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Supplementary Information for

Changes in temperature alter the relationship between biodiversity and ecosystem functioning

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Supporting Information Text

1. SI Materials and Methods

1.1. Identification of bacteria isolates. We identified the different isolates using 16S Polymerase Chain Reaction (PCR). A master-mix solution was prepared using 7.2 μl of DNA free water, 0.4 μl 27 forward primer, 0.4 μl 1492 reverse primer and 10 μl of Taq polymerase per sample. To create a template solution 2 μl of sample 100 x diluted in DNA free water was added to 18 μl of master-mix solution. Samples were then placed in a thermal cycler (Applied Biosystems Veriti Thermal Cycler). This procedure included 1 cycle at 94 °C for 4 minutes, 35 cycles at 94, 48 and 72 °C for 1 minute, 30s and 2 minutes, respectively, and finally, 1 cycle at 72 °C for 8 minutes. The PCR product was cleaned up using Exonuclease I and Antartic Phosphatase and high quality samples were Sanger sequenced using the 27F, 1492R primers (Core Genomic Facility, University of Sheffield). Sequences were trimmed in Genious (version 6.1.8) removing the bp from the 5′ end and trimming the 3′ end to a maximum length of 1000bp.

1.2. Species-levels thermal tolerance curves. Prior to characterising the growth curve, each species was acclimated for 24 h at each temperature. The acclimated strains were then inocculated at a common density into a 96-well plate with 200 μL of protozoan media. Plates were stored inside of plastic boxes with water soaked sponges to maintain humidity during the experiment and avoid changes in the volume due to evaporation. The optical density of each replicate was measured every 2 hours using a Biotek reader synergy 2 at 600 nm wavelength and measurements were corrected with a blank (to account for particulate organic matter in the protozoa medium). The optical density (OD) was monitored until each species reached carrying capacity.

Population growth rates (r (h^{-1})) and carrying capacities (OD_{600}) were quantified by fitting the logistic growth equation to the time-series of biomass measurements using non-linear least squares regression:

$$N_t = \frac{K}{1 + Ae^{-rt}}; A = \frac{K - N_0}{N_0} \quad [1]$$

where N_t is the biomass (OD_{600}) at time, t, K is the carrying capacity (OD_{600}), N_0 is the biomass at the start of the experiment and r is the rate of exponential population growth (h^{-1}). The thermal tolerance curve was quantified by fitting the four parameter Sharpe-Schoolfield equation to the mean population growth rate (across the 6 replicates at each assay temperature) measured along the thermal gradient for each taxa:

$$\ln(r(T)) = Ea(\frac{1}{kT_c} - \frac{1}{kT}) + \ln(r(T_c)) - \ln(1 + e^{E_h(\frac{1}{kT_h} - \frac{1}{kT})}) \quad [2]$$

where r(T), is population growth rate (h^{-1}), k is Boltzman′s constant ($8.62*10^{-5}$ eV K^{-1}), Ea is the activation energy (in eV) that characterises the steepness of the slope leading up to a thermal optimum, T is temperature in Kelvin (K), E_h characterizes temperature-induced inactivation of growth above T_h, the temperature where half the enzymes are rendered non functional and $r(T_c)$ is the rate of growth normalized to an arbitrary reference temperature, $T_c = 18$ °C, where no low or high temperature inactivation is experienced. Equation (2) yields a maximum growth rate at an optimum temperature:

$$T_{opt} = \frac{E_h T_h}{E_h + kT_h \ln(\frac{E_h}{E_a} - 1)} \quad [3]$$

The four-parameter Sharpe-Schoofield model assumes that there is a single rate limiting enzymatic reaction that is reversibly inhibited by temperature. The parameters of the equation (r(T_c), E_a, E_h, T_h, and T_{opt}) characterize the thermal tolerance curve. We consider these parameters to be thermal "traits" that play a key role in shaping the impacts of temperature change on community dynamics and ecosystem functioning (Fig. S6, Table S1).

1.3. Biodiversity ecosystem functioning experiment. The optical density of each community at each temperature level was measured every 2 hours using a Biotek reader synergy 2 at 600 nm wavelength and was monitored until each microcosm reached carrying capacity. In all microcosms, biomass increased exponentially and then reached a stationary phase. Ecosystem functioning was quantified as the asymptotic biomass (i.e. the yield) of the community in the stationary phase, determined by fitting the logistic growth equation to the biomass time-series. For richness = 1, the average yield (across the 6 replicates) of each of the 24 taxa grown in monoculture at each assay temperature and characterised in the "species-level thermal tolerance curves", were used.

The experiment structure was well defined by a power function:

$$\log_{10}Y(S) = b(\log_{10}S - \log_{10}S_c) + \log_{10}Y(S_c) \quad [4]$$

where $\log_{10}Y$ is the natural logarithm of ecosystem function (here yield) at a given level of species richness, S, b is the exponent, that captures the shape of the diversity functioning relationship, ($\log_{10}$S - $\log_{10}S_c$), is the natural log transformed centred species richness. Centring the species richness variabile means that the intercept, $\log_{10}Y(S_c)$, gives the yield at an average level of species richness, and decreases the correlation between the exponent and the intercept. The exponent can indicate that ecosystem function is either a decellerating function of species richness when $b < 1$ (i.e. there is some degree of functional redundancy) or that functioning increases linearly with richness when $b = 1$ (i.e. there is no functional redundancy

and each species has a positive contribution to ecosystem functioning). We quantified the effects of warming on the relationship between biodiversity and ecosystem functioning by fitting Eq. (4) to the experimental data using a linear mixed effects model via the "lmer" function in the "lme4" package of R software. We included "temperature" as a fixed categorical factor to assess how b and $\log_{10}Y(S_c)$ varied among the various temperature treatments. Because our experimental design entailed exposing each unique randomly assembled community at each level of species richness to the 8 temperature treatments, we included "community ID" nested within "richness" as a random effect on the intercept to account for non-independence among measurements made on the same communities across temperature treatments. To quantify the significance of differences in the parameters among all pairwise combinations of the 8 temperature treatments, we used post-doc Tukey tests via the "glht" function in the "multcomp" package for R statistical software (see Table S9).

1.4. Re-isolation of species. At the end of the biodiversity ecosystem functioning experiment we re-isolated the bacterial taxa from maximum richness treatments (S = 24) exposed to the ambient (20 °C) and the two extreme temperatures (10 & 40 °C). Samples from each community were prepared by spreading 10 μL serial dilutions onto R2 agar plates and incubated at ambient temperature (20 °C). A total of 2512 colonies were identified across all replicates and counted by visual inspection. Of these, 121 colonies were identified using 16S rRNA Sanger sequencing (see section 1.1) to confirm the taxonomic identity based on colony morphology.

