Supplementary Information for:

Agriculture and climate change reshape insect biodiversity worldwide

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Contents

Supplementary Methods

S1: Testing temperature thresholds to define "insect active" months

Insects are active during different times of the year depending on latitude, for example insects in temperate areas are less likely to be active during the winter months, whereas in the tropics insects are often active all year round. In this work, we followed Johansson *et al* in considering insects to be active in any months where the average daily-mean temperature is at or above 10°C[1]. This threshold was chosen based on a study of minimum developmental temperatures of 66 insect species[2]. To determine the potential impact of this choice of threshold on our results, we re-ran our main models for Hypothesis 2 using alternative values: 6 °C and 8 °C.

As the threshold temperature is reduced, more months in higher latitudes meet the threshold, and so the anomaly can be calculated for a greater area, but spatial patterns are consistent (Extended Data Figure 1; Figures S1-2). There was very little difference in responses of total insect abundance when using the different temperature thresholds (Figure S3-S4, threshold 10 Figure 2 main text). The finding that responses were *relatively* more negative in agriculture (especially intensive agriculture) compared to natural habitats was true across all models.

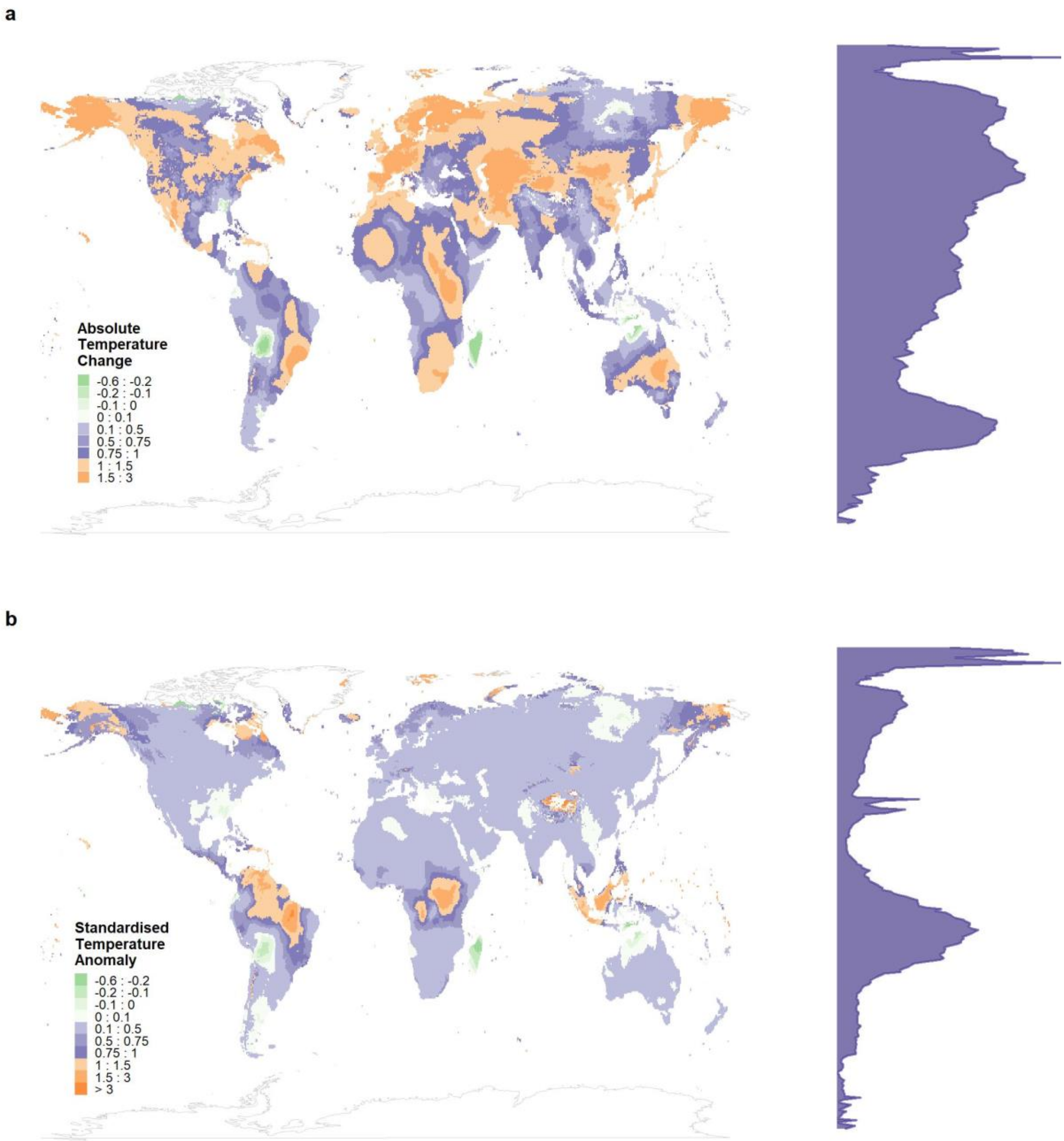
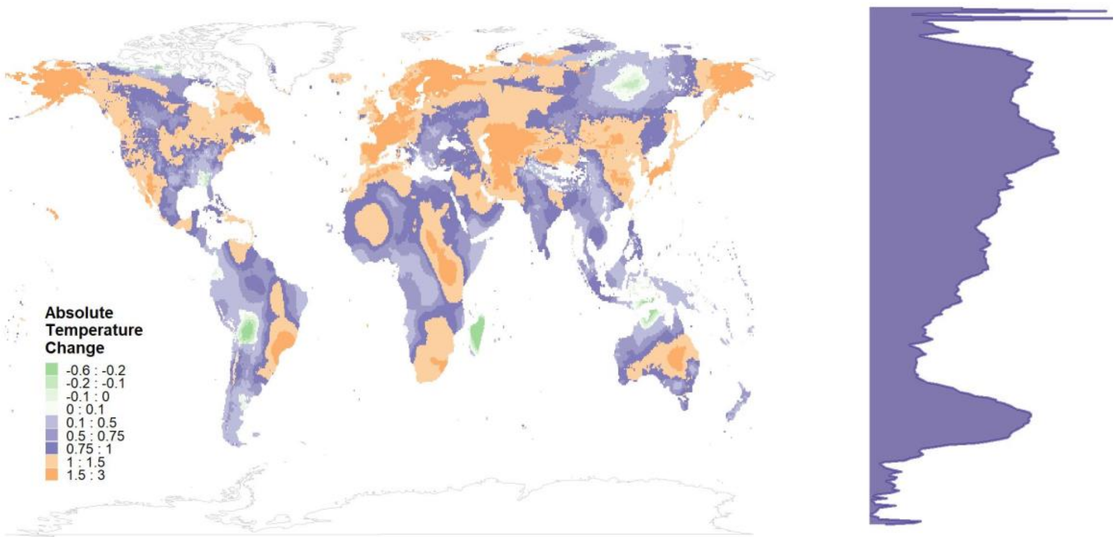


