

SUPPLEMENTARY INFORMATION

**Table S1** The percentage of sequences belonging to different bacterial phyla in the long-term warmed grassland (LWG) and the short-term warmed grassland (SWG)

Phylum	LWG (%)	SWG (%)
Proteobacteria	29	29
Acidobacteria	25	18
Actinobacteria	11	21
Chloroflexi	7	6
Verrucomicrobia	5.99	4.87
Gemmatimonadetes	3.57	2.90
Bacteroidetes	2.57	3.25
Firmicutes	2.44	3.52
Nitrospirae	2.41	1.74
WS3	1.54	1.32
Planktomyces	0.85	1.19
TM6	0.56	0.51
TM7	0.47	0.51
Chlamydiae	0.30	0.47
Elusimicrobia	0.30	0.17
OD1	0.29	0.23
Armatimonadetes	0.22	0.16
Cyanobacteria	0.18	0.14
Chlorobi	0.16	0.18
AD3	0.90	0.21
Fibrobacteres	0.08	0.07
Tenericutes	0.06	0.03
Spirochaetes	0.04	0.02
Undefined	4.85	3.94

**Table S2** The percentage of sequences belonging to different fungal functional groups in the long-term warmed grassland (LWG) and the short-term warmed grassland (SWG).

	LWG	SWG
Filamentous saprotrophs	66.40	61.08
AMF	6.28	5.44
Yeasts	1.87	7.83
White rot saprotrophs	1.02	0.05
Plant pathogens	0.77	0.52
Ectomycorrhizal fungi	0.39	1.51
Animal parasites	0.06	0.05
Mycoparasites	0.02	0.06
Unassigned	22.88	23.46

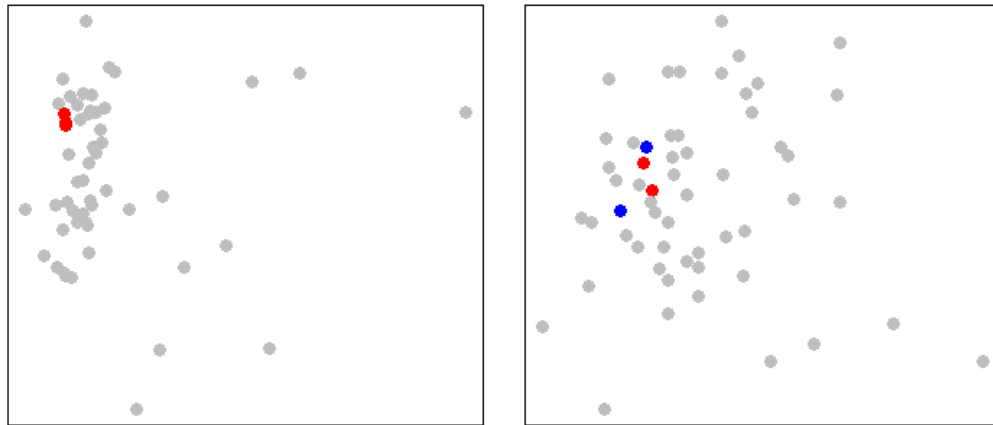
**Table S3** The results ANOVA analysis for differences in relative abundance of dominant bacterial and fungal groups (containing more than 2% of total number of sequences) from different soil warming levels in the long-term warmed grassland (LWG) and short-term warmed grassland (SWG).

