Supplemental Materials and Methods

Site monitoring and characterization of environmental indices

Thaw depth was measured using a metal depth probe. Constantan–copper thermocouples and CR1000 data loggers (Campbell Scientific) were used to measure and record soil temperature and moisture content at each depth every half hour in flux bases installed in each plot. Volumetric water content from the soil surface to 15 cm depth was measured using site-calibrated Campbell CS616 water content reflectometer probes and soil moisture data presented in this study were averaged over the growing season. To prepare soils for microbial and chemical analyses, visible roots and stones were removed by metal forceps. To measure soil C and nitrogen (N), soil samples (5 g) were dried at 70 °C, ground to powder, encapsulated in silver foil and fumigated with HCl for 24 h at room temperature to remove soil inorganic C (carbonates). Soil C and N concentrations were analyzed in the Colorado Plateau Stable Isotope Laboratory at the Northern Arizona University on a DELTA V Advantage isotope ratio mass spectrometer (Thermo Fisher Scientific), configured through a Finnigan CONFLO III (Thermo Fisher Scientific) and using a Carlo Erba NC2100 elemental analyser (CE Elantech).

Soil DNA isolation, metagenome library preparation, and sequencing

Soil DNA was extracted using a freeze-grinding plus sodium dodecyl sulfate (SDS) lysis method as described previously [1] and was purified by a MOBIO PowerSoil kit (MO BIO Laboratories, Inc., Carlsbad, CA, USA) according to manufacturer’s protocol. DNA quality was assessed based on spectrometry absorbance at wavelengths of 230nm, 260nm and 280nm detected by a NanoDrop ND-1000 Spectrophotometer (NanoDrop Products by Thermo Fisher Scientific). The absorbance ratios of 260/280 nm were around 1.8, and of 260/230 nm were larger than 1.7. The final DNA concentrations were quantified by PicoGreen using a FLUOstar Optima fluorescence plant reader (BMG Labtech, Jena, Germany). Dual-indexed DNA sequencing libraries were prepared using the Illumina Nextera XT DNA library prep kit according to manufacturer's instruction except that the protocol was terminated after isolation of cleaned double-stranded libraries. Prepared library DNA concentrations were determined with a Qubit HS DNA assay and libraries were run on a High Sensitivity DNA chip using the Bioanalyzer 2100 instrument (Agilent) to determine library average insert sizes. DNA libraries were sequenced at the Georgia Institute of Technology High Throughput DNA Sequencing Core on an Illumina HiSeq 2500 instrument in the rapid run mode for 300 cycles (150 bp, paired-end mode). Adapter trimming and demultiplexing of sequences (assignment of sequences to samples) were carried out by the Illumina 2500 instrument. Metagenomic sequences have been deposited in the European Nucleotide Archive.

[1] Zhou JZ, Bruns MA, and Tiedje JM (1996) DNA recovery from soils of diverse composition. Applied and Environmental Microbiology 2: 316-322.

Supplemental tables

Table S1: European Nucleotide Archive database accession IDs, sequencing depth, quality metrics, and average genome size for all twenty-four soil community metagenomes from the 4.5-year CiPEHR sample collection (May 2013). Estimated average genome size of each sample community metagenome was determined with MicrobeCensus. MicrobeCensus (Nayfach and Pollard 2015) is a tool that estimates average genome size by normalizing the number of reads matching to a set of conserved single copy marker genes by the total number of reads used in query.

Sample metagenome	ENA Sample ID	# Raw sequences	# Post-QC sequences	% Reads retained	Raw data size (Gbp)	Data size post-QC (Gbp)	Est. avg genome size
Fence 1, 15-25 cm, Control	ERS3336394	16921626	14009649	82.80%	5.08	3.02	6929393
Fence 2, 15-25 cm, Control	ERS3336395	27732641	22464651	81.00%	8.32	5.56	6699766
Fence 3, 15-25 cm, Control	ERS3336396	23357438	18245350	78.10%	7.01	4.79	6345230
Fence 4, 15-25 cm, Control	ERS3336397	28854107	20482564	71.00%	8.66	5.65	6288559
Fence 5, 15-25 cm, Control	ERS3336398	37835617	30044541	79.40%	11.35	6.35	6130808
Fence 6, 15-25 cm, Control	ERS3336399	21182813	15933022	75.20%	6.35	4.26	7500976
Fence 1, 15-25 cm, Warming	ERS3336400	24473078	19649679	80.30%	7.34	4.94	6806590
Fence 2, 15-25 cm, Warming	ERS3336401	29401318	24324617	82.70%	8.82	5.99	6327260
Fence 3, 15-25 cm, Warming	ERS3336402	31374460	22870499	72.90%	9.41	6.08	7035674
Fence 4, 15-25 cm, Warming	ERS3336403	20149558	15834600	78.60%	6.04	4.07	7438793
Fence 5, 15-25 cm, Warming	ERS3336404	23412481	18608517	79.50%	7.02	4.56	7009593
Fence 6, 15-25 cm, Warming	ERS3336405	38005737	31682650	83.40%	11.4	6.93	5873189
Fence 1, 45-55 cm, Control	ERS3336406	14057671	11455841	81.50%	4.22	2.88	4794725
Fence 2, 45-55 cm, Control	ERS3336407	20247622	16323195	80.60%	6.07	3.58	4785026
Fence 3, 45-55 cm, Control	ERS3336408	18636844	15863933	85.10%	5.59	3.78	5129050
Fence 4, 45-55 cm, Control	ERS3336409	18322419	15359809	83.80%	5.5	3.56	5186224
Fence 5, 45-55 cm, Control	ERS3336410	15207692	12794505	84.10%	4.56	3.22	5014540
Fence 6, 45-55 cm, Control	ERS3336411	19174175	16153340	84.20%	5.75	3.73	4131485
Fence 1, 45-55 cm, Warming	ERS3336412	24867267	20116318	80.90%	7.46	4.09	4248245
Fence 2, 45-55 cm, Warming	ERS3336413	26240894	20213517	77.00%	7.87	3.81	4162469
Fence 3, 45-55 cm, Warming	ERS3336414	22183927	18370879	82.80%	6.66	4	4878232
Fence 4, 45-55 cm, Warming	ERS3336415	19747772	16796376	85.10%	5.92	3.95	4282672
Fence 5, 45-55 cm, Warming	ERS3336416	12737442	10115066	79.40%	3.82	2.48	4954275
Fence 6, 45-55 cm, Warming	ERS3336417	18580029	15219345	81.90%	5.57	3.36	4799293

Table S2: The relative sequence abundances of archaeal clades in 4.5-year metagenomes. Percentages represent the proportion of metagenome-derived 16S sequences matching to each clade relative to the number of total bacterial and archaeal 16S sequences (i.e., proportion relative to total prokaryotic community).

Sample metagenome ID	Total Archaea	Cren- archaeota	Diaph- erotrites	Eury- archaeota	Nano- archaeaeota	Thaum- archaeota	Methano- peredens
Fence 1, 15-25 cm, control	1.687%	0.337%	0.000%	0.844%	0.000%	0.506%	0.000%
Fence 2, 15-25 cm, control	1.337%	0.000%	0.122%	0.243%	0.000%	0.972%	0.000%
Fence 3, 15-25 cm, control	1.600%	0.123%	0.000%	0.246%	0.000%	1.231%	0.000%
Fence 4, 15-25 cm, control	1.581%	0.063%	0.063%	0.316%	0.000%	1.138%	0.000%
Fence 5, 15-25 cm, control	2.005%	0.143%	0.191%	1.146%	0.000%	0.525%	0.000%
Fence 6, 15-25 cm, control	2.224%	0.000%	0.035%	0.000%	0.000%	2.189%	0.000%
Fence 1, 15-25 cm, warmed	1.738%	0.000%	0.087%	0.087%	0.087%	1.478%	0.000%
Fence 2, 15-25 cm, warmed	1.062%	0.000%	0.118%	0.000%	0.000%	0.944%	0.000%
Fence 3, 15-25 cm, warmed	1.626%	0.296%	0.000%	0.444%	0.000%	0.887%	0.000%
Fence 4, 15-25 cm, warmed	1.759%	0.000%	0.065%	0.000%	0.000%	1.694%	0.000%
Fence 5, 15-25 cm, warmed	1.831%	0.000%	0.000%	0.354%	0.000%	1.476%	0.000%
Fence 6, 15-25 cm, warmed	1.839%	0.225%	0.000%	1.389%	0.000%	0.225%	0.000%
Fence 1, 45-55 cm, control	1.883%	0.583%	0.053%	1.087%	0.000%	0.159%	0.505%
Fence 2, 45-55 cm, control	1.552%	0.038%	0.000%	1.514%	0.000%	0.000%	0.153%
Fence 3, 45-55 cm, control	1.655%	0.061%	0.000%	1.318%	0.000%	0.276%	0.000%
Fence 4, 45-55 cm, control	2.888%	0.380%	0.000%	2.507%	0.000%	0.000%	0.000%
Fence 5, 45-55 cm, control	2.761%	0.194%	0.000%	2.527%	0.000%	0.039%	0.000%
Fence 6, 45-55 cm, control	2.503%	0.000%	0.054%	2.448%	0.000%	0.000%	0.381%
Fence 1, 45-55 cm, warmed	4.189%	0.313%	0.030%	3.816%	0.015%	0.015%	3.026%
Fence 2, 45-55 cm, warmed	3.456%	0.377%	0.000%	3.063%	0.016%	0.000%	1.753%
Fence 3, 45-55 cm, warmed	2.604%	0.133%	0.019%	2.395%	0.038%	0.019%	0.000%
Fence 4, 45-55 cm, warmed	3.021%	0.407%	0.086%	2.529%	0.000%	0.000%	0.021%
Fence 5, 45-55 cm, warmed	2.716%	0.157%	0.079%	2.440%	0.000%	0.039%	0.118%
Fence 6, 45-55 cm, warmed	2.422%	0.153%	0.092%	2.115%	0.061%	0.000%	0.276%

Table S3: Metagenome-assembled genome (MAG) quality indicators and basic genome statistics. MAG completeness and contamination was determined using CheckM lineage workflow for either domain *Archaea* or *Bacteria*.