Figure S1: Maps of a. absolute temperature change and b. the standardised temperature anomaly calculated using a threshold of 6°C to define insect-active months. Density plots to the right of each map show the average temperature change at a given latitude. Some areas at the highest latitudes and elevations are blank as they do not have months that meet the insect-active temperature threshold.

a



b

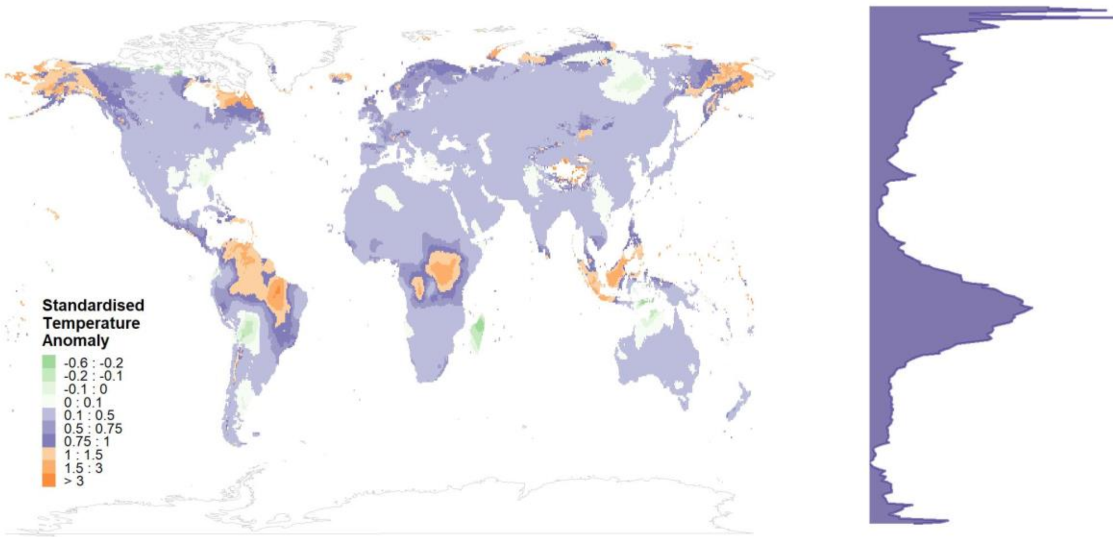


Figure S2: Maps of a. absolute temperature change and b. the standardised temperature anomaly calculated using a threshold of 8°C to define insect-active months. Density plots to the right of each map show the average temperature change at a given latitude. Some areas at the highest latitudes and elevations are blank as they do not have months that meet the insect-active temperature threshold.

