceae;Chloroflexus	28.16505676
SYSU GY2-88	Bacteria;Chloroflexi;Chloroflexia;Chloroflexales;Chloroflexaceae;Chloroflexus	28.16505676
SYSU GY2-135	Bacteria;Chloroflexi;Chloroflexia;Chloroflexales;Chloroflexaceae;Chloroflexus	28.16505676
SYSU GY2-39	Bacteria;Deinococcus-Thermus;Deinococci;Thermates;Thermaceae;Thermus	8.070469359
SYSU GY2-83	Bacteria;Chloroflexi;Chloroflexia;Chloroflexales;Chloroflexaceae;Chloroflexus	28.16505676
SYSU GY2-66	Bacteria;Deinococcus-Thermus;Deinococci;Thermates;Thermaceae;Thermus	8.070469359
SYSU GY2-76	Bacteria;Deinococcus-Thermus;Deinococci;Thermates;Thermaceae;Thermus	8.070469359
SYSU GY2-3	Bacteria;Deinococcus-Thermus;Deinococci;Thermates;Thermaceae;Thermus	8.070469359
SYSU GY2-67	Bacteria;Deinococcus-Thermus;Deinococci;Thermates;Thermaceae;Thermus	8.070469359
SYSU GY2-27	Bacteria;Deinococcus-Thermus;Deinococci;Thermates;Thermaceae;Thermus	8.070469359

SYSU GY2-33	Bacteria;Deinococcus-Thermus;Deinococci;Thermates;Thermaceae;Thermus	8.070469359
SYSU GY2-44	Bacteria;Deinococcus-Thermus;Deinococci;Thermates;Thermaceae;Thermus	8.070469359
SYSU GY2-9	Bacteria;Deinococcus-Thermus;Deinococci;Thermates;Thermaceae;Thermus	8.070469359
SYSU GY2-93	Bacteria;Deinococcus-Thermus;Deinococci;Thermates;Thermaceae;Thermus	8.070469359
SYSU GY2-120	Bacteria;Deinococcus-Thermus;Deinococci;Thermates;Thermaceae;Thermus	8.070469359
SYSU GY2-129	Bacteria;Deinococcus-Thermus;Deinococci;Thermates;Thermaceae;Thermus	8.070469359
SYSU GY2-141	Bacteria;Deinococcus-Thermus;Deinococci;Thermates;Thermaceae;Thermus	8.070469359
SYSU GY2-20	Bacteria;Deinococcus-Thermus;Deinococci;Thermates;Thermaceae;Thermus	8.070469359
SYSU GY2-31	Bacteria;Deinococcus-Thermus;Deinococci;Thermates;Thermaceae;Thermus	8.070469359
SYSU GY2-35	Bacteria;Deinococcus-Thermus;Deinococci;Thermates;Thermaceae;Thermus	8.070469359
SYSU GY2-40	Bacteria;Deinococcus-Thermus;Deinococci;Thermates;Thermaceae;Thermus	8.070469359
SYSU GY2-46	Bacteria;Deinococcus-Thermus;Deinococci;Thermates;Thermaceae;Thermus	8.070469359
SYSU GY2-60	Bacteria;Deinococcus-Thermus;Deinococci;Thermates;Thermaceae;Thermus	8.070469359
SYSU GY2-62	Bacteria;Deinococcus-Thermus;Deinococci;Thermates;Thermaceae;Thermus	8.070469359
SYSU GY2-69	Bacteria;Deinococcus-Thermus;Deinococci;Thermates;Thermaceae;Thermus	8.070469359
SYSU GY2-98	Bacteria;Firmicutes;Bacilli;Bacillales;Bacillaceae;Bacillus	0.066315891
SYSU GY2-155	Bacteria;Firmicutes;Bacilli;Bacillales;Bacillaceae;Bacillus	0.066315891
SYSU GY2-148	Bacteria;Firmicutes;Bacilli;Bacillales;Bacillaceae;Bacillus	0.066315891
SYSU GY2-14	Bacteria;Deinococcus-Thermus;Deinococci;Thermates;Thermaceae;Thermus	8.070469359
SYSU GY2-75	Bacteria;Deinococcus-Thermus;Deinococci;Thermates;Thermaceae;Thermus	8.070469359
SYSU GY2-48	Bacteria;Deinococcus-Thermus;Deinococci;Thermates;Thermaceae;Thermus	8.070469359
SYSU GY2-89	Bacteria;Deinococcus-Thermus;Deinococci;Thermates;Thermaceae;Thermus	8.070469359
SYSU GY2-97	Bacteria;Deinococcus-Thermus;Deinococci;Thermates;Thermaceae;Thermus	8.070469359
SYSU GY2-105	Bacteria;Deinococcus-Thermus;Deinococci;Thermates;Thermaceae;Thermus	8.070469359
SYSU GY2-140	Bacteria;Deinococcus-Thermus;Deinococci;Thermates;Thermaceae;Thermus	8.070469359
SYSU GY2-34	Bacteria;Deinococcus-Thermus;Deinococci;Thermates;Thermaceae;Thermus	8.070469359
SYSU GY2-47	Bacteria;Deinococcus-Thermus;Deinococci;Thermates;Thermaceae;Thermus	8.070469359
SYSU GY2-58	Bacteria;Deinococcus-Thermus;Deinococci;Thermates;Thermaceae;Thermus	8.070469359

SYSU GY3-13	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Acetobacteraceae;Eliaeraea	ND
SYSU GY3-101	Bacteria;Chloroflexi;Chloroflexia;Chloroflexales;Chloroflexaceae;Chloroflexus	28.16505676
SYSU GY3-23	Bacteria;Bacteroidetes;Flavobacteria;Flavobacteriales;Schleiferiaceae;Schleiferia	0.776593981
SYSU GY3-42	Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;Sandaracinobacter	0.773976248
SYSU GY3-136	Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;Sandaracinobacter	0.773976248
SYSU GY3-35	Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;Sandaracinobacter	0.773976248
SYSU GY3-37	Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;Sandaracinobacter	0.773976248
SYSU GY-37	Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;Sandaracinobacter	0.773976248
SYSU GY3-P8	Bacteria;Chloroflexi;Chloroflexia;Chloroflexales;Roseiflexaceae;Roseiflexus	7.817421882
SYSU GY3-138	Bacteria;Chloroflexi;Chloroflexia;Chloroflexales;Roseiflexaceae;Roseiflexus	7.817421882
SYSU GY3-144	Bacteria;Chloroflexi;Chloroflexia;Chloroflexales;Roseiflexaceae;Roseiflexus	ND
SYSU GY3-41	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Acetobacteraceae;Eliaeraea	1.166636126
SYSU GY3-147	Bacteria;Deinococcus-Thermus;Deinococci;Thermales;Thermaceae;Thermus	ND
SYSU GY3-17	Bacteria;Chloroflexi;Chloroflexia;Chloroflexales;Chloroflexaceae;Chloroflexus	28.16505676
SYSU GY3-112	Bacteria;Deinococcus-Thermus;Deinococci;Thermales;Thermaceae;Thermus	ND
SYSU GY3-6-2	Bacteria;Chloroflexi;Chloroflexia;Chloroflexales;Roseiflexaceae;Roseiflexus	7.817421882
SYSU GY3-63	Bacteria;Proteobacteria;Gammaproteobacteria;Xanthomonadales;Xanthomonadaceae;AF407725	ND
SYSU GY3-141	Bacteria;Proteobacteria;Gammaproteobacteria;Xanthomonadales;Xanthomonadaceae;AF407725	ND
SYSU GY3-81	Bacteria;Aquificae;Aquificae;Aquificales;Hydrogenothermaceae;Sulfurihydrogenibium	ND
SYSU GY3-83	Bacteria;Aquificae;Aquificae;Aquificales;Hydrogenothermaceae;Sulfurihydrogenibium	ND
SYSU GY3-67	Bacteria;Aquificae;Aquificae;Aquificales;Hydrogenothermaceae;Sulfurihydrogenibium	ND
SYSU GY3-146	Bacteria;Deinococcus-Thermus;Deinococci;Thermales;Thermaceae;Thermus	8.070469359
SYSU GY3-201	Bacteria;Deinococcus-Thermus;Deinococci;Thermales;Thermaceae;Thermus	8.070469359
SYSU GY3-61	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Tepidimonas	0.724239331
SYSU GY3-77	Bacteria;Acidobacteria;Solibacteres;Solibacterales;Bryobacteraceae;Paludibaculum	ND
SYSU GY3-85	Bacteria;Acidobacteria;Solibacteres;Solibacterales;Bryobacteraceae;Paludibaculum	ND
SYSU GY3-193	Bacteria;Deinococcus-Thermus;Deinococci;Thermales;Thermaceae;Thermus	8.070469359
SYSU GY3-150	Bacteria;Deinococcus-Thermus;Deinococci;Thermales;Thermaceae;Thermus	8.070469359