1.5. Linking thermal traits to the impacts of warming and species loss on ecosystem functioning. In this analysis, community yield was treated as the response variable, $<T_{\text{opt}}>_c$ was continuous predictor and temperature (10, 15, 20, 25, 27.5, 30, 35, 40 °C) and species richness (S = 2, 4, 8, 16) were treated as categorical factor variables. To account for the hierarchical nature of our experimental design we included "community ID" nested within "richness" as a random effect on the intercept. Note, we did not include the maximum level of species richness, S = 24, because there was no variation in $<T_{\text{opt}}>_c$ as each of the 10 replicates received an identical set of taxa. We started with the most complex model which included all variables and their interactions and carried out model simplification by sequentially removing terms and testing for their significance using likelihood ratio tests. Model simplification was stopped when all terms were significant at $p < 0.05$ (Table S8).

1.6. Partitioning the net biodiversity effect into selection and complementarity. Using information on the relative abundance of species isolated from the high diversity treatments at 10, 20 and 40 °C, the net effect of biodiversity was calculated as the difference betweeen the observed yield and the expected (weighted average yield of the monocultures). The complementarity effect was estimated as $\overline{N}\overline{\Delta RY}\overline{M}$, where N is the number of species, $\overline{\Delta RY}$ is the average change in the relative yield for all species in the mixture and $\overline{M}$ is the average monoculture yield. The selection effect was calculated as the covariance between the monoculture yield of species and their change in relative yield in the mixture (Ncov(ΔRY, M)).

Hence, NE, SE and CE were estimated at a local scale for each replicate (10 replicates per temperature) and the total effects were estimated for each temperature treatment (10, 20 and 40 °C) (Table S5). An analysis of variance (Anova) was performed to test for significant differences among temperature treatments for each mechanism (i.e. NE, SE, CE) (Table S10). To determine whether differences among all pairwise temperature levels were signficant, we used Tukey-Kramer post hoc tests (Table S11). We additionally test whether NE, SE and CE estimated for each temperature treatment were significantly different from zero using a *t*-tests (Table S12).

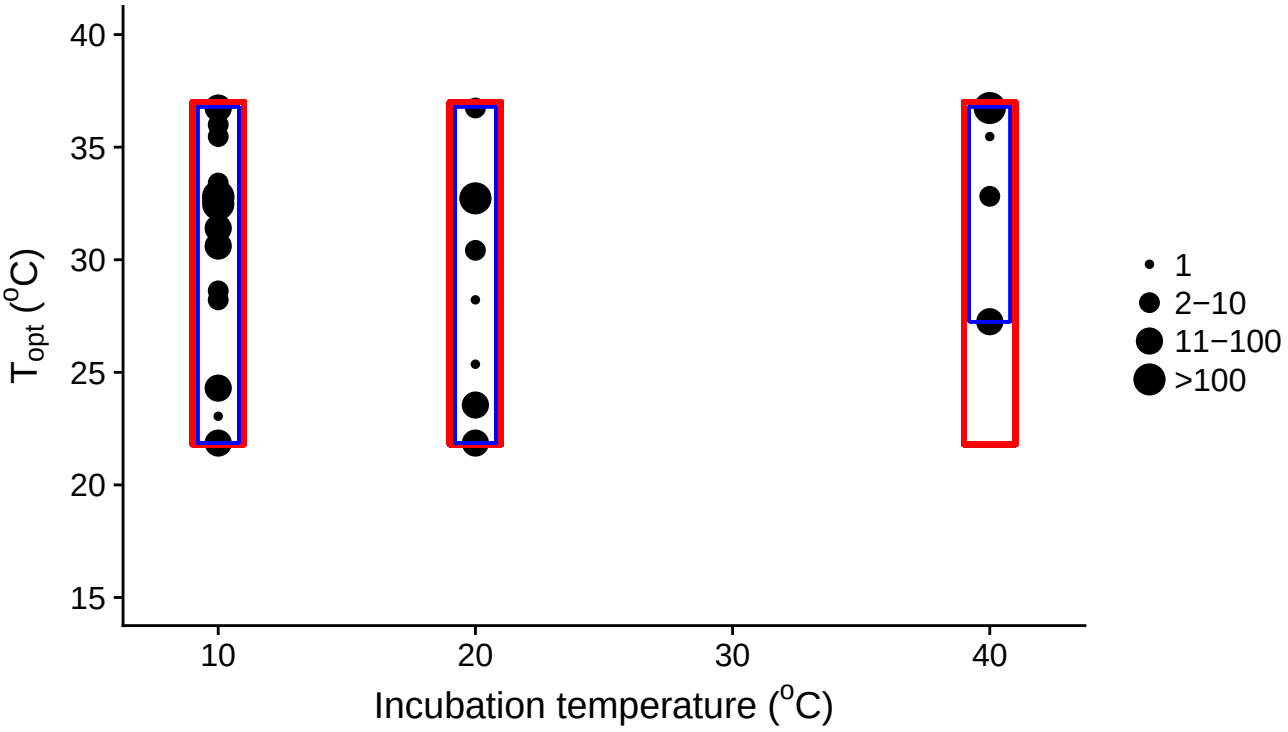

Fig. S1. **Temperature-driven selection of community composition linked to thermal tolerance traits.** At the end of the diversity experiment we re-isolated the bacterial taxa from maximum richness treatments (S = 24) that had been exposed to the ambient (20 °C) and the two extreme temperatures (10 & 40 °C). The red box represents the range of optimal temperatures of the 24 taxa and the blue box represents the optimal temperature of the taxa recovered at the end of the experiment. We found that the presence of taxa in the different temperature treatments was strongly associated with their thermal tolerance curves, with those present in the 40 °C treatments being species with the highest T_{opt}. Notably no taxa with $T_{opt} < 27$ °C were present at the end of experiments in the 40 °C treatments. These results demonstrate that "selection effects" played an important role in determining the effects of temperature community composition that likely influenced the diversity-functioning relationship. Point size corresponds to the number of colonies of a determined taxa that appeared at each incubation temperature.

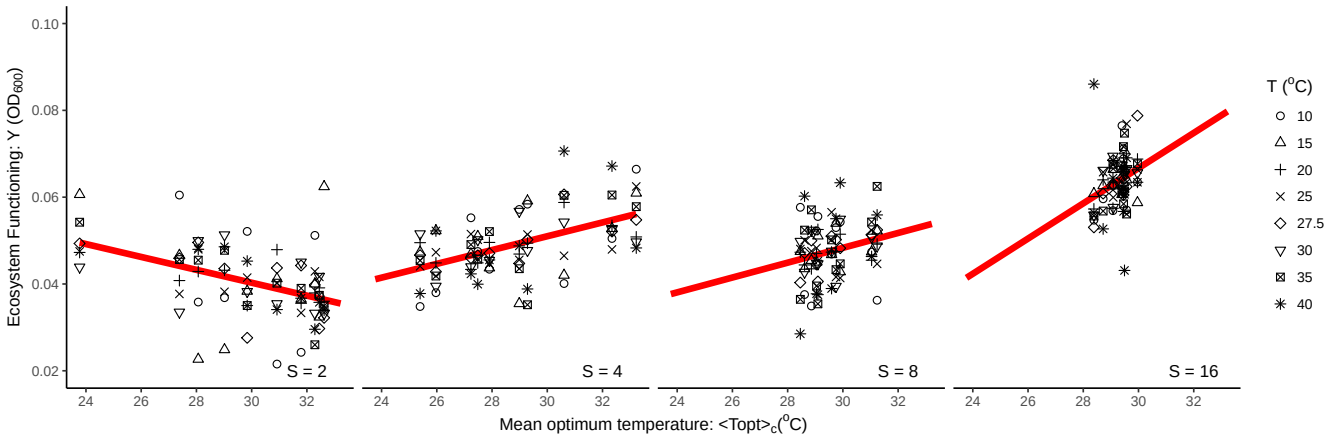

Fig. S2. Linking thermal traits to the impacts of warming and species loss on ecosystem functioning. Coupling between ecosystem functioning (community yield) and the community-mean optimum temperature $<T_{\text{opt}}>_{\text{c}}$ at different richness levels from 2 to 16. Analyses reveal that $<T_{\text{opt}}>_{\text{c}}$ becomes an increasingly important predictor of ecosystem function as species richness increases, highlighting a strong positive interaction between biodiversity and mean optimum temperature. The red lines represent the fitted curves derived from the linear mixed effect model. The different point shapes represents the level of temperature (T).