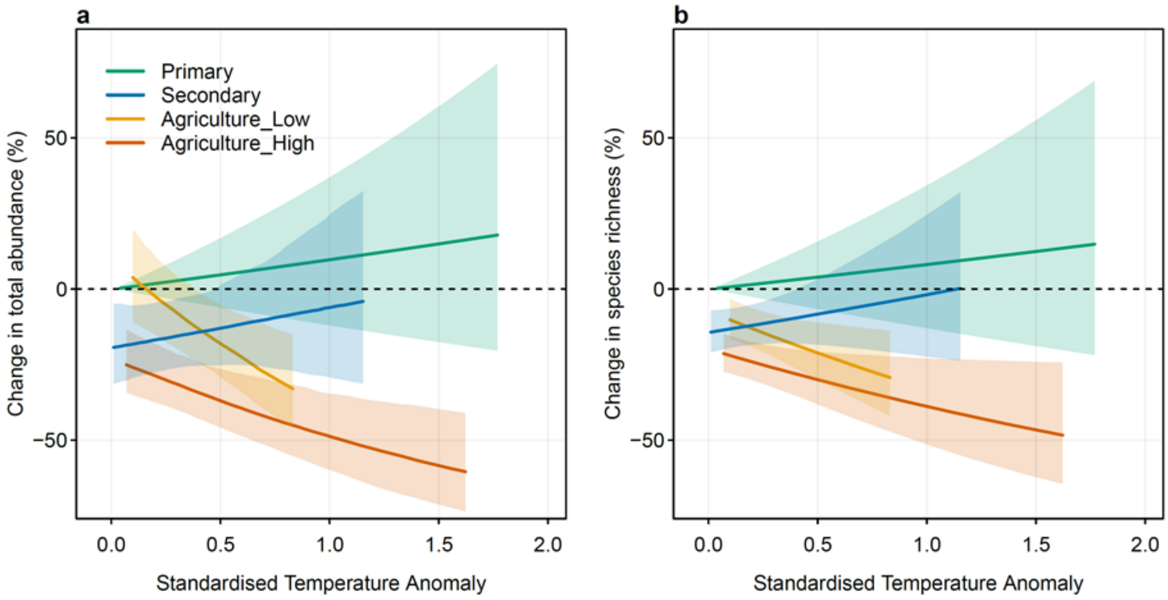


Figure S3: Response of a. insect total abundance and b. species richness to the interaction between land use and the standardised temperature anomaly when the anomaly is calculated using a threshold of 6°C to define insect-active months. Lines correspond to the median predicted value and shaded area represents the 95% confidence interval. Results are plotted for the central 95% of modelled anomaly values for each land use.

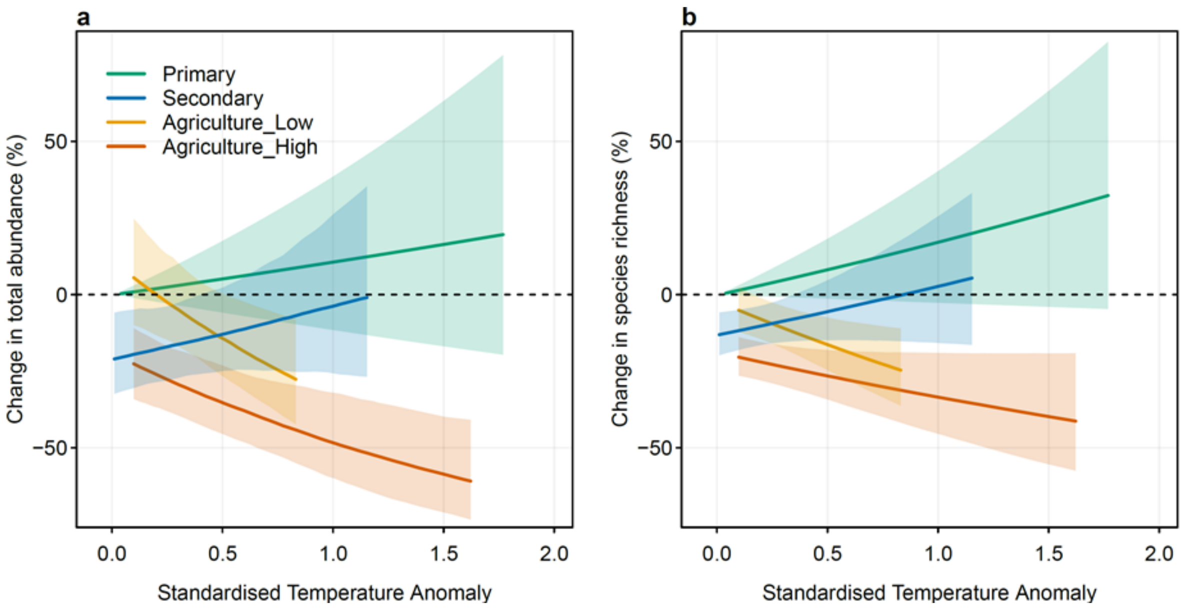


Figure S4: Response of a. insect total abundance and b. species richness to the interaction between land use and the standardised temperature anomaly when the anomaly is calculated using a threshold of 8°C to define insect-active months. Lines correspond to the median predicted value and shaded area represents the 95% confidence interval. Results are plotted for the central 95% of modelled anomaly values for each land use.