SYSU GY3-89	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Acetobacteraceae;Eliaeraea	ND
SYSU GY3-38	Bacteria;Deinococcus-Thermus;Deinococci;Thermates;Thermaceae;Thermus	8.070469359
SYSU GY3-121	Bacteria;Deinococcus-Thermus;Deinococci;Thermates;Thermaceae;Thermus	8.070469359
SYSU GY3-194	Bacteria;Deinococcus-Thermus;Deinococci;Thermates;Thermaceae;Thermus	8.070469359
SYSU GY3-33	Bacteria;Deinococcus-Thermus;Deinococci;Thermates;Thermaceae;Thermus	8.070469359
SYSU GY3-31	Bacteria;Deinococcus-Thermus;Deinococci;Thermates;Thermaceae;Thermus	8.070469359
SYSU GY3-36	Bacteria;Deinococcus-Thermus;Deinococci;Thermates;Thermaceae;Thermus	8.070469359
SYSU GY3-192	Bacteria;Deinococcus-Thermus;Deinococci;Thermates;Thermaceae;Thermus	8.070469359
SYSU GY3-96	Bacteria;Deinococcus-Thermus;Deinococci;Thermates;Thermaceae;Thermus	8.070469359
SYSU GY3-14	Bacteria;Deinococcus-Thermus;Deinococci;Thermates;Thermaceae;Thermus	8.070469359
SYSU GY3-44	Bacteria;Chloroflexi;Chloroflexia;Chloroflexales;Chloroflexaceae;Chloroflexus	28.16505676
SYSU GY3-188	Bacteria;Deinococcus-Thermus;Deinococci;Thermates;Thermaceae;Thermus	8.070469359
SYSU GY3-196	Bacteria;Deinococcus-Thermus;Deinococci;Thermates;Thermaceae;Thermus	8.070469359
SYSU GY3-197	Bacteria;Deinococcus-Thermus;Deinococci;Thermates;Thermaceae;Thermus	8.070469359
SYSU GY3-199	Bacteria;Deinococcus-Thermus;Deinococci;Thermates;Thermaceae;Thermus	8.070469359
SYSU GY3-19	Bacteria;Chloroflexi;EU335161;AB186887;AB186887;AB186887	ND
SYSU GY3-20	Bacteria;Chloroflexi;EU335161;AB186887;AB186887;AB186887	ND
SYSU GY3-116	Bacteria;Deinococcus-Thermus;Deinococci;Thermates;Thermaceae;Thermus	8.070469359
SYSU GY3-59	Bacteria;Deinococcus-Thermus;Deinococci;Thermates;Thermaceae;Thermus	8.070469359
SYSU GY3-191	Bacteria;Deinococcus-Thermus;Deinococci;Thermates;Thermaceae;Thermus	8.070469359
SYSU GY3-195	Bacteria;Deinococcus-Thermus;Deinococci;Thermates;Thermaceae;Thermus	8.070469359
SYSU GY3-102	Bacteria;Deinococcus-Thermus;Deinococci;Thermates;Thermaceae;Thermus	8.070469359
SYSU GY3-142	Bacteria;Chloroflexi;EU335161;AB186887;AB186887;AB186887	ND
SYSU GY3-15	Bacteria;Deinococcus-Thermus;Deinococci;Thermates;Thermaceae;Thermus	8.070469359
SYSU GY3-49	Bacteria;Chloroflexi;EU335161;AB186887;AB186887;AB186887	ND
SYSU GY3-52	Bacteria;Chloroflexi;EU335161;AB186887;AB186887;AB186887	ND
SYSU GY3-53	Bacteria;Chloroflexi;EU335161;AB186887;AB186887;AB186887	ND
SYSU GY3-24	Bacteria;Chloroflexi;EU335161;AB186887;AB186887;AB186887	ND

SYSU GY3-143	Bacteria;Chloroflexi;EU335161;AB186887;AB186887;AB186887	ND
SYSU GY3-97	Bacteria;Deinococcus-Thermus;Deinococci;Thermates;Thermaceae;Thermus	8.070469359
SYSU GY3-39	Bacteria;Deinococcus-Thermus;Deinococci;Thermates;Thermaceae;Thermus	8.070469359
SYSU GY3-40	Bacteria;Deinococcus-Thermus;Deinococci;Thermates;Thermaceae;Thermus	8.070469359
SYSU GY3-41-2	Bacteria;Deinococcus-Thermus;Deinococci;Thermates;Thermaceae;Thermus	8.070469359
SYSU GY3-46	Bacteria;Deinococcus-Thermus;Deinococci;Thermates;Thermaceae;Thermus	8.070469359
SYSU GY3-47	Bacteria;Deinococcus-Thermus;Deinococci;Thermates;Thermaceae;Thermus	8.070469359
SYSU GY3-50	Bacteria;Deinococcus-Thermus;Deinococci;Thermates;Thermaceae;Thermus	8.070469359
SYSU GY3-51	Bacteria;Deinococcus-Thermus;Deinococci;Thermates;Thermaceae;Thermus	8.070469359
SYSU GY3-54	Bacteria;Deinococcus-Thermus;Deinococci;Thermates;Thermaceae;Thermus	8.070469359
SYSU GY3-55	Bacteria;Deinococcus-Thermus;Deinococci;Thermates;Thermaceae;Thermus	8.070469359
SYSU GY3-56	Bacteria;Deinococcus-Thermus;Deinococci;Thermates;Thermaceae;Thermus	8.070469359
SYSU GY3-86	Bacteria;Deinococcus-Thermus;Deinococci;Thermates;Thermaceae;Thermus	8.070469359
SYSU GY3-18	Bacteria;Deinococcus-Thermus;Deinococci;Thermates;Thermaceae;Thermus	8.070469359
SYSU GY3-30	Bacteria;Deinococcus-Thermus;Deinococci;Thermates;Thermaceae;Thermus	8.070469359
SYSU GY3-32	Bacteria;Deinococcus-Thermus;Deinococci;Thermates;Thermaceae;Thermus	8.070469359
SYSU GY3-118	Bacteria;Deinococcus-Thermus;Deinococci;Thermates;Thermaceae;Thermus	8.070469359
SYSU GY3-120	Bacteria;Deinococcus-Thermus;Deinococci;Thermates;Thermaceae;Thermus	8.070469359
SYSU GY3-126	Bacteria;Deinococcus-Thermus;Deinococci;Thermates;Thermaceae;Thermus	8.070469359
SYSU GY3-129	Bacteria;Deinococcus-Thermus;Deinococci;Thermates;Thermaceae;Thermus	8.070469359
SYSU GY3-57	Bacteria;Deinococcus-Thermus;Deinococci;Thermates;Thermaceae;Thermus	8.070469359
SYSU GY3-60	Bacteria;Deinococcus-Thermus;Deinococci;Thermates;Thermaceae;Thermus	8.070469359
SYSU GY3-62	Bacteria;Deinococcus-Thermus;Deinococci;Thermates;Thermaceae;Thermus	8.070469359
SYSU GY3-64	Bacteria;Deinococcus-Thermus;Deinococci;Thermates;Thermaceae;Thermus	8.070469359
SYSU GY3-68	Bacteria;Deinococcus-Thermus;Deinococci;Thermates;Thermaceae;Thermus	8.070469359
SYSU GY3-69	Bacteria;Deinococcus-Thermus;Deinococci;Thermates;Thermaceae;Thermus	8.070469359
SYSU GY3-71	Bacteria;Deinococcus-Thermus;Deinococci;Thermates;Thermaceae;Thermus	8.070469359
SYSU GY3-74	Bacteria;Deinococcus-Thermus;Deinococci;Thermates;Thermaceae;Thermus	8.070469359