MAG ID	Source metagenome	CheckM lineage	Complete-ness	Contam-ination	Quality score	Genome size (bp)	# contigs
AK5YR.2.maxbin2.1	Fence 2, 15-25 cm, Control	Bacteria	84.95	2.74	71.25	6931655	809
AK5YR.2.maxbin2.12	Fence 2, 15-25 cm, Control	Bacteria	98.82	3.79	79.87	6459283	720
AK5YR.2.maxbin2.7	Fence 2, 15-25 cm, Control	Bacteria	78.45	1.72	69.85	2238819	480
AK5YR.2.metabat2.12	Fence 2, 15-25 cm, Control	Bacteria	82.41	1.72	73.81	2643895	488
AK5YR.2.metabat2.14	Fence 2, 15-25 cm, Control	Bacteria	100	4.31	78.45	3869809	450
AK5YR.2.metabat2.17	Fence 2, 15-25 cm, Control	Bacteria	63.34	0.16	62.54	2733095	601
AK5YR.2.metabat2.25	Fence 2, 15-25 cm, Control	Bacteria	84.09	3.03	68.94	7008488	1210
AK5YR.2.metabat2.9	Fence 2, 15-25 cm, Control	Bacteria	84.72	0	84.72	4096575	646
AK5YR.3.maxbin2.1	Fence 3, 15-25 cm, Control	Bacteria	81.27	1.72	72.67	6764200	1117
AK5YR.3.maxbin2.10	Fence 3, 15-25 cm, Control	Bacteria	63.17	0.47	60.82	1395498	405
AK5YR.3.maxbin2.4	Fence 3, 15-25 cm, Control	Bacteria	80.72	2.74	67.02	4881000	1011
AK5YR.3.metabat2.3	Fence 3, 15-25 cm, Control	Bacteria	94.83	1.88	85.43	3028190	352
AK5YR.3.metabat2.5	Fence 3, 15-25 cm, Control	Bacteria	83.75	0.66	80.45	7208858	1252
AK5YR.4.maxbin2.1	Fence 4, 15-25 cm, Control	Bacteria	82.41	0.78	78.51	6733584	1152
AK5YR.4.maxbin2.13	Fence 4, 15-25 cm, Control	Bacteria	81.9	0.31	80.35	3411634	759
AK5YR.4.maxbin2.3	Fence 4, 15-25 cm, Control	Bacteria	62.96	0	62.96	2234204	631
AK5YR.4.maxbin2.8	Fence 4, 15-25 cm, Control	Bacteria	99.53	3.45	82.28	6301634	799
AK5YR.4.metabat2.13	Fence 4, 15-25 cm, Control	Bacteria	70.69	2.07	60.34	2357896	463
AK5YR.4.metabat2.14	Fence 4, 15-25 cm, Control	Bacteria	80.49	0.69	77.04	4204278	628
AK5YR.4.metabat2.16	Fence 4, 15-25 cm, Control	Bacteria	64.05	0.31	62.5	2289783	406
AK5YR.4.metabat2.3	Fence 4, 15-25 cm, Control	Bacteria	66.38	0	66.38	5129989	831
AK5YR.4.metabat2.8	Fence 4, 15-25 cm, Control	Bacteria	75.97	1.57	68.12	7412611	1234
AK5YR.5.maxbin2.16	Fence 5, 15-25 cm, Control	Bacteria	65.72	0	65.72	4496059	1361
AK5YR.5.maxbin2.5	Fence 5, 15-25 cm, Control	Bacteria	76.96	1.72	68.36	4290350	906
AK5YR.5.maxbin2.6	Fence 5, 15-25 cm, Control	Bacteria	86.29	0.92	81.69	2512209	433
AK5YR.5.metabat2.1	Fence 5, 15-25 cm, Control	Bacteria	98.67	2.59	85.72	4232025	513
AK5YR.5.metabat2.13	Fence 5, 15-25 cm, Control	Bacteria	93.81	2.59	80.86	2510699	214
AK5YR.5.metabat2.15	Fence 5, 15-25 cm, Control	Bacteria	94.83	1.72	86.23	3551262	497
AK5YR.5.metabat2.16	Fence 5, 15-25 cm, Control	Bacteria	79.31	1.18	73.41	2244515	466
AK5YR.5.metabat2.17	Fence 5, 15-25 cm, Control	Bacteria	91.95	0	91.95	2486754	217
AK5YR.5.metabat2.26	Fence 5, 15-25 cm, Control	Bacteria	80.8	3.61	62.75	2860384	378
AK5YR.5.metabat2.27	Fence 5, 15-25 cm, Control	Bacteria	100	1.72	91.4	4178772	336
AK5YR.5.metabat2.28	Fence 5, 15-25 cm, Control	Bacteria	90.13	1.88	80.73	1916754	320
AK5YR.5.metabat2.29	Fence 5, 15-25 cm, Control	Bacteria	65.28	0.63	62.13	1773451	400
AK5YR.5.metabat2.32	Fence 5, 15-25 cm, Control	Bacteria	82.96	0	82.96	4210440	702
AK5YR.5.metabat2.5	Fence 5, 15-25 cm, Control	Bacteria	91.38	2.04	81.18	6007982	551
AK5YR.6.metabat2.1	Fence 6, 15-25 cm, Control	Bacteria	80.8	3.61	62.75	7320259	1173
AK5YR.6.metabat2.3	Fence 6, 15-25 cm, Control	Bacteria	89.66	3.16	73.86	2274186	525
AK5YR.7.maxbin2.1	Fence 1, 15-25 cm, Warmed	Bacteria	94.1	0	94.1	7017134	675
AK5YR.7.maxbin2.8	Fence 1, 15-25 cm, Warmed	Bacteria	74.71	1.88	65.31	4702110	1098
AK5YR.7.metabat2.1	Fence 1, 15-25 cm, Warmed	Bacteria	94.83	0	94.83	2749748	221
AK5YR.7.metabat2.7	Fence 1, 15-25 cm, Warmed	Bacteria	96.55	1.72	87.95	3581158	467
AK5YR.7.metabat2.9	Fence 1, 15-25 cm, Warmed	Bacteria	74.53	0.16	73.73	5288811	1054
AK5YR.8.maxbin2.3	Fence 2, 15-25 cm, Warmed	Bacteria	84.33	1.88	74.93	2447597	363
AK5YR.8.metabat2.9	Fence 2, 15-25 cm, Warmed	Bacteria	97.41	0.16	96.61	3306291	191
AK5YR.9.maxbin2.16	Fence 3, 15-25 cm, Warmed	Bacteria	68.02	1.13	62.37	2141514	656
AK5YR.9.maxbin2.2	Fence 3, 15-25 cm, Warmed	Bacteria	96.68	1.88	87.28	7080299	528

AK5YR.9.maxbin2.7	Fence 3, 15-25 cm, Warmed	Bacteria	71.96	0.86	67.66	2377888	618
AK5YR.9.metabat2.11	Fence 3, 15-25 cm, Warmed	Bacteria	62.54	0.16	61.74	3914657	752
AK5YR.9.metabat2.13	Fence 3, 15-25 cm, Warmed	Bacteria	86.78	1.72	78.18	8347157	627
AK5YR.9.metabat2.14	Fence 3, 15-25 cm, Warmed	Bacteria	81.43	0.57	78.58	8027617	1158
AK5YR.9.metabat2.26	Fence 3, 15-25 cm, Warmed	Bacteria	77.27	3.45	60.02	4722618	827
AK5YR.9.metabat2.30	Fence 3, 15-25 cm, Warmed	Bacteria	100	4.31	78.45	6142187	624
AK5YR.11.maxbin2.4	Fence 5, 15-25 cm, Warmed	Bacteria	80.25	2.19	69.3	4421421	1025
AK5YR.11.metabat2.10	Fence 5, 15-25 cm, Warmed	Bacteria	93.1	1.72	84.5	3244339	441
AK5YR.12.maxbin2.1	Fence 6, 15-25 cm, Warmed	Bacteria	97.41	2.8	83.41	6786960	457
AK5YR.12.maxbin2.14	Fence 6, 15-25 cm, Warmed	Bacteria	97.24	5.17	71.39	5820699	949
AK5YR.12.maxbin2.17	Fence 6, 15-25 cm, Warmed	Bacteria	93.89	1.72	85.29	3041336	528
AK5YR.12.maxbin2.3	Fence 6, 15-25 cm, Warmed	Bacteria	79	0.86	74.7	2782270	741
AK5YR.12.maxbin2.30	Fence 6, 15-25 cm, Warmed	Bacteria	76.96	1.72	68.36	2150201	393
AK5YR.12.maxbin2.7	Fence 6, 15-25 cm, Warmed	Bacteria	85.72	2.35	73.97	2191830	441
AK5YR.12.maxbin2.9	Fence 6, 15-25 cm, Warmed	Bacteria	81.43	3.92	61.83	2452804	471
AK5YR.12.metabat2.18	Fence 6, 15-25 cm, Warmed	Bacteria	84.72	1.72	76.12	2991341	373
AK5YR.12.metabat2.2	Fence 6, 15-25 cm, Warmed	Bacteria	95.69	2.74	81.99	3262588	251
AK5YR.12.metabat2.20	Fence 6, 15-25 cm, Warmed	Bacteria	94.83	0	94.83	3088664	447
AK5YR.12.metabat2.34	Fence 6, 15-25 cm, Warmed	Bacteria	69.37	0	69.37	4016944	865
AK5YR.12.metabat2.37	Fence 6, 15-25 cm, Warmed	Bacteria	92.24	3.61	74.19	4219648	491
AK5YR.12.metabat2.5	Fence 6, 15-25 cm, Warmed	Bacteria	77.04	2.04	66.84	2545634	522
AK5YR.13.maxbin2.4	Fence 1, 45-55 cm, Control	Bacteria	90.52	0	90.52	2635641	610
AK5YR.13.maxbin2.9	Fence 1, 45-55 cm, Control	Bacteria	90.36	0	90.36	2145657	452
AK5YR.13.metabat2.1	Fence 1, 45-55 cm, Control	Bacteria	86.05	3.45	68.8	2887148	411
AK5YR.13.metabat2.10	Fence 1, 45-55 cm, Control	Bacteria	84.48	0.5	81.98	3064316	398
AK5YR.13.metabat2.12	Fence 1, 45-55 cm, Control	Bacteria	74.71	0.5	72.21	2575935	556
AK5YR.13.metabat2.2	Fence 1, 45-55 cm, Control	Bacteria	84.09	0.31	82.54	2445485	329
AK5YR.13.metabat2.4	Fence 1, 45-55 cm, Control	Bacteria	94.83	1.72	86.23	2909792	148
AK5YR.13.metabat2.6	Fence 1, 45-55 cm, Control	Bacteria	74.83	1.88	65.43	2174775	443
AK5YR.14.maxbin2.1	Fence 2, 45-55 cm, Control	Bacteria	74.53	2.46	62.23	3524556	960
AK5YR.14.maxbin2.11	Fence 2, 45-55 cm, Control	Bacteria	77.66	2.04	67.46	1874466	425
AK5YR.14.maxbin2.12	Fence 2, 45-55 cm, Control	Bacteria	96.55	0	96.55	3046720	229
AK5YR.14.maxbin2.15	Fence 2, 45-55 cm, Control	Archaea	86.84	0	86.84	1452226	175
AK5YR.14.maxbin2.17	Fence 2, 45-55 cm, Control	Bacteria	91.38	1.72	82.78	2963116	555
AK5YR.14.metabat2.1	Fence 2, 45-55 cm, Control	Bacteria	91.38	0	91.38	2927082	472
AK5YR.14.metabat2.12	Fence 2, 45-55 cm, Control	Bacteria	93.1	2.93	78.45	4207425	510
AK5YR.14.metabat2.16	Fence 2, 45-55 cm, Control	Bacteria	93.1	2.59	80.15	2860032	368
AK5YR.14.metabat2.17	Fence 2, 45-55 cm, Control	Bacteria	88.32	1.88	78.92	1901843	258
AK5YR.14.metabat2.18	Fence 2, 45-55 cm, Control	Bacteria	98.28	0	98.28	3312935	183
AK5YR.14.metabat2.3	Fence 2, 45-55 cm, Control	Bacteria	61.76	0.16	60.96	953407	245
AK5YR.15.maxbin2.16	Fence 3, 45-55 cm, Control	Bacteria	95.69	1.72	87.09	2719254	287
AK5YR.15.metabat2.11	Fence 3, 45-55 cm, Control	Bacteria	86.21	0	86.21	2449717	435
AK5YR.15.metabat2.12	Fence 3, 45-55 cm, Control	Bacteria	82.45	1.72	73.85	3020330	589
AK5YR.15.metabat2.13	Fence 3, 45-55 cm, Control	Archaea	93.46	1.87	84.11	1611189	130
AK5YR.15.metabat2.14	Fence 3, 45-55 cm, Control	Bacteria	82.76	1.72	74.16	2467312	344
AK5YR.15.metabat2.16	Fence 3, 45-55 cm, Control	Bacteria	70.22	0.16	69.42	1961198	347
AK5YR.15.metabat2.20	Fence 3, 45-55 cm, Control	Bacteria	62.07	0	62.07	4718258	1001
AK5YR.15.metabat2.4	Fence 3, 45-55 cm, Control	Bacteria	97.49	2.07	87.14	4566485	508
AK5YR.16.maxbin2.1	Fence 4, 45-55 cm, Control	Bacteria	74.01	0	74.01	3419166	937
AK5YR.16.maxbin2.10	Fence 4, 45-55 cm, Control	Bacteria	77.56	0.31	76.01	3166771	623