S2: Testing differing baseline lengths in STA calculation

To determine the sensitivity of our results to the timespan of the baseline years for calculating the standardised temperature anomaly, we re-calculated the anomaly using three alternative baseline lengths and re-ran the total abundance and species richness models for Hypothesis 2. In the original calculation of the anomaly, a 30-year baseline from 1901 to 1930 was used, matching the length often used in studies of climate impact (e.g. refs [3–5]). Three additional baseline periods of different length were tested: 1. 1901-1905, 2. 1901-1910 and 3. 1901-1920. Maps of the anomalies based on these baselines can be seen in Figure S5. The anomalies calculated from these baselines were used within replicate models for Hypothesis 2, from which we replotted versions of Figure 2. The final model for this sensitivity test took the following form, with a separate model run for each baseline period:

Scaled abundance ~ Land Use-Intensity x Standardized Temperature Anomaly$_{baseline}$+ (1|Study) + (1|Block)

Species Richness ~ Land Use-Intensity x Standardized Temperature Anomaly$_{baseline}$+ (1|Study) + (1|Block) + (1|Site)

Spatial variation in temperature anomaly values and biodiversity responses were very similar across all baselines (Figures S6-S7).

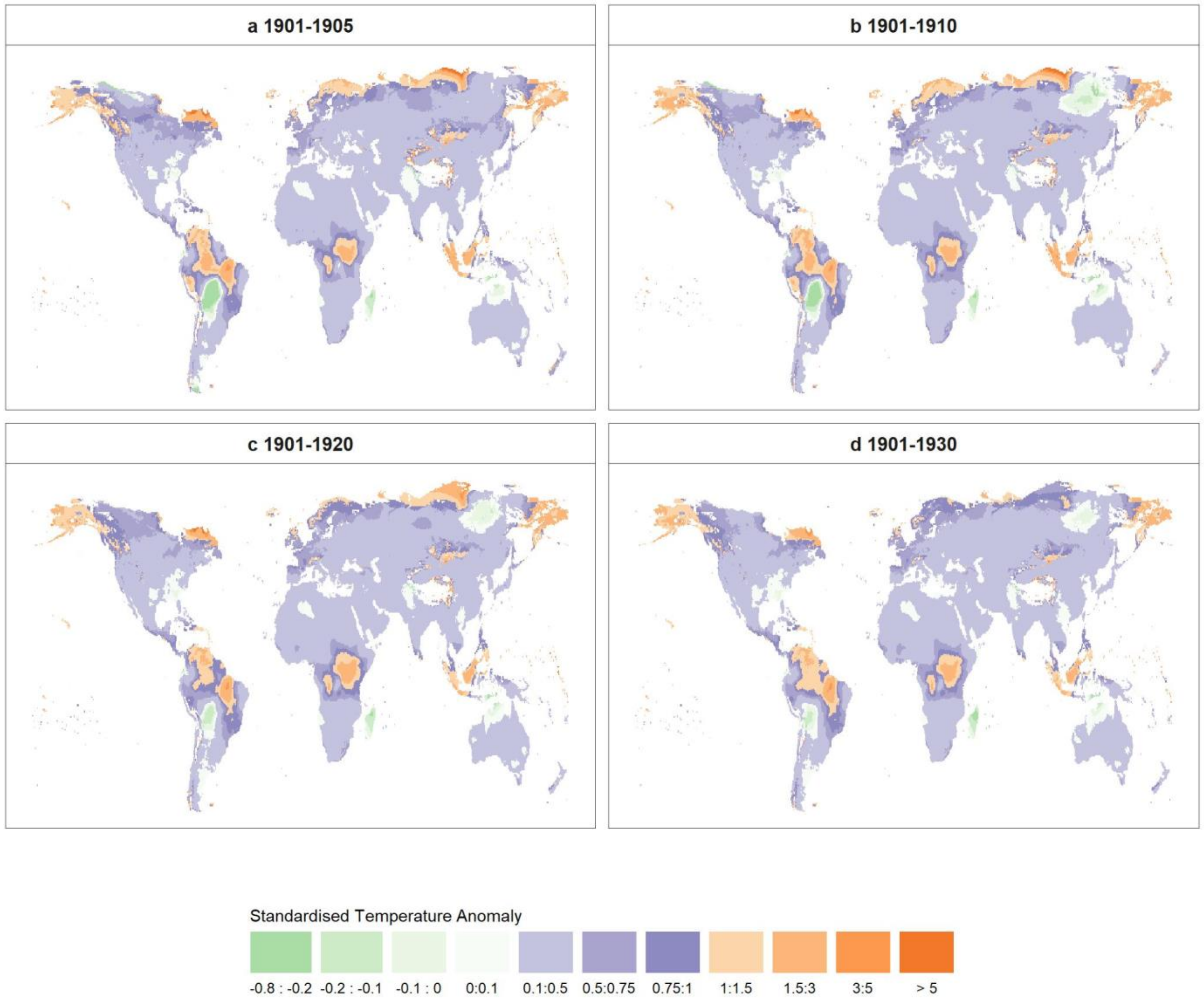


Figure S5: Maps of the standardised temperature anomaly calculated using baselines of different length. a. 1901-1905. b. 1901-1910. c. 1901-1920. d. 1901-1930 (Extended Data Figure 7). The anomaly represents climatic warming from these baselines until 2005.