SYSU GY3-94	Bacteria;Deinococcus-Thermus;Deinococci;Thermates;Thermaceae;Thermus	8.070469359
SYSU GY3-189	Bacteria;Deinococcus-Thermus;Deinococci;Thermates;Thermaceae;Thermus	8.070469359
SYSU GY3-190	Bacteria;Deinococcus-Thermus;Deinococci;Thermates;Thermaceae;Thermus	8.070469359
SYSU GY3-153	Bacteria;Deinococcus-Thermus;Deinococci;Thermates;Thermaceae;Thermus	8.070469359
SYSU GY3-P5	Bacteria;Firmicutes;Clostridia;Thermoanaerobacterales;Thermaerobacter;Thermaerobacter	ND
SYSU GY3-48	Bacteria;Deinococcus-Thermus;Deinococci;Thermates;Thermaceae;Thermus	8.070469359
SYSU GY3-108	Bacteria;Deinococcus-Thermus;Deinococci;Thermates;Thermaceae;Thermus	8.070469359
SYSU GY3-65	Bacteria;Deinococcus-Thermus;Deinococci;Thermates;Thermaceae;Thermus	8.070469359
SYSU GY3-78	Bacteria;Deinococcus-Thermus;Deinococci;Thermates;Thermaceae;Thermus	8.070469359
SYSU GY3-93	Bacteria;Deinococcus-Thermus;Deinococci;Thermates;Thermaceae;Thermus	8.070469359
SYSU GY3-95	Bacteria;Deinococcus-Thermus;Deinococci;Thermates;Thermaceae;Thermus	8.070469359
SYSU GY3-113	Bacteria;Deinococcus-Thermus;Deinococci;Thermates;Thermaceae;Thermus	8.070469359
SYSU GY3-2	Bacteria;Chloroflexi;Chloroflexia;Chloroflexales;Chloroflexaceae;Chloroflexus	28.16505676
SYSU GY3-34	Bacteria;Chloroflexi;Chloroflexia;Chloroflexales;Chloroflexaceae;Chloroflexus	28.16505676
SYSU GY3-127	Bacteria;Chloroflexi;Chloroflexia;Chloroflexales;Chloroflexaceae;Chloroflexus	28.16505676
SYSU GY3-104-2	Bacteria;Chloroflexi;Caldilineae;Caldilineales;Caldilineaceae;Caldilinea	0.221634687
SYSU GY3-87	Bacteria;Deinococcus-Thermus;Deinococci;Thermates;Thermaceae;Thermus	8.070469359
SYSU GY3-6	Bacteria;Chloroflexi;Caldilineae;Caldilineales;Caldilineaceae;Caldilinea	0.221634687
SYSU GY3-103	Bacteria;Firmicutes;Bacilli;Bacillales;Bacillaceae;Anoxybacillus	0.157063951
SYSU GY3-99	Bacteria;Deinococcus-Thermus;Deinococci;Thermates;Thermaceae;Thermus	8.070469359
SYSU GY3-11	Bacteria;Chloroflexi;Caldilineae;Caldilineales;Caldilineaceae;Caldilinea	0.221634687
SYSU GY3-12	Bacteria;Chloroflexi;Caldilineae;Caldilineales;Caldilineaceae;Caldilinea	0.221634687
SYSU GY3-181	Bacteria;Chloroflexi;Caldilineae;Caldilineales;Caldilineaceae;Caldilinea	0.221634687
SYSU GY3-21	Bacteria;Deinococcus-Thermus;Deinococci;Thermates;Thermaceae;Thermus	8.070469359
SYSU GY3-104-3	Bacteria;Firmicutes;Bacilli;Bacillales;Bacillaceae;Anoxybacillus	0.157063951
SYSU GY3-105	Bacteria;Firmicutes;Bacilli;Bacillales;Bacillaceae;Anoxybacillus	0.157063951
SYSU GY3-124	Bacteria;Deinococcus-Thermus;Deinococci;Thermates;Thermaceae;Thermus	8.070469359
SYSU GY3-128	Bacteria;Deinococcus-Thermus;Deinococci;Thermates;Thermaceae;Thermus	8.070469359

SYSU GY3-79	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Tepidicella	0.073296511
SYSU GY3-25	Bacteria;Deinococcus-Thermus;Deinococci;Thermales;Thermaceae;Thermus	8.070469359

Note: ND, not detected in high throughput sequencing files.

Supplementary Table 5. List of metabolites detected in the spent culture medium (SCM).

Compound	ratio(W1/CK)	p-value	ratio(W2/CK)	p-value	ratio(W3/CK)	p-value	ratio(W4/CK)	p-value
	4 h		8 h		12 h		24 h	
Deoxycytidine	1.275581901	0.612927201	3.518705798	0.012640955	4.873195604	0.001526261	78.85635509	0.014671813
2'-deoxyadenosine	1.39508061	0.293103876	2.478473306	0.012245001	4.41492471	0.000352319	45.67379558	0.010206931
5'-deoxyadenosine	1.39508061	0.293103876	2.478473306	0.012245001	4.41492471	0.000352319	45.67379558	0.010206931
Deoxyadenosine	1.39508061	0.293103876	2.478473306	0.012245001	4.41492471	0.000352319	45.67379558	0.010206931
Muramic acid	1.39508061	0.293103876	2.478473306	0.012245001	4.41492471	0.000352319	45.67379558	0.010206931
Isopentenyladenine	2.857357979	0.078494146	17.355568	0.064426391	13.37271281	0.034081622	44.80751871	0.007641073
Cytosine	1.783774649	0.027654827	9.474045045	0.000736749	9.421251864	5.43979E-06	35.67788317	0.010838476
Indole acetaldehyde	1.133372456	0.511957036	13.80787892	3.40488E-05	6.883256698	1.29762E-06	13.63361952	0.008854468
N4-acetyl aminobutanol	1.188106517	0.425617279	2.847008357	0.012633844	2.002956712	0.010623608	9.130807179	0.002266932
Nicotinamide ribose	0.907915333	0.767301258	3.143833582	0.028667145	3.323933579	0.023705742	8.120664675	7.2039E-05
Pantothenic acid (VB5)	1.230365944	0.342226141	2.538930324	0.007733578	1.633019045	0.04041704	7.039690987	0.002513511
N-acetyl Glutamic acid	1.179977589	0.335302688	7.270944921	0.001032418	5.096344776	5.98678E-05	6.803259741	8.51656E-05
hydroxy Pyruvate	0.692766823	0.152222532	4.898986021	0.00074515	3.213084986	0.000433992	5.757009189	2.89393E-05
Malonate	0.692766823	0.152222532	4.898986021	0.00074515	3.213084986	0.000433992	5.757009189	2.89393E-05
L-Histidinol	1.66067784	0.060517162	4.047844853	0.003773859	2.602849744	0.004103524	0.247720245	0.023809787
N-acetyl Ornithine	1.137072726	0.511228807	2.351479006	0.014716974	1.8726147	0.010022495	0.186095547	0.046480523
2-amino Butyric acid	1.151958987	0.473777701	0.30095251	0.025563996	0.404755824	0.036356965	0.179596299	0.013519223
D-α-amino Butyric acid	1.151958987	0.473777701	0.30095251	0.025563996	0.404755824	0.036356965	0.179596299	0.013519223
L-α-amino Butyric acid								
(homoalanine)	1.151958987	0.473777701	0.30095251	0.025563996	0.404755824	0.036356965	0.179596299	0.013519223
γ-amino Butyric acid	1.151958987	0.473777701	0.30095251	0.025563996	0.404755824	0.036356965	0.179596299	0.013519223
Dimethylglycine	1.151958987	0.473777701	0.30095251	0.025563996	0.404755824	0.036356965	0.179596299	0.013519223
2-amino-2-methylpropanoate	1.151958987	0.473777701	0.298962119	0.025072049	0.404755824	0.036356965	0.179596299	0.013519223
3-aminoisobutanoate	1.151958987	0.473777701	0.298962119	0.025072049	0.404755824	0.036356965	0.179596299	0.013519223