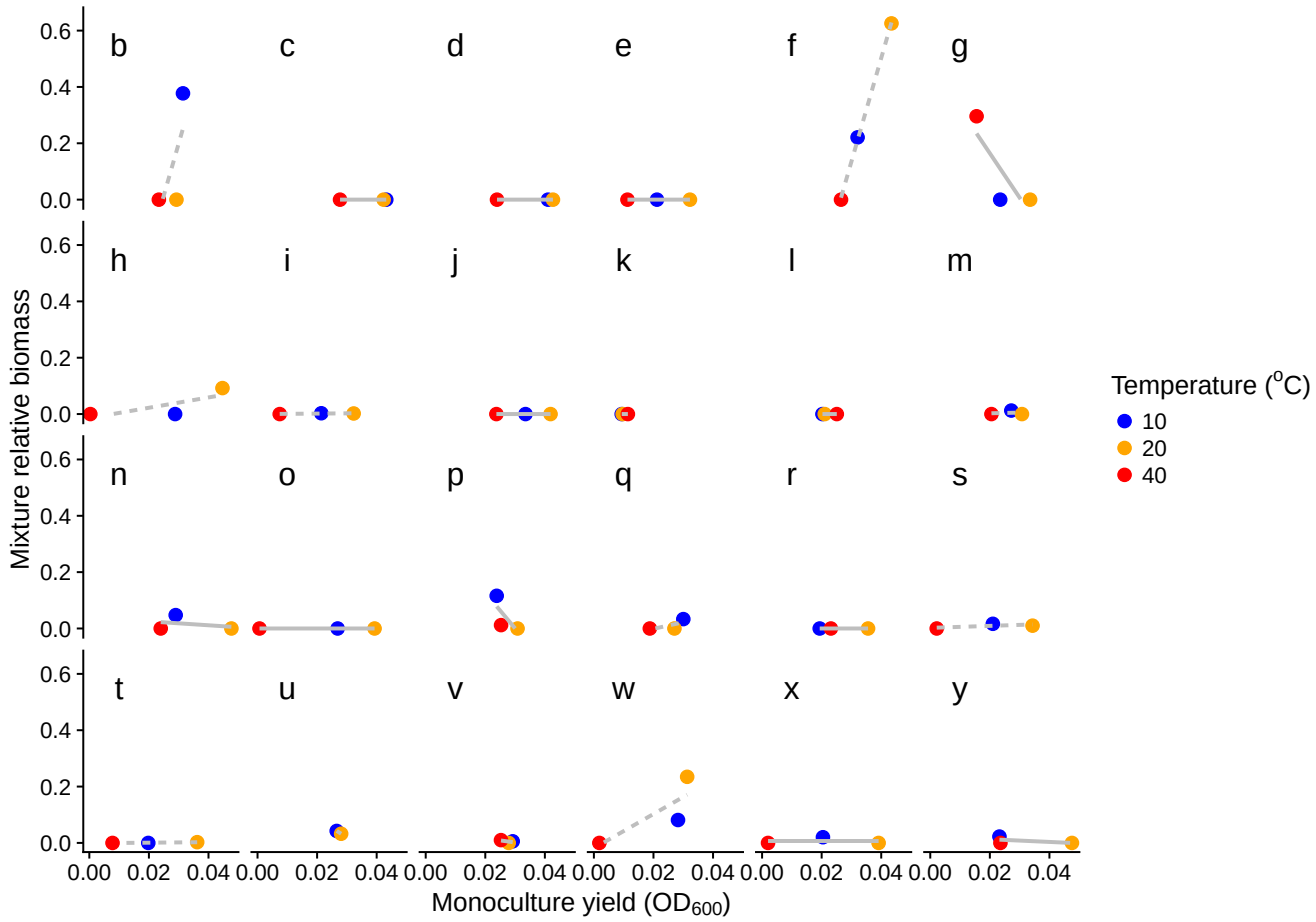

Fig. S3. Covariation between monoculture yields and mixture relative biomass. For species we assess the correlation between monoculture yield and the relative abundance of each species in the 24 species mixtures at the ambient (20 °C) and the two extreme temperatures (10 & 40 °C). Grey lines represent the fit of a linear model. Dashed grey lines represent cases where we obtained a positive slope (7 of the 24 species) and indicates that there is dominance by species in the mixture for those temperatures at which the species growth in monoculture was optimal.

