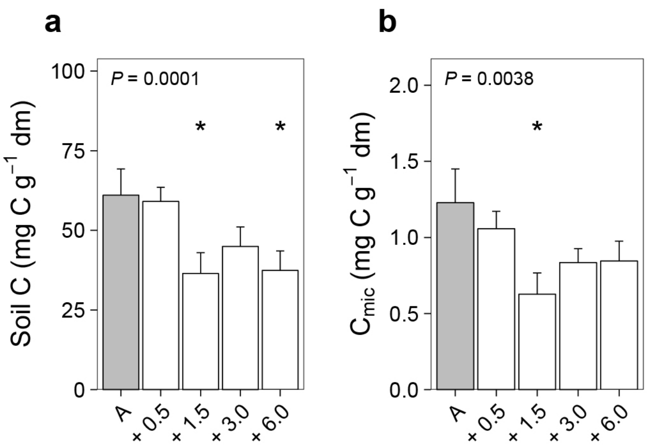
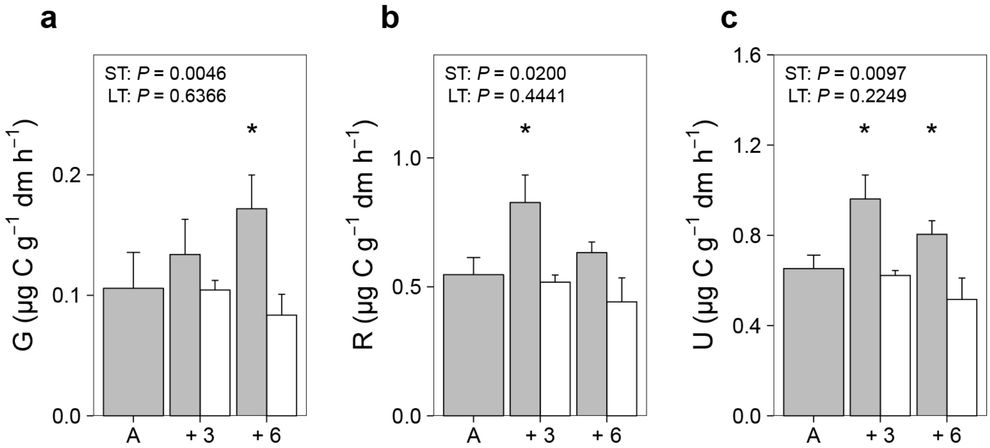
Microbial temperature sensitivity and biomass change explain soil carbon loss with warming

Tom W. N. Walker, Christina Kaiser, Florian Strasser, Craig W. Herbold, Niki I. W. Leblans, Dagmar Woebken, Ivan A. Janssens, Bjarni D. Sigurdsson and Andreas Richter

