Table S1. Environmental variables

Environmental variables	Control	Wetting	Drying	Warming	Warming + Wetting	Warming + Drying
Clay (%)[a]	65.33±4.36a[b]	66.97±3.94ab	72.40±2.70ab	60.32±6.70a	63.86±4.95a	78.67±2.32b
Silt (%)	11.85±0.87a	12.09±0.63a	10.48±1.35a	14.68±2.65a	12.16±1.34a	10.93±0.73a
Sandy (%)	22.82±3.61b	20.94±3.33b	17.11±2.81ab	25.01±4.25b	23.98±3.78b	10.39±2.70a
pH	7.85±0.07ab	7.86±0.03b	7.89±0.01b	7.91±0.01b	7.77±0.07a	7.90±0.02b
SWC (g kg^{-1})	32.48±1.50b	35.91±2.00b	28.30±3.90ab	28.40±2.15ab	34.48±2.09b	22.21±1.03a
ST (°C)	4.77±0.30a	4.82±0.50a	4.96±0.28ab	6.67±0.47c	6.36±0.11bc	7.38±0.57c
TC (g kg^{-1})	78.18±0.95a	75.78±3.95a	81.35±7.45a	75.05±7.59a	79.50±2.48a	79.90±4.82a
TN (g kg^{-1})	5.75±0.28a	5.55±0.34a	6.25±0.60a	5.55±0.79a	5.85±0.13a	5.88±0.37a
TP (g kg^{-1})	0.79±0.05ab	0.82±0.03ab	0.87±0.05b	0.75±0.06ab	0.83±0.02ab	0.71±0.04a
SOC (g kg^{-1})	63.10±1.04a	62.77±3.86a	67.09±4.57a	65.39±3.37a	65.02±1.79a	64.42±3.90a
NH$_4^+$ (mg kg^{-1})	27.29±4.20a	26.32±0.34a	30.50±3.13a	23.73±2.05a	21.30±3.59a	28.18±3.74a
NO$_3^-$ (mg kg^{-1})	10.27±0.47b	8.61±0.33a	11.61±0.35cd	10.47±0.41bc	10.11±0.35b	12.41±0.10d
SAP (mg kg^{-1})	7.68±0.17a	7.43±0.52a	6.83±0.41a	6.72±0.41a	7.60±0.20a	6.60±0.32a
DOC (mg kg^{-1})	280.31±6.07bd	245.69±11.58ab	304.60±10.41cd	268.92±8.47abc	240.28±10.49a	311.65±5.75d
DON (mg kg^{-1})	33.03±3.28a	29.01±2.56a	40.67±4.03a	31.11±1.42a	30.94±4.00a	37.33±4.81a
MBC (mg kg^{-1})	656.79±34.20bc	710.64±45.61c	567.29±36.49ab	552.57±19.10ab	688.57±36.11bc	477.64±25.37a
MBN (mg kg^{-1})	61.40±1.92bc	73.79±2.98c	55.70±5.72b	59.93±5.21b	66.24±3.07bc	42.93±0.72a
CO$_2$ (mg m^{-2} h^{-1})	647.96±48.93abc	710.36±28.40cd	587.56±23.87ab	635.76±42.97ac	772.54±46.49d	545.66±36.24a
CH$_4$ (μg m^{-2} h^{-1})	-56.05±5.70bcd	-42.76±2.76d	-75.71±5.29ab	-69.74±4.25ac	-54.84±8.29cd	-84.97±0.32a
N$_2$O (μg m^{-2} h^{-1})	11.59±4.43a	-2.01±0.83a	2.94±7.89a	3.69±1.12a	0.26±0.65a	-0.76±4.24a