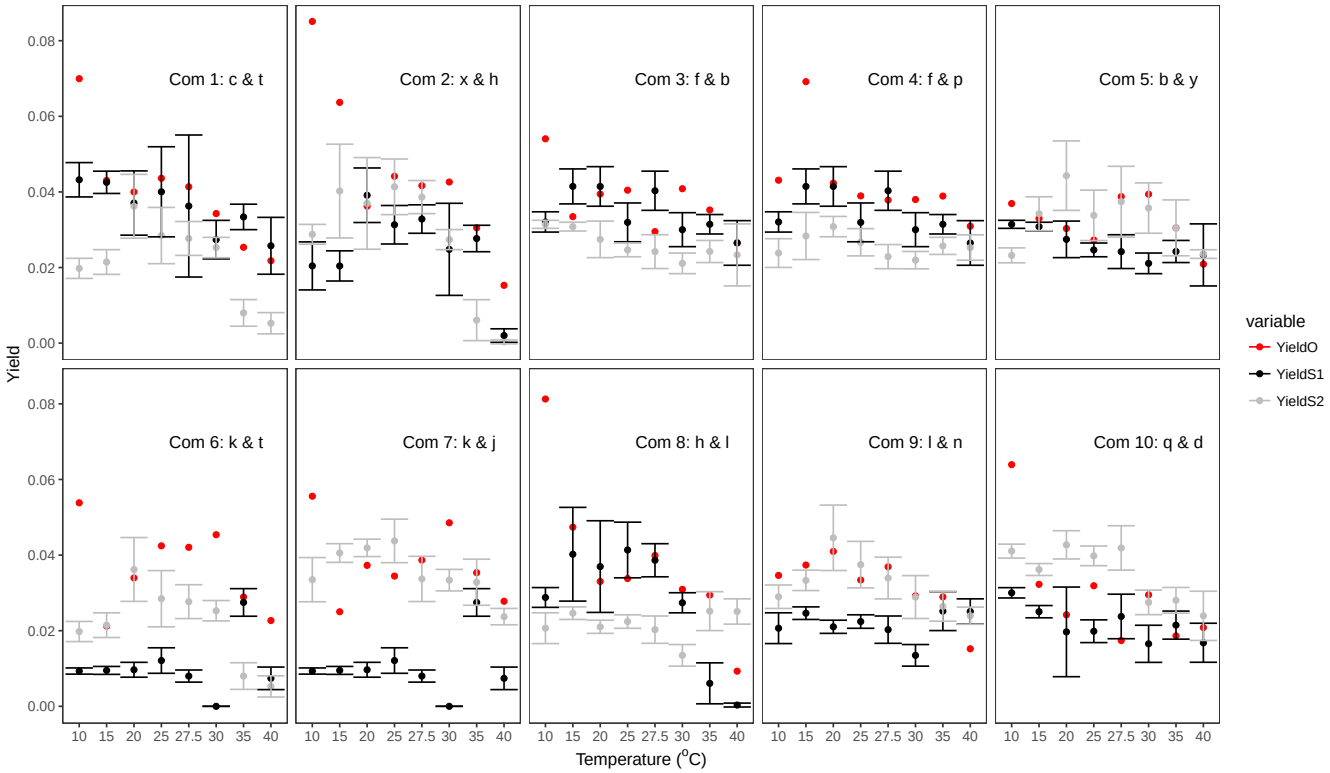

Fig. S4. **Temperature changes the nature of species interactions.** For 10 randomly assembled pairwise combinations of species we compare the yield of the mixture (red circles) to the yield of each species in monoculture (black and grey circles) across the thermal gradient. We see substantial variation in the outcome (i.e. which species dominates) and the nature (i.e. whether mixture yield exceeds monoculture yield) across the thermal gradient. These results imply that temperature change altered species interactions in the biodiversity-ecosystem functioning experiment. Error bars represent the standard deviation of the yield across 6 replicates of each species in monoculture.

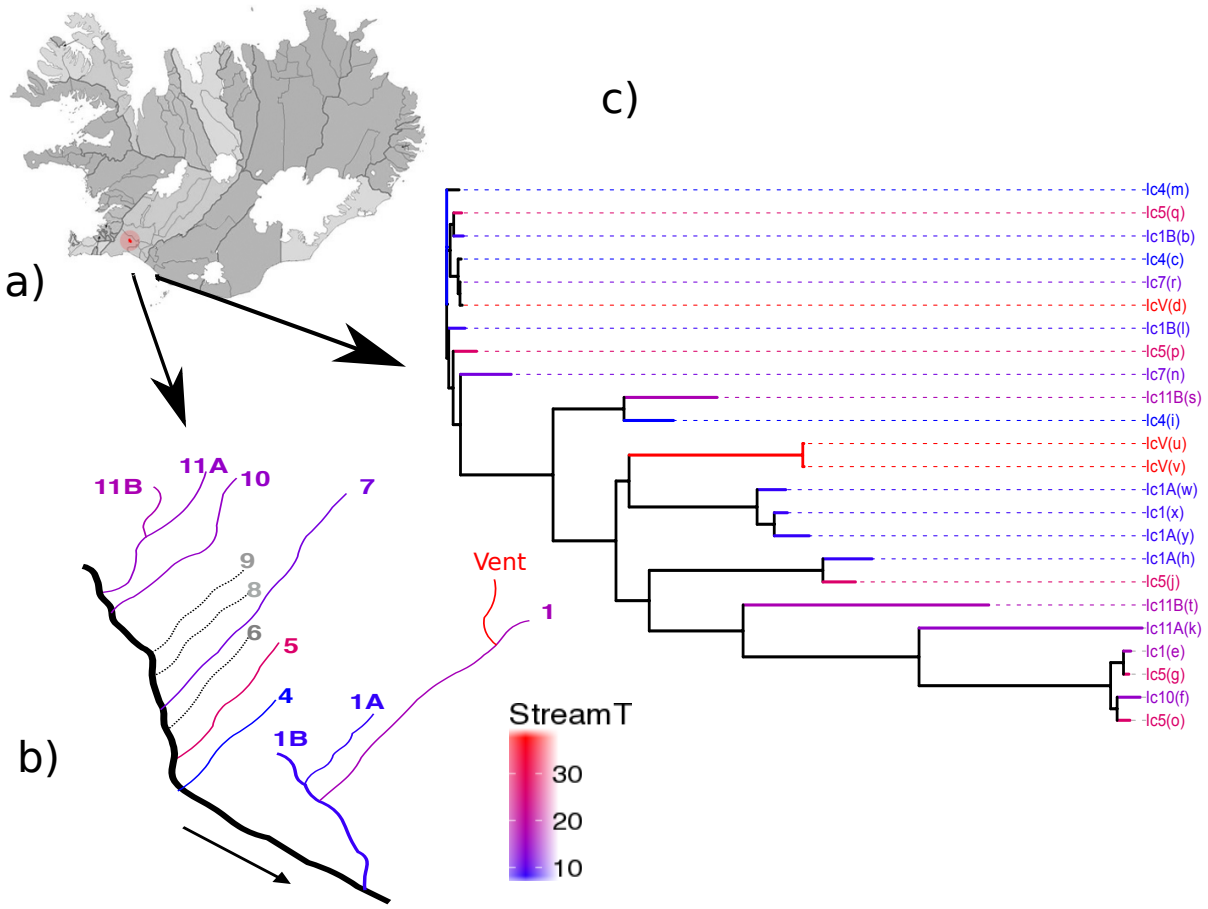

Fig. S5. **Overview of the study site and isolation process.** **a:** Map of Iceland showing geographic location of the field site, Hvergerdi Valley, 45 km east of Reykjavik. **b:** Map of the drainage basin in the Hvergerdi Valley, identifying the streams from which taxa were isolated. **c:** Phylogenetic tree with the 24 different strains isolated from the streams (see table S1 for taxonomic and associated information of each taxa). The colour code represents the temperature for the streams.