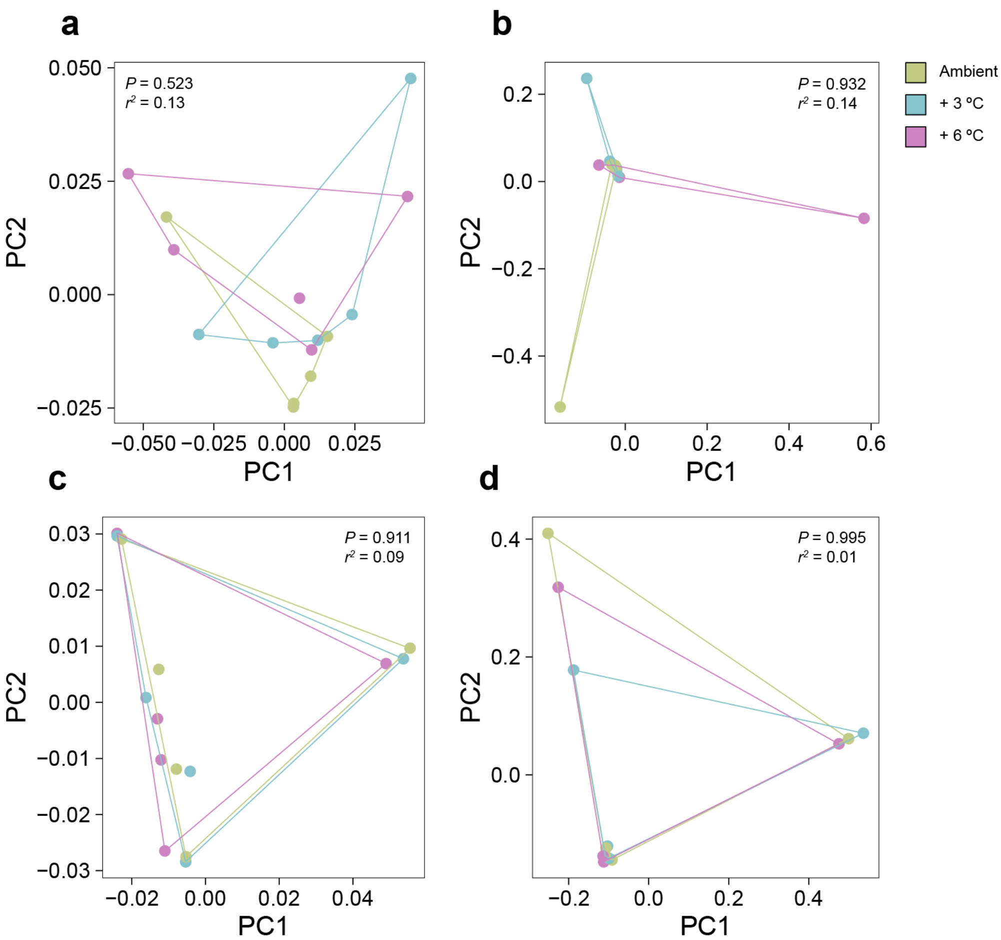
SUPPLEMENTARY INFORMATION



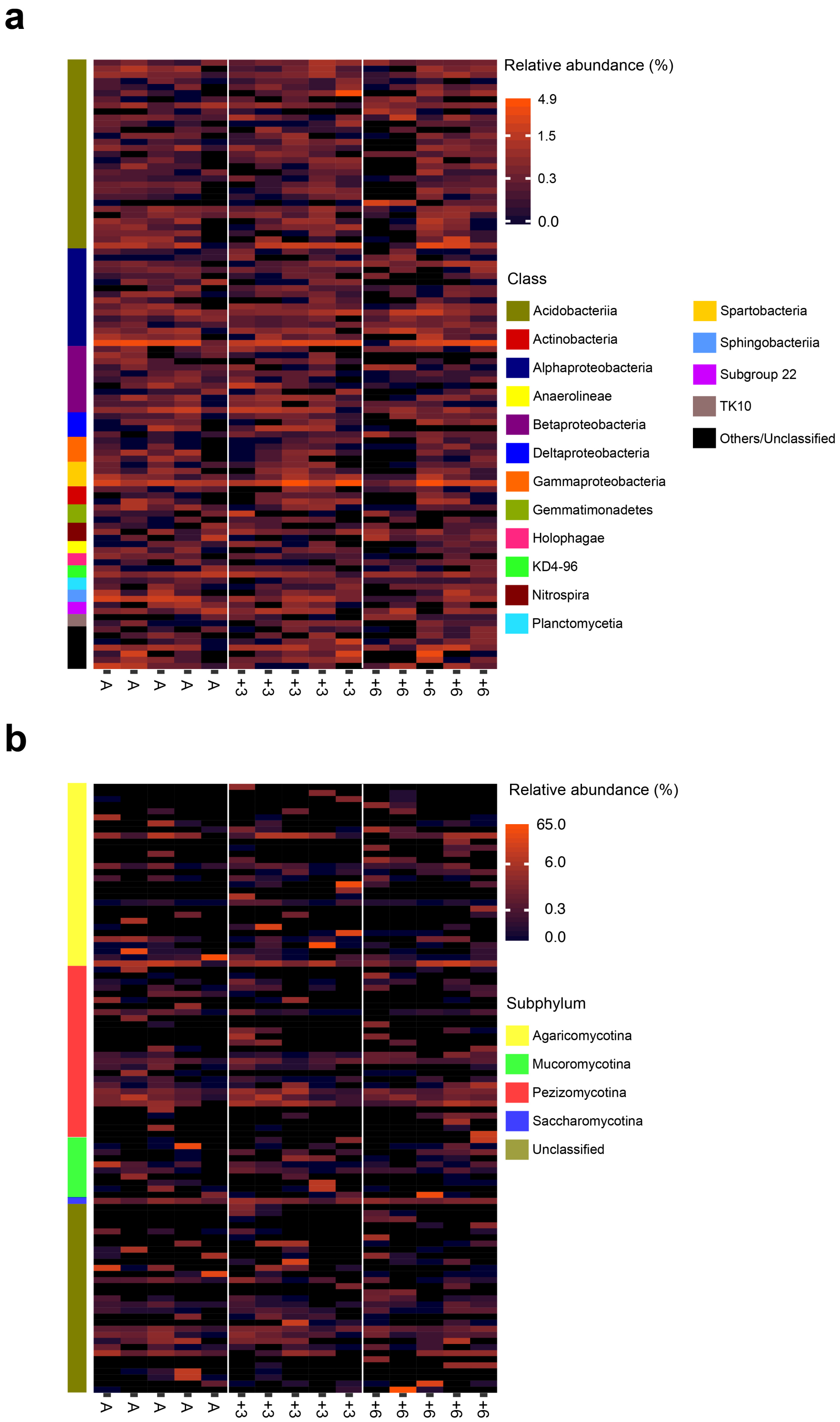
Supplementary Fig. S1. Soil carbon pool responses to long-term warming. Mean (± SE; n = 5) (a) soil carbon content (mg C g^{-1} soil dry mass); and (b) microbial biomass C (C_{mic}; mg C g^{-1} soil dry mass) of soils following exposure to at least 50 years of ambient temperature (A; grey bars) or warming of between 0.5 ºC and 6 ºC (white bars). Asterisks indicate significant differences between ambient and warmed temperatures.



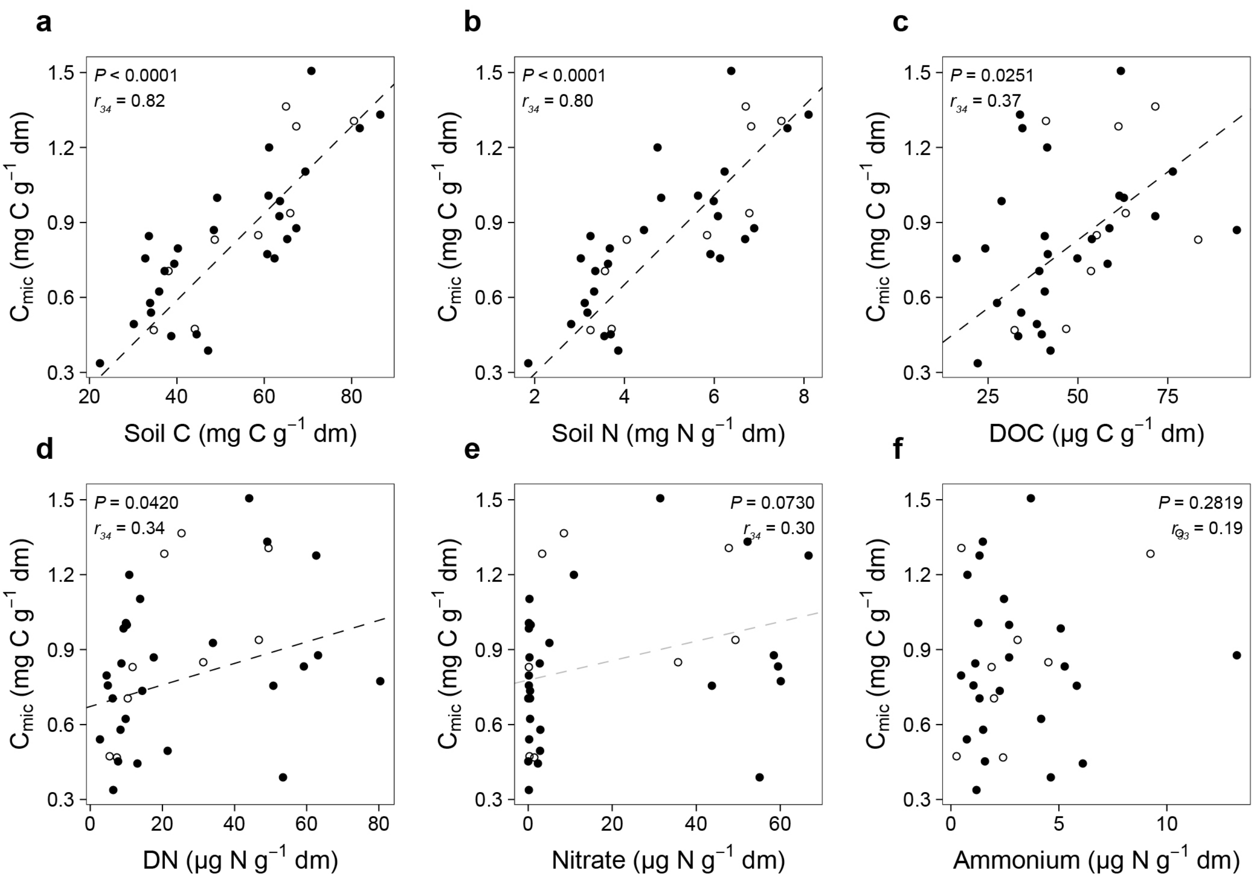
Supplementary Fig. S2. Soil microbial responses to laboratory warming. Mean (± SE; n = 5) (a) total microbial growth (G; µg C g^{-1} soil dry mass h^{-1}); (b) total microbial respiration (R; µg C g^{-1} soil dry mass h^{-1}); and (c) total microbial C uptake (U; µg C g^{-1} soil dry mass h^{-1}) of soils from ambient (A; grey bars), + 3 ºC or + 6 ºC (white bars) field temperature following six weeks of incubation at ambient temperature (11 ºC), + 3 ºC and + 6 ºC. *P*-values show significance of warming effects on ambient field soils only (ST; i.e. short-term warming) and ambient versus warmed field soils (LT: i.e. long-term warming), with asterisks indicating significant differences ($P < 0.05$) between ambient and warmed temperatures.