Grass ANPP (g m^{-2})	175.65±33.36a	221.96±14.67ab	188±23.94a	226.07±9.59ab	322.35±64.41b	152.73±11.71a
Sedge ANPP (g m^{-2})	37.60±5.78ab	51.16±19.70b	18.59±4.81a	15.14±6.83a	32.70±2.59ab	12.36±3.16a
Forb ANPP (g m^{-2})	146.26±3.30c	104.08±20.77ac	80.38±3.57a	93.99±14.06ab	134.75±2.96bc	58.92±11.08a
Other ANPP (g m^{-2})	0.00±0.00a	0.00±0.00a	0.69±0.69a	0.15±0.15a	0.03±0.03a	0.00±0.00a
ANPP (g m^{-2})	359.51±38.45bc	377.20±13.40bc	287.65±22.91ab	335.35±11.66ab	489.82±62.14c	224.01±17.29a
Total plant biomass	1088.11±125.49a	993.82±26.50a	995.78±102.15a	998.48±55.82a	1109.88±24.95a	943.96±123.53a
Root/shoot ratio	2.00±0.05bc	1.63±0.05c	2.44±0.08ab	1.98±0.24bc	1.32±0.25c	3.23±0.51a
Grass richness	6.50±0.65a	6.25±0.48a	5.75±0.63a	5.00±0.58a	7.00±0.58a	4.75±0.48a
Sedge richness	2.75±0.25ab	2.75±0.25ab	2.00±0.00a	2.75±0.25ab	3.00±0.00b	2.75±0.25ab
Forb richness	21.00±1.08bc	24.00±1.35c	20.25±0.63ac	19.00±1.22ab	23.00±0.00c	17.00±0.82a
Other plant richness	0.25±0.25a	0.00±0.00a	0.25±0.25a	0.00±0.00a	0.25±0.25a	0.00±0.00a
Plant richness	30.50±1.50bc	33.00±1.73c	28.25±1.31ac	26.75±1.38ab	33.25±0.75c	24.50±0.65a
Plant diversity	1.72±0.11a	1.55±0.15a	1.49±0.18a	1.45±0.15a	1.66±0.20a	1.12±0.13a
BNPP (g m^{-2})	726.73±88.42a	616.62±16.94a	707.89±79.09a	662.85±63.33a	595.44±75.55a	719.96±118.79a
GPP (μmol CO$_2$ m^{-2} s^{-1})	16.38±1.40a	20.27±0.73b	17.11±0.51ab	19.72±1.27b	24.04±0.35c	16.21±1.18a
NEE (μmol CO$_2$ m^{-2} s^{-1})	-10.08±0.74cd	-13.04±0.78b	-10.64±0.62cd	-11.78±1.17bc	-15.82±0.34a	-9.30±1.09d
ER (μmol CO$_2$ m^{-2} s^{-1})	6.30±0.72a	7.23±0.06ac	6.47±0.67a	7.94±0.37bc	8.22±0.12c	6.91±0.21ab
EMF	0.19±0.18bc	-0.11±0.04ac	-0.04±0.14ac	-0.24±0.12ab	0.34±0.10c	-0.36±0.07a

[a]Abbreviations: Clay, soil clay content, Silt, soil silt content, Sandy, soil sandy content; SWC, soil water content; ST, soil temperature; TC, soil total carbon; TN, soil total nitrogen; TP, soil total phosphorus; SOC, soil organic carbon; SAP, soil available phosphorus; DOC, dissolved organic carbon; DON, dissolved organic nitrogen; MBC, microbial biomass carbon; MBN, microbial biomass nitrogen; CO$_2$, soil CO$_2$ flux; CH$_4$, soil CH$_4$

flux; N$_2$O, soil N$_2$O flux; Grass ANPP, the aboveground net primary production of grass; Sedge ANPP, the aboveground net primary production of sedge; Forb ANPP, the aboveground net primary production of forb; Other ANPP, the aboveground net primary production of other functional groups of plant; ANPP, the aboveground net primary production of plant community; Total plant biomass, the sum of aboveground and belowground net primary production; Root/shoot ratio, the ratio of BNPP to ANPP; the Grass richness, species number of grass; Sedge richness, species number of sedge; Forb richness, species number of forb; Other plant richness, species number of other functional groups of plants; Plant richness, the species numbers of plant community; Plant diversity, the α-diversity of plant community based on Shannon index; BNPP, belowground net primary production; NEE, net ecosystem exchange; ER, ecosystem respiration; GPP, gross primary productivity; EMF, ecosystem multifunctionality.

[b]Mean values (± s.e.) are shown. The letters were calculated by post-hoc Tukey's honest significant difference test of a linear mixed-effects model. Different alphabetic letters indicate significant difference ($P < 0.050$).

Table S2. Treatment effects on environmental variables and microbial communities[a]

	Variables	Temperature	Precipitation	Interaction
	Clay (%)[b]	0.01	13.40**	3.36
	Silt (%)	3.01	2.06	0.84
	Sandy (%)	0.93	14.86***	5.57
	pH	0.41	4.94*	4.41*
	SWC (g kg^{-1})	5.95*	14.02***	1.20
	ST (°C)	68.11***	1.73	0.08
	TC (g kg^{-1})	0.01	0.77	0.57
	TN (g kg^{-1})	0.16	1.25	0.76
	TP (g kg^{-1})	5.95*	14.03***	1.20
	SOC (g kg^{-1})	0.12	0.39	0.81
	NH_4^+ (mg kg^{-1})	7.89**	6.38**	0.36
	NO_3^- (mg kg^{-1})	8.59**	38.08***	1.29
	SAP (mg kg^{-1})	2.93	3.80*	2.18
Environmental	DOC (mg kg^{-1})	0.11	40.86***	2.31
variables	DON (mg kg^{-1})	0.01	2.70	0.20
	CO_2 (mg m^{-2} h^{-1})	1.51	22.83***	1.95
	CH_4 (μg m^{-2} h^{-1})	12.34**	28.21***	0.44
	N_2O (μg m^{-2} h^{-1})	3.07	0.36	2.48
	Grass ANPP (g m^{-2})	1.00	5.07*	2.29
	Sedge ANPP (g m^{-2})	6.10*	6.92**	0.38
	Forb ANPP (g m^{-2})	4.68*	14.94***	5.33*
	Other ANPP (g m^{-2})	0.57	0.81	1.34
	ANPP (g m^{-2})	0.34	20.28***	4.46*
	Total plant biomass	0.58	18.46***	4.05*
	Root/shoot ratio	0.27	15.09***	1.88
	Grass richness	5.01*	5.32*	4.10*
	Sedge richness	8.57*	6.96*	3.75*
	Forb richness	9.17**	12.13***	0.82

