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Experimental warming leads to convergent succession of grassland archaeal community

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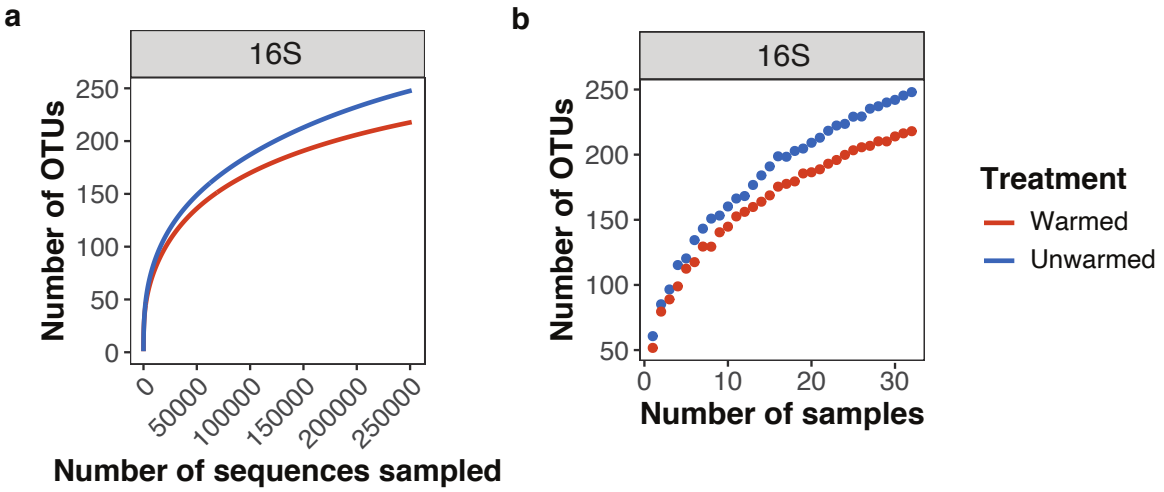

Figure S1. Rarefaction curves. The number of OTUs with an increasing number of sequences (**a**) and accumulation curves of the number of OTUs with an increasing number of samples (**b**) for archaeal 16S rRNA genes. The observed number of OTUs with warming treatment was significantly lower in comparison with unwarmed control in (**a**) (Paired *t*-test, one-sided, $p < 0.0001$). The number of samples does not have a substantial influence on the differences between warming and non-warming control, as shown in (**b**). After removing global singletons and resampling, the rarefaction curves approached asymptotes for both unwarmed and warmed samples, indicating that the sequencing depth was sufficient for assessing the effects of warming on these microbial communities.

Tables S1. Differences in taxon relative abundances between warming and control at the OTU level. Only OTUs showing significant difference between warming and control are included.

	Taxonomical classification					Relative abundance (%)	
	Order	Family	Genus	Response Ratio	95% confidence interval for RR	Warming Mean	Control Mean
95% Confidence Interval DOWN							
OTU1057	Methanobacteriales	Methanobacteriaceae	Methanobrevibacter	-2.23	1.54	0.00	0.01
OTU535	Methanobacteriales	Methanobacteriaceae	Methanobrevibacter	-2.83	2.47	0.00	0.01
OTU1314	unclassified_Euryarchaeota	unclassified_Euryarchaeota	unclassified_Euryarchaeota	-0.83	0.72	0.01	0.02
OTU218	unclassified_Euryarchaeota	unclassified_Euryarchaeota	unclassified_Euryarchaeota	-1.46	1.06	0.00	0.01
OTU333	unclassified_Euryarchaeota	unclassified_Euryarchaeota	unclassified_Euryarchaeota	-0.95	0.72	0.01	0.03
OTU122	Nitrososphaerales	Nitrososphaeraceae	Nitrososphaera	-2.03	1.75	0.00	0.03
OTU1363	Nitrososphaerales	Nitrososphaeraceae	Nitrososphaera	-2.00	0.87	0.01	0.06
OTU2	Nitrososphaerales	Nitrososphaeraceae	Nitrososphaera	-0.45	0.32	9.08	14.26
OTU291	Nitrososphaerales	Nitrososphaeraceae	Nitrososphaera	-2.48	2.29	0.00	0.00
OTU7967	Nitrososphaerales	Nitrososphaeraceae	Nitrososphaera	-0.79	0.78	0.00	0.01
OTU1341	unclassified_Archaea	unclassified_Archaea	unclassified_Archaea	-2.30	2.27	0.00	0.00
OTU729	unclassified_Archaea	unclassified_Archaea	unclassified_Archaea	-1.61	1.57	0.00	0.01
OTU1292	unclassified_Woesearchaeota	unclassified_Woesearchaeota	unclassified_Woesearchaeota	-2.94	2.63	0.00	0.01
95% Confidence Interval UP							
OTU75	unclassified_Euryarchaeota	unclassified_Euryarchaeota	unclassified_Euryarchaeota	0.91	0.69	0.10	0.04
OTU11	Nitrososphaerales	Nitrososphaeraceae	Nitrososphaera	0.75	0.60	1.27	0.60
OTU1884	Nitrososphaerales	Nitrososphaeraceae	Nitrososphaera	0.55	0.51	0.47	0.27
OTU363	Nitrososphaerales	Nitrososphaeraceae	Nitrososphaera	0.60	0.36	0.54	0.30
OTU396	Nitrososphaerales	Nitrososphaeraceae	Nitrososphaera	1.22	0.88	0.01	0.00
OTU4	Nitrososphaerales	Nitrososphaeraceae	Nitrososphaera	0.40	0.27	10.95	7.35
OTU119	unclassified_Archaea	unclassified_Archaea	unclassified_Archaea	1.68	1.41	0.10	0.02

Table S2. Significance tests of the effects of experimental warming on the archaeal community composition and structure across seven years by Adonia, ANOSIM, and MRPP.