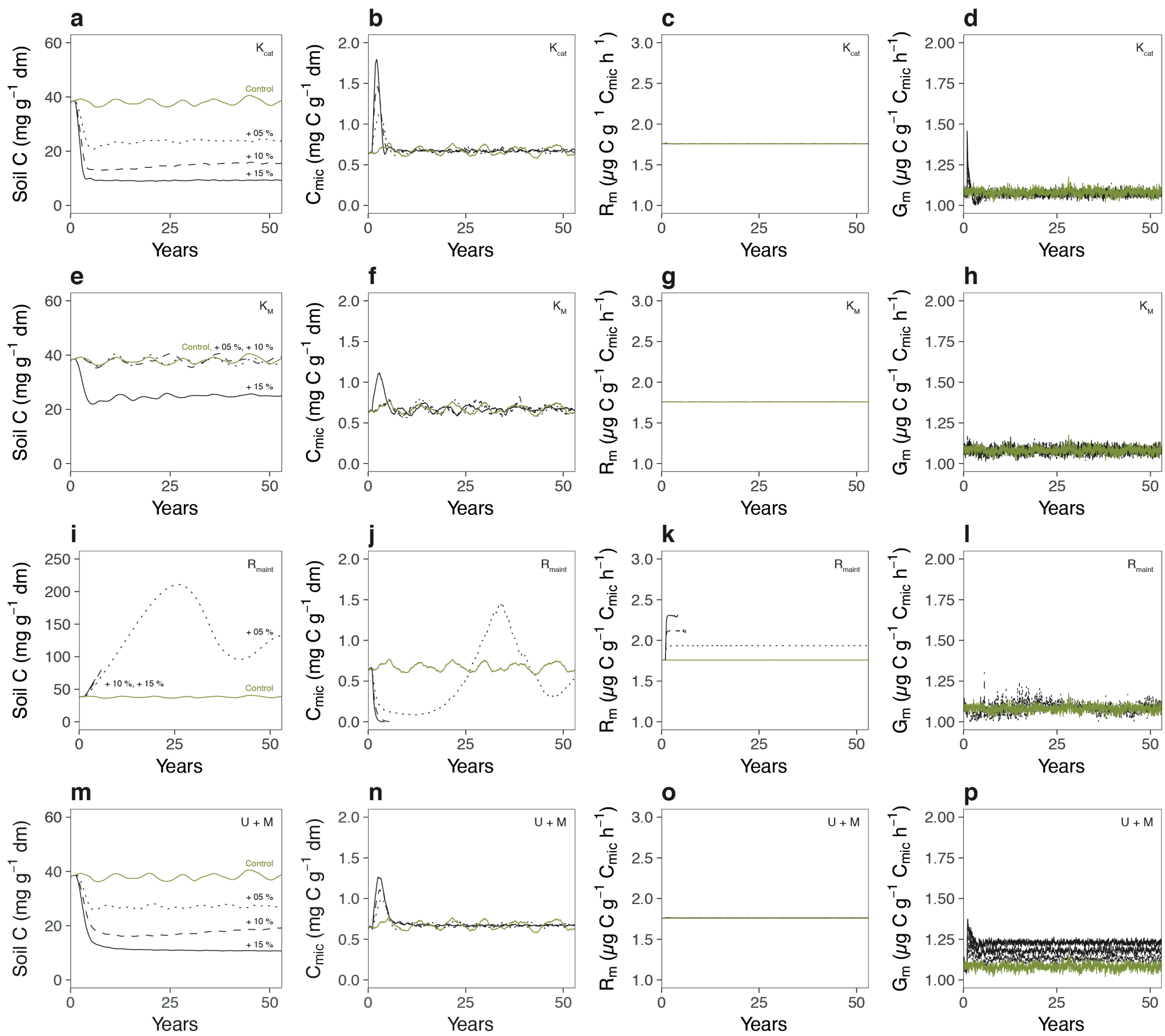
Supplementary Fig. S3. Long-term and short-term warming effects on soil microbial community composition. PCA plots showing the distribution of (a,c) bacterial/archaeal and (b,d) fungal OTUs across principal components (PCs) 1 and 2 for soils subjected to either (a,b) 50 years or (b,d) six-weeks of ambient temperature (A; green) or warming of 3 ºC (blue) and 6 ºC (purple). *P*-values illustrate the significance of differences between temperatures as determined by PERMANOVAs (Methods). Visual similarities between distributions illustrated in (c,d) emerged because transect identity, not incubation temperature, drove most variation observed between bacterial/archaeal (r^2 = 0.64, P = 0.001) and fungal (r^2 = 0.60, P = 0.017) OTUs.



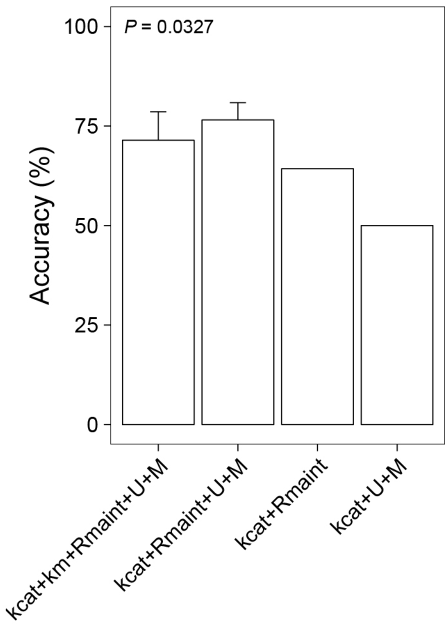
Supplementary Fig. S4. The relative abundance of microbial taxa under long-term warming, showing no consistent changes in microbial community structure with temperature. Heatmaps illustrating the relative abundance (%) of the 100 most abundant (a) bacterial and (b) fungal OTUs in soils exposed to more than 50 years of warming (A: ambient, + 3 ºC, + 6 ºC). OTUs (rows) are clustered by class for bacteria/archaea and by subphylum for fungi, and data are shown for all plots separately (columns) clustered by field temperature, with numbers representing different replicate blocks.