	Other plant richness	1.19	0.01	4.76*
	Plant richness	8.03**	14.60***	2.24
	Plant diversity	3.34	3.89*	1.65
	BNPP (g m^{-2})	1.09	0.79	0.86
	NEE (μmol CO$_2$ m^{-2} s^{-1})	2.43	18.45***	4.41*
	ER (μmol CO$_2$ m^{-2} s^{-1})	14.54***	8.13***	0.76
	GPP (μmol CO$_2$ m^{-2} s^{-1})	5.77*	15.36***	2.73
	EMF	3.24	6.36**	4.22*
Microbial biomass	MBC (mg kg^{-1})	8.76**	16.89***	1.52
	MBN (mg kg^{-1})	6.35*	26.46***	1.72
	Overall functional community	0.71	2.67*	1.14
	amyA	0.79	2.37*	1.04
	amyX	0.74	2.54	5.91*
	apu	0.10	1.78	0.43
	cda	1.10	2.50**	1.14
	glucoamylase	1.02	2.35**	1.04
	isopullulanase	0.13	1.01	0.93
	nplT	1.80	3.16***	2.86***
	pulA	1.02	2.82**	1.47
	ara	0.74	2.95*	1.15
	mannanase	1.09	3.39*	1.29
	xylA	0.83	1.78*	0.97
	xylanase	0.73	1.80*	1.08
	axe	0.72	2.48*	1.12
	cellobiase	1.12	1.88*	1.26
	GH7 cellulase	1.03	6.13**	0.82
Microbial functional communities	*endoglucanase*	0.97	2.32*	1.04
	exoglucanase	1.03	2.03*	0.96
	acetylglucosaminidase	0.88	2.99*	1.26
	chitin deacetylase	0.98	2.48*	1.43
	chitinase	0.79	2.53*	1.11
	glx	0.94	3.16**	1.40

	ligninase	0.58	1.92*	2.12*
	mnp	0.22	1.93	0.83
	phenol oxidase	1.19	2.49**	1.42
	fwdB	1.57	2.68	0.66
	ftr	0.47	4.35**	1.06
	hmd	2.02	2.29*	2.44
	mch	1.24	3.42*	1.02
	mtrH	2.68	5.90***	1.82
	mer	0.84	2.19*	1.66
	acs	3.14	0.56	0.96
	mtaB	0.57	5.34***	3.00*
	mtmB	2.44	6.97**	1.86
	mtbC	0.20	1.76	1.22
	mcrA	0.66	3.20*	0.92
	MT2	0.47	1.41	2.59**
	hdrB	1.46	3.54*	1.22
	mmoX	0.68	1.86	2.25*
	pmoA	1.02	2.82**	1.47
	Overall bacterial community	1.27	1.58*	1.04
	Unclassified	1.04	1.07	1.05
	Alphaproteobacteria	1.15	1.30	1.10
	Deltaproteobacteria	1.18	1.58	1.16
	Gammaproteobacteria	0.88	3.23	1.16
	Betaproteobacteria	1.98	2.94	1.48
	Acidobacteria	0.91	1.27	1.06
	Actinobacteria	1.73	1.26	0.80
	Planctomycetes	1.12	1.04	0.96
	Gemmatimonadetes	0.84*	1.11	1.07
Bacterial communities	*Bacteroidetes*	1.60	2.40**	1.37
	Firmicutes	0.43	0.70	0.75
	Chloroflexi	0.99	1.17	1.09
	Verrucomicrobia	1.29	1.54	1.08

	Candidate division WPS 1	0.71	1.12	0.96
	Armatimonadetes	1.10	2.23*	1.54
	Thaumarchaeota	1.04	2.83*	1.00
	Latescibacteria	0.34	1.22	1.07
	Nitrospirae	1.00	0.66	1.73
Fungal communities	Overall fungal community	0.94	1.24*	1.18
	Ascomycota	0.98	1.20	1.19
	Basidiomycota	0.99	1.31	1.16
	Unclassified	0.90	0.92	0.97
	Zygomycota	0.89	1.36	1.26
	Chytridiomycota	0.56	1.38	1.65*
	Glomeromycota	0.95	1.24*	1.26*

[a]ANOVA based on the linear mixed-effects model was used to test treatment effects on environmental variables. PerMANOVA is based on the linear mixed-effects model with a weighted Bray-Curtis dissimilarity matrix to test treatment effects on microbial communities. *F*-statistics are shown. Significance is indicated by *$P < 0.050$, **$P < 0.010$, ***$P < 0.001$.