4-aminobutanoate	1.151958987	0.473777701	0.298962119	0.025072049	0.404755824	0.036356965	0.179596299	0.013519223
α -keto Glutaric acid (Oxoglutaric acid)	0.997157209	0.988025222	0.080242842	0.02898861	0.159232688	0.03510424	0.090891411	0.005852645
L-glutamic acid	1.119840876	0.580704054	0.077332657	0.041604947	0.096773607	0.043300644	0.041828308	0.039074844
2-amino-2-methylpropanoate	1.118187088	0.582261734	0.121796407	0.009818818	0.184034517	0.046975053	0.036095081	0.034617086
3-aminoisobutanoate	1.118187088	0.582261734	0.121796407	0.009818818	0.184034517	0.046975053	0.036095081	0.034617086
D- α -aminobutyric acid	1.118187088	0.582261734	0.121796407	0.009818818	0.184034517	0.046975053	0.036095081	0.034617086
L-(+)-2-Aminobutyric acid	1.118187088	0.582261734	0.121796407	0.009818818	0.184034517	0.046975053	0.036095081	0.034617086
5'-Methylthioadenosine	0.997693195	0.991799608	0.409313149	0.053244526	0.331062712	0.034644512	0.010904041	0.040966945
4-Guanidinobutanoic acid	0.855665922	0.52589644	12.29090872	0.014152117	10.51650961	3.68725E-05	16.49021266	0.082465636
5-amino-1-[3,4-dihydroxy-5-(hydroxymethyl)oxolan-2-yl]imidazole-4-carboxamide	3.639715906	0.00628222	3.449020449	0.302305656	3.084503551	0.036719393	3.2996711	0.246876587
Putrescine	2.141896053	0.143502079	103.5827064	0.010566997	77.11744813	0.002413465	1.23679359	0.414736602
L-Histidine	1.181017928	0.36919145	2.071653071	0.018182106	1.523050139	0.033820853	1.113057314	0.559144325
13(S)-HPOT	0.965853491	0.593941183	0.871471244	0.144028469	0.778826866	0.005050769	0.982235445	0.752401271
N-acetyl Putrescine	1.202678012	0.410804131	2.359640024	0.015472336	1.794095397	0.04152126	0.978722199	0.924515201
3-hydroxy isovaleric acid	1.196164241	0.622202795	4.32403076	0.007884285	2.818673748	0.006928969	5.131755898	ND
L-aspartate	1.104928824	0.63229002	0.144665156	0.048936221	0.151836207	0.05019662	0.103504291	0.045865098
7-methyl Guanine	1.319495289	0.297089595	2.191051885	0.029321125	1.74013682	0.051158818	4.349613076	0.002704836
Galacturonic acid	0.492289209	0.068718096	0.454333956	0.019489525	0.612152626	0.055662939	0.634961998	0.068074484
5-oxo-proline	0.968112431	0.852101206	0.187743125	0.011336635	0.413077759	0.056783322	0.036371076	0.020862129
pyro Glutamic acid (5-oxoproline)	0.968112431	0.852101206	0.187743125	0.011336635	0.413077759	0.056783322	0.036371076	0.020862129
Pyrrolidonecarboxylic acid	0.968112431	0.852101206	0.187743125	0.011336635	0.413077759	0.056783322	0.036371076	0.020862129
Ile-Val	1.124929035	0.616070102	0.064375647	0.052243634	0.125063684	0.057657013	0.038172665	0.049724915
Val-Leu	1.124929035	0.616070102	0.064375647	0.052243634	0.125063684	0.057657013	0.038172665	0.049724915
Val-Ile	1.124929035	0.616070102	0.064375647	0.052243634	0.125063684	0.057657013	0.038172665	0.049724915

Leu-Val	1.124929035	0.616070102	0.064375647	0.052243634	0.125063684	0.057657013	0.038172665	0.049724915
N-acetyl Leucine	1.073523946	0.792969572	2.912855916	0.006819747	1.980938529	0.061791744	3.224652203	0.004891712
Pantothenic Acid	1.092135683	0.652456821	2.19218583	0.007219408	1.520708161	0.062792727	4.666709108	0.002023426
Asn-Pro	1.635587474	0.032948523	1.463452765	0.089499656	1.423812011	0.084665741	1.27045046	0.206202639
Ser-Thr	1.294384109	0.341042619	0.138537339	0.081356679	0.168945953	0.086386273	ND	ND
Thr-Ser	1.294384109	0.341042619	0.138537339	0.081356679	0.168945953	0.086386273	ND	ND
L-Phenylalanine	1.271443187	0.326476466	0.339910841	0.099637569	0.310396416	0.09324993	0.008284228	0.049597612
L-serine	1.119454938	0.589897855	0.417333943	0.097407282	0.419365444	0.096233274	0.044405976	0.039857296
Indole	1.263208929	0.454885282	0.415749248	0.120525155	0.380526591	0.102400373	5.092328311	0.003857233
IS-Trp	1.049760998	0.2838379	0.899342514	0.431529087	0.886349576	0.116515637	0.858581898	0.00805224
L-erythro-4-Hydroxyglutamate	1.284859561	0.321229202	2.022489261	0.019443472	1.507286112	0.129938353	2.359033113	0.012779067
Pterin	1.284859561	0.321229202	2.022489261	0.019443472	1.507286112	0.129938353	2.359033113	0.012779067
3-Indoleacetic Acid	0.81139784	0.448773124	1.85070727	0.027266676	1.425879126	0.138617677	2.788520828	0.005261224
5-hydroxy Indoleacetaldehyde	0.81139784	0.448773124	1.85070727	0.027266676	1.425879126	0.138617677	2.788520828	0.005261224
Indoleacetic acid	0.81139784	0.448773124	1.85070727	0.027266676	1.425879126	0.138617677	2.788520828	0.005261224
Guanosine 3',5'-cyclic monophosphate (cGMP)	1.32625179	0.257973379	1.824904617	0.041605837	1.515922347	0.165025751	1.555099701	0.110321201
L-lysine	1.117091197	0.658336797	0.646489944	0.258480008	0.554884567	0.188534968	0.024112387	0.049931873
Trimethylacetic acid	3.248741096	0.054330991	2.651000957	0.111731309	1.638125022	0.201722947	5.096506225	0.014261241
Glyceric acid	0.662582131	0.150833822	0.596183177	0.077224997	0.771027353	0.222234006	0.13634197	0.028318686
Leucinic acid;								
Hydroxyisocaproic acid	2.780690861	ND	7.505161606	0.01367008	4.048933888	0.275987425	1.574116782	ND
5-hydroxy Lysine	1.313915299	0.360185188	2.31469727	0.00846175	0.674721861	0.279636709	4.268782121	0.001826408
Choline	1.024692741	0.439552928	0.936297624	0.725549381	1.15690996	0.287321348	0.84098389	0.012041801
N1-Acetylspermidine	0.759570665	0.323228377	1.382486845	0.222666885	0.782177181	0.325456716	0.258549082	0.017098793
Imidazoleacetic acid	0.958534094	0.921974021	1.337258532	0.476172031	1.351598915	0.453076574	7.484013808	0.007624278
Histamine	1.326321705	0.279255122	1.88843376	0.028496721	1.203622203	0.457454555	1.753292928	0.052386431