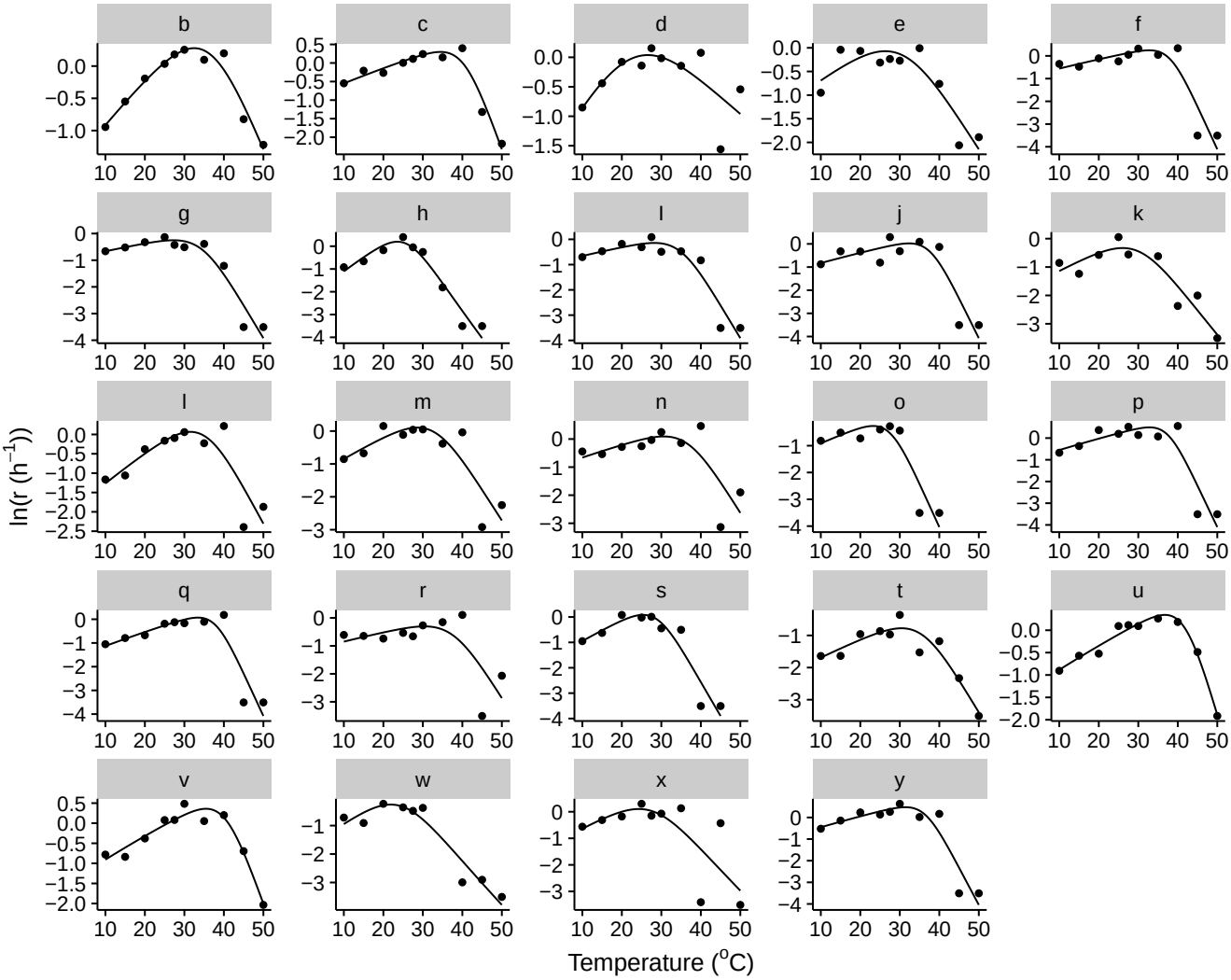

Fig. S6. **Thermal tolerance curves for each isolate fitted using the Sharpe-Schoofield model.** Y-axis represents the average natural log-tansformed population growth rate (ln$r$) quantified from the logistic growth curves of 6 replicates at each assay temperature. X-axis represents the growth temperature.

Table S1. Thermal tolerance traits for the 24 isolates

Isolate ID	ln($r(T_c)$)	E_a	E_h	T_h	quasi r^2	T_{opt}
Ic1B(b)	-0.34	0.50	1.87	309.89	0.92	32.32
Ic4(c)	-0.22	0.29	3.00	313.64	0.91	34.31
IcV(d)	0.07	0.75	1.29	297.66	0.25	26.42
Ic1(e)	-0.22	0.40	1.61	304.64	0.74	26.15
Ic10(f)	-0.23	0.29	3.68	311.20	0.77	32.58
Ic5(g)	-0.42	0.21	2.45	307.87	0.89	27.1
Ic1A(h)	0.09	0.88	2.94	298.74	0.91	23.4
Ic4(i)	-0.37	0.25	2.60	308.14	0.86	28.07
Ic5(j)	-0.46	0.32	3.43	310.78	0.76	32.17
Ic11A(k)	-0.57	0.49	2.04	303.39	0.79	25.86
Ic1B(l)	-0.63	0.56	2.28	308.53	0.59	31.37
Ic4(m)	-0.30	0.47	2.18	306.30	0.63	28.47
Ic7(n)	-0.29	0.32	2.37	309.94	0.39	30.46
Ic5(o)	0.41	0.43	3.17	300.69	0.74	23.08
Ic5(p)	-0.12	0.38	3.80	310.58	0.76	32.67
Ic5(q)	-0.64	0.42	3.66	310.98	0.77	33.26
Ic7(r)	-0.58	0.24	2.30	311.02	0.30	30.23
Ic11B(s)	-0.26	0.60	2.91	301.98	0.83	25.21
Ic11B(t)	-1.23	0.40	2.27	308.88	0.84	30.27
IcV(u)	-0.44	0.38	3.18	315.00	0.97	36.59
IcV(v)	-0.43	0.42	2.94	313.55	0.92	35.32
Ic1A(w)	-0.20	0.64	2.00	297.73	0.89	21.71
Ic1(x)	-0.01	0.54	1.94	301.12	0.32	24.15
Ic1A(y)	-0.04	0.36	3.45	309.47	0.82	31.26
Fit all sps	-0.01	0.60	1.00	298.84	0.92	28.76

Data shown are the parameters obtained from the Schoofield model and characterize the thermal tolerance curve for each taxa and an overall thermal tolerance curve derived by aggregating the growth rate data across species for each temperature (Fig. 1c). Isolate ID is the identity of each isolated taxa (see Table S1). ln($r(T_c)$) is the rate of growth normalized to an arbitrary reference temperature, $T_c = 18$ °C, where no low or high temperature inactivation is experienced. E_a is the activation energy (in eV) that characterises the steepness of the slope leading to a thermal optimum. E_h characterizes temperature-induced inactivation of growth above T_h, the temperature where half the enzymes are rendered non functional. The quasi r^2 represents the quality of the model fitting and T_{opt} is the optimal temperature at which the maximum growth rate is reached.

Table S2. Details of the linear mixed effects model analysis for the biodiversity - ecosystem functioning relationship.

Model	d.f.	AIC	Log Lik	Chisq	p
Random effects structure					
random = $\sim$ *1/Replicate*					
Fixed effects structure					
1.log$_{10}Y \sim$ *1 + log*$_{10}S$ ** T*	19	-1055.15	546.57	108.11	$< 0.001 * **$
2.log$_{10}Y \sim$ *1 + log*$_{10}S$ *+ T*	12	-961.04	492.52		

Random effects on intercept were determined at the level of replicates nested within richness level. The results of the model selection procedure on the fixed effect terms are given and the most parsimonious model is model 1 ($p < 0.01$). Analyses reveal that ecosystem functioning ($\log_{10}$Y) changed significantly through the different richness levels ($\log_{10}S$) and that the exponent and intercept were significantly different between selection temperatures. The degrees of freedom (d.f.), AIC, logLik, Chi square (Chisq) and p-value are given.