[b]Abbreviations: Clay, soil clay content, Silt, soil silt content, Sandy, soil sandy content; SWC, soil water content; ST, soil temperature; TC, soil total carbon; TN, soil total nitrogen; TP, soil total phosphorus; SOC, soil organic carbon; SAP, soil available phosphorus; DOC, dissolved organic carbon; DON, dissolved organic nitrogen; CO_2, soil CO_2 flux; CH_4, soil CH_4 flux; N_2O, soil N_2O flux; Grass ANPP, the aboveground net primary production of grass; Sedge ANPP, the aboveground net primary production of sedge; Forb ANPP, the aboveground net primary production of forb; Other ANPP, the

aboveground net primary production of other functional groups of plant; ANPP, the

aboveground net primary production of plant community; Total plant biomass, the sum

of aboveground and belowground net primary production; Root/shoot ratio, the ratio of

BNPP to ANPP; the Grass richness, species number of grass; Sedge richness, species

number of sedge; Forb richness, species number of forb; Other plant richness, species

number of other functional groups of plants; Plant richness, the species numbers of

plant community; Plant diversity, the α-diversity of plant community based on Shannon

index; BNPP, belowground net primary production; NEE, net ecosystem exchange; ER,

ecosystem respiration; GPP, gross primary productivity; EMF, ecosystem

multifunctionality; MBC, microbial biomass carbon; MBN, microbial biomass nitrogen.
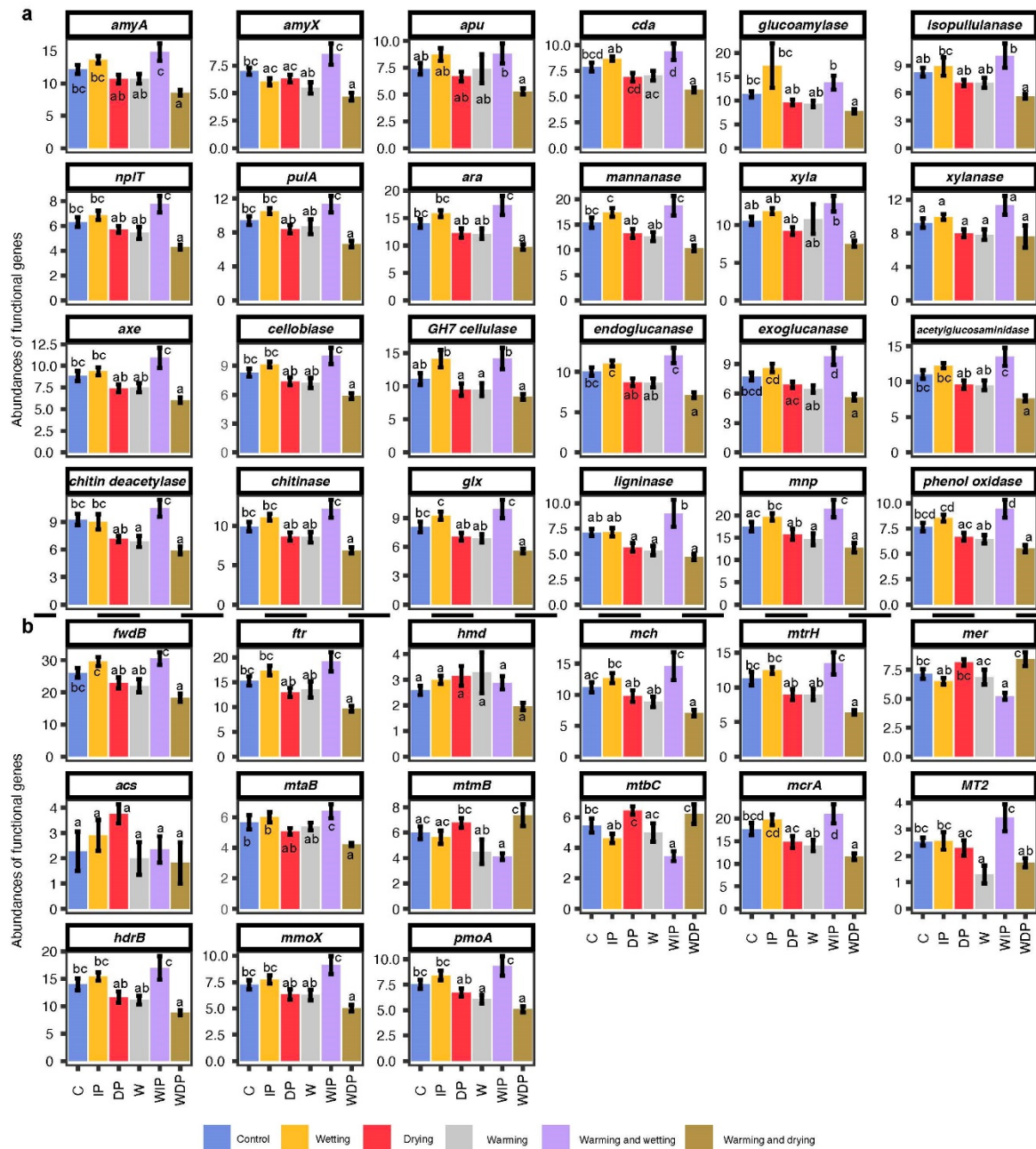
Fig. S1 The MBC-normalized abundances of microbial functional genes associated with carbon degradation (a) and methane cycling (b). Functional genes associated with starch degradation (*amyA*, *amyX*, *apu*, *cda*, *glucoamylase*, *isopullulanase*, *nplT,* and *pulA*); hemicellulose degradation (*ara*, *mannanase*, *xylA,* and *xylanase*); cellulose degradation (*axe, cellobiase, GH7 cellulase, endoglucanase,* and *exoglucanase*); chitin degradation (*acetylglucosaminidase, chitin deacetylase,* and *chitinase*); lignin degradation (*glx, ligninase, mnp,* and *phenol oxidase*); methanogenesis (*fwdB, ftr, hmd, mch, mtrH, mer, acs, mtaB,*

mtmB, mtbC, mcrA, MT2, and hdrB) and methane oxidation (*mmoX* and *pmoA*) are shown.