Datasets	**Adonis**		**ANOSIM**		**MRPP**	
	F	*P*	*R*	*P*	δ	*P*
OTU	3.923	**0.014**	0.018	**0.047**	0.344	**0.040**
UNOISE3	2.625	**0.023**	0.0093	0.082	0.434	0.066
DADA2	2.656	**0.016**	0.010	0.069	0.452	**0.043**
Deblur	2.229	0.051	0.0038	0.126	0.475	0.110

Results from three different non-parametric multivariate analyses are shown, including the permutational multivariate analysis of variance (Adonis), analysis of similarity (ANOSIM), and multiple response permutation procedure (MRPP) are shown (one-way tests). All of the three tests are based on Bray-Curtis dissimilarities among samples. Results from four different approaches of microbiome sequence error-correction are included (open-reference 97% operational taxonomic units (OTUs) clustering, UNOISE3, DADA2, and Deblur). For ANOSIM and MRPP, the permutation was constrained within each block in each year. Significant *p* values (<0.05) are shown in bold.

Table S3. Differences in functional gene abundances between warming and control by response ratios detected by GeoChip. Only genes showing significant differences between warming and control were included.

Category	Subcategory	Gene ID	Response Ratio	95% confidence interval for RR
C Cycling	Carbon degradation	aceA	-0.15	0.13
C Cycling	Carbon degradation	aceB	-0.15	0.13
C Cycling	Carbon degradation	amyA	-0.09	0.08
C Cycling	Carbon degradation	ara	-0.19	0.12
C Cycling	Carbon degradation	cda	-0.18	0.15
C Cycling	Carbon degradation	nplT	-0.12	0.11
C Cycling	Carbon degradation	rgl	-0.22	0.20
C Cycling	Carbon fixation	AACT_DiC4HB	-0.16	0.15
C Cycling	Carbon fixation	C_CoA_hydratase_DiC4HB	-0.15	0.12
C Cycling	Methane	fmdB_fwdB	-0.09	0.07
C Cycling	Methane	Ftr	-0.09	0.08
C Cycling	Methane	hdrB	-0.10	0.09
C Cycling	Methane	mcra	-0.11	0.08
C Cycling	Methane	mrtH	-0.12	0.10
N	Ammonification	urec	-0.16	0.10
N	Assimilatory N reduction	nasa	-0.11	0.09
N	Denitrification	narg	-0.11	0.10
N	Denitrification	norb	-0.17	0.17
N	Denitrification	nosz	-0.09	0.08
N	Nitrification	amoa	-0.13	0.11
N	Nitrification	amoa_quasi	-0.11	0.08
S	sulfite reduction	dsrB	-0.10	0.09
Metal Homeostasis	Arsenic	arsB	-0.10	0.07
Metal Homeostasis	Cadmium	cadBD	-0.15	0.12
Metal Homeostasis	Cadmium,Cobalt,Zinc	czcD	-0.16	0.13
Metal Homeostasis	Cobalt/Magnesium	corA	-0.07	0.06
Metal Homeostasis	Copper	CutA	-0.12	0.11
Metal Homeostasis	Iron	feoB	-0.10	0.10
Metal Homeostasis	Manganese	mntH_Nramp	-0.14	0.09
Metal Homeostasis	Potassium	trkA	-0.10	0.08
Metal Homeostasis	Sodium	natB	-0.14	0.10
Metal Homeostasis	Sodium	nhaP	-0.12	0.09
Stress	Envelope stress	pspA	-0.12	0.10
Stress	Glucose limitation	lrp	-0.14	0.09
Stress	Oxidative stress	sodA	-0.15	0.08
Stress	Phosphate limitation	pstA	-0.16	0.13
Stress	Phosphate limitation	pstC	-0.11	0.09
Organic Remediation	Herbicides related compound	trza	-0.13	0.13
Organic Remediation	Aromatics	nitrilase	-0.13	0.11
Secondary metabolism	Pigments	phytoene_synthase	-0.12	0.07
Other	CRISPR	Cas7	-0.16	0.10
Other	CRISPR	cmr3	-0.15	0.12
Other	CRISPR	csm2	-0.14	0.08
Other	CRISPR	csm3	-0.16	0.14
Other	CRISPR	csx3	-0.16	0.14