3-(2-hydroxyphenyl)propanoate	0.334802698	0.025626434	2.239651274	0.041713963	1.342945744	0.46138225	0.978822199	0.93546318
Ile-Lys	1.423092701	0.18444866	1.236384529	0.453147867	1.137450397	0.630648449	0.091230667	0.023243107
Eicosanoic acid (20:1)	0.878155833	0.049824681	0.902424549	0.220781084	0.970676015	0.714298359	1.147957417	0.227872526
Uracil	1.23482782	0.685641082	1.057865278	0.850399496	0.892640302	0.75339564	2.966260239	0.036086493
Citrulline	1.100157484	0.583945976	0.898891239	0.658492169	0.950692105	0.823038749	0.370343765	0.013489059
Adenine	1.285645229	0.12714525	4.993667914	0.005182231	0.986845747	0.956447516	8.906877185	0.000279769
Oxypurinol	1.29025128	0.371772788	ND	ND	ND	ND	2.039728865	0.046691207
Xanthine	1.29025128	0.371772788	ND	ND	ND	ND	2.039728865	0.046691207

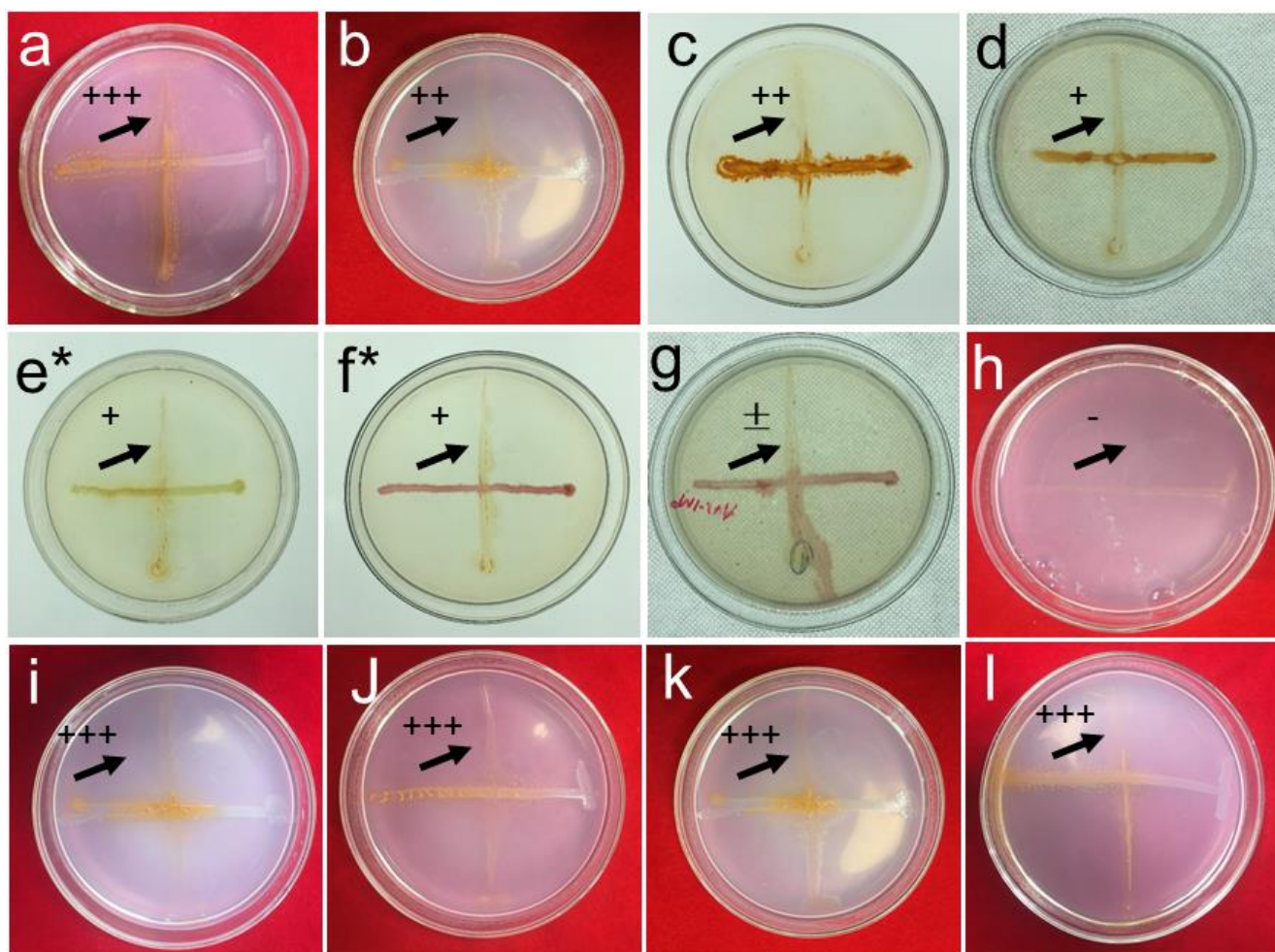
Note: Ratio >1, increase production as compared to 0 h;

<1, decrease production as compared to 0 h

ND, metabolite not detected

Supplementary Table 6. List of commercially available metabolites used in the growth promotion assay on nine representative *Chloroflexi* and *Bacteroidetes* strains.

Compound	CAS	Concentration	Concentration	Concentration
		1 (mg/ml)	2 (mg/ml)	3 (mg/ml)
Cytosine	71-30-7	1	0.1	0.01
Adenine	73-24-5	1	0.1	0.01
Uracil	66-22-8	1	0.1	0.01
2'-Deoxycytidine	207121-53-7	10	1	0.1
3'-Deoxycytidine	7057-33-2	10	1	0.1
Deoxycytidine	1186526-91-9	1	0.1	0.01
Indole	120-72-9	1	0.1	0.01
3-Indoleacetic acid	87-51-4	1	0.1	0.01
Isopentenyladenine	2365-40-4	1	0.1	0.01
Hydroxypyruvate	1113-60-6	0.1	0.01	0.001
Putrescine	110-60-1	10	0.01	0.001
N-acetyl Glutamic acid	19146-55-5	1	0.1	0.01
Muramic acid	1114-41-6	0.1	0.01	0.001
Pantothenic acid	599-54-2	10	1	0.1
Imidazole acetic acid	70615-26-8	10	1	0.1