Different alphabets on the bars were calculated by post-hoc Tukey's honest significant

difference test with a linear mixed-effects model ($P < 0.050$).
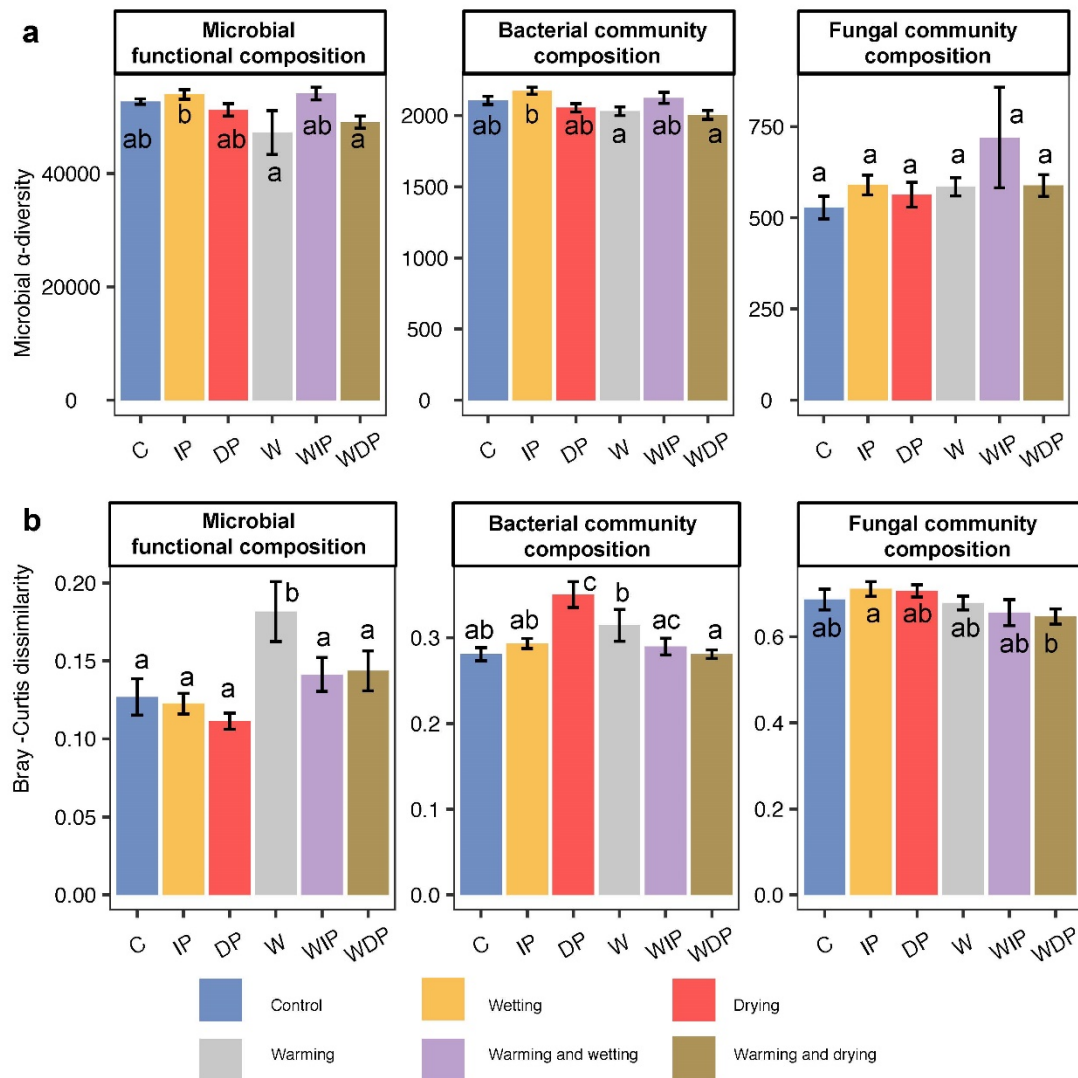
Fig. S2 α-diversity (a) and mean Bray-Curtis weighted dissimilarities (b) of soil microbial communities under different treatments. Different alphabets on the bars associated with α-diversity were calculated by post-hoc Tukey's honest significant difference test with a linear mixed-effects model ($P < 0.050$). Different alphabets on the bars associated with within-group dissimilarities were calculated by Kruskal-Wallis H-test ($P < 0.050$). The dissimilarity of within-group samples was calculated as mean Bray-Curtis weighted dissimilarities between pairs of replicates in a group.