Table S3. Results from the pairwise comparison of the Permutational Multivariate Analysis of Variance (PERMANOVA) to test the effect of temperature on community composition.

Temperature	F	R^2	p-value	p.adjusted
10-20	4.56	0.21	0.010	$0.030*$
10-40	9.22	0.34	0.001	$0.003 * **$
20-40	19.75	0.54	0.001	$0.003 * **$

The table shows the parameters obtained from the pairwise Permutational Multivariate Analysis of Variance (PERMANOVA) comparison to compare whether there is significant differences between all pairwise combinations of the temperature treatments (10, 20 and 40 °C). p is the p-value and p.adjusted is the adjusted p value using Bonferroni correction.

Table S4. Results from the Permutational Multivariate Analysis of Variance (PERMANOVA) analysis to test the effect of temperature on community composition

Parameter	d.f.	Sum of Sqs	Mean Sqs	F-value	R^2	p-value
Temperature	1	2.76	2.76	10.00	0.27	$0.001 * **$
Residuals	27	7.44	0.28		0.73	
Total	28	10.20			1.00	

The table shows the parameters obtained from Permutational Multivariate Analysis of Variance (PERMANOVA) test to analyse whether there is significant differences between the species composition at each temperature treatments (10, 20 and 40 °C).

Table S5. Local scale and total biodiversity partitions.

		Temperature treatments		
		10	20	40
Biodiversity effects				
NBE	$\sum_k^P \sum_j^T \sum_i^N \Delta \mathrm{R}_{ijk} Y_{ijk}$ [5]	0.50	0.16	0.38
TC	PTN$\overline{\overline{\Delta RY}}$ [6]	0.43	0.12	0.24
TS	PTNcov($\Delta \mathrm{RY}_{ijk}$, M_{ijk}) [7]	0.07	0.06	0.13
local $<NBE>$	$\sum_i^N \Delta \mathrm{R}_i Y_i$ [8]	0.050	0.018	0.038
local $<CE>$	N$\overline{\Delta RYM}$ [9]	0.043	0.012	0.024
local $<SE>$	Ncov($\Delta \mathrm{RY}_i$, M_i) [10]	0.007	0.006	0.014

NBE is the net biodiversity effect, TC is the total complementarity, TS is the total selection effect, local $<NBE>$ is the average local net biodiversity effect, local $<CE>$ is the average local complememtarity effect and local $<SE>$ is the average local selection effect. $\overline{\Delta RY}$ is the average change in the relative yield for all species in the mixture and M is the monoculture yield, i is the indexes of one of the number of species (N = 24), j is the indexes of one of T times (T = 1), k is the indexes of one of P places (P = 10).

Table S6. List of bacterial isolates used in the experiment.

Isolate ID	Genus	Family	Phylum	Stream	Temp stream	Accession number
Ic1B(b)	Aeromonas sp	Aeromonadaceae	Gammaproteobacteria	1B	8.2	MH801968
Ic4(c)	Aeromonas sp	Aeromonadaceae	Gammaproteobacteria	4	7.3	MH801970
IcV(d)	Aeromonas sp	Aeromonadaceae	Gammaproteobacteria	vent	38	MH801982
Ic1(e)	Chryseobacterium sp	Flavobacteriaceae	Bacteroidetes	1	16.5	MH801963
Ic10(f)	Chryseobacterium sp	Flavobacteriaceae	Bacteroidetes	10	16.5	MH801979
Ic5(g)	Chryseobacterium sp	Flavobacteriaceae	Bacteroidetes	5	16.5	MH801973
Ic1A(h)	Janthinobacterium sp	Janthinobacteriaceae	Betaproteobacteria	1A	8	MH801965
Ic4(i)	Erwinia sp	Enterobacteriaceae	Gammaproteobacteria	4	7.3	MH801971
Ic5(j)	Hebaspirillum sp	Betaproteobacteria	Oxalobacteriaceae	5	26.9	MH801976
Ic11A(k)	Flavobacterium sp	Flavobacteriaceae	Bacteroidetes	11A	14.4	MH801981
Ic1B(l)	Aeromonas sp	Aeromonadaceae	Gammaproteobacteria	1B	8.2	MH801969
Ic4(m)	Aeromonas sp	Aeromonadaceae	Gammaproteobacteria	4	7.3	MH801972
Ic7(n)	Aeromonas sp	Aeromonadaceae	Gammaproteobacteria	7	11.4	MH801974
Ic5(o)	Chryseobacterium sp	Flavobacteriaceae	Bacteroidetes	5	26.9	MH801975
Ic5(p)	Aeromonas sp	Aeromonadaceae	Gammaproteobacteria	5	26.9	MH801977
Ic5(q)	Aeromonas sp	Aeromonadaceae	Gammaproteobacteria	5	26.9	MH801978
Ic7(r)	Aeromonas sp	Aeromonadaceae	Gammaproteobacteria	7	11.4	MH801980
Ic11B(s)	Buttiauxella sp	Gammaproteobacteria	Enterobacteriaceae	11B	17.2	MH801983
Ic11B(t)	Bacillus sp	Bacillaceae	Bacilli	11B	17.2	MH801984
IcV(u)	Acinetobacter sp	Moraxellaceae	Gammaproteobacteria	vent	38	MH801985
IcV(v)	Acinetobacter sp	Moraxellaceae	Gammaproteobacteria	vent	38	MH801986
Ic1A(w)	Pseudomonas sp	Gammaproteobacteria	Pseudomonaceae	1A	8	MH801964
Ic1(x)	Pseudomonas sp	Gammaproteobacteria	Pseudomonaceae	1	16.5	MH801967
Ic1A(y)	Pseudomonas sp	Gammaproteobacteria	Pseudomonaceae	1A	8	MH801966

Isolate identification codes, taxonomic information, stream ID, average daily water temperature at the time of sampling and GenBank accession numbers are given.

