Figure S1. Schematic of experimental design used for assessing the effect of heterogeneity in C_t on DEMENT outputs. Letters denoting parts of figure 1 in the main text are retained to facilitate cross-comparison of scenarios, so are not contiguous within the plot. C_t is the same across all taxa, and is set to $0°C^{-1}$ (A), $0.011 °C^{-1}$ (A_i), or $-0.011 °C^{-1}$ (A_{ii}). These "homogeneous" values correspond to the mean starting cross-taxon average C_t of the adjacent heterogeneous scenario in the figure: -0.022 to $0.022 °C^{-1}$ (scenarios A and B); o to $0.022 °C^{-1}$ (scenarios A_i and G); -0.022 to $0 °C^{-1}$ (scenarios A_{ii} and H)

Table S1. Effect of changing the reference CUE and enzyme costs against CUE on the stability and concievability of DEMENT outputs under three warming scenarios. CUE_ref is the CUE at 15°C, prior to calculating enzyme costs. C_t describes whether CUE is homogeneous or heterogeneous between taxa. CUE_enz is the maximum cost against CUE for enzyme production (with transporter costs parameterized the same). Stable is the fraction of runs where the microbial community constrained litter accumulation until the end. The median MBC, SOC:MBC ratio, and SOC are shown, along with the biomass-weighted CUE of the active community at the end of this time. CN, CP, and NP refer to median elemental ratios of microbial biomass. Italicized values are those not deemed to be within the range of biologically plausible values.

| CUE_ref	C_t	Temperature	CUE_enz	Stable	MedianMBC	Median SOC:MBC	Median SOC	Final CUE	CN	CP	NP
	homogeneous	H	-0.1	0.71	57	*3.4*	198	0.44	4.5	49	9.3
0.58	NA	C	-0.1	0.97	67	*2.3*	142	0.41	4.6	43	9.3
	heterogeneous	H	-0.1	0.86	107	*1.4*	144	0.53	4.7	43	9
	homogeneous	H	-0.1	0.98	36	9.2	331	0.32	4.5	43	9.4
0.48	NA	C	-0.1	0.93	37	7.6	241	0.31	4.3	39	9.1
	heterogeneous	H	-0.1	0.9	70	*2.1*	137	0.42	4.6	42	9.3
	homogeneous	H	-0.2	0.64	20	54	*1041*	0.23	4.5	41	9.2
0.48	NA	C	-0.2	0.81	18	*131*	687	0.15	3.6	35	9.5
	heterogeneous	H	-0.2	0.97	34	19	325	0.26	3.9	37	9.3
	homogeneous	H	-0.1	0.95	20	32	637	0.23	4.4	39	9
0.38	NA	C	-0.1	0.95	20	33	492	0.22	3.8	37	9.3
	heterogeneous	H	-0.1	0.98	38	7.2	219	0.32	4.1	38	9.2
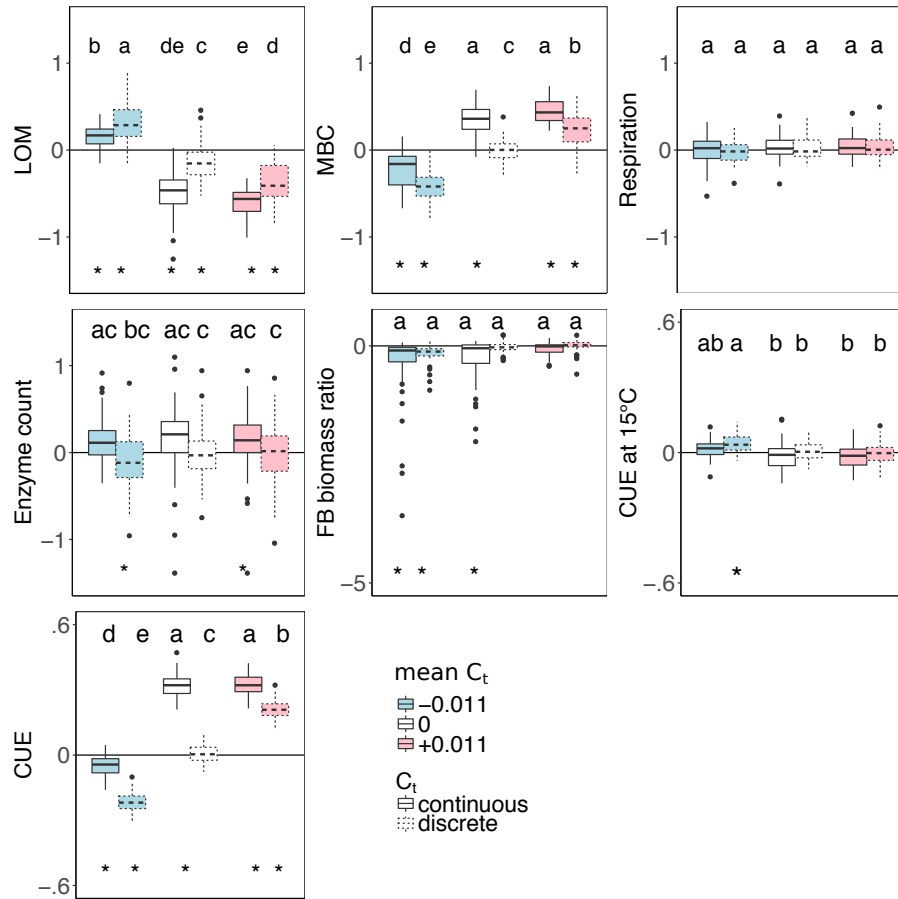
Figure S2. Effect of 5°C warming on C stocks and flows in simulations, reported as the natural log of the ratio of the values in heated compared to control conditions. Here, the CUE temperature response is allowed to vary (heterogeneous) or is fixed (homogeneous) at the mean cross-taxon value as in Figure 3, but the variability is either constrained to all negative values (mean of -0.011 °C^{-1}; range -0.022 to 0°C^{-1}), or all positive values (mean of 0.011 °C^{-1}; range 0 to 0.022°C^{-1})