AK5YR.16.maxbin2.17	Fence 4, 45-55 cm, Control	Archaea	97.9	0	97.9	2071984	46
AK5YR.16.maxbin2.3	Fence 4, 45-55 cm, Control	Bacteria	71.55	0	71.55	2127275	490
AK5YR.16.metabat2.1	Fence 4, 45-55 cm, Control	Bacteria	93.89	1.72	85.29	2404926	285
AK5YR.16.metabat2.11	Fence 4, 45-55 cm, Control	Bacteria	87.7	2.07	77.35	3327915	470
AK5YR.16.metabat2.13	Fence 4, 45-55 cm, Control	Bacteria	67.16	0.63	64.01	2992352	698
AK5YR.16.metabat2.14	Fence 4, 45-55 cm, Control	Bacteria	100	1.72	91.4	3247612	94
AK5YR.16.metabat2.17	Fence 4, 45-55 cm, Control	Bacteria	63.24	0.57	60.39	1287653	291
AK5YR.16.metabat2.21	Fence 4, 45-55 cm, Control	Bacteria	71.43	1.72	62.83	2597850	452
AK5YR.16.metabat2.25	Fence 4, 45-55 cm, Control	Bacteria	90.44	0.34	88.74	3896438	495
AK5YR.16.metabat2.7	Fence 4, 45-55 cm, Control	Bacteria	84.48	0	84.48	1705289	290
AK5YR.17.maxbin2.1	Fence 5, 45-55 cm, Control	Bacteria	81.9	4.29	60.45	4127436	1154
AK5YR.17.maxbin2.11	Fence 5, 45-55 cm, Control	Bacteria	96.55	1.72	87.95	2378607	416
AK5YR.17.maxbin2.16	Fence 5, 45-55 cm, Control	Bacteria	73.51	1.88	64.11	4033749	996
AK5YR.17.maxbin2.4	Fence 5, 45-55 cm, Control	Bacteria	85.89	3.61	67.84	3152720	715
AK5YR.17.metabat2.1	Fence 5, 45-55 cm, Control	Archaea	96.26	0	96.26	1593083	82
AK5YR.17.metabat2.10	Fence 5, 45-55 cm, Control	Bacteria	73.51	2.35	61.76	2088182	374
AK5YR.17.metabat2.12	Fence 5, 45-55 cm, Control	Bacteria	62.65	0	62.65	2448597	466
AK5YR.17.metabat2.16	Fence 5, 45-55 cm, Control	Bacteria	86.79	1.21	80.74	3880390	482
AK5YR.17.metabat2.2	Fence 5, 45-55 cm, Control	Bacteria	93.1	3.45	75.85	2705578	251
AK5YR.18.maxbin2.15	Fence 6, 45-55 cm, Control	Bacteria	76.49	0.16	75.69	1484817	364
AK5YR.18.maxbin2.8	Fence 6, 45-55 cm, Control	Bacteria	94.83	2.07	84.48	4452424	679
AK5YR.18.metabat2.10	Fence 6, 45-55 cm, Control	Bacteria	72.41	1.02	67.31	2144487	454
AK5YR.18.metabat2.19	Fence 6, 45-55 cm, Control	Bacteria	89.5	0.16	88.7	2915605	495
AK5YR.18.metabat2.21	Fence 6, 45-55 cm, Control	Bacteria	89.37	1.72	80.77	2481013	268
AK5YR.18.metabat2.5	Fence 6, 45-55 cm, Control	Bacteria	82.76	0.5	80.26	2344929	420
AK5YR.18.metabat2.7	Fence 6, 45-55 cm, Control	Archaea	95.33	0.93	90.68	1655771	98
AK5YR.19.maxbin2.10	Fence 1, 45-55 cm, Warmed	Bacteria	78.92	2.3	67.42	2187609	512
AK5YR.19.maxbin2.18	Fence 1, 45-55 cm, Warmed	Bacteria	80.69	1.72	72.09	2316475	573
AK5YR.19.maxbin2.22	Fence 1, 45-55 cm, Warmed	Archaea	81.24	0	81.24	2337627	337
AK5YR.19.maxbin2.5	Fence 1, 45-55 cm, Warmed	Bacteria	98.28	2.07	87.93	3129873	272
AK5YR.19.metabat2.10	Fence 1, 45-55 cm, Warmed	Bacteria	100	0.86	95.7	2625374	332
AK5YR.19.metabat2.14	Fence 1, 45-55 cm, Warmed	Archaea	81.25	2.34	69.55	1127689	197
AK5YR.19.metabat2.17	Fence 1, 45-55 cm, Warmed	Bacteria	93.97	0	93.97	2445731	224
AK5YR.19.metabat2.21	Fence 1, 45-55 cm, Warmed	Bacteria	96.55	3.45	79.3	3211898	430
AK5YR.19.metabat2.25	Fence 1, 45-55 cm, Warmed	Bacteria	62.38	0.16	61.58	2427514	525
AK5YR.19.metabat2.30	Fence 1, 45-55 cm, Warmed	Bacteria	69.59	0	69.59	1550092	344
AK5YR.19.metabat2.8	Fence 1, 45-55 cm, Warmed	Bacteria	63.17	0	63.17	1620299	321
AK5YR.20.metabat2.3	Fence 2, 45-55 cm, Warmed	Bacteria	99.14	3.45	81.89	3283277	202
AK5YR.20.metabat2.7	Fence 2, 45-55 cm, Warmed	Bacteria	66.38	0	66.38	1813899	354
AK5YR.20.metabat2.9	Fence 2, 45-55 cm, Warmed	Bacteria	94.2	0.16	93.4	2812684	338
AK5YR.21.maxbin2.18	Fence 3, 45-55 cm, Warmed	Bacteria	87.62	1.72	79.02	2986873	333
AK5YR.21.maxbin2.2	Fence 3, 45-55 cm, Warmed	Bacteria	88.79	0.31	87.24	2831058	417
AK5YR.21.maxbin2.5	Fence 3, 45-55 cm, Warmed	Bacteria	92.53	1.18	86.63	2673271	482
AK5YR.21.maxbin2.8	Fence 3, 45-55 cm, Warmed	Bacteria	93.1	0	93.1	4148668	513
AK5YR.21.metabat2.10	Fence 3, 45-55 cm, Warmed	Bacteria	75.86	1.72	67.26	2729910	568
AK5YR.21.metabat2.11	Fence 3, 45-55 cm, Warmed	Archaea	74.55	0.93	69.9	2480889	528
AK5YR.21.metabat2.13	Fence 3, 45-55 cm, Warmed	Bacteria	93.1	0.34	91.4	4257681	486
AK5YR.21.metabat2.14	Fence 3, 45-55 cm, Warmed	Bacteria	85.11	1.72	76.51	2541403	297
AK5YR.21.metabat2.17	Fence 3, 45-55 cm, Warmed	Bacteria	85.34	0	85.34	2409094	436
AK5YR.21.metabat2.23	Fence 3, 45-55 cm, Warmed	Bacteria	92.24	0	92.24	2169025	59

AK5YR.21.metabat2.25	Fence 3, 45-55 cm, Warmed	Bacteria	82.18	0	82.18	2901203	491
AK5YR.21.metabat2.5	Fence 3, 45-55 cm, Warmed	Archaea	67.06	0.93	62.41	1112371	211
AK5YR.21.metabat2.8	Fence 3, 45-55 cm, Warmed	Bacteria	98.28	1.72	89.68	3274953	247
AK5YR.22.maxbin2.4	Fence 4, 45-55 cm, Warmed	Bacteria	92.24	0	92.24	3163516	422
AK5YR.22.metabat2.11	Fence 4, 45-55 cm, Warmed	Bacteria	86.21	0	86.21	3042565	411
AK5YR.22.metabat2.12	Fence 4, 45-55 cm, Warmed	Bacteria	68.16	0	68.16	1719663	398
AK5YR.22.metabat2.14	Fence 4, 45-55 cm, Warmed	Bacteria	86.05	0	86.05	2603937	532
AK5YR.22.metabat2.16	Fence 4, 45-55 cm, Warmed	Bacteria	68.81	0.5	66.31	805369	94
AK5YR.22.metabat2.18	Fence 4, 45-55 cm, Warmed	Bacteria	74.92	2.59	61.97	2611838	288
AK5YR.22.metabat2.2	Fence 4, 45-55 cm, Warmed	Archaea	98.13	0.93	93.48	1663619	154
AK5YR.22.metabat2.5	Fence 4, 45-55 cm, Warmed	Bacteria	91.38	2.59	78.43	3321573	349
AK5YR.22.metabat2.9	Fence 4, 45-55 cm, Warmed	Bacteria	70.42	0.16	69.62	1897201	408
AK5YR.23.maxbin2.10	Fence 5, 45-55 cm, Warmed	Archaea	96.26	1.55	88.51	2342076	327
AK5YR.23.maxbin2.5	Fence 5, 45-55 cm, Warmed	Bacteria	71.08	0	71.08	1981316	546
AK5YR.23.maxbin2.8	Fence 5, 45-55 cm, Warmed	Bacteria	80.3	1.52	72.7	3136795	825
AK5YR.23.metabat2.1	Fence 5, 45-55 cm, Warmed	Bacteria	90.2	0	90.2	3073885	418
AK5YR.23.metabat2.11	Fence 5, 45-55 cm, Warmed	Bacteria	84.48	0.86	80.18	3011590	467
AK5YR.23.metabat2.4	Fence 5, 45-55 cm, Warmed	Bacteria	87.24	0.16	86.44	2157427	301
AK5YR.23.metabat2.5	Fence 5, 45-55 cm, Warmed	Bacteria	83.33	2.23	72.18	2976523	538
AK5YR.24.maxbin2.14	Fence 6, 45-55 cm, Warmed	Archaea	68.07	1.4	61.07	1274598	312
AK5YR.24.maxbin2.15	Fence 6, 45-55 cm, Warmed	Bacteria	85.29	0	85.29	2583362	570
AK5YR.24.maxbin2.17	Fence 6, 45-55 cm, Warmed	Bacteria	81.03	3.61	62.98	2315733	541
AK5YR.24.maxbin2.9	Fence 6, 45-55 cm, Warmed	Archaea	66.85	0.93	62.2	1197383	311
AK5YR.24.metabat2.15	Fence 6, 45-55 cm, Warmed	Bacteria	79.14	0.89	74.69	2715553	586
AK5YR.24.metabat2.6	Fence 6, 45-55 cm, Warmed	Bacteria	90.44	3.95	70.69	3077374	519
AK5YR.24.metabat2.9	Fence 6, 45-55 cm, Warmed	Bacteria	96.55	0	96.55	3260802	443

Table S4: Taxonomic classifications of metagenome-assembled genomes (MAGs), derived from GTDB-Tk.

MAG ID	GTDBTk taxonomic classification
AK5YR.2.maxbin2.1	d__Bacteria;p__Acidobacteriota;c__Acidobacteriae;o__Acidobacteriales;f__Koribacteraceae;g__;s__
AK5YR.2.maxbin2.7	d__Bacteria;p__Dormibacterota;c__Dormibacteria;o__UBA8260;f__UBA8260;g__UBA8260;s__
AK5YR.2.maxbin2.12	d__Bacteria;p__Actinobacteriota;c__Actinobacteria;o__Streptosporangiales;f__Streptosporangiaceae;g__UBA8262;s__
AK5YR.2.metabat2.9	d__Bacteria;p__Actinobacteriota;c__Thermoleophilia;o__Solirubrobacterales;f__Solirubrobacteraceae;g__;s__
AK5YR.2.metabat2.12	d__Bacteria;p__Acidobacteriota;c__Thermoanaerobaculia;o__UBA5066;f__UBA5066;g__;s__
AK5YR.2.metabat2.14	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Steroidobacterales;f__Steroidobacteraceae;g__;s__
AK5YR.2.metabat2.17	d__Bacteria;p__Actinobacteriota;c__Acidimicrobiia;o__Acidimicrobiales;f__;g__;s__
AK5YR.2.metabat2.25	d__Bacteria;p__Acidobacteriota;c__Acidobacteriae;o__Solibacterales;f__Solibacteraceae;g__Solibacter;s__
AK5YR.3.maxbin2.1	d__Bacteria;p__Acidobacteriota;c__Acidobacteriae;o__Acidobacteriales;f__Koribacteraceae;g__;s__
AK5YR.3.maxbin2.4	d__Bacteria;p__Acidobacteriota;c__Acidobacteriae;o__Acidobacteriales;f__Koribacteraceae;g__;s__
AK5YR.3.maxbin2.10	d__Bacteria;p__Dormibacterota;c__Dormibacteria;o__UBA8260;f__UBA8260;g__UBA8260;s__
AK5YR.3.metabat2.3	d__Bacteria;p__Dormibacterota;c__Dormibacteria;o__UBA8260;f__UBA8260;g__;s__
AK5YR.3.metabat2.5	d__Bacteria;p__Acidobacteriota;c__Acidobacteriae;o__Solibacterales;f__Solibacteraceae;g__Solibacter;s__
AK5YR.4.maxbin2.1	d__Bacteria;p__Acidobacteriota;c__Acidobacteriae;o__Acidobacteriales;f__Koribacteraceae;g__;s__