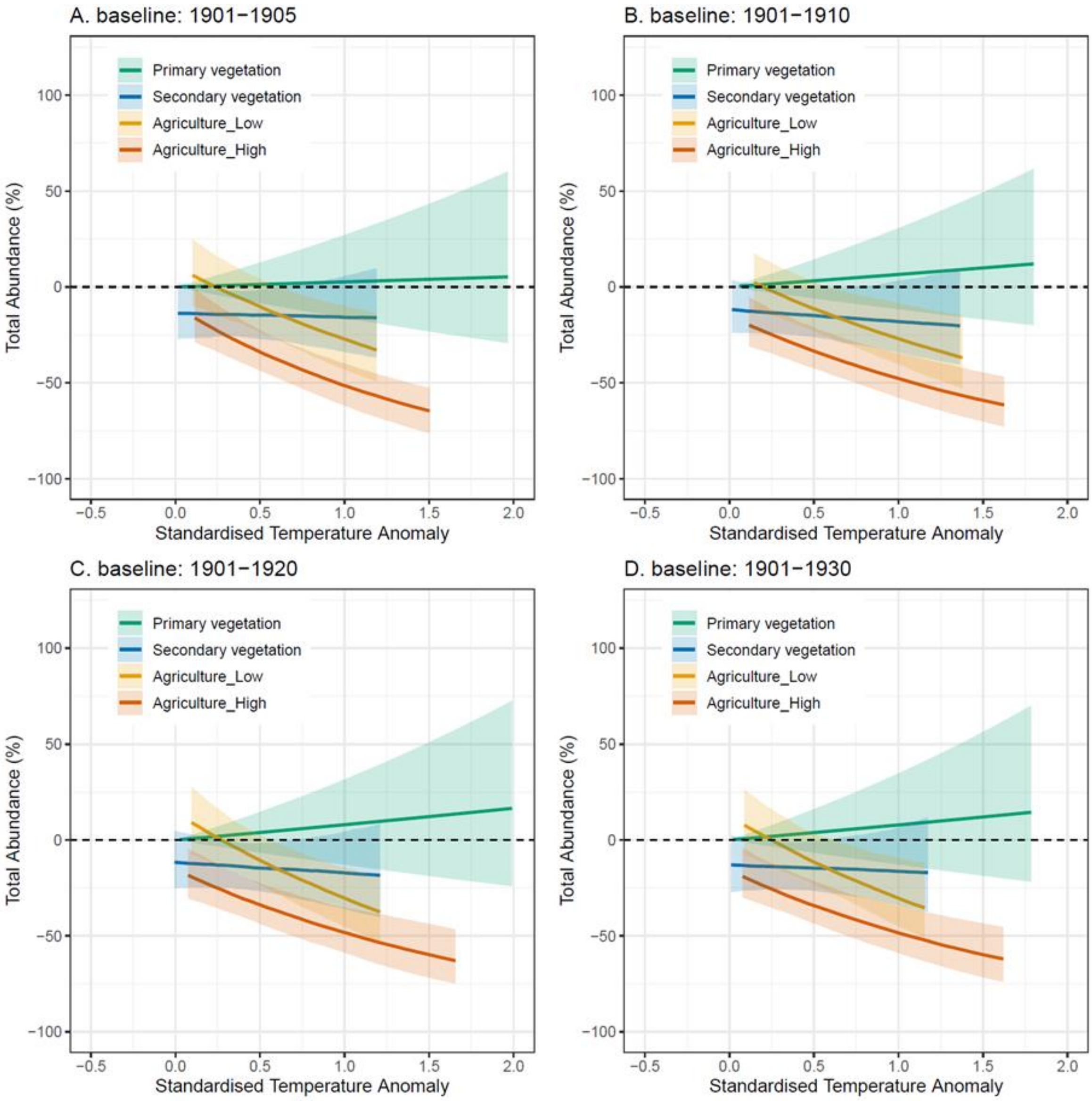


Figure S6: Response of insect abundance to the interaction between land use and the standardised temperature anomaly calculated from baselines of different lengths. A. 1901-1905. B. 1901-1910. C. 1901-1920. D. 1901-1930 (as in Figure 2 in the main text). Values represent the percentage difference compared to primary vegetation with no temperature change (i.e., a standardised temperature anomaly value of 0). Lines correspond to median predicted values and shaded area to 95% confidence intervals. Modelled values are plotted for the central 95% of sampled values of the standardised temperature anomaly for each land use.