Table S3. Correlations between carbon fluxes and relative abundances of microbial

functional genes

Carbon fluxes	Category	Subcategory	Gene	r	P
	Carbon degradation	Starch	*amyA*	0.65	0.001**[b]
	Carbon degradation	Starch	*amyX*	0.30	0.588
	Carbon degradation	Starch	*apu*	0.29	0.588
	Carbon degradation	Starch	*cda*	0.63	0.002**
	Carbon degradation	Starch	*glucoamylase*	0.23	0.749
	Carbon degradation	Starch	*isopullulanase*	0.48	0.035*
	Carbon degradation	Starch	*nplT*	0.55	0.011*
	Carbon degradation	Starch	*pulA*	0.61	0.003**
	Carbon degradation	Hemicellulose	*ara*	0.65	0.001**
	Carbon degradation	Hemicellulose	*mannanase*	0.68	< 0.001***
	Carbon degradation	Hemicellulose	*xylA*	0.62	0.002**
CO_2[a]	Carbon degradation	Hemicellulose	*xylanase*	0.35	0.320
	Carbon degradation	Cellulose	*axe*	0.66	0.001**
	Carbon degradation	Cellulose	*cellobiase*	0.61	0.003**
	Carbon degradation	Cellulose	*GH7 cellulase*	0.62	0.003**
	Carbon degradation	Cellulose	*endoglucanase*	0.64	0.002**
	Carbon degradation	Cellulose	*exoglucanase*	0.61	0.003**
	Carbon degradation	Chitin	*acetylglucosaminidase*	0.64	0.002**
	Carbon degradation	Chitin	*chitin deacetylase*	0.59	0.004**
	Carbon degradation	Chitin	*chitinase*	0.64	0.002**
	Carbon degradation	Lignin	*glx*	0.63	0.002**
	Carbon degradation	Lignin	*ligninase*	0.55	0.011*
	Carbon degradation	Lignin	*mnp*	0.53	0.014*
	Carbon degradation	Lignin	*phenol oxidase*	0.61	0.003**
	Methane	Methanogenesis	*fwdB*	0.48	0.050
CH_4	Methane	Methanogenesis	*ftr*	0.64	0.001**
	Methane	Methanogenesis	*hmd*	0.21	0.999

Methane	Methanogenesis	*mch*	0.48	0.050
Methane	Methanogenesis	*mtrH*	0.66	< 0.001***
Methane	Methanogenesis	*mer*	0.42	0.098
Methane	Methanogenesis	*acs*	0.03	0.999
Methane	Methanogenesis	*mtaB*	0.13	0.999
Methane	Methanogenesis	*mtmB*	0.05	0.999
Methane	Methanogenesis	*mtbC*	0.49	0.039*
Methane	Methanogenesis	*mcrA*	0.56	0.008**
Methane	Methanogenesis	*MT2*	0.21	0.999
Methane	Methanogenesis	*hdrB*	0.57	0.006**
Methane	Methanotrophy	*mmoX*	0.45	0.078
Methane	Methanotrophy	*pmoA*	0.42	0.100

[a]Abbreviations: CO_2, soil CO_2 flux; CH_4, soil CH_4 flux.

[b]Significance is indicated by *$P < 0.050$; **$P < 0.010$; ***$P < 0.001$

Table S4. Correlations between carbon fluxes and the MBC-normalized abundances of major bacterial and fungal taxa

		CO_2[a]		CH_4		NEE	
		r	P	r	P	r	P
Bacterial phylum	*Acidobacteria*	0.27	0.366	0.44	0.046*[b]	-0.39	0.100
	Actinobacteria	0.02	0.935	0.17	0.564	-0.04	0.908
	Bacteroidetes	0.47	0.024*	0.55	< 0.001***	-0.35	0.169
	Candidate division WPS 1	0.11	0.736	0.14	0.635	0.05	0.902
	Firmicutes	-0.10	0.736	-0.04	0.908	0.12	0.705
	Gemmatimonadetes	-0.05	0.898	0.08	0.793	-0.32	0.221
	Latescibacteria	0.16	0.594	0.23	0.434	-0.56	< 0.001***
	Nitrospirae	-0.18	0.564	-0.05	0.902	-0.19	0.550
	Proteobacteria	0.57	< 0.001***	0.71	< 0.001***	-0.53	0.013*
	Verrucomicrobia	0.23	0.434	0.17	0.564	-0.17	0.564
Bacterial genus	*Agromyces*	-0.06	0.875	0.12	0.685	0.04	0.908
	Asanoa	0.15	0.632	0.19	0.550	0.00	0.987
	Blastococcus	0.06	0.882	0.19	0.550	0.02	0.947
	Bradyrhizobium	0.26	0.366	0.42	0.068	-0.25	0.398
	Nitrosospira	0.32	0.221	0.48	0.036*	-0.44	0.052
	Oryzihumus	0.22	0.465	0.33	0.210	-0.04	0.908
	Phyllobacterium	-0.12	0.692	0.30	0.249	-0.04	0.908
	Pseudonocardia	0.33	0.210	0.41	0.077	-0.16	0.594