AK5YR.4.maxbin2.3	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Steroidobacterales;f__Steroidobacteraceae;g__;s__
AK5YR.4.maxbin2.8	d__Bacteria;p__Actinobacteriota;c__Actinobacteria;o__Streptosporangiales;f__Streptosporangiaceae;g__UBA8262;s__
AK5YR.4.maxbin2.13	d__Bacteria;p__Actinobacteriota;c__Acidimicrobiia;o__Acidimicrobiales;f__;g__;s__
AK5YR.4.metabat2.3	d__Bacteria;p__Acidobacteriota;c__Acidobacteriae;o__Acidobacteriales;f__Koribacteraceae;g__;s__
AK5YR.4.metabat2.8	d__Bacteria;p__Acidobacteriota;c__Acidobacteriae;o__Solibacterales;f__Solibacteraceae;g__Solibacter;s__
AK5YR.4.metabat2.13	d__Bacteria;p__Dormibacterota;c__Dormibacteria;o__UBA8260;f__UBA8260;g__;s__
AK5YR.4.metabat2.14	d__Bacteria;p__Acidobacteriota;c__Acidobacteriae;o__Acidobacteriales;f__Koribacteraceae;g__;s__
AK5YR.4.metabat2.16	d__Bacteria;p__Actinobacteriota;c__Thermoleophilia;o__Solirubrobacterales;f__Solirubrobacteraceae;g__;s__
AK5YR.5.maxbin2.5	d__Bacteria;p__Acidobacteriota;c__Acidobacteriae;o__Acidobacteriales;f__Koribacteraceae;g__;s__
AK5YR.5.maxbin2.6	d__Bacteria;p__Dormibacterota;c__Dormibacteria;o__UBA8260;f__UBA8260;g__UBA8260;s__
AK5YR.5.maxbin2.16	d__Bacteria;p__Acidobacteriota;c__Acidobacteriae;o__Solibacterales;f__Solibacteraceae;g__Solibacter;s__
AK5YR.5.metabat2.1	d__Bacteria;p__Acidobacteriota;c__Acidobacteriae;o__Acidobacteriales;f__Koribacteraceae;g__;s__
AK5YR.5.metabat2.5	d__Bacteria;p__Acidobacteriota;c__Acidobacteriae;o__Acidobacteriales;f__Koribacteraceae;g__;s__
AK5YR.5.metabat2.13	d__Bacteria;p__Actinobacteriota;c__Thermoleophilia;o__Solirubrobacterales;f__Solirubrobacteraceae;g__;s__
AK5YR.5.metabat2.15	d__Bacteria;p__Actinobacteriota;c__Acidimicrobiia;o__Acidimicrobiales;f__UBA7543;g__UBA7543;s__
AK5YR.5.metabat2.16	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Steroidobacterales;f__Steroidobacteraceae;g__;s__
AK5YR.5.metabat2.17	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Betaproteobacteriales;f__Gallionellaceae;g__Gallionella;s__
AK5YR.5.metabat2.26	d__Bacteria;p__Acidobacteriota;c__Acidobacteriae;o__Acidobacteriales;f__Acidobacteriaceae;g__Terracidiphilus;s__
AK5YR.5.metabat2.27	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Steroidobacterales;f__Steroidobacteraceae;g__;s__
AK5YR.5.metabat2.28	d__Bacteria;p__Actinobacteriota;c__Acidimicrobiia;o__Acidimicrobiales;f__RAAP-2;g__RAAP-2;s__
AK5YR.5.metabat2.29	d__Bacteria;p__UBP10;c__GR-WP33-30;o__UBA7539;f__UBA7539;g__UBA7539;s__
AK5YR.5.metabat2.32	d__Bacteria;p__Actinobacteriota;c__Thermoleophilia;o__Solirubrobacterales;f__Solirubrobacteraceae;g__Conexibacter;s__
AK5YR.6.metabat2.1	d__Bacteria;p__Actinobacteriota;c__Actinobacteria;o__Streptosporangiales;f__Streptosporangiaceae;g__UBA9676;s__
AK5YR.6.metabat2.3	d__Bacteria;p__Dormibacterota;c__Dormibacteria;o__UBA8260;f__UBA8260;g__;s__
AK5YR.7.maxbin2.1	d__Bacteria;p__Acidobacteriota;c__Acidobacteriae;o__Acidobacteriales;f__Koribacteraceae;g__;s__
AK5YR.7.maxbin2.8	d__Bacteria;p__Actinobacteriota;c__Actinobacteria;o__Streptosporangiales;f__Streptosporangiaceae;g__UBA8262;s__
AK5YR.7.metabat2.1	d__Bacteria;p__Verrucomicrobiota;c__Verrucomicrobiae;o__Chthoniobacterales;f__UBA10450;g__;s__
AK5YR.7.metabat2.7	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Steroidobacterales;f__Steroidobacteraceae;g__;s__
AK5YR.7.metabat2.9	d__Bacteria;p__Actinobacteriota;c__Actinobacteria;o__Streptosporangiales;f__Streptosporangiaceae;g__UBA9676;s__
AK5YR.8.maxbin2.3	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Betaproteobacteriales;f__Gallionellaceae;g__Gallionella;s__
AK5YR.8.metabat2.9	d__Bacteria;p__Dormibacterota;c__Dormibacteria;o__UBA8260;f__UBA8260;g__;s__
AK5YR.9.maxbin2.2	d__Bacteria;p__Acidobacteriota;c__Acidobacteriae;o__Acidobacteriales;f__Koribacteraceae;g__;s__
AK5YR.9.maxbin2.7	d__Bacteria;p__Actinobacteriota;c__Acidimicrobiia;o__Acidimicrobiales;f__UBA7543;g__UBA7543;s__
AK5YR.9.maxbin2.16	d__Bacteria;p__Actinobacteriota;c__Acidimicrobiia;o__Acidimicrobiales;f__;g__;s__
AK5YR.9.metabat2.11	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Steroidobacterales;f__Steroidobacteraceae;g__;s__
AK5YR.9.metabat2.13	d__Bacteria;p__Acidobacteriota;c__Acidobacteriae;o__Solibacterales;f__Solibacteraceae;g__;s__
AK5YR.9.metabat2.14	d__Bacteria;p__Acidobacteriota;c__Acidobacteriae;o__Solibacterales;f__Solibacteraceae;g__Solibacter;s__
AK5YR.9.metabat2.26	d__Bacteria;p__Actinobacteriota;c__Actinobacteria;o__Streptosporangiales;f__Streptosporangiaceae;g__UBA8262;s__
AK5YR.9.metabat2.30	d__Bacteria;p__Actinobacteriota;c__Actinobacteria;o__Streptosporangiales;f__Streptosporangiaceae;g__UBA8262;s__
AK5YR.11.maxbin2.4	d__Bacteria;p__Acidobacteriota;c__Acidobacteriae;o__Acidobacteriales;f__Koribacteraceae;g__;s__
AK5YR.11.metabat2.10	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Steroidobacterales;f__Steroidobacteraceae;g__;s__
AK5YR.12.maxbin2.1	d__Bacteria;p__Acidobacteriota;c__Acidobacteriae;o__Acidobacteriales;f__Koribacteraceae;g__;s__
AK5YR.12.maxbin2.3	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Steroidobacterales;f__Steroidobacteraceae;g__;s__
AK5YR.12.maxbin2.7	d__Bacteria;p__Actinobacteriota;c__Acidimicrobiia;o__Acidimicrobiales;f__RAAP-2;g__RAAP-2;s__
AK5YR.12.maxbin2.9	d__Bacteria;p__Dormibacterota;c__Dormibacteria;o__UBA8260;f__UBA8260;g__UBA8260;s__
AK5YR.12.maxbin2.14	d__Bacteria;p__Actinobacteriota;c__Actinobacteria;o__Streptosporangiales;f__Streptosporangiaceae;g__UBA8262;s__
AK5YR.12.maxbin2.17	d__Bacteria;p__Actinobacteriota;c__Thermoleophilia;o__Solirubrobacterales;f__Solirubrobacteraceae;g__;s__
AK5YR.12.maxbin2.30	d__Bacteria;p__Actinobacteriota;c__Thermoleophilia;o__Solirubrobacterales;f__Solirubrobacteraceae;g__;s__
AK5YR.12.metabat2.2	d__Bacteria;p__Acidobacteriota;c__Acidobacteriae;o__Acidobacteriales;f__Acidobacteriaceae;g__Terracidiphilus;s__
AK5YR.12.metabat2.5	d__Bacteria;p__Acidobacteriota;c__Thermoanaerobaculia;o__UBA5066;f__UBA5066;g__;s__

AK5YR.12.metabat2.18	d__Bacteria;p__Acidobacteriota;c__Acidobacteriae;o__Acidobacteriales;f__Acidobacteriaceae;g__Terracidiphilus;s__
AK5YR.12.metabat2.20	d__Bacteria;p__Actinobacteriota;c__Acidimicrobiia;o__Acidimicrobiales;f__UBA7543;g__UBA7543;s__
AK5YR.12.metabat2.34	d__Bacteria;p__Acidobacteriota;c__Acidobacteriae;o__Solibacterales;f__Solibacteraceae;g__Solibacter;s__
AK5YR.12.metabat2.37	d__Bacteria;p__Acidobacteriota;c__Acidobacteriae;o__Acidobacteriales;f__Koribacteraceae;g__;s__
AK5YR.13.maxbin2.4	d__Bacteria;p__Actinobacteriota;c__Acidimicrobiia;o__Acidimicrobiales;f__UBA8190;g__;s__
AK5YR.13.maxbin2.9	d__Bacteria;p__Dormibacterota;c__Dormibacteria;o__UBA8260;f__UBA8260;g__;s__
AK5YR.13.metabat2.1	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Chitinophagales;f__Chitinophagaceae;g__65-1;s__
AK5YR.13.metabat2.2	d__Bacteria;p__Gemmatimonadota;c__Gemmatimonadetes;o__Gemmatimonadales;f__Gemmatimonadaceae;g__UBA4720;s__
AK5YR.13.metabat2.4	d__Bacteria;p__Chloroflexota;c__Ellin6529;o__CSP1-4;f__CSP1-4;g__;s__
AK5YR.13.metabat2.6	d__Bacteria;p__Acidobacteriota;c__Thermoanaerobaculia;o__UBA5066;f__UBA5066;g__;s__
AK5YR.13.metabat2.10	d__Bacteria;p__UBP10;c__GR-WP33-30;o__UBA7539;f__UBA7539;g__UBA7539;s__
AK5YR.13.metabat2.12	d__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Xanthobacteraceae;g__Pseudolabrys;s__
AK5YR.14.maxbin2.1	d__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Xanthobacteraceae;g__Pseudolabrys;s__
AK5YR.14.maxbin2.11	d__Bacteria;p__Dormibacterota;c__Dormibacteria;o__UBA8260;f__UBA8260;g__;s__
AK5YR.14.maxbin2.12	d__Bacteria;p__Chloroflexota;c__Ellin6529;o__CSP1-4;f__CSP1-4;g__;s__
AK5YR.14.maxbin2.15	d__Archaea;p__Halobacterota;c__Methanosarcinia;o__UBA590;f__UBA590;g__UBA590;s__
AK5YR.14.maxbin2.17	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Chitinophagales;f__Chitinophagaceae;g__65-1;s__
AK5YR.14.metabat2.1	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Betaproteobacteriales;f__SG8-39;g__2-12-FULL-64-23;s__
AK5YR.14.metabat2.3	d__Bacteria;p__Actinobacteriota;c__Thermoleophilia;o__20CM-4-69-9;f__20CM-4-69-9;g__;s__
AK5YR.14.metabat2.12	d__Bacteria;p__Actinobacteriota;c__Actinobacteria;o__Actinomycetales;f__Dermatophilaceae;g__UBA4719;s__
AK5YR.14.metabat2.16	d__Bacteria;p__Acidobacteriota;c__Thermoanaerobaculia;o__UBA5066;f__UBA5066;g__;s__
AK5YR.14.metabat2.17	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Betaproteobacteriales;f__Gallionellaceae;g__Gallionella;s__
AK5YR.14.metabat2.18	d__Bacteria;p__UBP10;c__GR-WP33-30;o__UBA7539;f__UBA7539;g__UBA7539;s__
AK5YR.15.maxbin2.16	d__Bacteria;p__Dormibacterota;c__Dormibacteria;o__UBA8260;f__UBA8260;g__;s__
AK5YR.15.metabat2.4	d__Bacteria;p__Actinobacteriota;c__Actinobacteria;o__Actinomycetales;f__Dermatophilaceae;g__UBA4719;s__
AK5YR.15.metabat2.11	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Chitinophagales;f__Chitinophagaceae;g__65-1;s__
AK5YR.15.metabat2.12	d__Bacteria;p__Actinobacteriota;c__Thermoleophilia;o__Solirubrobacterales;f__Solirubrobacteraceae;g__Conexibacter;s__
AK5YR.15.metabat2.13	d__Archaea;p__Halobacterota;c__Methanosarcinia;o__UBA590;f__UBA590;g__UBA590;s__
AK5YR.15.metabat2.14	d__Bacteria;p__Actinobacteriota;c__Thermoleophilia;o__Solirubrobacterales;f__Solirubrobacteraceae;g__;s__
AK5YR.15.metabat2.16	d__Bacteria;p__Actinobacteriota;c__Acidimicrobiia;o__Acidimicrobiales;f__RAAP-2;g__RAAP-2;s__
AK5YR.15.metabat2.20	d__Bacteria;p__Acidobacteriota;c__Acidobacteriae;o__Solibacterales;f__Solibacteraceae;g__Solibacter;s__
AK5YR.16.maxbin2.1	d__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Xanthobacteraceae;g__Pseudolabrys;s__
AK5YR.16.maxbin2.3	d__Bacteria;p__Dormibacterota;c__Dormibacteria;o__UBA8260;f__UBA8260;g__UBA8260;s__
AK5YR.16.maxbin2.10	d__Bacteria;p__Acidobacteriota;c__Acidobacteriae;o__Acidobacteriales;f__Acidobacteriaceae;g__Terracidiphilus;s__
AK5YR.16.maxbin2.17	d__Archaea;p__Halobacterota;c__Methanosarcinia;o__UBA590;f__UBA590;g__UBA590;s__
AK5YR.16.metabat2.1	d__Bacteria;p__Actinobacteriota;c__Acidimicrobiia;o__Acidimicrobiales;f__RAAP-2;g__RAAP-2;s__
AK5YR.16.metabat2.7	d__Bacteria;p__Dormibacterota;c__Dormibacteria;o__UBA8260;f__;g__;s__
AK5YR.16.metabat2.11	d__Bacteria;p__Actinobacteriota;c__Actinobacteria;o__Actinomycetales;f__Dermatophilaceae;g__UBA4719;s__
AK5YR.16.metabat2.13	d__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Xanthobacteraceae;g__Bradyrhizobium;s__
AK5YR.16.metabat2.14	d__Bacteria;p__Dormibacterota;c__Dormibacteria;o__UBA8260;f__UBA8260;g__;s__
AK5YR.16.metabat2.17	d__Bacteria;p__Dormibacterota;c__Dormibacteria;o__UBA8260;f__UBA8260;g__;s__
AK5YR.16.metabat2.21	d__Bacteria;p__Verrucomicrobiota;c__Verrucomicrobiae;o__Pedosphaerales;f__Pedosphaeraceae;g__UBA11358;s__
AK5YR.16.metabat2.25	d__Bacteria;p__Actinobacteriota;c__Actinobacteria;o__Actinomycetales;f__Dermatophilaceae;g__UBA4719;s__
AK5YR.17.maxbin2.1	d__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Xanthobacteraceae;g__Pseudolabrys;s__
AK5YR.17.maxbin2.4	d__Bacteria;p__UBP10;c__GR-WP33-30;o__UBA7539;f__UBA7539;g__UBA7539;s__
AK5YR.17.maxbin2.11	d__Bacteria;p__Dormibacterota;c__Dormibacteria;o__UBA8260;f__;g__;s__
AK5YR.17.maxbin2.16	d__Bacteria;p__Acidobacteriota;c__Acidobacteriae;o__Acidobacteriales;f__Acidobacteriaceae;g__Terracidiphilus;s__
AK5YR.17.metabat2.1	d__Archaea;p__Halobacterota;c__Methanosarcinia;o__UBA590;f__UBA590;g__UBA590;s__
AK5YR.17.metabat2.2	d__Bacteria;p__Chloroflexota;c__Ellin6529;o__CSP1-4;f__CSP1-4;g__;s__
AK5YR.17.metabat2.10	d__Bacteria;p__Actinobacteriota;c__Acidimicrobiia;o__Acidimicrobiales;f__RAAP-2;g__RAAP-2;s__