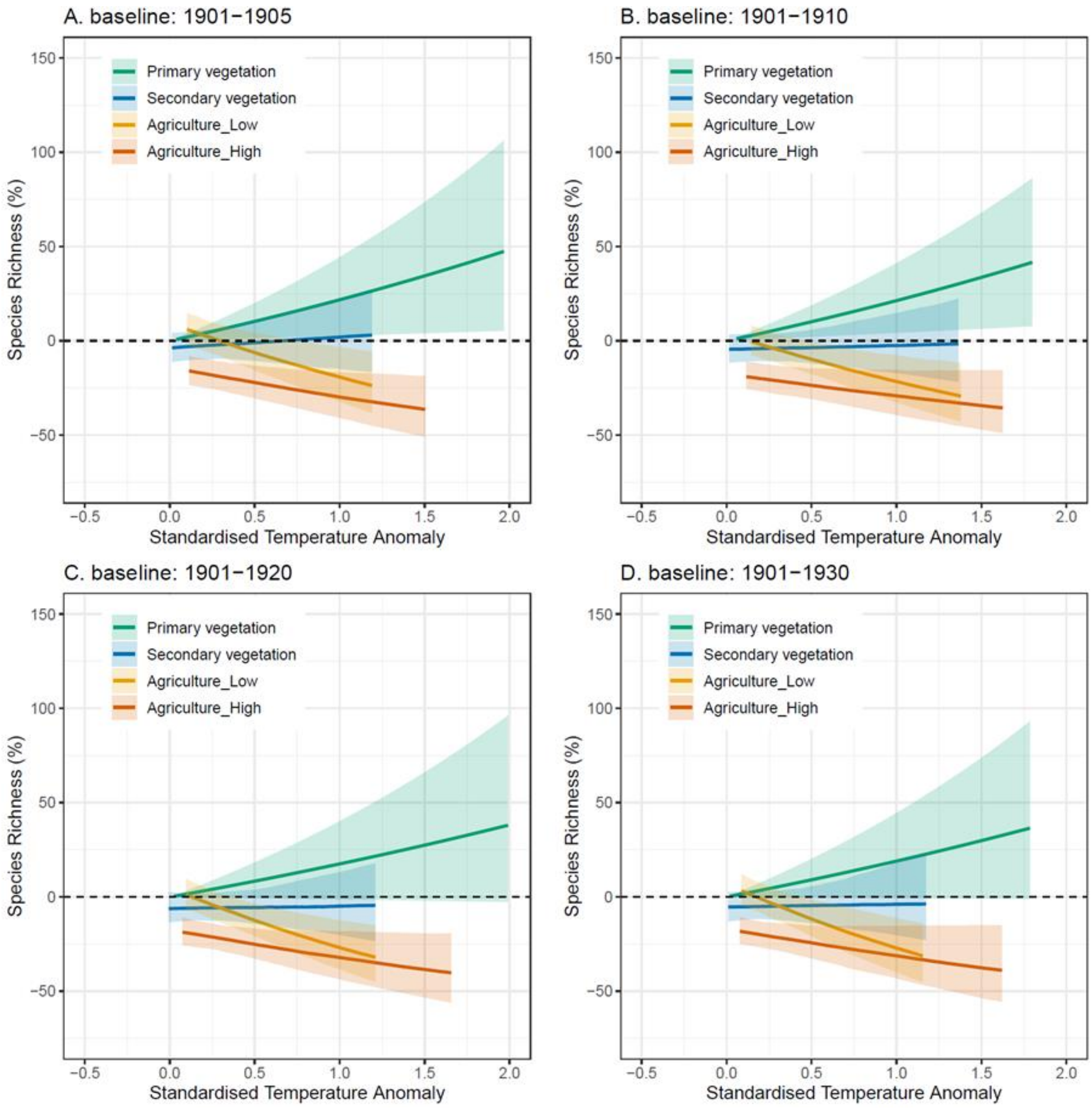


Figure S7: Response of insect species richness to the interaction between land use and standardised temperature anomaly calculated from baselines of different lengths. A. 1901-1905. B. 1901-1910. C. 1901-1920. D. 1901-1930. Values represent the percentage difference compared to primary vegetation with no temperature change (i.e., a standardised temperature anomaly value of 0). Lines correspond to median predicted values and shaded area to 95% confidence intervals. Modelled values are plotted for the central 95% of sampled values of the standardised temperature anomaly for each land use.

S3: Testing the influence of observations based on few weather stations

CRU TS mean temperature and maximum temperature data[6] are used to determine the standardised temperature anomalies used in this study. Mean and maximum temperature estimates are generally based on weather-station observations, except where such observations are missing, in which case estimates are filled based on the 1961-1990 mean monthly terrestrial climatology[7]. Where estimates are based on recent climate estimates, monthly variation in temperatures will be reduced, which could bias our results.