35 **Table S4.** Differences in functional gene abundances between warming and control by response
36 ratios detected by metagenome EcoFUN-MAP. Only genes showing significant differences
37 between warming and control were included.
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Category	Subcategory	Gene ID	Response Ratio	95% confidence interval for RR
S Cycling	Sulfide Oxidation	fccAB	-0.16	0.11
S Cycling	Sulfite reduction	CysI	-0.09	0.07
Organic Contaminant Degradation	Aromatics	AmiE	-0.18	0.09
Organic Contaminant Degradation	Aromatics	mdlA	-0.15	0.13
Organic Contaminant Degradation	Chlorinated solvents	dehH109	-0.22	0.13
Organic Contaminant Degradation	Other Hydrocarbons	Xamo	-0.35	0.30
Metal Homeostasis	Arsenic	aoxB	-0.23	0.15
Microbial Defense	CRISPR	csx17	-0.84	0.77
C Cycling	Carbon Degradation	ara	0.15	0.10
C Cycling	Carbon Degradation	aceB	0.04	0.04
C Cycling	Carbon Degradation	vdh	0.14	0.13
C Cycling	Carbon Degradation	pme	0.29	0.15
P Cycling	Polyphosphate degradation	ppx	0.05	0.04
Electron transport	Photosynthetic	phytoene_synthase	0.15	0.08
Metal Homeostasis	Sodium	mrpA	0.12	0.09
Metal Homeostasis	Arsenic	arsB	0.29	0.07
Organic Contaminant Degradation	Aromatics	catB	0.12	0.11
Organic Contaminant Degradation	Herbicides related compound	trzN	0.57	0.45
Plant Growth Promotion	Anti-pathogen	xylA	0.12	0.08
Stress	Oxygen limitation	narH	0.17	0.08
Stress	Oxygen limitation	narI	0.18	0.10
Stress	Oxidative stress	katA	0.15	0.12
Stress	Oxygen limitation	narJ	0.17	0.17
Stress	Cold shock	desR	1.07	1.03

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Table S5. Correlations between the structure of functional gene groups and ecosystem functioning. The numbers denote the significance levels (two-sided) of Pearson's correlation coefficients after adjusted by the false discovery rate (FDR). Only genes involved in C and N cycling were included.

Analysis	Genes	GPP	ER	NEE	Rh	Ra
GeoChip	*aceB*	0.760	0.856	0.856	0.973	0.621
GeoChip	acetylglucosaminidase	0.656	0.753	0.670	1.000	1.000
GeoChip	*ara*	***0.020***	***0.029***	0.103	1.000	1.000
GeoChip	*cda*	***0.020***	***0.020***	0.193	1.000	1.000
GeoChip	chitinase	0.369	0.504	0.795	1.000	0.955
GeoChip	*nplT*	0.959	1.000	0.940	0.305	0.259
GeoChip	xylanase	***0.020***	***0.020***	0.281	1.000	0.897
GeoChip	AACT_DiC4HB	0.569	0.569	0.836	0.878	0.796
GeoChip	PEPC	0.183	0.226	0.955	0.978	0.999
GeoChip	sucA_DiC4HB	1.000	1.000	1.000	1.000	0.955
GeoChip	suc_CoA_red_DiC4HB	1.000	0.970	1.000	0.933	1.000
GeoChip	*mtmB*	1.000	1.000	1.000	1.000	1.000
GeoChip	*narb*	0.290	0.365	0.702	0.858	1.000
GeoChip	*nasa*	1.000	1.000	1.000	1.000	1.000
GeoChip	*narg*	1.000	1.000	1.000	1.000	1.000
GeoChip	*amoA*	***0.039***	0.121	0.470	1.000	0.569
EFM	*ara*	0.548	0.360	0.885	0.550	0.863
EFM	*aceB*	0.916	0.368	0.758	0.742	0.758
EFM	*vdh*	0.876	0.904	0.482	0.606	0.360
EFM	*pme*	0.984	0.857	0.965	0.309	0.886

Table S6. Correlations between the structure of functional gene groups and ecosystem functioning. The numbers denote the R value of Pearson's correlation coefficients. Only genes involved in C and N cycling were included.

Analysis	Genes	GPP	ER	NEE	Rh	Ra
GeoChip	*aceB*	0.033	0.006	0.006	-0.022	0.056
GeoChip	acetylglucosaminidase	0.032	0.003	0.028	-0.047	-0.049
GeoChip	*ara*	***0.457***	***0.374***	***0.252***	-0.117	-0.067
GeoChip	*cda*	***0.366***	***0.327***	0.163	-0.115	-0.071
GeoChip	chitinase	0.105	0.081	0.013	-0.033	-0.014
GeoChip	*nplT*	-0.018	-0.039	-0.021	0.117	0.171
GeoChip	xylanase	***0.341***	***0.326***	0.138	-0.065	-0.003
GeoChip	AACT_DiC4HB	0.068	0.061	0.007	0.000	0.020
GeoChip	PEPC	0.131	0.143	-0.013	-0.018	-0.022
GeoChip	sucA_DiC4HB	-0.106	-0.109	-0.043	-0.025	-0.010
GeoChip	suc_CoA_red_DiC4HB	-0.049	-0.044	-0.066	-0.015	-0.110
GeoChip	*mtmB*	0.000	0.000	0.000	0.000	0.000
GeoChip	*narb*	0.139	0.118	0.025	0.007	-0.056
GeoChip	*nasa*	0.000	0.000	0.000	0.000	0.000
GeoChip	*narg*	0.000	0.000	0.000	0.000	0.000
GeoChip	*amoA*	***0.282***	***0.241***	0.091	-0.042	0.074
EFM	*ara*	0.042	0.078	-0.060	0.050	-0.041
EFM	*aceB*	-0.067	0.071	-0.007	0.009	0.003
EFM	*vdh*	-0.035	-0.044	0.066	0.029	0.088
EFM	*pme*	-0.134	-0.025	-0.127	0.109	-0.048

Table S7. Coefficient of determination (R) between deterministic process and each factor. The relative importance of the deterministic process was estimated by iCAMP. The correlation was analyzed by modified Mantel test based on linear model (LM) (two-way tests). Each environmental factor was log-transformed before fitting the model. The correlation was determined based on the difference (with a triangle before the name) or the mean (without a triangle) of a factor between each pair of samples. Factors marked with '.SM' are measured in the sampling month, while the remaining were annual means. SP: soil properties; PL: plant-related; WT: water-related; TP: temperature; ST: spatial coordinate-related.