Supplementary Fig. S5. Associations between microbial biomass and soil carbon and nitrogen pools. Microbial biomass C (C_{mic}; mg C g^{-1} soil dry mass) against (a) soil carbon content (mg C g^{-1} soil dry mass), (b) soil nitrogen content (mg N g^{-1} soil dry mass), (c) dissolved organic carbon (DOC; µg C g^{-1} soil dry mass), (d) dissolved nitrogen (DN; µg N g^{-1} soil dry mass), (e) nitrate nitrogen (µg N g^{-1} soil dry mass), and (f) ammonium nitrogen (µg N g^{-1} soil dry mass). Pearson correlations were performed on field and incubation data irrespective of warming intensity (warmed: black points, ambient: white points), with black lines showing significant (P < 0.05) correlations and grey lines showing marginally significant (P < 0.1) correlations.



Supplementary Fig. S6. Simulated responses to microbial physiology. Mean (n = 3) modelled responses of (a,e,I,m) soil carbon content (mg g^{-1} soil dry mass), (b,f,j,n) microbial biomass C (C_{mic}; mg C g^{-1} soil dry mass), (c,g,k,o) mass-specific microbial respiration (R; μg C g^{-1} C_{mic} h^{-1}) and (d,h,l,p) mass-specific microbial growth (G_m; μg C g^{-1} C_{mic} h^{-1}) to 50 years of accelerated microbial physiology (black lines) or a control scenario (green lines). We modelled 5 % (dotted line), 10 % (dashed line) and 15 % (solid line) increases in (a-d) extracellular enzyme efficiency (K_{cat}), (e-h) extracellular enzyme substrate affinity (K_M), (i-l) maintenance respiration (R_{maint}) or (m-p) maximum uptake and mortality (U+M). For (i-l), increases of more than 5 % caused a collapse of microbial biomass within 5 years.



Supplementary Fig. S7. Accuracy of multiple parameter model scenarios. Mean accuracy (% ± SE) of model scenarios involving combinations of extracellular enzyme efficiency (k_{cat}, k_M), maintenance respiration (R_{maint}), maximal uptake (U) and mortality (M). Accuracy was calculated as the percentage of output parameters matching the direction of equivalent empirical responses to warming on both short-term (i.e. six weeks) and long-term (i.e. at least 50 years) timescales (Methods). *P*-value indicates significance ($P < 0.05$) of differences between scenarios.

Table S1. Comparison of key carbon and nitrogen pools and fluxes between the model at steady state and observations from ambient temperature field plots.

Flux, pool or factor	Unit	Model at steady-state*	Ambient soil**
Soil C	mg C g^{-1} soil	37.45 (0.573)	61.04 (18.470)
Soil C:N	Ratio	17.55 (0.122)	10.56 (0.923)
Microbial biomass C	mg C g^{-1} soil	0.654 (0.032)	1.228 (0.496)
Microbial C per soil C	mg microbial C mg^{-1} soil C	0.017 (0.001)	0.020 (0.002)
Heterotrophic respiration	µg C g^{-1} soil $hour^{-1}$	1.149 (0.029)	1.062 (0.396)
Biomass-specific respiration	µg C mg^{-1} microbial biomass C $hour^{-1}$	1.758 (0.000)	0.898 (0.212)
Microbial growth	µg C g^{-1} soil $hour^{-1}$	0.707 (0.017)	0.341 (0.117)
Turnover rate (biomass-specific growth)	fraction of microbial biomass day^{-1}	0.026 (0.000)	0.007 (0.001)
Carbon use efficiency		0.381 (0.001)	0.244 (0.028)

*Simulated: means (± SD) of carbon pools and fluxes (averaged over a 1.5 year period) of three replicate control model scenarios. Values were aggregated over the grid volume and calculated on a per gram soil basis assuming a bulk density of 0.73 g dry soil cm^{-3} (data not shown).
**Measured.

Table S2. Parameter settings used for the spin-up runs and control scenario. Parameters in bold/italic were altered for "warmed" scenarios as described in Table S3.

Parameter	Description	Unit	Value
Enzyme kinetics[+]			
$\boldsymbol{k_{cat\_PS}}$	catalytic efficiency (kcat) of enzymes degrading primary substrate (plant material)	fmol C $enzyme^{-1}$ $hour^{-1}$	1.722
$\boldsymbol{k_{cat\_CMR}}$	kcat of enzymes degrading C-rich microbial remains	fmol C $enzyme^{-1}$ $hour^{-1}$	1.722
$\boldsymbol{k_{cat\_NMR}}$	kcat of enzymes degrading N-rich microbial remains	fmol C $enzyme^{-1}$ $hour^{-1}$	1.890
$\boldsymbol{K_{M\_PS}}$	K_M (substrate concentration at which reaction rate is half-maximal) of primary substrate	nmol C mm^{-3}	8
$\boldsymbol{K_{M\_CMR}}$	K_M C-rich microbial remains	nmol C mm^{-3}	8
$\boldsymbol{K_{M\_NMR}}$	K_M N-rich microbial remains	nmol C mm^{-3}	8
k_{enz}	First order rate constant for inactivation of enzymes	$hour^{-1}$	0.0009375
Microbial physiology[ξ]			
$\boldsymbol{R_{maint}}$	Maintenance respiration	Fraction of biomass $hour^{-1}$	0.001725
R_{ge}	Respiration for growth and enzyme production	Fraction of C used for growth/enzyme production	0.030000
$\boldsymbol{U_{max}}$	Basic maximum uptake rate (to be multiplied with individual surface:volume ratio)	Fraction of biomass $hour^{-1}$	0.001159
$\boldsymbol{M}$	Mortality rate	Probability to die $hour^{-1}$	0.00106875
E_{fr}[£]	Fraction of C uptake used for enzyme production (after deduction of maintenance respiration)		0.00156250
Maximum cell size and colony density[α]			
C_{max}	Size at which a microbial cell divides and colonizes a neighbouring microsite	fmol C $cell^{-1}$	4
C_{min}	Lower cell limit (below it, cells die from starving)	fmol C $cell^{-1}$	0.4
C_{col}	Maximal density of microbial cells in each microsite	Cells μm^{-1}	0.032
Microbial cell composition and stoichiometry[δ]			
F_{DOM}	Cell solubles	Fraction of biomass	0.06
F_{CC}	C-rich complex compounds (f.e. cell wall compounds, lipids, starch)	Fraction of biomass	0.52
F_{NC}	N-rich complex compounds (proteins, DNA, RNA)	Fraction of biomass	0.42
M_{cn}[β]	C/N ratio of microbial cells	Ratio	9.03
Initial values (for the spin-up)			
C_{enz}	Extracellular enzymes	nmol C mm^{-3}	4
C_{CMR}	C-rich microbial remains	nmol C mm^{-3}	400
C_{NMR}	N-rich microbial remains	nmol C mm^{-3}	80
C_{DOM}*	Bioavailable dissolved organic matter	nmol C mm^{-3}	56
C_{PS}	Primary substrate (plant material)	nmol C mm^{-3}	16000
Continuous input of organic matter			
I_{PS}	Input of plant-derived organic matter	nmol C mm^{-3} $hour^{-1}$	0.072
CN_{PS}	C/N ratio of PS_{input}		40
Translocation of solubles			
D_0	Diffusion rate of soluble organic compounds[γ]	cm^2 sec^{-1}	7.5×10^{-9}
F_L	Fraction of diffusing soluble compounds that is lost by leaching		0.000375
W	Water level	μm^3 μm^{-3}	0.18
Model dimensions			
L_{MS}	Microsite length	µm	5
L_G	Soil grid length	Microsites	200
L_{TS}	Time step length	min	30