Table S7. Experimental design

Richness	Replicate	Isolates ID	Vol (μl)
S2	1	c,t	12
S2	2	x,h	12
S2	3	f,b	12
S2	4	f,p	12
S2	5	b,y	12
S2	6	k,t	12
S2	7	k,j	12
S2	8	h,l	12
S2	9	l,n	12
S2	10	q,d	12
S4	1	d,p,o,w	6
S4	2	v,p,b,f	6
S4	3	q,m,y,x	6
S4	4	h,w,y,s	6
S4	5	h,y,f,w	6
S4	6	i,h,e,b	6
S4	7	g,t,m,u	6
S4	8	u,c,l,g	6
S4	9	i,m,e,q	6
S4	10	f,g,w,r	6
S8	1	v,h,y,t,b,k,i,r	3
S8	2	u,d,f,v,w,l,q,p	3
S8	3	v,r,w,m,g,u,i,h	3
S8	4	k,y,l,q,h,o,r,c	3
S8	5	j,o,w,g,n,s,u,f	3
S8	6	l,o,b,f,j,r,v,y	3
S8	7	b,s,p,q,o,v,t,g	3
S8	8	i,t,j,b,g,d,c,w	3
S8	9	n,l,u,e,x,y,k,j	3
S8	10	j,d,c,t,k,m,g,o	3
S16	1	h,j,n,u,f,s,t,m,l,b,d,o,x,v,i,q	1.5
S16	2	s,x,j,r,t,f,m,d,u,g,b,q,l,e,n,p	1.5
S16	3	m,f,t,p,q,d,o,h,s,k,l,i,r,j,b,x	1.5
S16	4	s,q,l,t,j,f,c,y,g,i,k,x,w,e,v,d	1.5
S16	5	q,g,l,r,c,v,h,p,x,y,s,m,w,f,i,	1.5
S16	6	l,r,j,h,q,e,n,d,t,x,u,b,i,k,m,y	1.5
S16	7	l,k,s,n,o,h,f,r,y,e,c,t,m,v,x,q	1.5
S16	8	j,k,e,b,p,c,y,l,q,i,h,d,x,f,g,t	1.5
S16	9	g,o,n,c,b,w,r,l,j,i,x,h,q,t,d,k	1.5
S16	10	s,l,e,q,d,r,m,k,g,h,i,u,p,b,n,	1.5
S24	1	all 24 sps	1
S24	2	all 24 sps	1
S24	3	all 24 sps	1
S24	4	all 24 sps	1
S24	5	all 24 sps	1
S24	6	all 24 sps	1
S24	7	all 24 sps	1
S24	8	all 24 sps	1
S24	9	all 24 sps	1
S24	10	all 24 sps	1

The table shows the experimental design of the diversity experiment. Richness represents the number of species assembled. Replicate identifies each of the 10 independent communities at each diversity level. Isolate IDs, give the identity of each isolate assembled into each community (we have only used the letter in brackets of the isolates ID in order to simplify the experimental design, see table S1 for further information about the bacterial isolates) and, finally, the volume describes the volume of media for each isolate added to each of the communities.

Table S8. Model selection results linking the species thermal traits to the observed ecosystem functioning in the biodiversity experiment

Random effects structure
random = $\sim$ *1S/Replicate*
Fixed effects structure
Model 1 Y $\sim$ $<T_{opt}>_c$ * T * S
Model 2 Y $\sim$ $<T_{opt}>_c$ + T + S + $<T_{opt}>_c$:T + $<T_{opt}>_c$:S + T:S
Model 3 Y $\sim$ $<T_{opt}>_c$ + T + S + $<T_{opt}>_c$:T + $<T_{opt}>_c$:S

Parameters	d.f.	AIC	logLik	Chisq	p-value
Model 3	24	-2043.1	1045.5		
Model 2	45	-2099.1	1094.6	98.11	$< 0.001 * **$
Model 1	66	-2087.7	1109.8	30.59	0.08

We used a linear mixed effects model to assess whether the community-mean optimum temperature, $<T_{\mathrm{opt}}>_{\mathrm{c}}$, was a significant predictor of ecosystem functioning across the various temperature (T) and diversity levels (S). To test for the significance of all terms in the model we sequentially removed terms from the most complex model that included all variables and their interactions using likelihood ratio tests. We found that the most parsimonious model included all variables and all two-way interactions, but did not include the 3-way interaction between $<T_{\mathrm{opt}}>_{\mathrm{c}}$: T : S.

Table S9. Multiple comparison contrast analysis for the power function between biodiversity and ecosystem function

Linear Hypotheses	Estimate	SE	t value	p-value
$log_{10}Y\ (S_c)$.T10 vs. $log_{10}Y\ (S_c)$.T15 == 0	-1.33	0.02	-80.74	$< 0.01 **$
$log_{10}Y\ (S_c)$.T10 vs. $log_{10}Y\ (S_c)$.T20 == 0	-1.36	0.02	-82.35	$< 0.01 **$
$log_{10}Y\ (S_c)$.T10 vs. $log_{10}Y\ (S_c)$.T25 == 0	-1.36	0.02	-82.60	$< 0.01 **$
$log_{10}Y\ (S_c)$.T10 vs. $log_{10}Y\ (S_c)$.T27.5 == 0	-1.36	0.02	-82.40	$< 0.01 **$
$log_{10}Y\ (S_c)$.T10 vs. $log_{10}Y\ (S_c)$.T30 == 0	-1.39	0.02	-84.34	$< 0.01 **$
$log_{10}Y\ (S_c)$.T10 vs. $log_{10}Y\ (S_c)$.T35 == 0	-1.38	0.02	-84.34	$< 0.01 **$
$log_{10}Y\ (S_c)$.T10 vs. $log_{10}Y\ (S_c)$.T40 == 0	-1.44	0.02	-86.70	$< 0.01 **$
$log_{10}Y\ (S_c)$.T15 vs. $log_{10}Y\ (S_c)$.T20 == 0	-0.03	0.01	-1.78	0.86
$log_{10}Y\ (S_c)$.T15 vs. $log_{10}Y\ (S_c)$.T25 == 0	-0.03	0.01	-1.96	0.75
$log_{10}Y\ (S_c)$.T15 vs. $log_{10}Y\ (S_c)$.T27.5 == 0	-0.03	0.01	-1.83	0.83
$log_{10}Y\ (S_c)$.T15 vs. $log_{10}Y\ (S_c)$.T30 == 0	-0.06	0.01	-3.98	$< 0.01 *$
$log_{10}Y\ (S_c)$.T15 vs. $log_{10}Y\ (S_c)$.T35 == 0	-0.05	0.01	-3.06	0.09
$log_{10}Y\ (S_c)$.T15 vs. $log_{10}Y\ (S_c)$.T40 == 0	-0.11	0.02	-7.39	$< 0.01 **$
$log_{10}Y\ (S_c)$.T20 vs. $log_{10}Y\ (S_c)$.T25 == 0	-0.003	0.01	-0.18	1.00
$log_{10}Y\ (S_c)$.T20 vs. $log_{10}Y\ (S_c)$.T27.5 == 0	-0.001	0.01	-0.05	1.00
$log_{10}Y\ (S_c)$.T20 vs. $log_{10}Y\ (S_c)$.T30 == 0	-0.03	0.01	-2.20	0.56
$log_{10}Y\ (S_c)$.T20 vs. $log_{10}Y\ (S_c)$.T35 == 0	-0.02	0.01	-1.29	0.99
$log_{10}Y\ (S_c)$.T20 vs. $log_{10}Y\ (S_c)$.T40 == 0	-0.08	0.02	-5.63	$< 0.01 **$
$log_{10}Y\ (S_c)$.T25 vs. $log_{10}Y\ (S_c)$.T27.5 == 0	0.001	0.01	0.12	1.00
$log_{10}Y\ (S_c)$.T25 vs. $log_{10}Y\ (S_c)$.T30 == 0	-0.03	0.01	-2.03	0.70
$log_{10}Y\ (S_c)$.T25 vs. $log_{10}Y\ (S_c)$.T35 == 0	-0.02	0.01	-1.12	1.00
$log_{10}Y\ (S_c)$.T25 vs. $log_{10}Y\ (S_c)$.T40 == 0	-0.08	0.02	-5.46	$< 0.01 **$
$log_{10}Y\ (S_c)$.T27.5 vs. $log_{10}Y\ (S_c)$.T30 == 0	-0.03	0.01	-2.15	0.61
$log_{10}Y\ (S_c)$.T27.5 vs. $log_{10}Y\ (S_c)$.T35 == 0	-0.02	0.01	-1.23	0.99
$log_{10}Y\ (S_c)$.T27.5 vs. $log_{10}Y\ (S_c)$.T40 == 0	-0.08	0.02	-5.58	$< 0.01 **$
$log_{10}Y\ (S_c)$.T30 vs. $log_{10}Y\ (S_c)$.T35 == 0	0.01	0.01	0.91	1.00
$log_{10}Y\ (S_c)$.T30 vs. $log_{10}Y\ (S_c)$.T40 == 0	-0.05	0.02	-3.45	$0.03*$
$log_{10}Y\ (S_c)$.T35 vs. $log_{10}Y\ (S_c)$.T40 == 0	-0.07	0.02	-4.34	$< 0.01 **$
b.T10 vs. b.T15 == 0	0.22	0.03	7.00	$< 0.01 **$
b.T10 vs. b.T20 == 0	0.13	0.03	4.21	$< 0.01 **$
b.T10 vs. b.T25 == 0	0.19	0.03	5.94	$< 0.01 **$
b.T10 vs. b.T27.5 == 0	0.19	0.03	5.82	$< 0.01 **$
b.T10 vs. b.T30 == 0	0.18	0.03	5.71	$< 0.01 **$
b.T10 vs. b.T35 == 0	0.30	0.03	9.53	$< 0.01 **$
b.T10 vs. b.T40 == 0	0.33	0.03	10.18	$< 0.01 **$
b.T15 vs. b.T20 == 0	-0.09	0.03	-3.27	$0.05*$
b.T15 vs. b.T25 == 0	-0.03	0.03	-1.27	0.99
b.T15 vs. b.T27.5 == 0	-0.04	0.03	-1.38	0.98
b.T15 vs. b.T30 == 0	-0.04	0.03	-1.51	0.96
b.T15 vs. b.T35 == 0	0.08	0.03	3.00	0.10
b.T15 vs. b.T40 == 0	0.11	0.03	3.84	$< 0.01 **$
b.T20 vs. b.T25 == 0	0.05	0.03	2.01	0.71
b.T20 vs. b.T27.5 == 0	0.05	0.03	1.89	0.80
b.T20 vs. b.T30 == 0	0.05	0.03	1.75	0.87
b.T20 vs. b.T35 == 0	0.17	0.03	6.23	$< 0.01 **$
b.T20 vs. b.T40 == 0	0.20	0.03	7.02	$< 0.01 **$
b.T25 vs. b.T27.5 == 0	-0.003	0.03	-0.11	1.00
b.T25 vs. b.T30 == 0	-0.007	0.03	-0.25	1.00
b.T25 vs. b.T35 == 0	0.11	0.03	4.28	$< 0.01 **$
b.T25 vs. b.T40 == 0	0.14	0.03	5.10	$< 0.01 **$
b.T27.5 vs. b.T30 == 0	-0.004	0.03	-0.13	1.00
b.T27.5 vs. b.T35 == 0	0.12	0.03	4.37	$< 0.01 **$
b.T27.5 vs. b.T40 == 0	0.15	0.03	5.18	$< 0.01 **$
b.T30 vs. b.T35 == 0	0.12	0.03	4.50	$< 0.01 **$
b.T30 vs. b.T40 == 0	0.15	0.03	5.31	$< 0.01 **$
b.T35 vs. b.T40 == 0	0.03	0.03	0.88	1.00