		Archaea	
	ID	*R*	*p*
SP	NO_3-N	0.009	0.462
SP	NH_4-N	0.061	0.338
SP	TN	0.258	**0.039**
SP	TOC	0.236	0.062
SP	pH	-0.080	0.304
PL	Total plant biomass	-0.362	**0.049**
PL	C_4 plant biomass	-0.087	0.322
PL	C_3 plant biomass	-0.355	**0.017**
PL	Plant richness	0.178	0.148
WT	Soil moisture SM	-0.071	0.376
WT	Soil moisture	-0.202	0.162
WT	Precipitation SM	-0.110	0.341
WT	Precipitation	0.065	0.421
WT	SPEI	0.213	0.183
TP	Soil temp	-0.111	0.272
ST	x	-0.324	**0.024**
ST	y	0.034	0.374
ST	PCNM1	0.113	0.274
ST	PCNM2	-0.374	**0.011**
ST	PCNM3	-0.241	**0.034**
ST	PCNM4	0.132	0.130
ST	PCNM5	0.138	0.179
SP	ΔNO3-N	0.036	0.376
SP	ΔNH4-N	-0.144	0.159
SP	ΔTN	-0.062	0.316
SP	ΔTOC	0.029	0.386
SP	ΔpH	0.101	0.187
PL	ΔT plant biomass	0.082	0.301
PL	ΔC4 plant biomass	0.022	0.442
PL	ΔC3 plant biomass	0.215	0.104
PL	ΔPlant richness	-0.210	**0.029**
WT	ΔSoil moisture SM	-0.024	0.451
WT	ΔSoil moisture	-0.056	0.346
TP	ΔSoil temp	-0.143	0.186
ST	Δx	0.216	0.052
ST	Δy	-0.033	0.183
ST	ΔPCNM1	-0.111	0.218
ST	ΔPCNM2	0.364	**0.010**
ST	ΔPCNM3	0.249	**0.038**
ST	ΔPCNM4	-0.126	0.230
ST	ΔPCNM5	-0.150	0.114

Table S8. OTU contribution to warming-induced changes in drift (DR) and homogeneous selection (HoS).

ID	Mean relative abundance	Bin	OTU contribution to DR (%)	OTU contribution to HoS (%)
OTU1148	0.0000	Bin1	0.0000	0.0008
OTU3468	0.0000	Bin1	0.0000	0.0001
OTU4373	0.0000	Bin1	0.0000	0.0001
OTU5265	0.0000	Bin1	0.0000	0.0000
OTU4161	0.0000	Bin1	0.0000	0.0003
OTU9284	0.0000	Bin1	0.0000	0.0003
OTU7498	0.0000	Bin1	0.0000	0.0001
OTU2263	0.0000	Bin1	0.0000	0.0001
OTU15	0.0022	Bin1	0.0008	0.0429
OTU4477	0.0000	Bin1	0.0000	0.0001
OTU67	0.0000	Bin1	0.0000	0.0001
OTU1363	0.0003	Bin1	0.0000	0.0166
OTU73	0.0005	Bin1	0.0001	0.0028
OTU9020	0.0001	Bin1	0.0000	0.0005
OTU11231	0.0000	Bin1	0.0000	0.0003
OTU7171	0.0005	Bin1	0.0001	0.0082
OTU33	0.0014	Bin1	0.0004	0.0130
OTU2834	0.0009	Bin1	0.0003	0.0108
OTU7967	0.0001	Bin1	0.0000	0.0017
OTU5652	0.0121	Bin1	0.0035	0.0213
OTU363	0.0042	Bin1	0.0015	0.0723
OTU825	0.0006	Bin1	0.0001	0.0118
OTU8485	0.0002	Bin1	0.0001	0.0022
OTU2101	0.0002	Bin1	0.0000	0.0032
OTU31	0.0022	Bin1	0.0005	0.0201
OTU9535	0.0009	Bin1	0.0003	0.0006
OTU10	0.0186	Bin1	0.0049	0.0975
OTU9436	0.0003	Bin1	0.0001	0.0050
OTU7966	0.0168	Bin1	0.0051	0.0746
OTU122	0.0002	Bin2	0.0015	0.0000
OTU291	0.0000	Bin2	0.0002	0.0000
OTU1884	0.0037	Bin2	0.0105	0.0000
OTU436	0.0028	Bin2	0.0025	0.0000
OTU6949	0.0499	Bin2	0.0416	0.0000
OTU9474	0.0000	Bin2	0.0001	0.0000
OTU4	0.0915	Bin2	0.1888	0.0000
OTU10223	0.0001	Bin2	0.0001	0.0000
OTU5	0.1417	Bin2	0.1644	0.0000
OTU3067	0.0029	Bin2	0.0039	0.0000
OTU9993	0.0000	Bin2	0.0000	0.0000
OTU2	0.1167	Bin2	0.2613	0.0000
OTU7274	0.0024	Bin2	0.0024	0.0000
OTU9259	0.0004	Bin2	0.0007	0.0000
OTU9403	0.0000	Bin2	0.0000	0.0000
OTU6336	0.0007	Bin2	0.0025	0.0000
OTU1	0.3759	Bin2	0.2431	0.0000
OTU10875	0.0000	Bin2	0.0000	0.0000
OTU10541	0.0011	Bin2	0.0002	0.0000
OTU10654	0.0011	Bin2	0.0014	0.0000
OTU10542	0.0007	Bin2	0.0001	0.0000
OTU9	0.0305	Bin2	0.0033	0.0000
OTU262	0.0131	Bin2	0.0054	0.0000
OTU3	0.0774	Bin1	0.0235	0.3363
OTU11	0.0094	Bin1	0.0035	0.2032
OTU9502	0.0000	Bin1	0.0000	0.0001