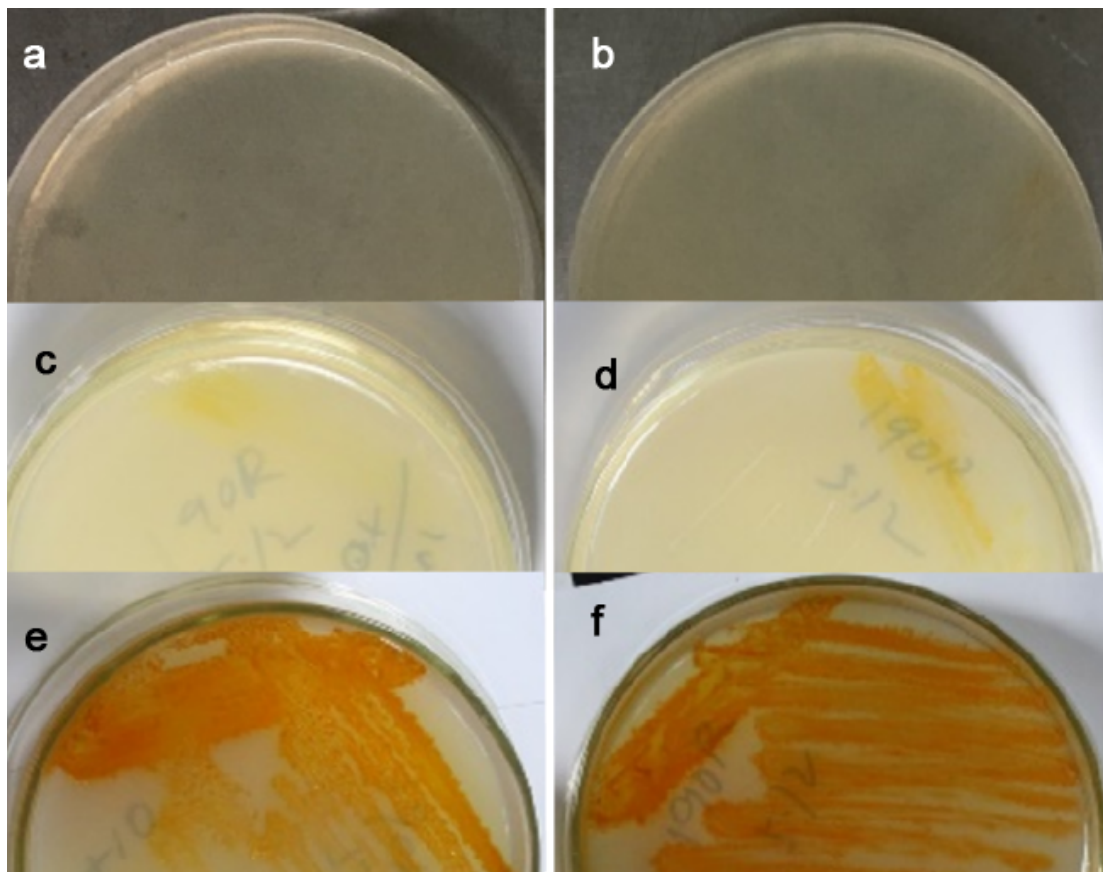
Supplementary Figure 1. Cross-streak analyses for growth promotion using eleven key node bacteria on *Chloroflexus* sp. SYSU G00190R. The putative key nodes bacteria were streaked on the horizontal direction while the indicator *Chloroflexus* sp. SYSU G00190R on the vertical direction. Both strains are incubated at either 45°C or 55°C for 1 week under dark conditions. The enhancement of growth was represented by the (+) sign.

Note: +++, good activity; ++, moderate activity; +, weak activity; -, no growth enhancement

*incubation at 45°C.

Key node strains:

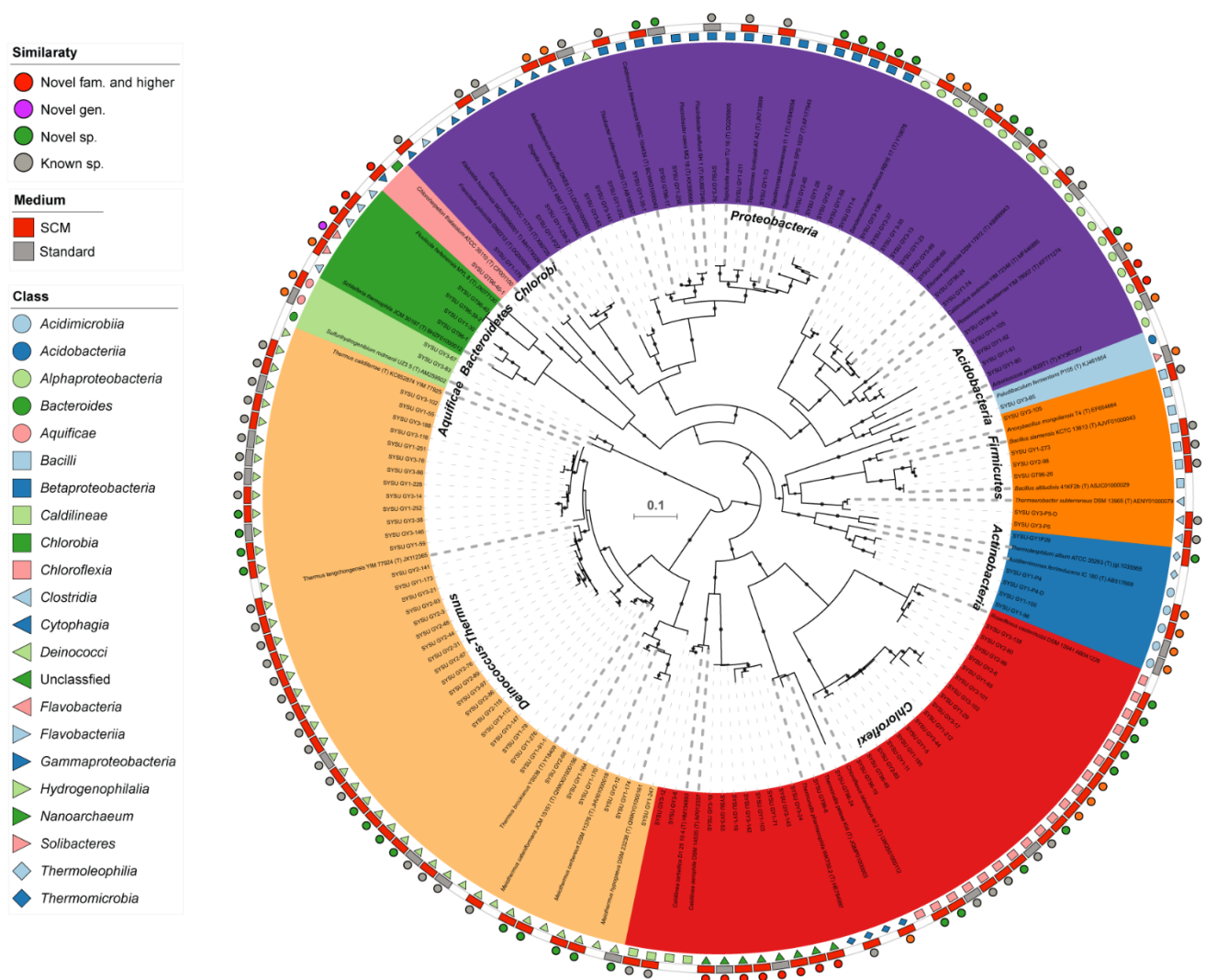
- (a) *Tepidimonas* sp. SYSU G00190W (*Tepidimonas ignava* SPS-1037^T, 99.79% 16S rRNA gene sequence identity)
- (b) *Tepidimonas* sp. SYSU G00470 (*Tepidimonas taiwanensis* I1-1^T, 98.27%)
- (c) *Geobacillus* sp. SYSU G00408 (*Geobacillus vulcani* 3S-1^T, 99.88%)
- (d) *Geobacillus* sp. SYSU G00405 (*Geobacillus kaustophilus* NBRC 102445^T, 100%)
- (e) *Sphingomonas* sp. SYSU G00007^T
- (f) *Meiothermus* sp. SYSU GA4201 (*Meiothermus hypogaeus* DSM 23238^T, 99.35%)
- (g) *Meiothermus* sp. SYSU GA4201 (*Meiothermus hypogaeus* DSM 23238^T, 99.35%)
- (h) *Thermus* sp. SYSU G00458. (*Thermus arciformis* CGMCC 1.6992^T, 99.87%)
- (i) *Tepidimonas ignava* SPS-1037^T
- (j) *Tepidimonas taiwanensis* I1-1^T
- (k) *Tepidimonas sediminis* YIM 72259^T
- (l) *Tepidimonas alkaliphilus* YIM 72238^T



Supplementary Figure 2. Comparison of the growth of the indicator *Chloroflexus* sp. strain G00190R in R2A agar and media supplemented with cell free extract or spent culture supernatants of *Tepidimonas* sp. strain 190W following incubation at 55°C for 3 days of incubation