		CO₂		CH₄		NEE	

	Rhizobacter	0.48	0.024*	0.52	0.013*	-0.48	0.024*
	Variovorax	0.54	0.013*	0.51	0.013*	-0.38	0.115
Fungal phylum	*Ascomycota*	0.26	0.366	0.23	0.434	-0.44	0.046*
	Basidiomycota	0.17	0.564	0.30	0.257	-0.02	0.940
	Chytridiomycota	-0.09	0.763	-0.13	0.661	0.13	0.661
	Glomeromycota	-0.09	0.763	-0.18	0.564	0.17	0.564
	Zygomycota	0.29	0.302	0.47	0.024*	-0.30	0.249
Fungal genus	*Chalara*	0.23	0.434	0.24	0.404	-0.26	0.366
	Davidiella	-0.16	0.594	-0.10	0.750	-0.19	0.564
	Eurotiales	0.12	0.705	-0.11	0.705	-0.22	0.447
	Eurotiomycetes	0.07	0.839	0.13	0.661	0.10	0.761
	Herpotrichiellaceae	-0.04	0.908	-0.02	0.940	-0.17	0.564
	Hygrocybe	-0.03	0.935	0.18	0.564	0.13	0.661
	Leptosphaeria	0.25	0.384	0.32	0.221	-0.02	0.935
	Ramariopsis	0.36	0.158	0.05	0.908	-0.41	0.076
	Tetracladium	0.16	0.594	0.24	0.415	-0.26	0.366
	Tricholoma	-0.01	0.978	-0.15	0.632	0.09	0.763

[a]Abbreviations: CO₂, soil CO₂ flux; CH₄, soil CH₄ flux; NEE, net ecosystem exchange

[b]Significance is indicated by *$P < 0.050$; **$P < 0.010$; ***$P < 0.001$
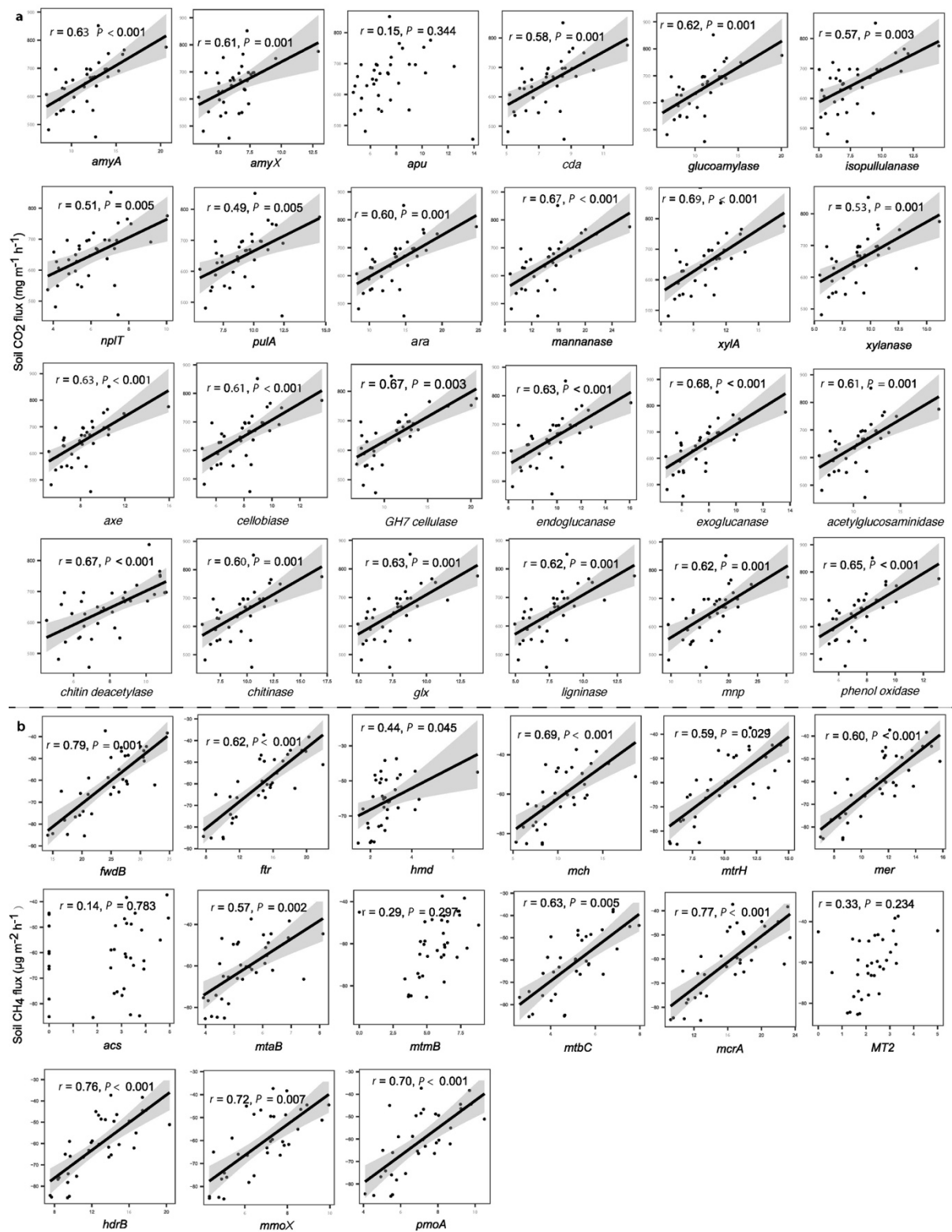
Fig. S3 Correlations between soil carbon fluxes and the MBC-normalized abundances of microbial functional genes. Correlations between soil CO₂ flux and the MBC-normalized abundances of microbial functional genes associated with starch degradation (*amyA*, *amyX*, *apu*, *cda*, *glucoamylase*, *isopullulanase*, *nplT,* and *pulA*), hemicellulose degradation (*ara*,