OTU11277	0.0000	Bin1	0.0000	0.0001
OTU96	0.0003	Bin1	0.0001	0.0058
OTU3778	0.0002	Bin1	0.0000	0.0031
OTU47	0.0008	Bin1	0.0003	0.0077
OTU396	0.0001	Bin1	0.0000	0.0024
OTU971	0.0000	Bin1	0.0000	0.0011
OTU4078	0.0000	Bin1	0.0000	0.0001
OTU55	0.0006	Bin1	0.0001	0.0110
OTU428	0.0000	Bin1	0.0000	0.0006
OTU2734	0.0000	Bin1	0.0000	0.0008
OTU2804	0.0000	Bin1	0.0000	0.0003
OTU5138	0.0000	Bin1	0.0000	0.0001
OTU2835	0.0000	Bin1	0.0000	0.0010
OTU6811	0.0000	Bin1	0.0000	0.0001
OTU3713	0.0000	Bin4	0.0000	0.0000
OTU9647	0.0000	Bin3	0.0000	0.0000
OTU1314	0.0001	Bin3	0.0002	0.0004
OTU4344	0.0000	Bin3	0.0000	0.0000
OTU170	0.0002	Bin3	0.0002	0.0005
OTU190	0.0004	Bin3	0.0005	0.0002
OTU81	0.0005	Bin3	0.0004	0.0012
OTU2359	0.0000	Bin3	0.0000	0.0000
OTU1714	0.0000	Bin3	0.0000	0.0000
OTU827	0.0001	Bin3	0.0001	0.0001
OTU333	0.0002	Bin3	0.0004	0.0009
OTU1232	0.0001	Bin3	0.0001	0.0001
OTU9508	0.0000	Bin3	0.0000	0.0000
OTU21	0.0031	Bin4	0.0021	0.0014
OTU1097	0.0000	Bin4	0.0000	0.0000
OTU195	0.0001	Bin4	0.0002	0.0001
OTU229	0.0001	Bin4	0.0003	0.0001
OTU2097	0.0000	Bin4	0.0001	0.0000
OTU546	0.0000	Bin4	0.0001	0.0000
OTU9407	0.0000	Bin4	0.0000	0.0000
OTU6647	0.0000	Bin4	0.0001	0.0000
OTU25	0.0020	Bin4	0.0025	0.0011
OTU507	0.0003	Bin4	0.0001	0.0001
OTU218	0.0001	Bin4	0.0003	0.0001
OTU7542	0.0000	Bin4	0.0000	0.0000
OTU1847	0.0000	Bin4	0.0001	0.0000
OTU10814	0.0000	Bin4	0.0000	0.0000
OTU1237	0.0001	Bin4	0.0000	0.0000
OTU196	0.0002	Bin4	0.0000	0.0001
OTU1080	0.0000	Bin4	0.0000	0.0000
OTU4597	0.0000	Bin4	0.0001	0.0000
OTU119	0.0006	Bin4	0.0022	0.0002
OTU478	0.0001	Bin4	0.0002	0.0001
OTU664	0.0000	Bin4	0.0001	0.0000
OTU802	0.0000	Bin4	0.0001	0.0000
OTU372	0.0000	Bin4	0.0000	0.0000
OTU75	0.0007	Bin4	0.0014	0.0000
OTU3202	0.0000	Bin4	0.0001	0.0000
OTU56	0.0016	Bin4	0.0018	0.0002
OTU2892	0.0000	Bin4	0.0000	0.0000
OTU751	0.0000	Bin5	0.0000	0.0000
OTU3418	0.0000	Bin5	0.0000	0.0000
OTU2337	0.0000	Bin5	0.0001	0.0001
OTU10549	0.0000	Bin5	0.0000	0.0000
OTU2779	0.0000	Bin5	0.0001	0.0000
OTU3571	0.0000	Bin5	0.0000	0.0000
OTU8544	0.0000	Bin5	0.0000	0.0000
OTU589	0.0000	Bin5	0.0000	0.0000