[+]Within the range reported[1,2]
[ξ] Maintenance respiration and maximum uptake rates derived from ranges of specific maintenance rates and maximum relative growth rates[3]
[α] Refs[4-7]
[£]Ratio of enzyme production is 0:64:0.18:0.18 for plant-derived organic matter: C-rich microbial remains: N-rich microbial remains degrading enzymes
[δ8]

[β]Microbial C/N ratio is calculated from the chemical composition of the total biomass, assuming that F_{dom}, F_{CC} and F_{NC} have C:N ratios of 15,150 and 5, respectively[9]
*C_{DOM} has an initial C/N ratio of 8.
[γ] Effective diffusion rate is calculated by multiplying the basic diffusion rate (D0) with an impedance factor that is related to the water level (IF = 0.67 x W – 0.102, where IF is the impedance factor and W is the volumetric water content in μm/μm. Adapted from ref. [10] based on a bulk density of 0.73). The distance a particle can travel per time step in a random walk ("jumpsize") is then calculated based on the effective diffusion rate (~10 μm, which corresponds to 2 microsites in this model). For details see ref. [11].

Table S3 (overleaf). Short-term and long-term responses of modelled pools and fluxes to sudden changes in microbial and biochemical parameters that accompany rising soil temperatures. Scenarios considered singular and combined increases to enzyme kinetics (k_{cat}, k_M) and/or microbial activity (maintenance respiration (R_{maint}), maximum microbial uptake (U_{max}), and microbial mortality). All scenarios started from the same spin-up run (see Supplementary Tables S1 and S2 for spin-up parameter settings and resulting steady state conditions, respectively). Parameter changes induced in scenarios are expressed as fractions of spin-up (i.e. control) parameters (e.g. 0.05 represents a 5 % increase relative the control value shown in Supplementary Table S1). The control scenario was allowed to run without constraint from the spin-up with no induced parameter changes. Responses are presented as proportional differences between each scenario and the control scenario within the same time period (i.e. -0.05 represents a 5 % decrease). Model outputs were aggregated over the whole grid and means (± SE, n = 3) were taken for three time periods: (i) 40 to 50 days (approx. six weeks; short-term response); (ii) 1.5 to 3 years (peak short-term response); and (iii) 49.5 to 50.5 years (long-term response) (Methods). Soil C: total carbon stock (mg C g^{-1} soil); C/N: soil carbon to nitrogen ratio; C_{mic}: microbial biomass carbon (mg C g^{-1} soil); DOC: dissolved organic carbon (ug C g^{-1} soil); CUE: community carbon use efficiency, calculated as CUE = (U_{DOC}-R-P_{ENZ})/U_{DOC}, where U_{DOC} is total amount of DOC taken up by all microbes on the grid, R is the total amount of carbon respired and P_{ENZ} is the total amount of carbon released as extracellular enzymes; R: total microbial respiration (ug C g^{-1} soil h^{-1}); G: total microbial growth (ug C g^{-1} soil h^{-1}); R_{mic}: mass-specific microbial respiration (mg C g C_{mic} h^{-1}); G_{mic}: mass-specific microbial growth (fraction of C_{mic} day^{-1}). Coloured bars visualize relative changes within each time period (blue: positive change, orange: negative change), scaled for each response separately.

Short-term response (40-50 days after change)
(relative difference to control as fraction of the control scenario)