To test this, we investigated the contribution of the number of weather-stations to the baseline temperature estimates at the sites sampled for insect biodiversity. We further tested whether locations supported by fewer weather-stations had a strong influence on our model results. Specifically, we re-ran the models for Hypothesis 2 using subsets of the dataset where sites within grid cells (within the 0.5 × 0.5° grid) where temperature estimates are supported by few weather stations are removed. We did this for both the abundance and the species richness models, for the complete dataset and also for the data subsets for tropical and non-tropical regions. The tropical realm is more affected by sparse weather-station data than the temperate realm. The number of weather stations supporting the temperature estimates ranges between 0 and 8, with fewer stations available in some regions including areas of the tropics and at high latitudes (Figure S8). Most sites in the complete dataset are within regions with 8 contributing stations (Number of sites with *n* stations: 0 = 148, 1 = 178, 2 = 505, 3 = 750, 4 = 147, 5 = 66, 6 = 21, 7 = 66, 8 = 4188).

Importantly, all models were very robust to excluding sites supported by the fewest weather stations (i.e., zero or one weather stations). Sequentially removing sites supported by few stations, from the removal of sites represented by zero weather stations up to sites represented by five weather stations, showed that the abundance results for the complete dataset were qualitatively similar throughout, with the lowest insect biodiversity where agriculture (especially intensive agriculture) coincides with rapid recent climate change (Figure S9). When only sites with four or more stations are included, then the decline in abundance within low-intensity agriculture is no longer present, and primary sites show more of an increase in abundance (Figure S9).

Similar patterns were also seen for the global species richness results (Figures S10). For species richness, the negative effect of climate change in high-intensity agriculture was lost with the removal of fewer sites. When the dataset contains only sites supported by more than 3 stations, the relationship between richness and climate anomaly in high-intensity agriculture is flat.

Within each plot, the central 95% region of the anomaly for which data are available is presented, as more sites are removed, this range is reduced. This removal of data at the more extreme values of the anomaly, likely from the tropical realm and where greater biodiversity losses are likely (Figure S11), will result in a reduced response being presented as these sites are removed. This leads to a spatial bias towards non-tropical sites as sites supported by fewer stations are removed.

When assessing the subsets of data for sites found within the tropical and non-tropical regions, responses of both total abundance and species richness to the interactive effect of land use and climate change were robust to the removal of sites with no or very few weather stations (Figures S12-15). As more sites are removed, the responses in some land uses change, however the range of anomaly values that remains within the dataset quickly becomes reduced in these subsets as you can see from the area covered by the lines in each plot. This is particularly evident for the tropical realm however after sites supported by 3 or fewer stations are removed (Figure S16). In the tropical realm, when sites supported by 3 or fewer stations are removed from the dataset, the coverage of the data across the anomaly values is much reduced (Figure

S12-13). This is not such an issue for the non-tropical sites (Figures S14-15). The number of sites remaining within the dataset in each iteration of the analysis is presented in each figure legend.

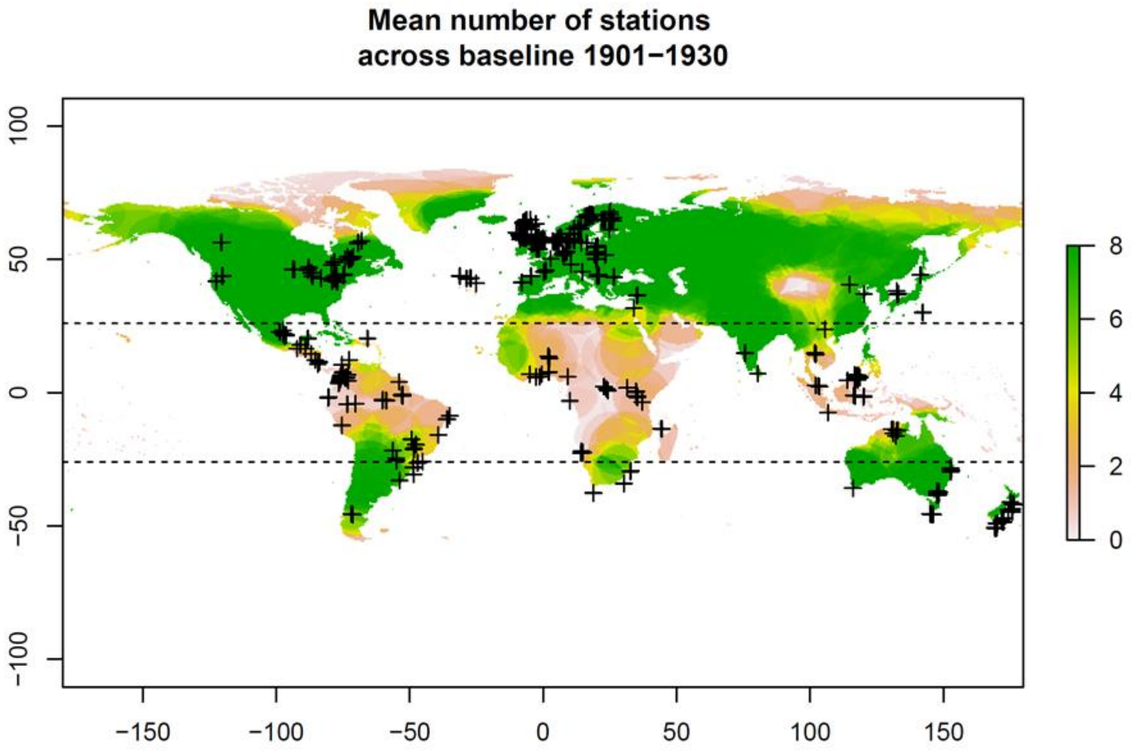


Figure S8: Map showing the mean number of weather stations across the baseline period 1901-1930. This information is taken from the 'stn' variable supplied alongside the mean temperature data from the CRU TS dataset. Crosses show the locations of the sites sampled in the PREDICTS database and used in this study.