OTU2028	0.0000	Bin5	0.0000	0.0000
OTU535	0.0000	Bin5	0.0001	0.0000
OTU9214	0.0000	Bin5	0.0000	0.0000
OTU10460	0.0000	Bin5	0.0000	0.0000
OTU889	0.0000	Bin5	0.0001	0.0000
OTU1057	0.0001	Bin5	0.0002	0.0000
OTU1625	0.0000	Bin5	0.0000	0.0000
OTU1295	0.0000	Bin5	0.0000	0.0000
OTU556	0.0000	Bin6	0.0001	0.0003
OTU11479	0.0000	Bin6	0.0000	0.0001
OTU5809	0.0000	Bin6	0.0001	0.0002
OTU1978	0.0000	Bin6	0.0000	0.0000
OTU65	0.0001	Bin6	0.0003	0.0007
OTU5415	0.0000	Bin6	0.0000	0.0000
OTU663	0.0000	Bin6	0.0000	0.0000
OTU4802	0.0000	Bin6	0.0000	0.0000
OTU1047	0.0000	Bin6	0.0000	0.0001
OTU775	0.0000	Bin6	0.0000	0.0000
OTU4616	0.0000	Bin6	0.0000	0.0000
OTU2203	0.0000	Bin6	0.0000	0.0000
OTU1985	0.0000	Bin6	0.0001	0.0003
OTU8343	0.0000	Bin6	0.0000	0.0001
OTU3303	0.0000	Bin6	0.0000	0.0001
OTU90	0.0003	Bin6	0.0008	0.0023
OTU793	0.0000	Bin6	0.0000	0.0001
OTU126	0.0001	Bin6	0.0000	0.0002
OTU770	0.0000	Bin6	0.0000	0.0001
OTU1518	0.0000	Bin6	0.0000	0.0000
OTU1381	0.0000	Bin6	0.0001	0.0002
OTU2614	0.0000	Bin6	0.0000	0.0001
OTU484	0.0000	Bin6	0.0000	0.0001
OTU2526	0.0000	Bin6	0.0000	0.0001
OTU203	0.0000	Bin6	0.0001	0.0002
OTU1224	0.0000	Bin6	0.0001	0.0001
OTU9609	0.0000	Bin6	0.0000	0.0000
OTU1313	0.0000	Bin6	0.0000	0.0001
OTU2151	0.0000	Bin6	0.0001	0.0001
OTU4390	0.0000	Bin6	0.0000	0.0001
OTU891	0.0000	Bin6	0.0000	0.0000
OTU6806	0.0000	Bin6	0.0000	0.0000
OTU3427	0.0000	Bin6	0.0000	0.0000
OTU1899	0.0000	Bin6	0.0000	0.0000
OTU284	0.0000	Bin6	0.0000	0.0001
OTU2023	0.0000	Bin6	0.0000	0.0000
OTU2630	0.0000	Bin6	0.0000	0.0001
OTU2177	0.0000	Bin6	0.0000	0.0000
OTU1350	0.0000	Bin6	0.0000	0.0000
OTU4044	0.0000	Bin6	0.0000	0.0001
OTU386	0.0000	Bin6	0.0000	0.0001
OTU8771	0.0000	Bin6	0.0000	0.0001
OTU611	0.0001	Bin6	0.0002	0.0005
OTU6490	0.0000	Bin6	0.0000	0.0001
OTU754	0.0000	Bin6	0.0000	0.0000
OTU232	0.0001	Bin6	0.0000	0.0000
OTU209	0.0001	Bin6	0.0000	0.0000
OTU6056	0.0000	Bin6	0.0000	0.0000
OTU898	0.0000	Bin6	0.0001	0.0002
OTU3433	0.0000	Bin6	0.0000	0.0000
OTU11386	0.0000	Bin6	0.0000	0.0000
OTU1463	0.0000	Bin6	0.0000	0.0000
OTU2039	0.0000	Bin6	0.0000	0.0000
OTU11410	0.0000	Bin6	0.0000	0.0000