	Parameter change (fraction of control)						Soil C		C/N		Cmic		DOC		CUE		R		G		R_{sub}		R_{mic}		G_{mic}	
	Scenario #	K_{cat}	K_m	R_{maint}	U_{max}	M	aver.	stderr	aver.	stderr	aver.	stderr	aver.	stderr	aver.	stderr	aver.	stderr	aver.	stderr	aver.	stderr	aver.	stderr	aver.	stderr
Contr.	0						0.00	0.00	0.00	0.00	0.00	0.02	0.00	0.01	0.00	0.00	0.00	0.02	0.00	0.02	0.00	0.02	0.00	0.00	0.00	0.01
Enzyme kinetics	1	0.05					0.00	0.00	0.00	0.00	0.11	0.01	0.01	0.01	0.05	0.01	0.12	0.01	0.21	0.00	0.12	0.01	0.00	0.00	0.09	0.01
	2	0.10					-0.01	0.00	-0.01	0.00	0.26	0.01	-0.01	0.02	0.10	0.01	0.27	0.01	0.49	0.02	0.27	0.01	0.00	0.00	0.18	0.01
	3	0.15					-0.01	0.00	-0.01	0.00	0.37	0.01	0.00	0.02	0.13	0.00	0.38	0.01	0.70	0.02	0.39	0.02	0.00	0.00	0.24	0.00
	4		0.05				0.00	0.00	0.00	0.00	0.00	0.01	0.01	0.01	0.00	0.00	0.01	0.01	0.01	0.01	0.01	0.01	0.00	0.00	0.01	0.01
	5		0.10				0.00	0.00	0.00	0.00	0.07	0.05	0.01	0.00	0.04	0.02	0.07	0.05	0.14	0.08	0.08	0.05	0.00	0.00	0.06	0.03
	6		0.15				0.00	0.00	0.00	0.00	-0.03	0.01	0.00	0.00	0.00	0.01	-0.03	0.01	-0.02	0.03	-0.03	0.01	0.00	0.00	0.00	0.02
	7		1.00				0.00	0.00	0.00	0.00	-0.08	0.00	0.01	0.01	-0.01	0.00	-0.09	0.00	-0.10	0.01	-0.09	0.01	0.00	0.00	-0.01	0.00
Microbial physiology	8			0.05			0.00	0.00	0.00	0.00	-0.05	0.01	0.02	0.00	-0.09	0.01	0.01	0.01	-0.13	0.02	0.01	0.01	0.06	0.00	-0.08	0.01
	9			0.10			0.00	0.00	0.00	0.00	-0.14	0.01	0.06	0.01	-0.16	0.01	-0.03	0.01	-0.25	0.00	-0.03	0.02	0.13	0.00	-0.13	0.01
	10			0.15			0.00	0.00	0.00	0.00	-0.16	0.02	0.05	0.01	-0.26	0.01	0.00	0.02	-0.36	0.02	0.00	0.02	0.19	0.00	-0.24	0.01
	11				0.05	0.05	0.00	0.00	0.00	0.00	-0.02	0.01	0.03	0.01	0.06	0.00	-0.01	0.01	0.08	0.01	-0.01	0.02	0.00	0.00	0.10	0.01
	12				0.10	0.10	0.00	0.00	0.00	0.00	0.00	0.02	0.06	0.01	0.09	0.01	0.00	0.02	0.16	0.03	0.00	0.02	0.00	0.00	0.16	0.01
	13				0.15	0.15	0.00	0.00	0.00	0.00	-0.01	0.00	0.07	0.02	0.14	0.01	0.00	0.00	0.24	0.01	0.00	0.00	0.00	0.00	0.24	0.01
Mixed Scenarios	14	0.10		0.05			0.00	0.00	0.00	0.00	0.16	0.01	0.02	0.01	0.01	0.01	0.24	0.01	0.26	0.01	0.25	0.02	0.07	0.00	0.08	0.01
	15	0.15		0.10			-0.01	0.00	-0.01	0.00	0.20	0.02	0.06	0.01	-0.04	0.00	0.36	0.02	0.28	0.02	0.37	0.02	0.13	0.00	0.07	0.00
	16	0.10			0.05	0.05	0.00	0.00	-0.01	0.00	0.24	0.01	0.03	0.00	0.14	0.00	0.25	0.01	0.55	0.01	0.25	0.01	0.00	0.00	0.25	0.00
	17	0.15			0.10	0.10	0.00	0.00	-0.01	0.00	0.38	0.02	0.04	0.02	0.20	0.00	0.39	0.02	0.90	0.02	0.40	0.02	0.01	0.00	0.37	0.01
	18	0.10		0.05	0.05	0.05	0.00	0.00	0.00	0.00	0.16	0.02	0.06	0.01	0.05	0.00	0.25	0.01	0.35	0.01	0.25	0.01	0.07	0.00	0.16	0.00
	19	0.15		0.10	0.05	0.05	0.00	0.00	0.00	0.00	0.19	0.02	0.08	0.01	0.00	0.00	0.35	0.02	0.36	0.02	0.36	0.02	0.14	0.00	0.15	0.01
	20	0.15		0.05	0.10	0.10	-0.01	0.00	-0.01	0.00	0.32	0.00	0.08	0.00	0.13	0.00	0.42	0.01	0.74	0.01	0.44	0.01	0.08	0.00	0.32	0.01
	21	0.15		0.10	0.10	0.10	-0.01	0.00	-0.01	0.00	0.22	0.01	0.10	0.01	0.04	0.00	0.40	0.01	0.49	0.02	0.41	0.02	0.14	0.00	0.22	0.01
	22	0.15		0.10	0.05	0.10	-0.01	0.00	-0.01	0.00	0.19	0.02	0.11	0.02	0.04	0.00	0.36	0.02	0.45	0.02	0.37	0.03	0.15	0.00	0.22	0.00
	23	0.15		0.10	0.10	0.05	0.00	0.00	0.00	0.00	0.20	0.02	0.09	0.01	-0.01	0.01	0.36	0.03	0.35	0.03	0.37	0.03	0.14	0.00	0.13	0.02
	24	0.10	0.20	0.05	0.05	0.05	0.00	0.00	-0.01	0.00	0.15	0.02	0.06	0.02	0.05	0.00	0.23	0.02	0.33	0.03	0.24	0.02	0.07	0.00	0.16	0.01
	25	0.12	0.20	0.05	0.05	0.05	0.00	0.00	0.00	0.00	0.18	0.02	0.07	0.01	0.07	0.01	0.26	0.02	0.41	0.02	0.27	0.02	0.07	0.00	0.19	0.02
	26	0.12	1.00	0.05	0.05	0.05	-0.01	0.00	-0.01	0.00	0.16	0.02	0.04	0.01	0.05	0.01	0.25	0.03	0.35	0.04	0.25	0.03	0.07	0.00	0.16	0.02
	27	0.12		0.05	0.05	0.05	-0.01	0.00	-0.01	0.00	0.22	0.02	0.06	0.01	0.07	0.01	0.30	0.02	0.45	0.03	0.31	0.02	0.07	0.00	0.19	0.01

Peak short-term response (1.5 - 3 years after change)
(relative difference to control as fraction of the control scenario)