	LWG		SWG	
	P adj.	Transformation	P adj.	Transformation
<b>Bacteria</b>				
Alphaproteobacteria	1		1	log
Betaproteobacteria	0.01	box-cox	<0.001	box-cox
Gammaproteobacteria	1	log	0.6	
Deltaproteobacteria	0.22	log	1	
Acidobacteria	1	log	1	
Actinobacteria	0.44	log	1	
Chloroflexi	1	box-cox	<0.001	
Verrucomicrobia	0.9	log	1	
Gemmatimonadetes	1		1	box-cox
Bacteroidetes	1		<0.001	box-cox
Firmicutes	1	log	0.07	box-cox
<b>Fungi</b>				
Filamentous sapr.	<0.001	box-cox	0.002	box-cox
AMF	<0.001	log	0.01	log
Yeasts	1		0.9	

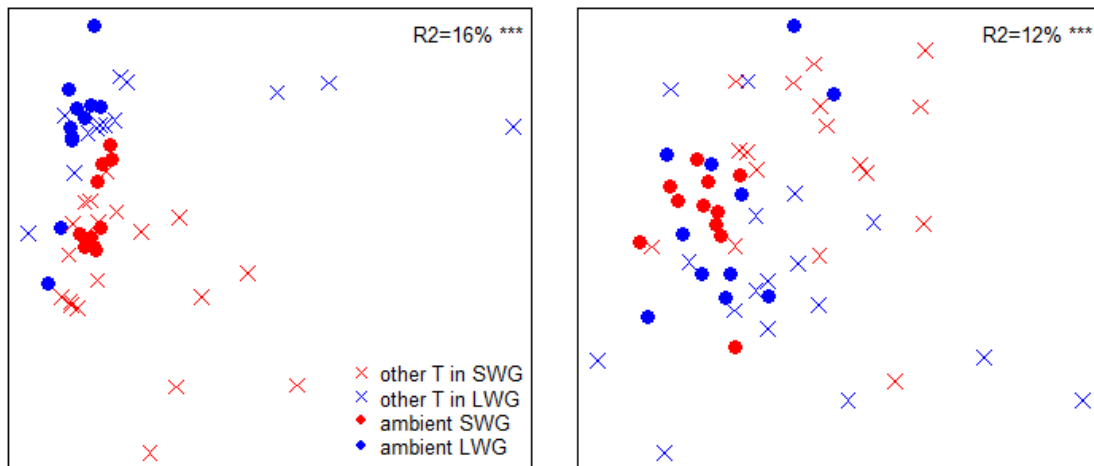
**Table S4** The differences in the relative abundance of dominant bacterial and fungal groups at different warming levels based on the post-hoc Tukey test (adjusted P values) in the long-term warmed grassland (LGW) and short-term warmed grassland (SWG).

	$W_0 - W_{low}$	$W_0 - W_{med}$	$W_0 - W_{high}$	$W_0 - W_{extr}$
<b>LGW bacteria</b>				
Betaproteobacteria	0.42	1.00	0.24	0.01
<b>SWG bacteria</b>				
Betaproteobacteria	0.42	1.00	0.01	<0.001
Bacteroidetes	1.00	1.00	0.05	<0.001
Chloroflexi	1.00	0.65	1.00	<0.001
<b>LGW fungi</b>				
Fil. saprotrophs	1.00	1.00	1.00	<0.001
AMF	1.00	1.00	0.87	<0.001
<b>SWG fungi</b>				
Fil. saprotrophs	0.18	0.01	<0.001	0.41
AMF	1.00	0.16	0.03	0.03

\*  $W_0$  – ambient (+0°C to +1°C),  $W_{low}$  (+2°C to +3°C),  $W_{med}$  (+3°C to +5°C),  $W_{high}$  (+6°C to +9°C),  $W_{high'}$  (+7°C to +11°C),  $W_{extr}$  (+15°C to +19°C)



**Figure S1** NMDS ordination based on Bray-Curtis distances for: bacterial (left) and fungal (right) samples in the study. For bacterial communities red points indicate three technical replicates of the same sample and for fungal communities red and blue points indicate two technical replicates of two different samples. Relatively close clustering of technical replicates show the reproducibility of the sample preparation and sequencing procedure.



**Figure S2** The differences between bacterial (left) and fungal (right) communities at ambient temperatures in the two grasslands (LWG: long-term warmed grassland; SWG: short-term warmed grassland) based on NMDS and PERMANOVA analyses. \*\*\*  $P < 0.001$