AK5YR.17.metabat2.12	d__Bacteria;p__Actinobacteriota;c__Actinobacteria;o__Actinomycetales;f__Dermatophilaceae;g__UBA4719;s__
AK5YR.17.metabat2.16	d__Bacteria;p__Actinobacteriota;c__Actinobacteria;o__Actinomycetales;f__Dermatophilaceae;g__UBA4719;s__
AK5YR.18.maxbin2.8	d__Bacteria;p__Actinobacteriota;c__Actinobacteria;o__Actinomycetales;f__Dermatophilaceae;g__UBA4719;s__
AK5YR.18.maxbin2.15	d__Bacteria;p__Actinobacteriota;c__Thermoleophilia;o__20CM-4-69-9;f__20CM-4-69-9;g__;s__
AK5YR.18.metabat2.5	d__Bacteria;p__Actinobacteriota;c__Actinobacteria;o__Actinomycetales;f__Dermatophilaceae;g__UBA4719;s__
AK5YR.18.metabat2.7	d__Archaea;p__Halobacterota;c__Methanosarcinia;o__UBA590;f__UBA590;g__UBA590;s__
AK5YR.18.metabat2.10	d__Bacteria;p__Actinobacteriota;c__Thermoleophilia;o__UBA2241;f__UBA2241;g__UBA2241;s__
AK5YR.18.metabat2.19	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Betaproteobacteriales;f__SG8-39;g__2-12-FULL-64-23;s__
AK5YR.18.metabat2.21	d__Bacteria;p__Actinobacteriota;c__Thermoleophilia;o__Solirubrobacterales;f__Solirubrobacteraceae;g__;s__
AK5YR.19.maxbin2.5	d__Bacteria;p__Acidobacteriota;c__Thermoanaerobaculia;o__UBA5066;f__UBA5066;g__;s__
AK5YR.19.maxbin2.10	d__Bacteria;p__Acidobacteriota;c__Thermoanaerobaculia;o__UBA5066;f__UBA5066;g__;s__
AK5YR.19.maxbin2.18	d__Bacteria;p__Desulfobacterota;c__Syntrophia;o__Syntrophales;f__UBA5619;g__UBA5619;s__
AK5YR.19.maxbin2.22	d__Archaea;p__Halobacterota;c__Methanosarcinia;o__Methanosarcinales;f__Methanoperedenaceae;g__Methanoperedens;s__
AK5YR.19.metabat2.8	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Betaproteobacteriales;f__Gallionellaceae;g__Gallionella;s__
AK5YR.19.metabat2.10	d__Bacteria;p__Dormibacterota;c__Dormibacteria;o__UBA8260;f__;g__;s__
AK5YR.19.metabat2.14	d__Archaea;p__Halobacterota;c__Methanosarcinia;o__UBA590;f__UBA590;g__UBA590;s__
AK5YR.19.metabat2.17	d__Bacteria;p__Gemmatimonadota;c__Gemmatimonadetes;o__Gemmatimonadales;f__Gemmatimonadaceae;g__UBA4720;s__
AK5YR.19.metabat2.21	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Betaproteobacteriales;f__SG8-39;g__2-12-FULL-64-23;s__
AK5YR.19.metabat2.25	d__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Xanthobacteraceae;g__Pseudolabrys;s__
AK5YR.19.metabat2.30	d__Bacteria;p__Chloroflexota;c__Ellin6529;o__CSP1-4;f__CSP1-4;g__;s__
AK5YR.20.metabat2.3	d__Bacteria;p__Acidobacteriota;c__Aminicenantia;o__Aminicenantales;f__UBA4085;g__;s__
AK5YR.20.metabat2.7	d__Bacteria;p__Desulfobacterota;c__Syntrophia;o__Syntrophales;f__UBA5619;g__UBA5619;s__
AK5YR.20.metabat2.9	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Betaproteobacteriales;f__Gallionellaceae;g__Sideroxydans;s__
AK5YR.21.maxbin2.2	d__Bacteria;p__Dormibacterota;c__Dormibacteria;o__UBA8260;f__UBA8260;g__UBA8260;s__
AK5YR.21.maxbin2.5	d__Bacteria;p__Actinobacteriota;c__Acidimicrobiia;o__Acidimicrobiales;f__UBA8190;g__;s__
AK5YR.21.maxbin2.8	d__Bacteria;p__Acidobacteriota;c__Acidobacteriae;o__Acidobacteriales;f__Acidobacteriaceae;g__Terracidiphilus;s__
AK5YR.21.maxbin2.18	d__Bacteria;p__Gemmatimonadota;c__Gemmatimonadetes;o__Gemmatimonadales;f__Gemmatimonadaceae;g__UBA4720;s__
AK5YR.21.metabat2.5	d__Archaea;p__Halobacterota;c__Methanosarcinia;o__UBA590;f__UBA590;g__UBA590;s__
AK5YR.21.metabat2.8	d__Bacteria;p__UBP10;c__GR-WP33-30;o__UBA7539;f__UBA7539;g__UBA7539;s__
AK5YR.21.metabat2.10	d__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Xanthobacteraceae;g__Pseudolabrys;s__
AK5YR.21.metabat2.11	d__Archaea;p__Halobacterota;c__Methanosarcinia;o__Methanosarcinales;f__Methanosarcinaceae;g__Methanosarcina;s__
AK5YR.21.metabat2.13	d__Bacteria;p__Actinobacteriota;c__Actinobacteria;o__Actinomycetales;f__Dermatophilaceae;g__UBA4719;s__
AK5YR.21.metabat2.14	d__Bacteria;p__Actinobacteriota;c__Acidimicrobiia;o__Acidimicrobiales;f__RAAP-2;g__RAAP-2;s__
AK5YR.21.metabat2.17	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Chitinophagales;f__Chitinophagaceae;g__65-1;s__
AK5YR.21.metabat2.23	d__Bacteria;p__Dormibacterota;c__Dormibacteria;o__UBA8260;f__UBA8260;g__;s__
AK5YR.21.metabat2.25	d__Bacteria;p__Actinobacteriota;c__Actinobacteria;o__Actinomycetales;f__Dermatophilaceae;g__UBA4719;s__
AK5YR.22.maxbin2.4	d__Bacteria;p__Actinobacteriota;c__Acidimicrobiia;o__Acidimicrobiales;f__UBA8190;g__;s__
AK5YR.22.metabat2.2	d__Archaea;p__Halobacterota;c__Methanosarcinia;o__UBA590;f__UBA590;g__UBA590;s__
AK5YR.22.metabat2.5	d__Bacteria;p__Acidobacteriota;c__Acidobacteriae;o__Acidobacteriales;f__Acidobacteriaceae;g__Terracidiphilus;s__
AK5YR.22.metabat2.9	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Betaproteobacteriales;f__SG8-39;g__2-12-FULL-64-23;s__
AK5YR.22.metabat2.11	d__Bacteria;p__UBP10;c__GR-WP33-30;o__UBA7539;f__UBA7539;g__UBA7539;s__
AK5YR.22.metabat2.12	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__vadinHA17;g__LD21;s__
AK5YR.22.metabat2.14	d__Bacteria;p__Gemmatimonadota;c__Gemmatimonadetes;o__Gemmatimonadales;f__Gemmatimonadaceae;g__;s__
AK5YR.22.metabat2.16	d__Bacteria;p__Patescibacteria;c__Microgenomatia;o__Levybacterales;f__UBA12049;g__;s__
AK5YR.22.metabat2.18	d__Bacteria;p__Chloroflexota;c__Ellin6529;o__CSP1-4;f__CSP1-4;g__;s__
AK5YR.23.maxbin2.5	d__Bacteria;p__Actinobacteriota;c__Acidimicrobiia;o__Acidimicrobiales;f__UBA8190;g__;s__
AK5YR.23.maxbin2.8	d__Bacteria;p__Actinobacteriota;c__Actinobacteria;o__Actinomycetales;f__Dermatophilaceae;g__UBA4719;s__
AK5YR.23.maxbin2.10	d__Archaea;p__Halobacterota;c__Methanosarcinia;o__UBA590;f__UBA590;g__UBA590;s__
AK5YR.23.metabat2.1	d__Bacteria;p__UBP10;c__GR-WP33-30;o__UBA7539;f__UBA7539;g__UBA7539;s__
AK5YR.23.metabat2.4	d__Bacteria;p__Dormibacterota;c__Dormibacteria;o__UBA8260;f__UBA8260;g__;s__

AK5YR.23.metabat2.5	d__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Xanthobacteraceae;g__Pseudolabrys;s__
AK5YR.23.metabat2.11	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Betaproteobacteriales;f__SG8-39;g__2-12-FULL-64-23;s__
AK5YR.24.maxbin2.9	d__Archaea;p__Halobacterota;c__Methanosarcinia;o__UBA590;f__UBA590;g__UBA590;s__
AK5YR.24.maxbin2.14	d__Archaea;p__Halobacterota;c__Methanosarcinia;o__UBA590;f__UBA590;g__UBA590;s__
AK5YR.24.maxbin2.15	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Chitinophagales;f__Chitinophagaceae;g__65-1;s__
AK5YR.24.maxbin2.17	d__Bacteria;p__Dormibacterota;c__Dormibacteria;o__UBA8260;f__;g__;s__
AK5YR.24.metabat2.6	d__Bacteria;p__Acidobacteriota;c__Thermoanaerobaculia;o__UBA5066;f__UBA5066;g__;s__
AK5YR.24.metabat2.9	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Betaproteobacteriales;f__SG8-39;g__2-12-FULL-64-23;s__
AK5YR.24.metabat2.15	d__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Xanthobacteraceae;g__Pseudolabrys;s__

Table S5: Taxonomic classifications of metagenome-assembled genomes (MAGs) derived from Microbial Genome Atlas (MiGA), and MAG European Nucleotide Archive (ENA) accession IDs.

MAG ID	Accession ID	MiGA taxonomic classification
AK5YR.2.maxbin2.1	ERZ908899	d:Bacteria p:Acidobacteria c:Acidobacteriia
AK5YR.2.maxbin2.7	ERZ908986	d:Bacteria p:Firmicutes
AK5YR.2.maxbin2.12	ERZ908985	d:Bacteria p:Actinobacteria c:Actinobacteria
AK5YR.2.metabat2.9	ERZ908991	d:Bacteria p:Firmicutes
AK5YR.2.metabat2.12	ERZ908987	d:Bacteria p:Firmicutes
AK5YR.2.metabat2.14	ERZ908988	d:Bacteria p:Proteobacteria c:Gammaproteobacteria
AK5YR.2.metabat2.17	ERZ908989	d:Bacteria p:Actinobacteria
AK5YR.2.metabat2.25	ERZ908990	d:Bacteria p:Acidobacteria c:Solibacteres o:Solibacterales f:Solibacteraceae
AK5YR.3.maxbin2.1	ERZ909031	d:Bacteria p:Acidobacteria c:Acidobacteriia
AK5YR.3.maxbin2.4	ERZ909033	d:Bacteria p:Acidobacteria c:Acidobacteriia
AK5YR.3.maxbin2.10	ERZ909032	d:Bacteria p:Firmicutes
AK5YR.3.metabat2.3	ERZ909034	d:Bacteria p:Firmicutes
AK5YR.3.metabat2.5	ERZ909035	d:Bacteria p:Acidobacteria c:Solibacteres o:Solibacterales f:Solibacteraceae
AK5YR.4.maxbin2.1	ERZ909036	d:Bacteria p:Acidobacteria c:Acidobacteriia
AK5YR.4.maxbin2.3	ERZ909038	d:Bacteria p:Proteobacteria c:Gammaproteobacteria
AK5YR.4.maxbin2.8	ERZ909039	d:Bacteria p:Actinobacteria c:Actinobacteria
AK5YR.4.maxbin2.13	ERZ909037	d:Bacteria p:Actinobacteria
AK5YR.4.metabat2.3	ERZ909043	d:Bacteria p:Acidobacteria c:Acidobacteriia
AK5YR.4.metabat2.8	ERZ909044	d:Bacteria p:Acidobacteria c:Solibacteres o:Solibacterales f:Solibacteraceae
AK5YR.4.metabat2.13	ERZ909040	d:Bacteria p:Firmicutes
AK5YR.4.metabat2.14	ERZ909041	d:Bacteria p:Acidobacteria c:Acidobacteriia
AK5YR.4.metabat2.16	ERZ909042	d:Bacteria p:Firmicutes
AK5YR.5.maxbin2.5	ERZ909046	d:Bacteria p:Acidobacteria c:Acidobacteriia
AK5YR.5.maxbin2.6	ERZ909047	d:Bacteria p:Firmicutes
AK5YR.5.maxbin2.16	ERZ909045	d:Bacteria p:Acidobacteria c:Solibacteres o:Solibacterales f:Solibacteraceae
AK5YR.5.metabat2.1	ERZ909048	d:Bacteria p:Acidobacteria c:Acidobacteriia
AK5YR.5.metabat2.5	ERZ909058	d:Bacteria p:Acidobacteria c:Acidobacteriia
AK5YR.5.metabat2.13	ERZ909049	d:Bacteria p:Actinobacteria c:Thermoleophilia
AK5YR.5.metabat2.15	ERZ909050	d:Bacteria p:Actinobacteria c:Acidimicrobiia