	Parameter change (fraction of control)						Soil C		C/N		Cmic		DOC		CUE		R		G		R_{sub}		R_{mic}		G_{mic}	
	Scenario #	K_{cat}	K_m	R_{maint}	U_{max}	M	aver.	stderr	aver.	stderr	aver.	stderr	aver.	stderr	aver.	stderr	aver.	stderr	aver.	stderr	aver.	stderr	aver.	stderr	aver.	stderr
control	0						0.00	0.01	0.00	0.00	0.00	0.01	0.00	0.01	0.00	0.00	0.00	0.01	0.00	0.01	0.00	0.02	0.00	0.00	0.00	0.00
Enzyme kinetics	1	0.05					-0.28	0.01	-0.15	0.01	0.52	0.01	0.01	0.00	-0.01	0.00	0.52	0.01	0.51	0.01	1.11	0.04	0.00	0.00	-0.01	0.00
	2	0.10					-0.52	0.00	-0.30	0.00	0.67	0.01	0.05	0.00	-0.03	0.00	0.67	0.01	0.60	0.01	2.47	0.01	0.00	0.00	-0.04	0.00
	3	0.15					-0.67	0.00	-0.42	0.00	0.58	0.01	0.08	0.00	-0.04	0.00	0.58	0.01	0.47	0.01	3.83	0.03	0.00	0.00	-0.07	0.00
	4		0.05				0.00	0.00	0.00	0.00	0.02	0.02	-0.02	0.00	0.00	0.00	0.02	0.02	0.02	0.02	0.02	0.02	0.00	0.00	0.00	0.00
	5		0.10				-0.19	0.09	-0.10	0.05	0.34	0.16	0.00	0.01	-0.01	0.00	0.34	0.16	0.32	0.15	0.73	0.35	0.00	0.00	-0.01	0.01
	6		0.15				0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	-0.01	0.00	0.00	0.00	0.00	0.00
	7		1.00				0.09	0.00	0.04	0.00	-0.18	0.01	0.00	0.00	0.00	0.00	-0.18	0.01	-0.18	0.01	-0.25	0.01	0.00	0.00	0.00	0.00
Microbial physiology	8			0.05			0.26	0.00	0.14	0.00	-0.74	0.00	0.45	0.00	-0.08	0.01	-0.71	0.01	-0.75	0.01	-0.77	0.00	0.10	0.00	-0.04	0.01
	9			0.10			0.38	0.00	0.19	0.00	-0.94	0.00	0.91	0.01	-0.19	0.01	-0.93	0.00	-0.95	0.00	-0.95	0.00	0.20	0.00	-0.13	0.02
	10			0.15			0.28	0.09	0.09	0.07	-0.99	0.00	0.48	0.16	-0.72	0.06	-0.99	0.00	-0.99	0.00	-0.99	0.00	0.31	0.00	-0.34	0.05
	11				0.05	0.05	-0.14	0.01	-0.09	0.01	0.36	0.01	0.01	0.01	0.03	0.00	0.36	0.01	0.43	0.01	0.58	0.03	0.00	0.00	0.05	0.00
	12				0.10	0.10	-0.24	0.01	-0.16	0.00	0.56	0.01	0.05	0.00	0.06	0.00	0.56	0.01	0.71	0.01	1.07	0.03	0.00	0.00	0.09	0.00
	13				0.15	0.15	-0.36	0.00	-0.25	0.00	0.72	0.02	0.05	0.01	0.08	0.00	0.72	0.02	0.95	0.02	1.68	0.04	0.00	0.00	0.13	0.00
Mixed Scenarios	14	0.10		0.05			-0.20	0.01	-0.06	0.00	0.17	0.00	0.09	0.00	-0.07	0.00	0.29	0.00	0.16	0.00	0.62	0.02	0.10	0.00	-0.01	0.00
	15	0.15		0.10			-0.08	0.00	0.03	0.00	-0.23	0.01	0.23	0.01	-0.12	0.00	-0.08	0.01	-0.25	0.01	0.01	0.01	0.21	0.00	-0.02	0.00
	16	0.10			0.05	0.05	-0.60	0.00	-0.38	0.00	0.70	0.01	0.05	0.00	0.00	0.00	0.70	0.01	0.70	0.01	3.28	0.02	0.00	0.00	0.00	0.00
	17	0.15			0.10	0.10	-0.76	0.00	-0.52	0.00	0.41	0.01	0.13	0.00	0.01	0.00	0.42	0.01	0.43	0.01	4.89	0.02	0.00	0.00	0.01	0.00
	18	0.10		0.05	0.05	0.05	-0.33	0.01	-0.15	0.01	0.39	0.01	0.15	0.01	-0.04	0.00	0.53	0.01	0.44	0.01	1.28	0.04	0.10	0.00	0.03	0.00
	19	0.15		0.10	0.05	0.05	-0.23	0.01	-0.05	0.00	0.08	0.01	0.23	0.01	-0.09	0.00	0.30	0.02	0.12	0.01	0.70	0.03	0.21	0.00	0.04	0.00
	20	0.15		0.05	0.10	0.10	-0.63	0.00	-0.36	0.00	0.48	0.00	0.23	0.00	-0.03	0.00	0.63	0.00	0.54	0.00	3.36	0.05	0.10	0.00	0.04	0.00
	21	0.15		0.10	0.10	0.10	-0.37	0.01	-0.14	0.00	0.23	0.01	0.31	0.01	-0.07	0.00	0.48	0.01	0.32	0.01	1.36	0.02	0.21	0.00	0.07	0.00
	22	0.15		0.10	0.05	0.10	-0.37	0.01	-0.14	0.00	0.26	0.01	0.30	0.02	-0.07	0.00	0.52	0.01	0.35	0.01	1.41	0.02	0.21	0.00	0.08	0.00
	23	0.15		0.10	0.10	0.05	-0.23	0.01	-0.05	0.01	0.06	0.02	0.23	0.01	-0.09	0.00	0.28	0.02	0.10	0.02	0.67	0.05	0.21	0.00	0.04	0.00
	24	0.10	0.20	0.05	0.05	0.05	-0.31	0.01	-0.14	0.01	0.35	0.02	0.14	0.01	-0.04	0.00	0.49	0.02	0.40	0.02	1.16	0.04	0.10	0.00	0.03	0.00
	25	0.12	0.20	0.05	0.05	0.05	-0.40	0.01	-0.19	0.01	0.43	0.01	0.18	0.01	-0.05	0.00	0.58	0.01	0.47	0.01	1.64	0.03	0.10	0.00	0.02	0.00
	26	0.12	1.00	0.05	0.05	0.05	-0.33	0.01	-0.15	0.00	0.33	0.01	0.16	0.01	-0.04	0.00	0.47	0.01	0.37	0.01	1.20	0.02	0.10	0.00	0.02	0.00
	27	0.12		0.05	0.05	0.05	-0.43	0.01	-0.21	0.00	0.46	0.02	0.18	0.01	-0.05	0.00	0.60	0.02	0.49	0.02	1.82	0.02	0.10	0.00	0.02	0.00

Long-term response (49.5-50.5 years after change)
(relative difference to control as fraction of the control scenario)