Data shown are the contrast analysis for the biodiversity-ecosystem functioning relationship. This analysis tests whether exponent (b) and the intercept ($\log_{10}Y(S_c)$) are significantly different between all pairwise combinations of temperature treatments. The standard error (SE), t value and p-value were estimated for all possible pairwise combinations are given.

Table S10. Results from the analysis of variance (ANOVA) on the local scale biodiversity partitions.

	Net Effect					Sel effect					Comp effect				
Resp	d.f.	SumSqs	MeanSqs	F	p	d.f.	SumSqs	MeanSqs	F	p	d.f.	SumSqs	MeanSqs	F	p
Temp	2	0.005	0.002	207.6	< 0.001	2	$3*10^{-4}$	$1.64*10^{-4}$	3.1	0.06	2	0.005	0.002	48.8	< 0.001
Res	26	$3*10^{-4}$	$1*10^{-5}$			26	0.001	$5.29*10^{-5}$			26	0.001	$4.8*10^{-5}$		

ANOVAs were carried to determine whether the net biodiversity effects (NE), selection effects (SE) and complementarity effects (CE) were significantly different between temperature treatments (10, 20 and 40 °C). Analyses reveals that there is a significant effect of temperature for all biodiversity partitions ($p < 0.05$) except for selection effects ($p = 0.06$).

Table S11. Posthoc Tukey tests for the biodiversity partitions.

	Net Effect				Sel effect				Comp effect			
Temperature	diff	lwr	upr	p	diff	lwr	upr	p	diff	lwr	upr	p
20-10	-0.03	-0.04	-0.03	$< 0.001 * **$	-0.001	-0.01	0.01	0.94	-0.03	-0.04	-0.02	$< 0.001 * **$
40-10	-0.01	-0.02	-0.01	$< 0.001 * **$	0.005	-0.002	0.01	0.13	-0.02	-0.03	-0.02	$< 0.001 * **$
40-20	0.02	0.02	0.02	$< 0.001 * **$	0.005	-0.003	0.01	0.25	0.01	0.01	0.02	$< 0.01 * **$

Post hoc Tukey tests were carried to assess whether the net biodiversity effect (NE), the selection effect (SE), and complementarity effect (CE) differed among all pairwise combinations of the temperature treatments. Analyses reveal significant differences across temperature treatments for NE and CE, but not for SE.

Table S12. One sample t-test to assess whether the net biodiversity effect, the selection effect and the complementarity effects were significantly different from zero.

	Net Effect				Sel effect				Comp effect			
Temperature	t	df	CI[95%]	p	t	df	CI[95%]	p	t	df	CI[95%]	p
10	49.21	9	0.047 to 0.052	$< 0.001 * **$	3.45	9	0.003 to 0.012	$< 0.01 * *$	23.47	9	0.038 to 0.047	$< 0.001 * **$
20	13.6	8	0.015 to 0.021	$< 0.001 * **$	4.72	8	0.003 to 0.009	$< 0.01 * *$	5.71	8	0.007 to 0.016	$< 0.001 * **$
40	35.90	9	0.035 to 0.040	$< 0.001 * **$	4.58	9	0.007 to 0.02	$< 0.01 * *$	9.10	9	0.018 to 0.031	$< 0.001 * **$

Data shown are the parameters obtained from the t statistical test to analyse whether the net biodiversity effects (NE), selection effects (SE) and complementarity effects (CE) values obtained at the different temperature treatments levels (10, 20 and 40 °C) were or not significantly different from zero. t is the t-value, df the degrees of difference, CI the confidence intervale at 96 % and p the p-value. Analyses suggest that there are that there is a positive effects at all temperature treatments for the three mechanisms studied (NE, SE, CE).