AK5YR.5.metabat2.16	ERZ909051	d:Bacteria p:Proteobacteria c:Gammaproteobacteria
AK5YR.5.metabat2.17	ERZ909052	d:Bacteria p:Proteobacteria c:Betaproteobacteria o:Nitrosomonadales f:Gallionellaceae
AK5YR.5.metabat2.26	ERZ909053	d:Bacteria p:Acidobacteria c:Acidobacteriia
AK5YR.5.metabat2.27	ERZ909054	d:Bacteria p:Proteobacteria c:Gammaproteobacteria
AK5YR.5.metabat2.28	ERZ909055	d:Bacteria p:Actinobacteria
AK5YR.5.metabat2.29	ERZ909056	d:Bacteria p:Proteobacteria
AK5YR.5.metabat2.32	ERZ909057	d:Bacteria p:Firmicutes
AK5YR.6.metabat2.1	ERZ909059	d:Bacteria p:Actinobacteria c:Actinobacteria
AK5YR.6.metabat2.3	ERZ909060	d:Bacteria p:Firmicutes
AK5YR.7.maxbin2.1	ERZ909061	d:Bacteria p:Acidobacteria c:Acidobacteriia
AK5YR.7.maxbin2.8	ERZ909062	d:Bacteria p:Actinobacteria c:Actinobacteria
AK5YR.7.metabat2.1	ERZ909063	d:Bacteria p:Verrucomicrobia c:Verrucomicrobiae
AK5YR.7.metabat2.7	ERZ909064	d:Bacteria p:Proteobacteria c:Gammaproteobacteria
AK5YR.7.metabat2.9	ERZ909065	d:Bacteria p:Actinobacteria c:Actinobacteria
AK5YR.8.maxbin2.3	ERZ909066	d:Bacteria p:Proteobacteria c:Betaproteobacteria o:Nitrosomonadales f:Gallionellaceae
AK5YR.8.metabat2.9	ERZ909067	d:Bacteria p:Firmicutes
AK5YR.9.maxbin2.2	ERZ909070	d:Bacteria p:Acidobacteria c:Acidobacteriia
AK5YR.9.maxbin2.7	ERZ909071	d:Bacteria p:Actinobacteria c:Acidimicrobiia
AK5YR.9.maxbin2.16	ERZ909069	d:Bacteria p:Actinobacteria
AK5YR.9.metabat2.11	ERZ909072	d:Bacteria p:Proteobacteria c:Gammaproteobacteria
AK5YR.9.metabat2.13	ERZ909073	d:Bacteria p:Acidobacteria c:Solibacteres
AK5YR.9.metabat2.14	ERZ909074	d:Bacteria p:Acidobacteria c:Solibacteres o:Solibacterales f:Solibacteraceae
AK5YR.9.metabat2.26	ERZ909075	d:Bacteria p:Actinobacteria c:Actinobacteria
AK5YR.9.metabat2.30	ERZ909076	d:Bacteria p:Actinobacteria c:Actinobacteria
AK5YR.11.maxbin2.4	ERZ908903	d:Bacteria p:Acidobacteria c:Acidobacteriia
AK5YR.11.metabat2.10	ERZ908904	d:Bacteria p:Proteobacteria c:Gammaproteobacteria
AK5YR.12.maxbin2.1	ERZ908905	d:Bacteria p:Acidobacteria c:Acidobacteriia
AK5YR.12.maxbin2.3	ERZ908908	d:Bacteria p:Proteobacteria c:Gammaproteobacteria
AK5YR.12.maxbin2.7	ERZ908910	d:Bacteria p:Actinobacteria
AK5YR.12.maxbin2.9	ERZ908911	d:Bacteria p:Firmicutes
AK5YR.12.maxbin2.14	ERZ908906	d:Bacteria p:Actinobacteria c:Actinobacteria
AK5YR.12.maxbin2.17	ERZ908907	d:Bacteria p:Actinobacteria c:Thermoleophilia
AK5YR.12.maxbin2.30	ERZ908909	d:Bacteria p:Firmicutes
AK5YR.12.metabat2.2	ERZ908913	d:Bacteria p:Acidobacteria c:Acidobacteriia
AK5YR.12.metabat2.5	ERZ908917	d:Bacteria p:Firmicutes
AK5YR.12.metabat2.18	ERZ908912	d:Bacteria p:Acidobacteria c:Acidobacteriia
AK5YR.12.metabat2.20	ERZ908914	d:Bacteria p:Actinobacteria c:Acidimicrobiia
AK5YR.12.metabat2.34	ERZ908915	d:Bacteria p:Acidobacteria c:Solibacteres o:Solibacterales f:Solibacteraceae
AK5YR.12.metabat2.37	ERZ908916	d:Bacteria p:Acidobacteria c:Acidobacteriia
AK5YR.13.maxbin2.4	ERZ908918	d:Bacteria p:Actinobacteria c:Acidimicrobiia
AK5YR.13.maxbin2.9	ERZ908919	d:Bacteria p:Firmicutes
AK5YR.13.metabat2.1	ERZ908920	d:Bacteria p:Bacteroidetes c:Chitinophagia
AK5YR.13.metabat2.2	ERZ908923	d:Bacteria p:Gemmatimonadetes c:Gemmatimonadetes
AK5YR.13.metabat2.4	ERZ908924	d:Bacteria p:Chloroflexi
AK5YR.13.metabat2.6	ERZ908925	d:Bacteria p:Firmicutes
AK5YR.13.metabat2.10	ERZ908921	d:Bacteria p:Proteobacteria
AK5YR.13.metabat2.12	ERZ908922	d:Bacteria p:Proteobacteria c:Alphaproteobacteria o:Rhizobiales
AK5YR.14.maxbin2.1	ERZ908926	d:Bacteria p:Proteobacteria c:Alphaproteobacteria o:Rhizobiales
AK5YR.14.maxbin2.11	ERZ908927	d:Bacteria p:Firmicutes
AK5YR.14.maxbin2.12	ERZ908928	d:Bacteria p:Chloroflexi

AK5YR.14.maxbin2.15	ERZ908929	d:Archaea p:Euryarchaeota c:Methanomicrobia
AK5YR.14.maxbin2.17	ERZ908930	d:Bacteria p:Bacteroidetes c:Chitinophagia
AK5YR.14.metabat2.1	ERZ908931	d:Bacteria p:Proteobacteria c:Betaproteobacteria
AK5YR.14.metabat2.3	ERZ908936	d:Bacteria p:Firmicutes
AK5YR.14.metabat2.12	ERZ908932	d:Bacteria p:Actinobacteria c:Actinobacteria o:Micrococcales f:Intrasporangiaceae
AK5YR.14.metabat2.16	ERZ908933	d:Bacteria p:Acidobacteria
AK5YR.14.metabat2.17	ERZ908934	d:Bacteria p:Proteobacteria c:Betaproteobacteria o:Nitrosomonadales f:Gallionellaceae
AK5YR.14.metabat2.18	ERZ908935	d:Bacteria p:Proteobacteria
AK5YR.15.maxbin2.16	ERZ908937	d:Bacteria p:Firmicutes
AK5YR.15.metabat2.4	ERZ908944	d:Bacteria p:Actinobacteria c:Actinobacteria o:Micrococcales f:Intrasporangiaceae
AK5YR.15.metabat2.11	ERZ908938	d:Bacteria p:Bacteroidetes c:Chitinophagia
AK5YR.15.metabat2.12	ERZ908939	d:Bacteria p:Firmicutes
AK5YR.15.metabat2.13	ERZ908940	d:Archaea p:Euryarchaeota c:Methanomicrobia
AK5YR.15.metabat2.14	ERZ908941	d:Bacteria p:Actinobacteria c:Thermoleophilia
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AK5YR.16.maxbin2.10	ERZ908946	d:Bacteria p:Acidobacteria c:Acidobacteriia
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AK5YR.16.metabat2.7	ERZ908956	d:Bacteria p:Firmicutes
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AK5YR.16.metabat2.14	ERZ908952	d:Bacteria p:Firmicutes
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AK5YR.16.metabat2.21	ERZ908954	d:Bacteria p:Verrucomicrobia
AK5YR.16.metabat2.25	ERZ908955	d:Bacteria p:Actinobacteria c:Actinobacteria o:Micrococcales f:Intrasporangiaceae
AK5YR.17.maxbin2.1	ERZ908957	d:Bacteria p:Proteobacteria c:Alphaproteobacteria o:Rhizobiales
AK5YR.17.maxbin2.4	ERZ908960	d:Bacteria p:Proteobacteria
AK5YR.17.maxbin2.11	ERZ908958	d:Bacteria p:Firmicutes
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AK5YR.23.metabat2.11	ERZ909021	d:Bacteria p:Proteobacteria c:Betaproteobacteria
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AK5YR.24.maxbin2.15	ERZ909025	d:Bacteria p:Bacteroidetes c:Chitinophagia o:Chitinophagales
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AK5YR.24.metabat2.15	ERZ909028	d:Bacteria p:Proteobacteria c:Alphaproteobacteria o:Rhizobiales

Supplemental figures

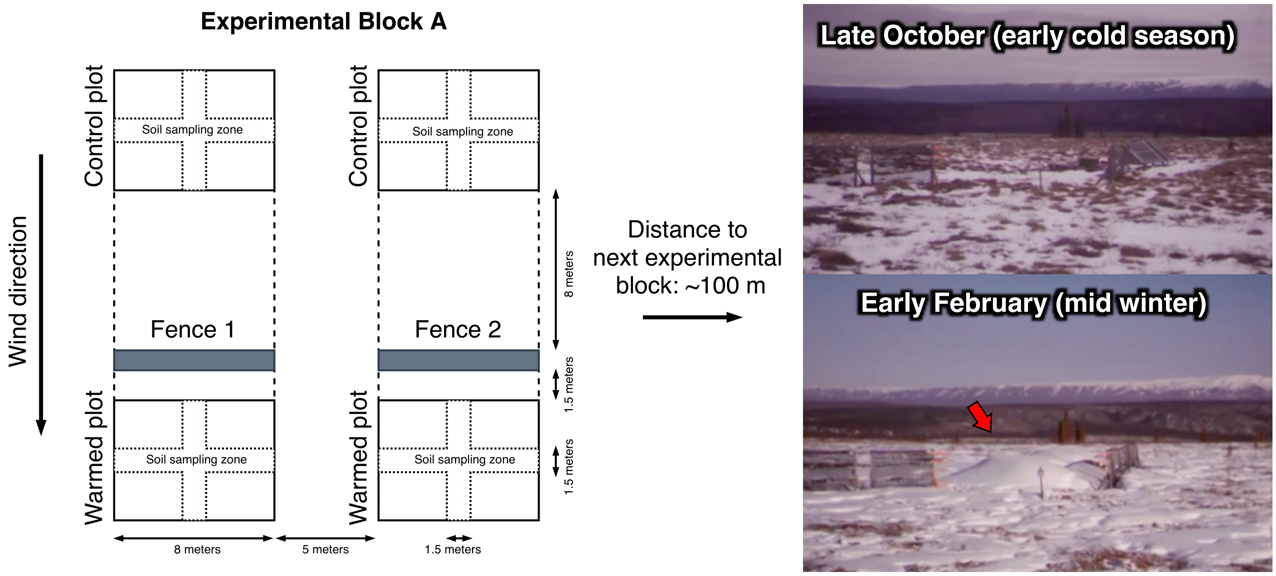

Figure S1: Example diagram of experimental blocks at the CiPEHR experimental warming site in Alaska, USA and photographs demonstrating snow accumulation that occurs during winter months. Diagram (left) represents an example of one of three experimental blocks. Each of the three experimental blocks were separated by at least 100 meters. Snow fence images were taken in October 2012 and February 2013.