	Parameter change (fraction of control)						Soil C		C/N		Cmic		DOC		CUE		R		G		R_{sub}		R_{mic}		G_{mic}	
	Scenario #	K_{cat}	K_m	R_{maint}	U_{max}	M	aver.	stderr	aver.	stderr	aver.	stderr	aver.	stderr	aver.	stderr	aver.	stderr	aver.	stderr	aver.	stderr	aver.	stderr	aver.	stderr
control	0						0.00	0.01	0.00	0.00	0.00	0.04	0.00	0.03	0.00	0.00	0.00	0.04	0.00	0.04	0.00	0.04	0.00	0.00	0.00	0.00
Enzyme kinetics	1	0.05					-0.38	0.01	-0.03	0.01	0.08	0.01	0.01	0.01	0.00	0.00	0.08	0.01	0.07	0.01	0.74	0.03	0.00	0.00	-0.01	0.00
	2	0.10					-0.59	0.01	-0.08	0.01	0.08	0.02	0.07	0.01	-0.01	0.00	0.08	0.02	0.07	0.02	1.66	0.01	0.00	0.00	-0.01	0.00
	3	0.15					-0.75	0.00	-0.21	0.00	0.10	0.01	0.12	0.01	0.00	0.00	0.10	0.01	0.09	0.01	3.46	0.04	0.00	0.00	-0.01	0.00
	4		0.05				-0.03	0.01	-0.01	0.00	0.01	0.05	-0.01	0.02	0.00	0.00	0.01	0.05	0.01	0.05	0.04	0.04	0.00	0.00	0.00	0.00
	5		0.10				-0.23	0.13	-0.02	0.01	0.10	0.02	-0.03	0.03	0.00	0.00	0.10	0.02	0.10	0.03	0.50	0.23	0.00	0.00	0.00	0.00
	6		0.15				-0.02	0.00	-0.02	0.00	0.00	0.03	-0.02	0.02	0.00	0.00	0.00	0.03	0.01	0.03	0.02	0.03	0.00	0.00	0.00	0.01
	7		1.00				0.07	0.00	-0.04	0.00	-0.01	0.05	-0.04	0.03	0.00	0.00	-0.01	0.05	-0.01	0.05	-0.08	0.04	0.00	0.00	0.00	0.00
Microbial physiology	8			0.05			2.44	0.22	0.45	0.03	-0.21	0.16	-0.18	0.01	-0.05	0.00	-0.13	0.18	-0.20	0.17	-0.74	0.06	0.10	0.00	0.02	0.00
	9			0.10			-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
	10			0.15			-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
	11				0.05	0.05	-0.29	0.00	-0.13	0.00	0.08	0.03	0.03	0.01	0.03	0.00	0.08	0.03	0.13	0.03	0.52	0.04	0.00	0.00	0.05	0.00
	12				0.10	0.10	-0.50	0.00	-0.26	0.00	0.09	0.03	0.10	0.02	0.05	0.00	0.09	0.03	0.19	0.03	1.16	0.05	0.00	0.00	0.09	0.00
	13				0.15	0.15	-0.72	0.00	-0.48	0.00	0.08	0.00	0.18	0.00	0.08	0.00	0.09	0.00	0.23	0.00	2.86	0.03	0.00	0.00	0.14	0.00
Mixed Scenarios	14	0.10		0.05			-0.06	0.02	0.25	0.01	0.03	0.04	0.00	0.00	-0.06	0.00	0.13	0.04	0.04	0.04	0.20	0.07	0.10	0.00	0.01	0.01
	15	0.15		0.10			0.40	0.04	0.46	0.01	-0.05	0.03	0.10	0.01	-0.12	0.00	0.15	0.04	-0.06	0.03	-0.18	0.04	0.21	0.00	-0.01	0.01
	16	0.10			0.05	0.05	-0.76	0.00	-0.31	0.00	0.08	0.01	0.15	0.00	0.02	0.00	0.08	0.01	0.12	0.01	3.55	0.02	0.00	0.00	0.04	0.00
	17	0.15			0.10	0.10	-0.83	0.00	-0.37	0.00	0.07	0.00	0.18	0.00	0.05	0.00	0.08	0.00	0.17	0.00	5.39	0.04	0.00	0.00	0.09	0.00
	18	0.10		0.05	0.05	0.05	-0.33	0.00	0.13	0.00	0.00	0.01	0.12	0.01	-0.03	0.00	0.11	0.01	0.05	0.00	0.65	0.01	0.10	0.00	0.05	0.00
	19	0.15		0.10	0.05	0.05	-0.06	0.01	0.34	0.00	-0.14	0.01	0.20	0.02	-0.09	0.00	0.03	0.01	-0.11	0.02	0.10	0.01	0.21	0.00	0.04	0.01
	20	0.15		0.05	0.10	0.10	-0.74	0.00	-0.17	0.00	-0.02	0.01	0.32	0.01	-0.01	0.00	0.08	0.01	0.07	0.01	3.14	0.02	0.10	0.00	0.09	0.00
	21	0.15		0.10	0.10	0.10	-0.30	0.01	0.24	0.00	-0.08	0.04	0.24	0.02	-0.06	0.00	0.11	0.05	0.01	0.05	0.58	0.05	0.21	0.00	0.10	0.00
	22	0.15		0.10	0.05	0.10	-0.29	0.01	0.24	0.01	-0.09	0.03	0.24	0.02	-0.06	0.00	0.10	0.03	0.00	0.03	0.56	0.03	0.21	0.00	0.10	0.00
	23	0.15		0.10	0.10	0.05	-0.05	0.02	0.34	0.01	-0.15	0.06	0.19	0.01	-0.09	0.00	0.03	0.07	-0.11	0.07	0.09	0.10	0.21	0.00	0.04	0.00
	24	0.10	0.20	0.05	0.05	0.05	-0.30	0.01	0.13	0.01	0.02	0.01	0.10	0.01	-0.03	0.00	0.12	0.01	0.07	0.02	0.60	0.03	0.10	0.00	0.05	0.00
	25	0.12	0.20	0.05	0.05	0.05	-0.41	0.01	0.10	0.00	-0.03	0.00	0.14	0.02	-0.03	0.00	0.06	0.00	0.01	0.00	0.81	0.02	0.10	0.00	0.04	0.00
	26	0.12	1.00	0.05	0.05	0.05	-0.31	0.01	0.10	0.00	-0.03	0.04	0.09	0.03	-0.03	0.00	0.06	0.05	0.01	0.05	0.55	0.07	0.10	0.00	0.05	0.00
	27	0.12		0.05	0.05	0.05	-0.43	0.00	0.11	0.00	-0.04	0.03	0.17	0.02	-0.03	0.00	0.06	0.03	0.00	0.03	0.85	0.06	0.10	0.00	0.04	0.01

Table S4. Statistical test outputs for *P*-values reported in Main Text.

	Warming effect		
	LR	d.f.	*P*
Long-term field warming			
Soil C	15.84	1,8	0.0001
Microbial biomass (C_{mic})	8.40	1,8	0.0038
Total microbial respiration (R)	0.84	1,8	0.3603
Total microbial growth (G)	0.21	1,4	0.6479
Total microbial uptake (U)	1.16	1,8	0.2822
Microbial carbon use efficiency (CUE)	0.70	1,4	0.4028
Microbial turnover rate (T_m)	8.64	1,4	0.0033
Mass-specific microbial respiration (R_m)	6.37	1,4	0.0116
Mass-specific microbial growth (G_m)	8.64	1,8	0.0033
Mass-specific microbial uptake (U_m)	7.71	1,4	0.0055
Laboratory warming (short-term)			
Total microbial respiration (R)	7.82	2,5	0.0200
Total microbial growth (G)	10.74	2,5	0.0046
Total microbial uptake (U)	9.26	2,5	0.0097
Microbial turnover rate (T_m)	8.23	2,5	0.0163
Mass-specific microbial respiration (R_m)	8.36	2,5	0.0153
Mass-specific microbial growth (G_m)	8.23	2,5	0.0163
Mass-specific microbial uptake (U_m)	9.21	2,5	0.0100
Laboratory incubation (long-term)			
Total microbial respiration (R)	1.63	2,5	0.4441
Total microbial growth (G)	0.90	2,5	0.6366
Total microbial uptake (U)	2.98	2,5	0.2249

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