OTU5006	0.0000	Bin6	0.0000	0.0001
OTU1347	0.0000	Bin6	0.0000	0.0000
OTU762	0.0000	Bin6	0.0001	0.0001
OTU7468	0.0000	Bin6	0.0000	0.0000
OTU9213	0.0000	Bin6	0.0000	0.0000
OTU2434	0.0000	Bin6	0.0000	0.0000
OTU8591	0.0000	Bin6	0.0000	0.0000
OTU5275	0.0000	Bin6	0.0000	0.0000
OTU4334	0.0000	Bin6	0.0000	0.0000
OTU3096	0.0000	Bin6	0.0000	0.0000
OTU1563	0.0000	Bin6	0.0000	0.0001
OTU4992	0.0000	Bin6	0.0000	0.0000
OTU4410	0.0000	Bin6	0.0000	0.0000
OTU1450	0.0000	Bin6	0.0000	0.0000
OTU765	0.0000	Bin6	0.0000	0.0000
OTU3756	0.0000	Bin6	0.0001	0.0002
OTU8715	0.0000	Bin6	0.0000	0.0000
OTU1341	0.0000	Bin6	0.0001	0.0002
OTU1996	0.0000	Bin6	0.0000	0.0000
OTU5983	0.0000	Bin6	0.0000	0.0000
OTU2213	0.0000	Bin6	0.0000	0.0000
OTU1292	0.0000	Bin6	0.0002	0.0004
OTU2154	0.0000	Bin6	0.0000	0.0000
OTU1114	0.0000	Bin6	0.0000	0.0000
OTU2441	0.0000	Bin6	0.0000	0.0000
OTU864	0.0000	Bin6	0.0000	0.0000
OTU2133	0.0000	Bin6	0.0000	0.0001
OTU897	0.0000	Bin6	0.0000	0.0001
OTU2657	0.0000	Bin7	0.0000	0.0000
OTU489	0.0000	Bin7	0.0001	0.0001
OTU8460	0.0000	Bin7	0.0000	0.0000
OTU511	0.0000	Bin7	0.0001	0.0000
OTU729	0.0000	Bin7	0.0002	0.0000
OTU10458	0.0000	Bin7	0.0000	0.0000
OTU1528	0.0000	Bin7	0.0000	0.0000
OTU5621	0.0000	Bin7	0.0000	0.0000
OTU752	0.0000	Bin7	0.0001	0.0000
OTU2498	0.0000	Bin7	0.0000	0.0000
OTU4543	0.0000	Bin7	0.0000	0.0000
OTU5020	0.0000	Bin7	0.0000	0.0000
OTU651	0.0001	Bin7	0.0002	0.0003
OTU8147	0.0000	Bin7	0.0000	0.0000
OTU2243	0.0000	Bin7	0.0000	0.0000
OTU2560	0.0000	Bin7	0.0000	0.0000
OTU4879	0.0000	Bin7	0.0000	0.0000
OTU3043	0.0000	Bin7	0.0000	0.0000
OTU635	0.0001	Bin7	0.0001	0.0001
OTU1115	0.0000	Bin7	0.0001	0.0001
OTU1699	0.0000	Bin7	0.0001	0.0001
OTU615	0.0000	Bin7	0.0000	0.0000
OTU5792	0.0000	Bin7	0.0000	0.0000
OTU7157	0.0000	Bin7	0.0000	0.0000
OTU5099	0.0000	Bin7	0.0000	0.0000
OTU413	0.0001	Bin7	0.0000	0.0001
OTU6019	0.0000	Bin7	0.0000	0.0000
OTU4249	0.0000	Bin7	0.0000	0.0000
OTU5107	0.0000	Bin7	0.0000	0.0000
OTU8664	0.0000	Bin8	0.0000	0.0000
OTU8611	0.0000	Bin8	0.0000	0.0000
OTU9669	0.0000	Bin8	0.0000	0.0000
OTU2948	0.0000	Bin8	0.0000	0.0000
OTU4509	0.0000	Bin8	0.0000	0.0000

OTU4828	0.0001	Bin8	0.0003	0.0003
OTU3671	0.0000	Bin8	0.0001	0.0001
OTU4927	0.0000	Bin8	0.0000	0.0000
OTU2644	0.0000	Bin8	0.0000	0.0000
OTU3328	0.0000	Bin8	0.0000	0.0000
OTU4126	0.0000	Bin8	0.0000	0.0000
OTU4668	0.0000	Bin8	0.0000	0.0000
OTU479	0.0001	Bin8	0.0001	0.0000
OTU2012	0.0000	Bin8	0.0000	0.0000
OTU376	0.0001	Bin8	0.0000	0.0002
OTU1972	0.0000	Bin8	0.0001	0.0000
OTU1825	0.0000	Bin8	0.0000	0.0000
OTU7689	0.0000	Bin8	0.0000	0.0000
OTU1408	0.0000	Bin8	0.0000	0.0000
OTU2172	0.0000	Bin8	0.0001	0.0001
OTU4288	0.0000	Bin8	0.0000	0.0000
OTU8594	0.0000	Bin8	0.0000	0.0000
OTU1977	0.0000	Bin8	0.0001	0.0001
OTU3510	0.0000	Bin8	0.0000	0.0000
OTU2602	0.0000	Bin8	0.0000	0.0000
OTU10136	0.0000	Bin8	0.0000	0.0000
OTU4816	0.0000	Bin8	0.0000	0.0000
OTU8661	0.0000	Bin8	0.0000	0.0000
OTU7009	0.0000	Bin8	0.0000	0.0000
OTU6115	0.0000	Bin8	0.0000	0.0000
OTU2257	0.0000	Bin8	0.0000	0.0000
OTU4116	0.0000	Bin8	0.0000	0.0000
OTU7267	0.0000	Bin8	0.0000	0.0000
OTU6939	0.0000	Bin8	0.0000	0.0000
OTU8945	0.0000	Bin8	0.0000	0.0000
OTU4446	0.0000	Bin8	0.0000	0.0000
OTU1715	0.0000	Bin8	0.0000	0.0000
OTU6276	0.0000	Bin8	0.0000	0.0000
OTU7276	0.0000	Bin8	0.0000	0.0000
OTU4104	0.0000	Bin8	0.0000	0.0000
OTU7268	0.0000	Bin8	0.0000	0.0000
OTU1269	0.0000	Bin8	0.0000	0.0000
OTU6270	0.0000	Bin8	0.0000	0.0000
OTU4207	0.0000	Bin8	0.0000	0.0000
OTU2640	0.0000	Bin8	0.0000	0.0000
OTU4009	0.0000	Bin8	0.0000	0.0000
OTU10471	0.0000	Bin8	0.0000	0.0000
OTU3984	0.0000	Bin8	0.0001	0.0000
OTU2766	0.0000	Bin7	0.0000	0.0000
OTU5478	0.0000	Bin7	0.0000	0.0000
OTU5470	0.0000	Bin7	0.0000	0.0000

Table S9. Potential predictors (independent variables, X) for each factor (dependent variable, Y) in partial least squares (PLS) analysis. All the listed predictors were tested, and the optimum model was based on forward selection as detailed in Methods. Soil temperature, moisture, and pH were not considered as dependent variables, given their key determinants are out of the scope of this study.