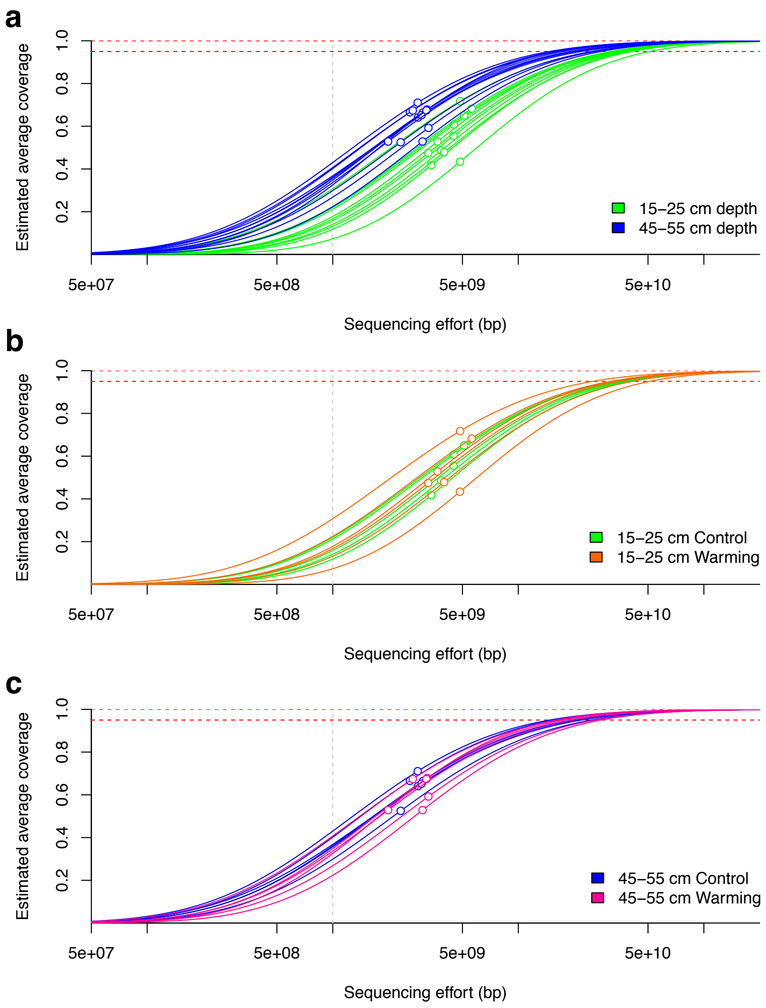

Figure S2: Curves representing soil microbial community complexity as determined by Nonpareil. Nonpareil is a statistical tool that uses read redundancy to estimate metagenome dataset complexity and the amount of sequencing effort needed to achieve a desired level of coverage (Rodriguez-R *et al.,* 2018). Different plots are shown to compare (a) all 5-year sample metagenomes, (b) 15-25 cm sample metagenomes only, and (c) 45-55 cm sample metagenomes only. Circles on curves represent the coverage of the actual sequencing depth for each dataset in relation to the entire curve (projection for complete coverage after the circle). Curves positioned on the right represent more sequence diverse metagenomes than curves positioned on the left.

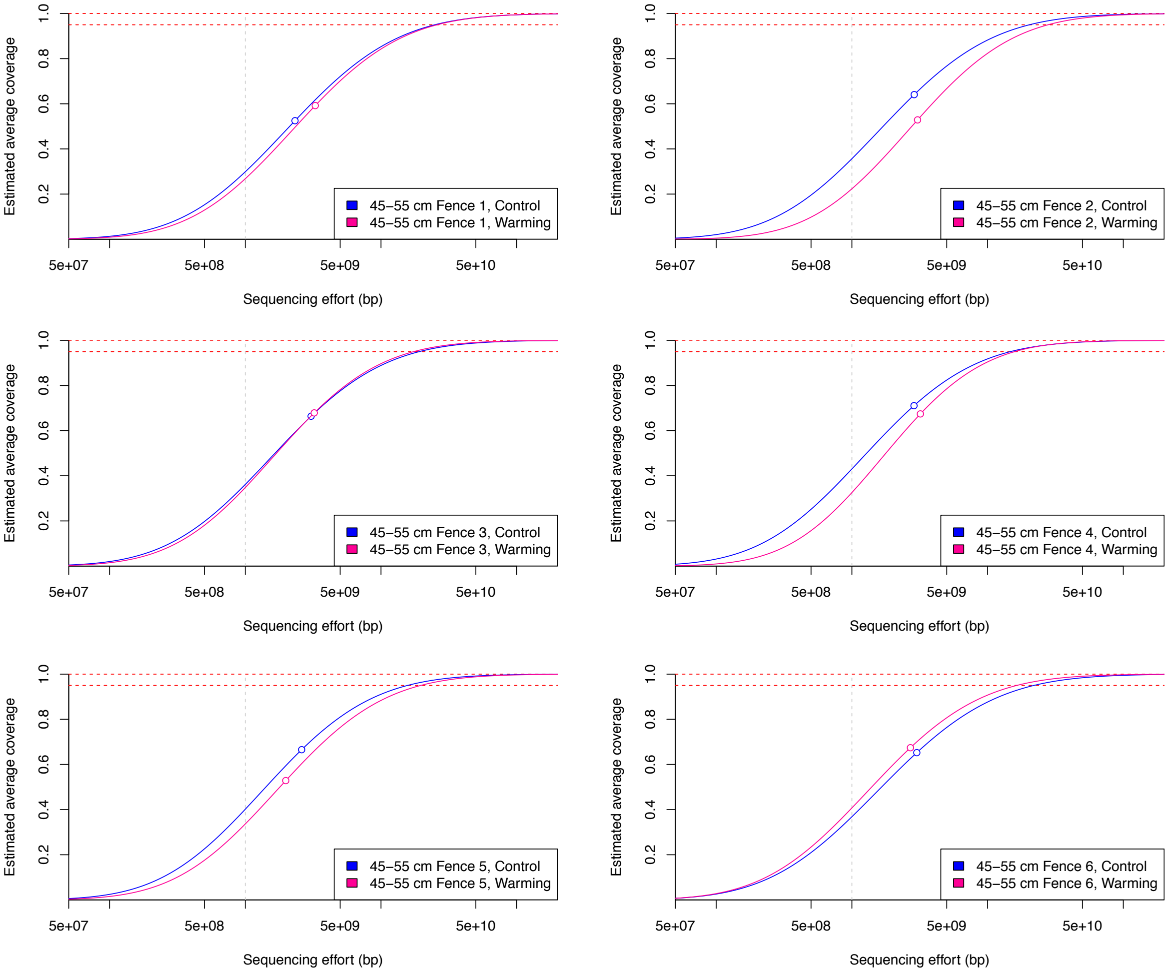

Figure S3: Curves representing pairwise comparisons of warmed and unwarmed soil communities after 4.5 years of experimentation at 45-55 cm. Each plot shows the differences between warmed and unwarmed samples corresponding to the six different fences (i.e., experimental plots). See Figure S1 legend for additional details.

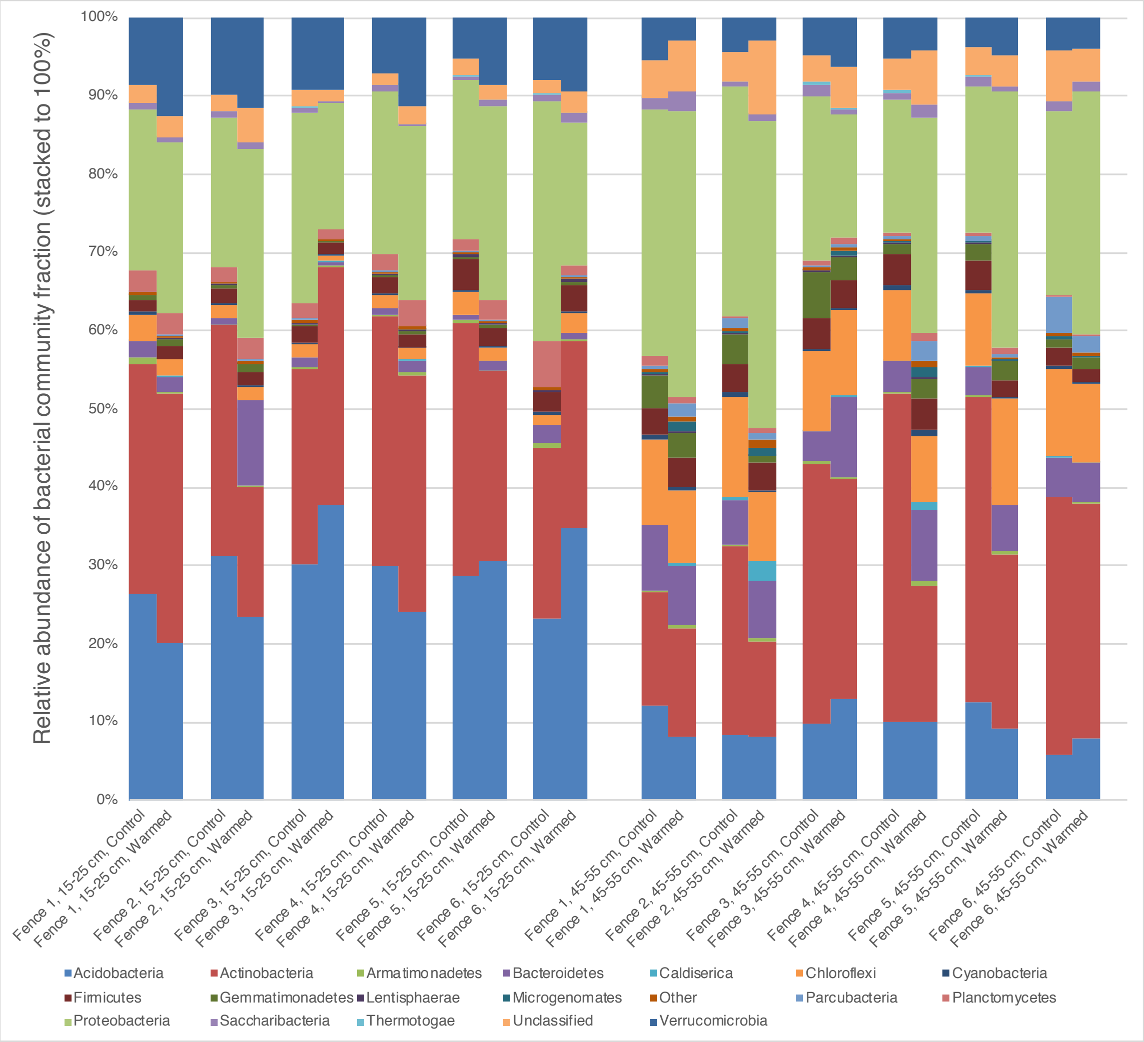

Figure S4: Bacterial community phylum-level composition for 4.5-year sample metagenomes. Underlying data is based on 16S rRNA gene-encoding fragments recovered from metagenomic datasets processed with Parallel-META version 2. Values represent the abundance of each bacterial phylum as a proportion of the total bacterial community. Only bacterial phyla with a mean relative abundance ≥ 0.1% are shown.

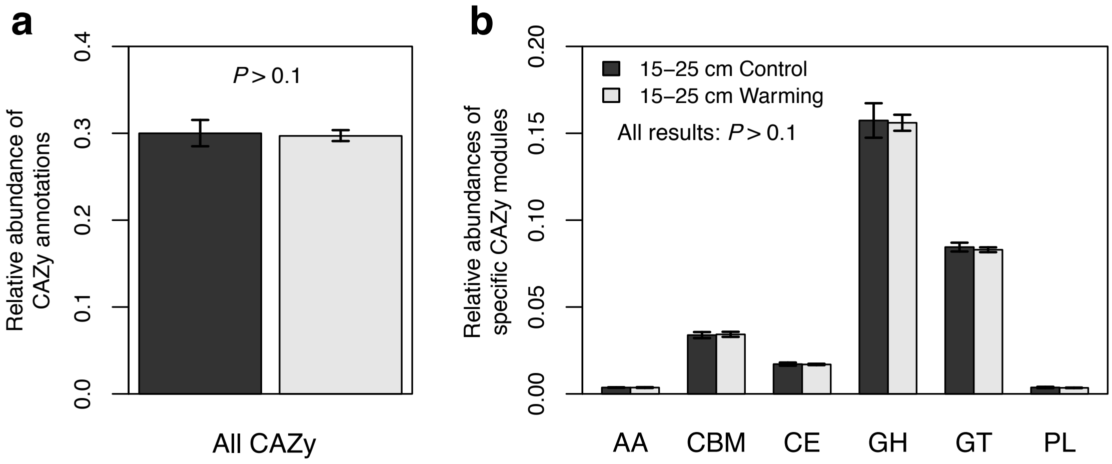

Figure S5: Shifts in carbohydrate utilization (CAZy) genes as an effect of experimental warming after 1.5 years. Relative abundances of **(a)** all CAZy annotations, and **(b)** CAZy modules: Auxiliary Activities (AA), Carbohydrate Binding (CBM), Carbohydrate Esterases (CE), Glycoside Hydrolases (GH), GlycosylTransferases (GT), and Polysaccharide Lyases (PL). Underlying values represent the mean relative abundance of each category for warmed vs. unwarmed soils. The abundances of CAZy functions were determined by normalizing the number of annotations matching to each broad definition by the number of annotations matching to the more comprehensive SwissProt database