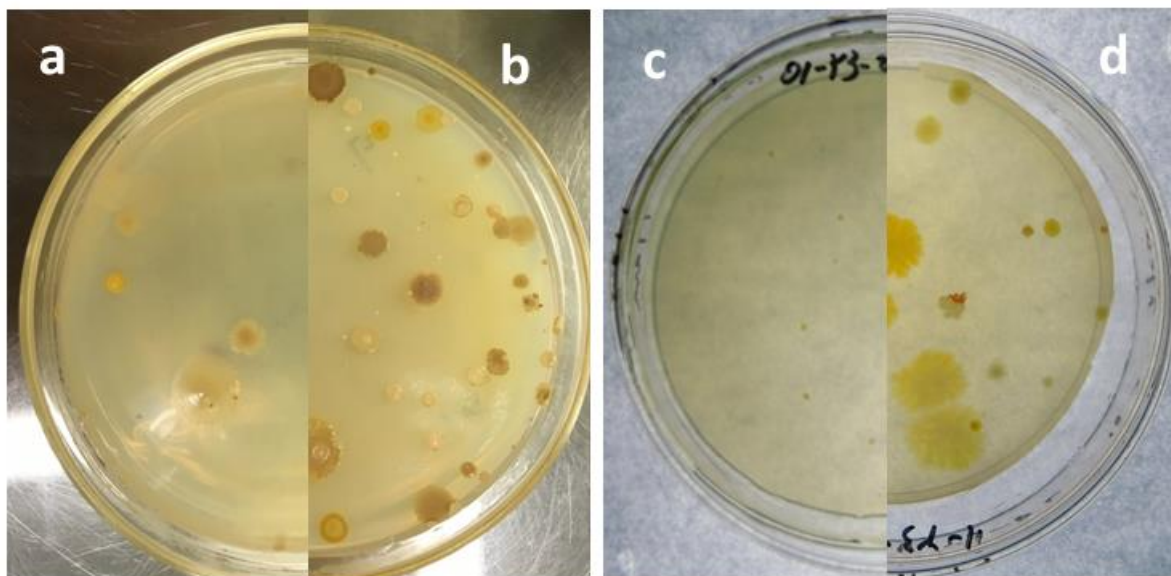
Note:

- a. R2A agar
- b. R2A agar + cell free extract
- c. R2A agar + 1% supernatant
- d. R2A agar + 5% supernatant
- e. R2A agar + 10% supernatant
- f. R2A agar + 20% supernatant



Supplementary Figure 3. Maximum likelihood tree showing the phylogenetic positions of the cultivated isolates determined in this study.

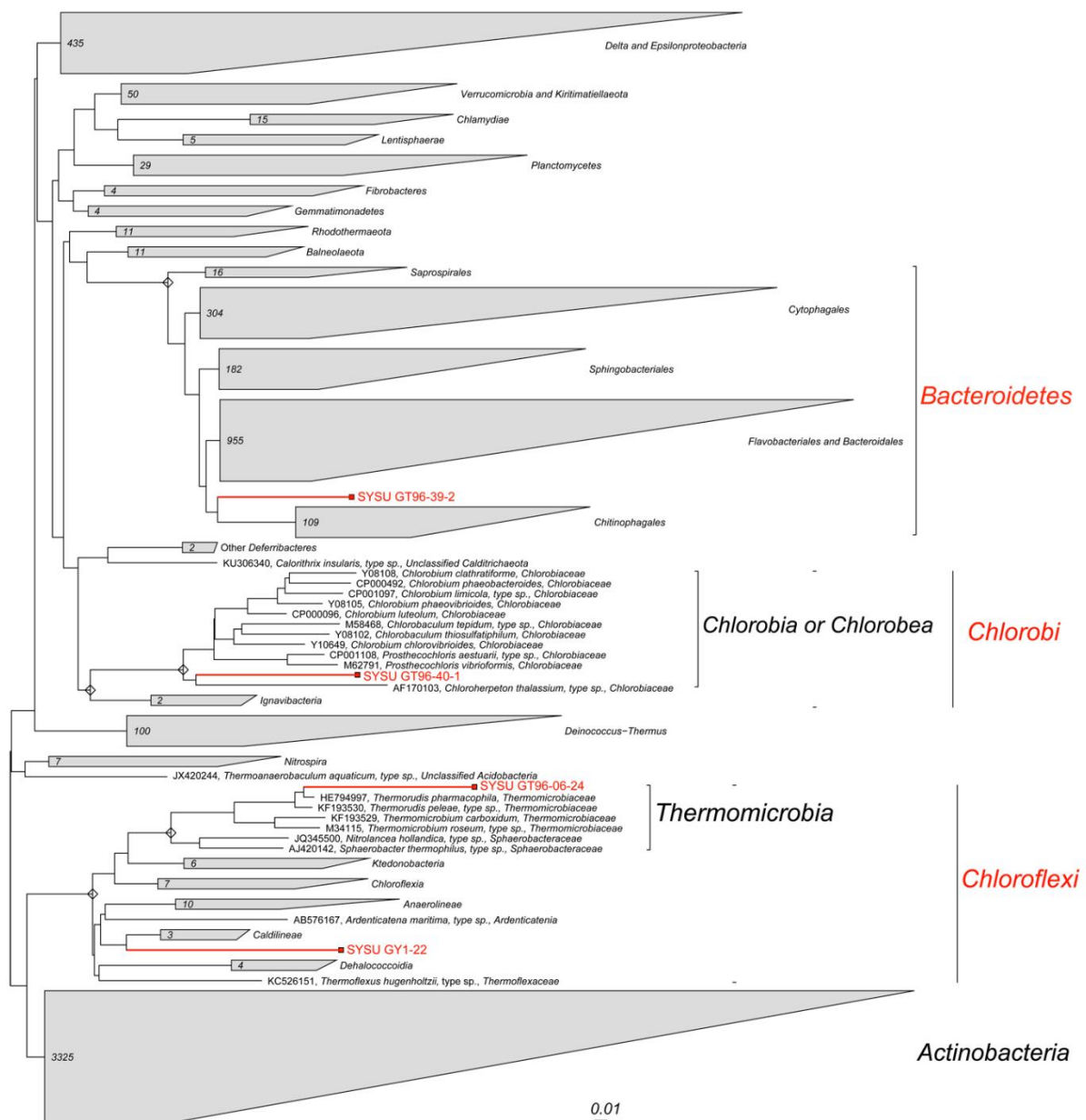
The filled circles in the outermost ring represent the taxonomic ranks of the isolates based on the 16S rRNA sequence identities. Bootstrap values higher than 50 are marked in black circles at the nodes of the phylogenetic tree.