Table S2. Median (or median-standardized interquartile range (IQRm)) output values for DEMENT model runs where C_t was either always positive, or always negative, marked according to warming effect (+/-) and model structure effects (letters) determined using Bonferoni-corrected post-hoc tests following linear mixed effect models. Symbols: "+" warming increased value; "-" warming decreased value). Letters: differences between warmed scenarios. In some instances, values differ slightly from those in Table 1 because some seeds failed to lead to constrained LOM accumulation and so were removed here.

Figure 1 scenario C_t (^{o}C^{-1})	A_{ii} -0.011	H -0.022 to 0	A_i +0.011	G 0 to 0.011
LOM IQRm	0.29	0.23	0.21	0.30
SOM IQRm	0.26	0.15	0.21	0.19
Surviving taxa	11a+	9b	10a	8b
Enzyme count	16.5b	19a	15b-	18a
Shannon's H	1.92a	1.61a	1.86ac	1.64bc-
MBC (mg cm^{-3})	26.5b+	32.3a+	13.6d-	17.2c-
LOM (mg cm^{-3})	411.5c-	334.6d-	841.8a+	706.5b+
CUE at 15°C	0.23bc	0.23c	0.24a+	0.23b
CUE at 20°C	0.29b+	0.32a+	0.19d-	0.22c-
FB biomass ratio	0.85a	0.81ac	0.73bc	0.68b
Respiration (mg cm^{-3} day^{-1})	0.94c	0.96ac	0.90b	0.94abc
FB richness ratio	0.51a	0.46ac	0.40bc	0.43ac
CUE bacteria	0.27b	0.36a+	0.27b	0.25c-
CUE fungus	0.22c	0.29a+	0.23b+	0.18d-