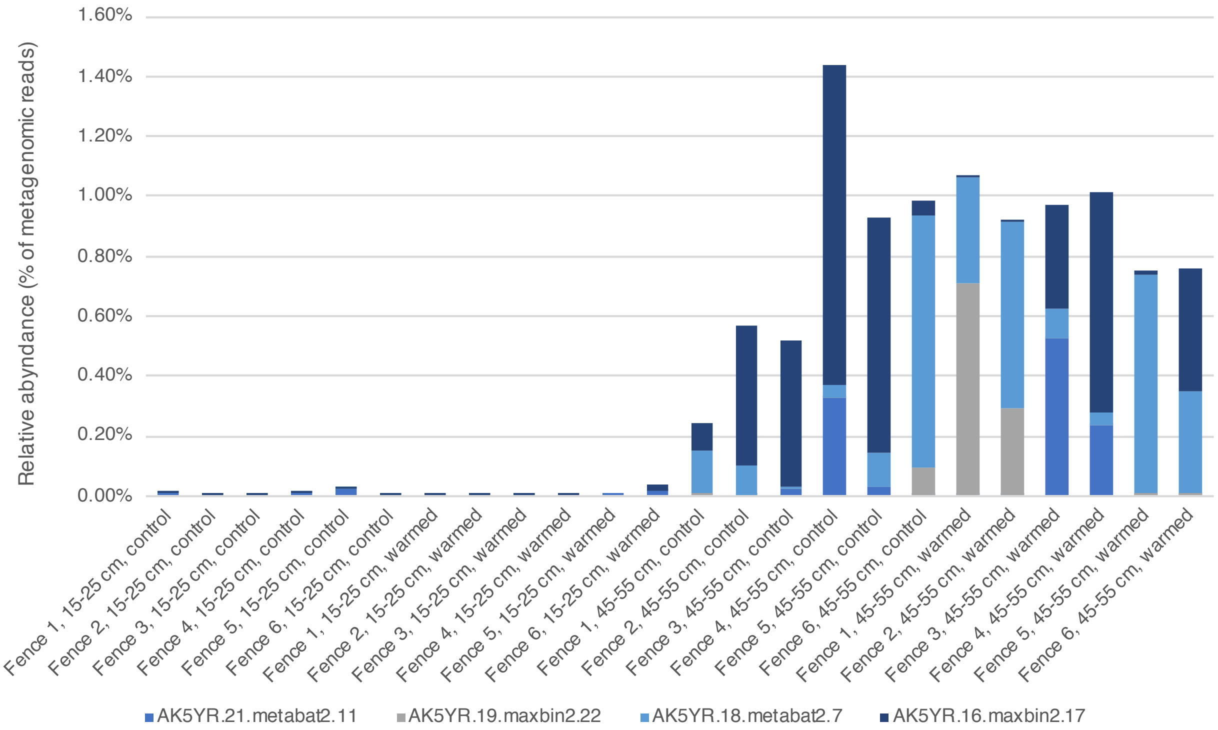

Figure S6. Sequence-based abundances of archaeal metagenome-assembled genomes (MAGs) in 4.5-year Alaskan tundra metagenomes determined by read mapping. Results were obtained by the number of sequences that matched MAG contigs (using a default megablast search) at ≥ 100 bp and ≥ 97% nucleotide, divided by the number of reads used as query. Note: Although 13 archaeal MAGs were recovered in total, they were de-replicated into four that were non-redundant (see materials and methods for de-replication procedure). For each non-redundant MAG, the version with the highest quality score (Calculated as completeness (from CheckM) – 5 * contamination (also from CheckM)) (Parks et al., 2017) was used for read mapping.

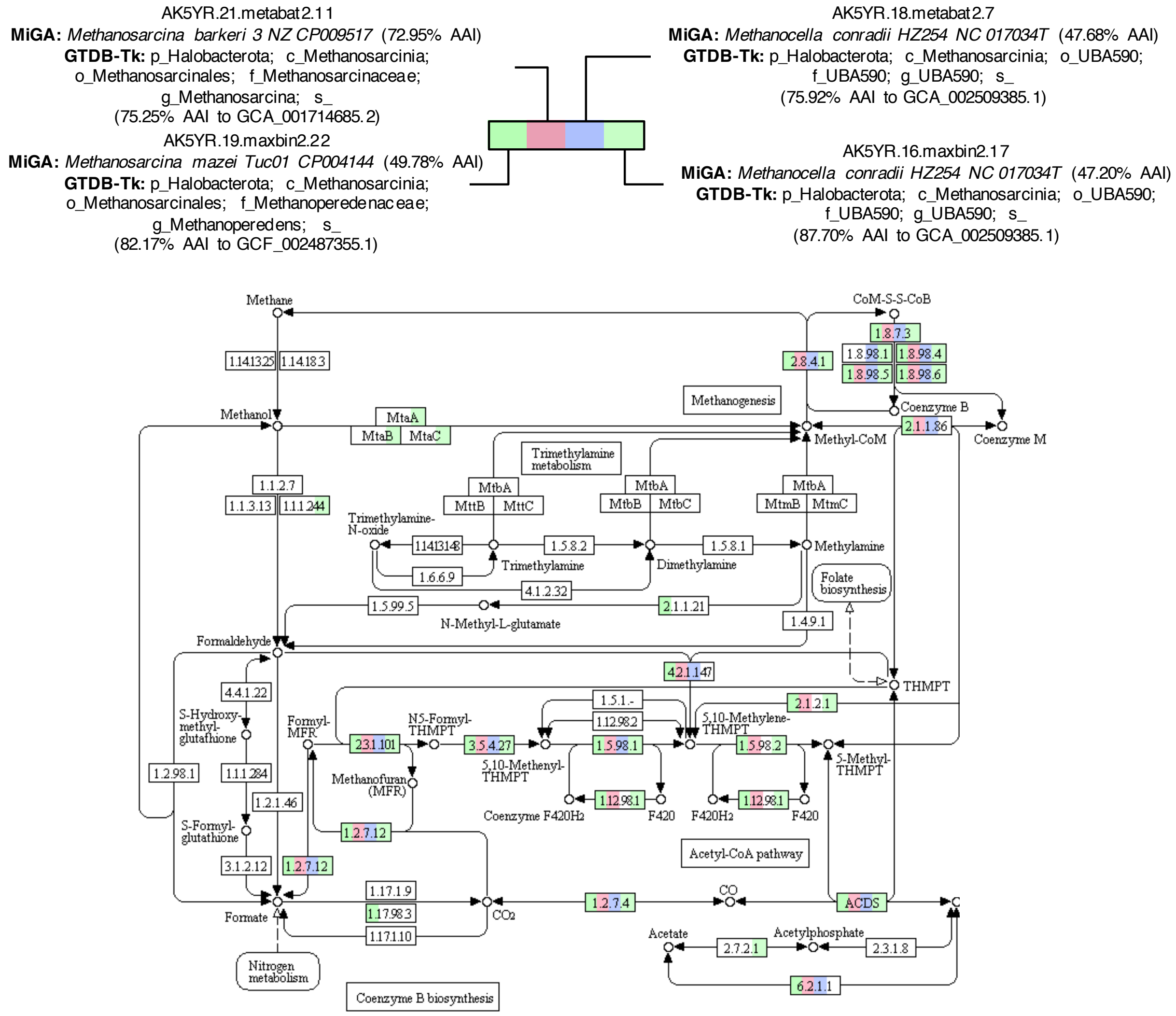

Figure S7: Taxonomic assignment and methane generating functions of recovered archaeal MAGs. Diagram represents partial KEGG reference pathway 'Methane metabolism' (map00680). Coloration of boxes is used to denote the presence of each function in each of the four non-redundant methanogenic MAGs (see top key). Although 13 archaeal MAGs were recovered in total, they were de-replicated into four that were non-redundant (see materials and methods for de-replication procedure). MAG taxonomic assignment was determined by using The Microbial Genomes Atlas (MiGA) webserver (http://enve-omics.ce.gatech.edu:3000) (Rodriguez-R et al., 2018) as well at GTDB-Tk (Parks et al., 2018). For MiGA classification, the percentage accompanying each taxonomic classification reflects the highest AAI (average amino acid identity) with a collection of isolate genome references. AAI was also calculated between each archaeal MAG and the closest related uncultured genome based on the GTDB-Tk phylogenetic tree (see Dataset S4); the NCBI assembly IDs for each of these uncultured relative genomes are provided. GCA_002509385.1 was derived from boreal peatland in Minnesota, USA (at 25 cm depth). GCA_001714685.2 was derived from permafrost sediment in Miers Valley Antarctica. GCF_002487355.1 was enriched from a mixture of freshwater sediment and anaerobic wastewater sludge in Brisbane, Australia

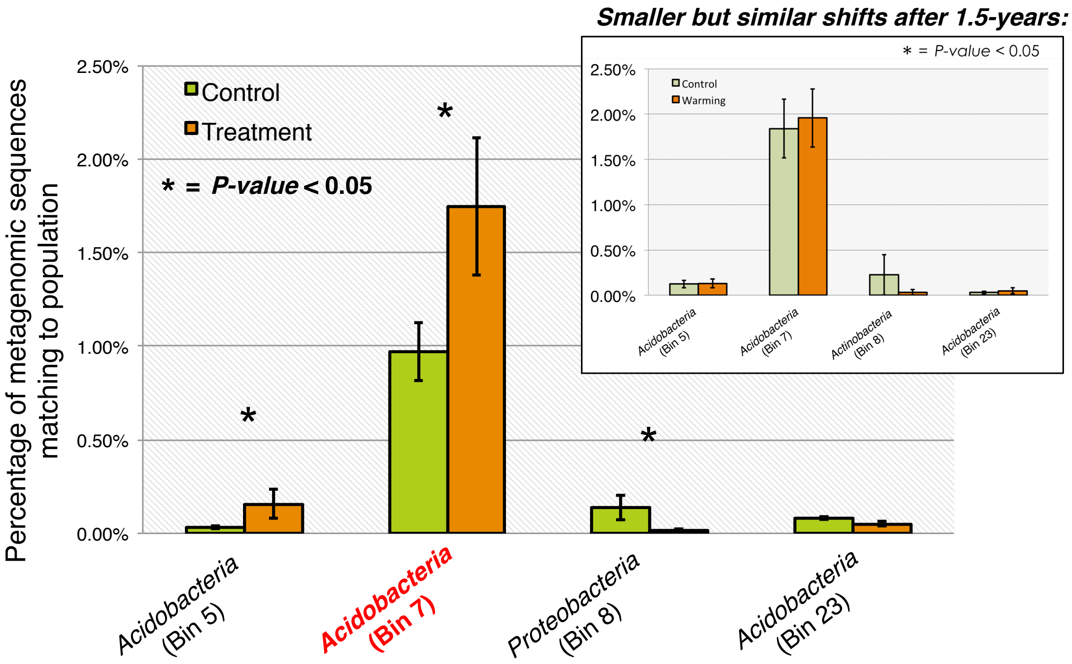

Figure S8: Shifts in the relative abundances of dominant MAGs at 15-25 cm after 1.5 and 4.5 years of experimental warming. MAG relative abundances were determined by dividing the number of short-reads matching each MAG at > 80 bp and > 98% nucleotide identity by the total number of reads used as query. MAG IDs reflect those assigned to MAGs in Johnston et al., 2016. Bars reflect the mean relative abundance for each sample group (unwarmed, warmed) at 15-25 cm (*n* = 6). Bars represent the standard error of the mean.

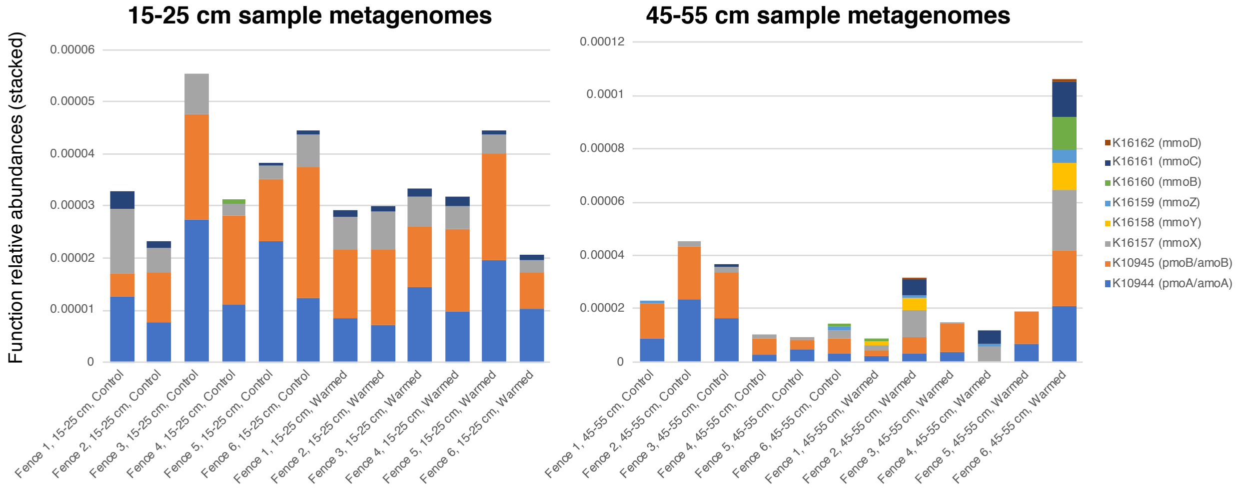

Figure S9: Relative abundances of Kegg Orthology (KO) terms/annotations associated with aerobic methane oxidation for all twenty-four 4.5-year metagenomes. Relative abundances were derived by normalizing the number of sequences matching to references belonging to each KO term by the total number of annotated sequences in each metagenome.