No.	Dependent variable (Y)	Potential predictors (independent variables, X, in PLS)
1	Soil total C	Warming, Soil total N, Soil NH_4^+-N, Soil NO_3^--N, Soil pH, Soil moisture, Soil Temperature, Total plant biomass, C_3 plant biomass
2	Soil total N	Soil total C, Warming, Soil NH_4^+-N, Soil NO_3^--N, Soil pH, Soil moisture, Soil Temperature, Total plant biomass, C_3 plant biomass
3	Soil NH_4^+-N	Soil total C, Warming, Soil total N, Soil NO_3^--N, Soil pH, Soil moisture, Soil Temperature, Total plant biomass, C_3 plant biomass
4	Soil NO_3^--N	Soil total C, Warming, Soil total N, Soil NH_4^+-N, Soil pH, Soil moisture, Soil Temperature, Total plant biomass, C_3 plant biomass
5	Soil pH	Soil total C, Warming, Soil total N, Soil NH_4^+-N, Soil NO_3^--N, Soil moisture, Soil Temperature, Total plant biomass, C_3 plant biomass
6	Soil moisture	Soil total C, Warming, Soil total N, Soil NH_4^+-N, Soil NO_3^--N, Soil pH, Soil Temperature, Total plant biomass, C_3 plant biomass
7	Soil Temperature	Soil total C, Warming, Soil total N, Soil NH_4^+-N, Soil NO_3^--N, Soil pH, Soil moisture, Soil Temperature, Total plant biomass, C_3 plant biomass
8	Total plant biomass	Soil total C, Warming, Soil total N, Soil NH_4^+-N, Soil NO_3^--N, Soil pH, Soil moisture, Soil Temperature, C_3 plant biomass, archaeal alpha-diversity (PD, richness), Archaeal beta-diversity (PCs), Relevant functional gene abundances*, R_a, R_h
9	C_3 plant biomass	Soil total C, Warming, Soil total N, Soil NH_4^+-N, Soil NO_3^--N, Soil pH, Soil moisture, Soil Temperature, Total plant biomass, Archaeal alpha-diversity (PD, richness), Archaeal beta-diversity (PCs), Relevant functional gene abundances*, R_a, R_h
10	Archaeal alpha-diversity	Soil total C, Warming, Soil total N, Soil NH_4^+-N, Soil NO_3^--N, Soil pH, Soil moisture, Soil Temperature, Total plant biomass, C_3 plant biomass, Archaeal beta-diversity (PCs), Relevant functional gene abundances*
11	Archaeal beta-diversity (PCs)	Soil total C, Warming, Soil total N, Soil NH_4^+-N, Soil NO_3^--N, Soil pH, Soil moisture, Soil Temperature, Total plant biomass, C_3 plant biomass, Archaeal alpha-diversity (PD, richness), Relevant functional gene abundances*
12	Relevant functional gene abundances*	Soil total C, Warming, Soil total N, Soil NH_4^+-N, Soil NO_3^--N, Soil pH, Soil moisture, Soil Temperature, Total plant biomass, C_3 plant biomass, Archaeal alpha-diversity (PD, richness), Archaeal beta-diversity (PCs), ER, NEE, R_a, R_h
13	Ecosystem respiration (ER)	Soil total C, Warming, Soil total N, Soil NH_4^+-N, Soil NO_3^--N, Soil pH, Soil moisture, Soil Temperature, Total plant biomass, C_3 plant biomass, Archaeal alpha-diversity (PD, richness), Archaeal beta-diversity (PCs), Relevant functional gene abundances*, NEE, R_a, R_h
14	Net ecosystem exchange (NEE)	Soil total C, Warming, Soil total N, Soil NH_4^+-N, Soil NO_3^--N, Soil pH, Soil moisture, Soil Temperature, Total plant biomass, C_3 plant

		biomass, Archaeal alpha-diversity (PD, richness), Archaeal beta-diversity (PCs), Relevant functional gene abundances*, ER, R_a, R_h
15	Autotrophic respiration (R_a)	Soil total C, Warming, Soil total N, Soil NH_4^+-N, Soil NO_3^--N, Soil pH, Soil moisture, Soil Temperature, Total plant biomass, C_3 plant biomass, Archaeal alpha-diversity (PD, richness), Archaeal beta-diversity (PCs), Relevant functional gene abundances*, ER, NEE, , R_a, R_h
16	Heterotrophic respiration (R_h)	Soil total C, Warming, Soil total N, Soil NH_4^+-N, Soil NO_3^--N, Soil pH, Soil moisture, Soil Temperature, Total plant biomass, C_3 plant biomass, Archaeal alpha-diversity (PD, richness), Archaeal beta-diversity (PCs), Relevant functional gene abundances*, ER, NEE, R_a, R_h

* Relevant functional gene abundances include the abundances of C degradation, C fixation, methane, ammonification, assimilatory N reduction, denitrification, dissimilatory N reduction, nitrification, N fixation.