mannanase, *xylA,* and *xylanase*), cellulose degradation (*axe*, *cellobiase*, *GH7 cellulase*, *endoglucanase,* and *exoglucanase*), chitin degradation (*acetylglucosaminidase*, *chitin deacetylase,* and *chitinase*), lignin degradation (*glx*, *ligninase*, *mnp,* and *phenol oxidase*) (a)**.** Correlations between soil CH_4 flux and the MBC-normalized abundances of microbial functional genes associated with methanogenesis (*fwdB*, *ftr*, *hmd*, *mch*, *mtrH*, *mer, acs, mtaB*, *mtmB, mtbC, mcrA, MT2,* and *hdrB*) and methanotrophy (*mmoX* and *pmoA*) (b)**.**

Table S5. Linkages between soil carbon fluxes and microbial functional genes, plant variables, and soil variables based on multiple regression on distance matrices

	Functional composition[a]	Plant	Soil	Model R^2	F values	Model P-value
CO_2	249.17 (0.038)*[b]	13.56 (0.002)**	6.15 (0.149)	0.23	63.55	0.001***
CH_4	29.45 (0.019)*	0.83 (0.070)	2.38 (0.001)***	0.19	49.87	0.001***
NEE	6.20 (0.048)*	0.13 (0.277)	0.08 (0.448)	0.08	20.43	0.043*

[a]Microbial functional composition associated with carbon degradation was used to detect linkages with soil CO_2 flux and net ecosystem exchange (NEE); microbial functional composition associated with methane cycling was used to reveal linkages with soil CH_4 flux. Soil variables include soil clay content, soil silt content, soil sandy content, soil pH, soil water content, soil total carbon, soil total nitrogen, soil total phosphorus, soil organic carbon, soil nitrate, soil ammonia, soil available phosphorus, dissolved organic carbon and dissolved organic nitrogen. Plant variables include aboveground and belowground net primary production and plant Shannon diversity.

[b]Regression coefficients are shown. The values in brackets are P-values from permutation tests. Significance is indicated by *$P < 0.050$; **$P < 0.010$; ***$P < 0.001$.

Table S6. R^2 values and standardized coefficients of predictors based on linear mixed-effects models

CO_2[a]		CH_4		NEE	
R^2.f	0.53	R^2.f	0.60	R^2.f	0.62
R^2.fr	0.69	R^2.fr	0.60	R^2.fr	0.73
Carbon degradation	0.69***[b]	Methanogenesis	0.74***	Carbon degradation	0.19***
ANPP	0.58*	Methanotrophy	0.34	ANPP	0.10***
SOC	0.54	SWC	0.06	BNPP	-0.02
		ST	0.00		

[a]Abbreviations: CO_2, soil CO_2 flux; CH_4, soil CH_4 flux; NEE, net ecosystem exchange; R^2.f, model R^2 values considering fixed effects for carbon fluxes (see *Materials and Methods* for details); R^2.fr, model R^2 values considering both fixed and random effects; carbon degradation, the MBC-normalized abundance of functional genes associated with carbon degradation; methanogenesis: the MBC-normalized abundance of functional genes associated with methanogenesis; methanotrophy: the MBC-normalized abundance of functional genes associated with methanotrophy; ANPP, aboveground net primary production; SOC, soil organic carbon; SWC, soil water content; ST, soil temperature; BNPP, belowground net primary production. The abundance of functional genes associated with carbon degradation, ANPP and SOC were used to predict soil CO_2 flux; The abundance of functional genes associated with methanogenesis and methanotrophy, SWC and ST were used to predict soil CH_4 flux; The MBC-normalized

abundance of functional genes associated with carbon degradation, ANPP and BNPP were used to predict NEE. All square-root VIFs are less than 2.

[b]Standardized coefficient values are shown. Significance of standardized coefficient was calculated by ANOVA and indicated by $*P < 0.050$; $**P < 0.010$; $***P < 0.001$.

Table S7. Procrustes analyses between microbial functional and taxonomic compositions

	Sum of squares[a]	r	P
GeoChip - 16S[b]	0.997	0.05	0.885
GeoChip - ITS	0.986	0.11	0.528
16S - ITS	0.878	0.34	0.019

[a] Sum of squares, Procrustes sum of squares (m12 squared); *r*, the correlation coefficient in symmetric Procrustes rotation; *P*, the significance of a Procrustes analysis calculated by permutation tests.

[b]GeoChip - 16S, the Procrustes analysis between microbial functional composition and bacterial community composition; GeoChip - ITS, the Procrustes analysis between microbial functional composition and fungal community composition; 16S - ITS, the Procrustes analysis between bacterial community composition and fungal community composition.