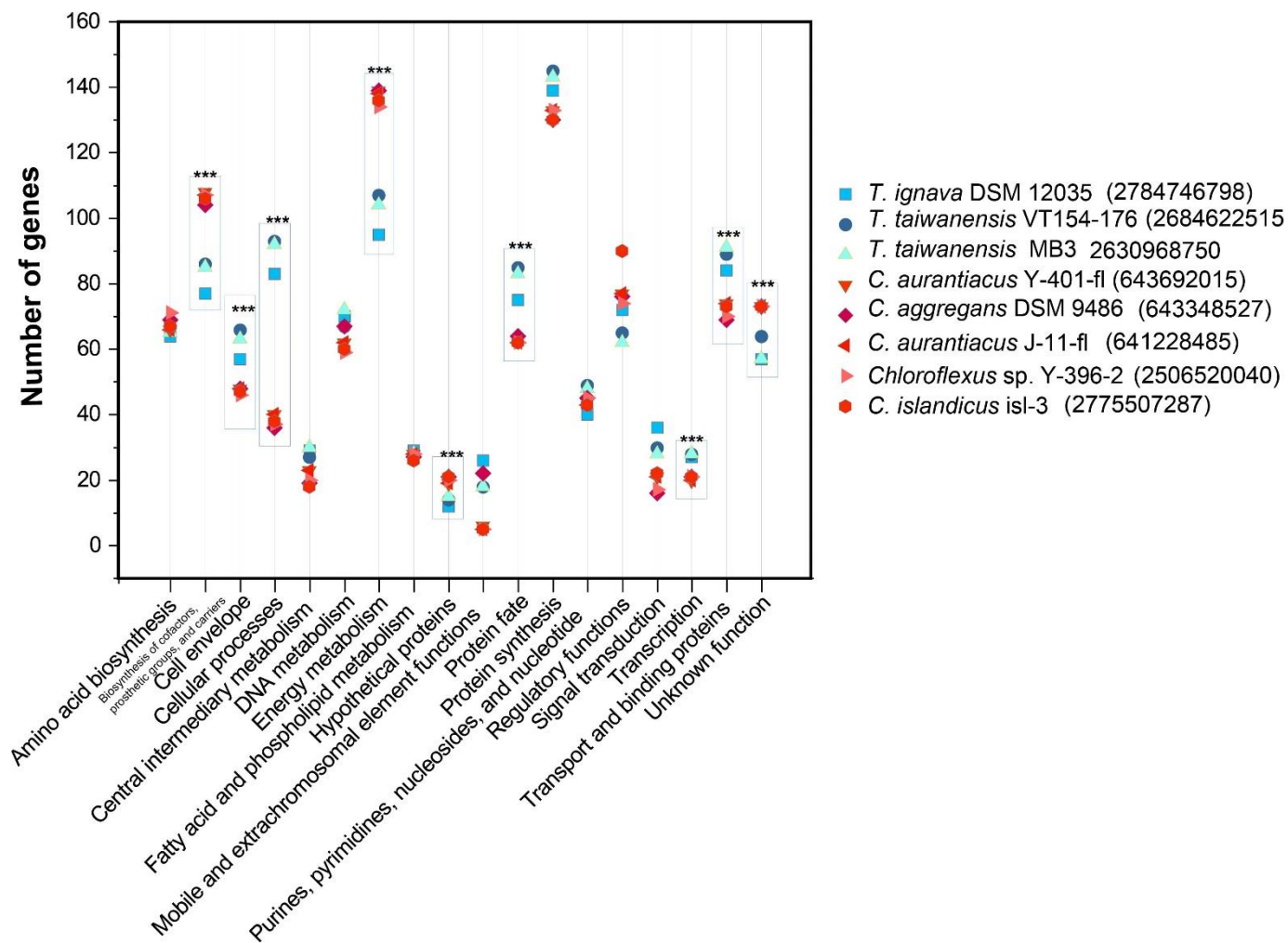
Supplementary Figure 4. Representative isolation plates comparing the difference between traditional (a, c) and SCM-based (b, d) isolation methods. The pictures of the isolation plates shown below are taken after plating the Y3 samples and incubating for 1 week at 55°C

Media used:

- (a) R2A agar
- (b) R2A agar + 10% spent culture supernatant
- (c) *Thermus* 162 agar
- (d) *Thermus* 162 agar + 10% spent culture supernatant



Supplementary Figure 5. Phylogenetic positions of the four strains representing putative novel lineages in the ARB all species tree.

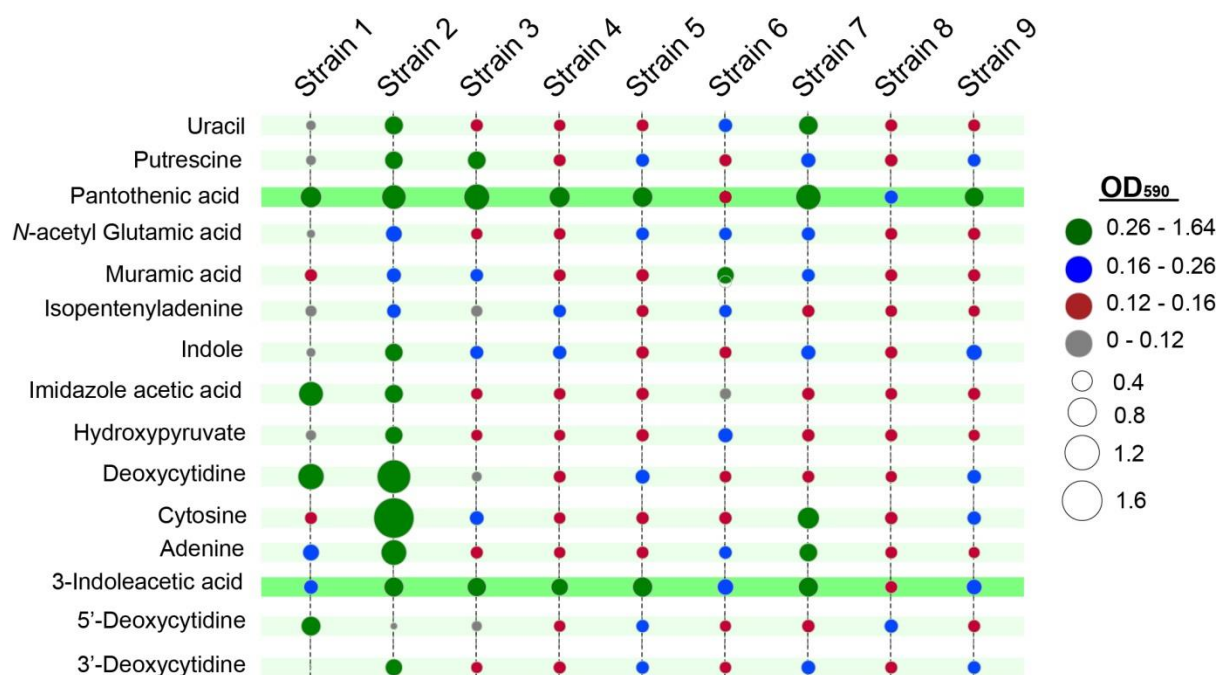


TIGRfam functional categories

Supplementary Figure 6. Functional annotation of the genomes of *Tepidimonas* and *Chloroflexus* spp.

Categorization of the function of each protein-coding gene was based on the TIGR assignments.

*** suggests significant differences between these two microbial groups at $p < 0.001$. The colours of these labels show the related species.



Supplementary Figure 7. Growth promotion assay of metabolites.

Each metabolite was tested in 3 concentration gradients (Table S6) and the most effective concentration as represented by the highest OD for each metabolite is selected for the interpretation of the growth effect. The circle represents the growth OD of each representative strain by the tested metabolite. Color circle depicts range (listed on the figure caption) on which the growth OD falls and the size the general depiction of the actual OD for each strain. The horizontal background line represents the metabolites with common growth promoting effect.

- Strain 1: **SYSU GY1-5** [*Chloroflexus islandicus* isl-2^T, 98.67% 16S rRNA gene sequence identity, *Chloroflexi*];
 Strain 2: **SYSU GY3-101** [*Chloroflexus islandicus* isl-2^T, 93.39%, *Chloroflexi*];
 Strain 3: **SYSU GY2-6** [*Roseiflexus castenholzii* DSM 13941^T, 96.24%, *Chloroflexi*];
 Strain 4: **SYSU GY2-90** [*Roseiflexus castenholzii* DSM 13941^T, 96.07%, *Chloroflexi*];
 Strain 5: **SYSU GY3-144** [uncultured *Roseiflexus* clone DTM38 (EF205514), 95.69%, *Chloroflexi*];
 Strain 6: **SYSU GY1-22** [uncultured bacterium SK47 (AY753393), 99.35%, *Chloroflexi*];
 Strain 7: **SYSU GY2-54** [uncultured bacterium SK47 (AY753393), 99.23%, *Chloroflexi*];
 Strain 8: **SYSU GT96-06-24** [uncultured *Chloroflexi* clone AE1b_G7, 98.8%, *Chloroflexi*];
 Strain 9: **SYSU GT96-39-2** [uncultured bacterium clone NBDTU1 (FJ529921), 89.23%, *Bacteroidetes*].