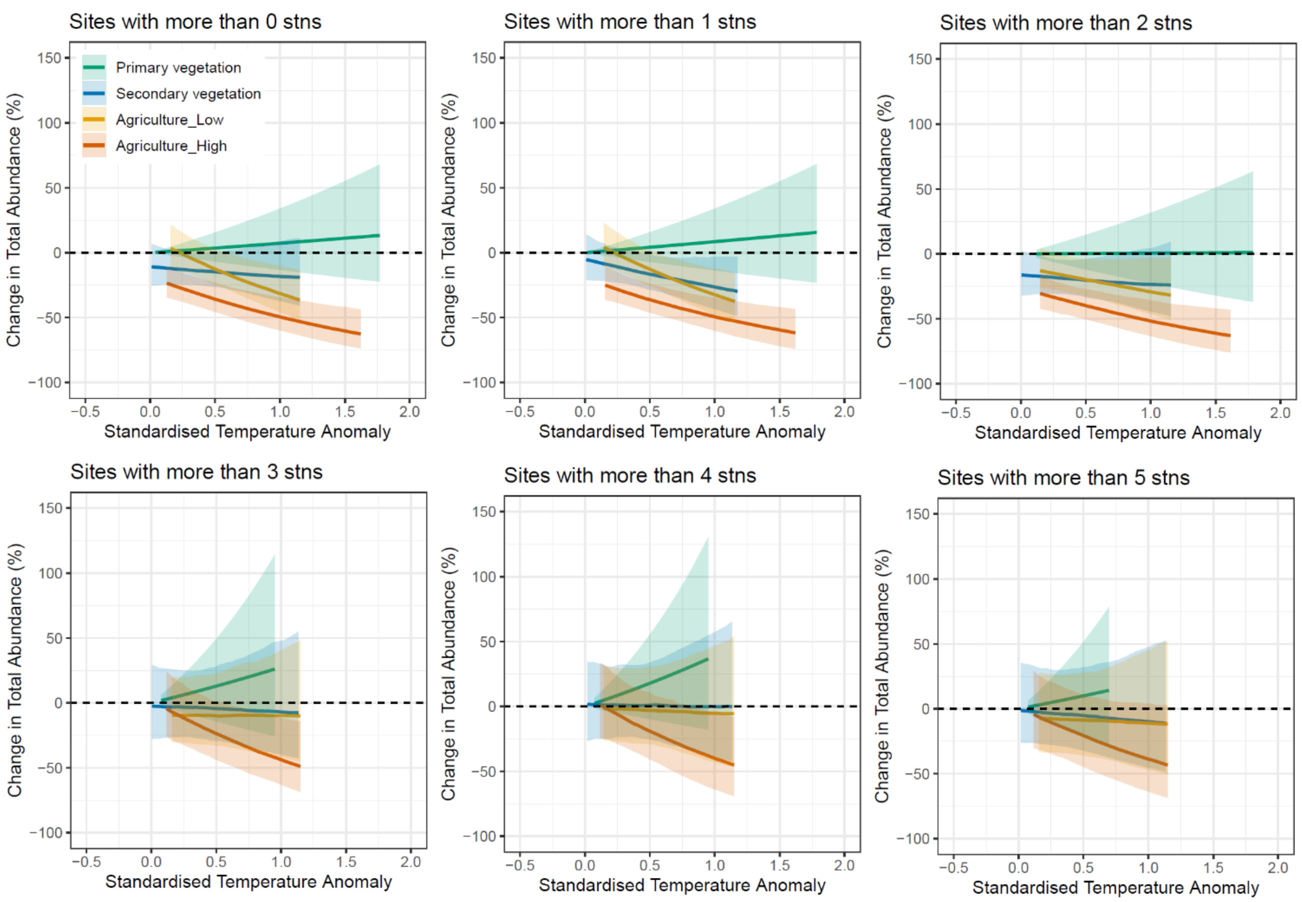


Figure S9: Results from total abundance model runs where sites with few observations contributing to the CRU TS temperature data are sequentially removed. First, sites supported by an average of 0 observations are removed and the models run, followed by 1, 2, 3 up to 5. At the point where sites are supported by more than 5 stations, only 231 of the 4120 sites are from the tropics. Number of sites supported by more than *n* stations: 0 = 5,608, more than 1 = 5,434, more than 2 = 5,021, more than 3 = 4,289, more than 4 = 4,201, more than 5 = 4,135. Lines correspond to the median predicted value and shaded area represents the 95% confidence interval.

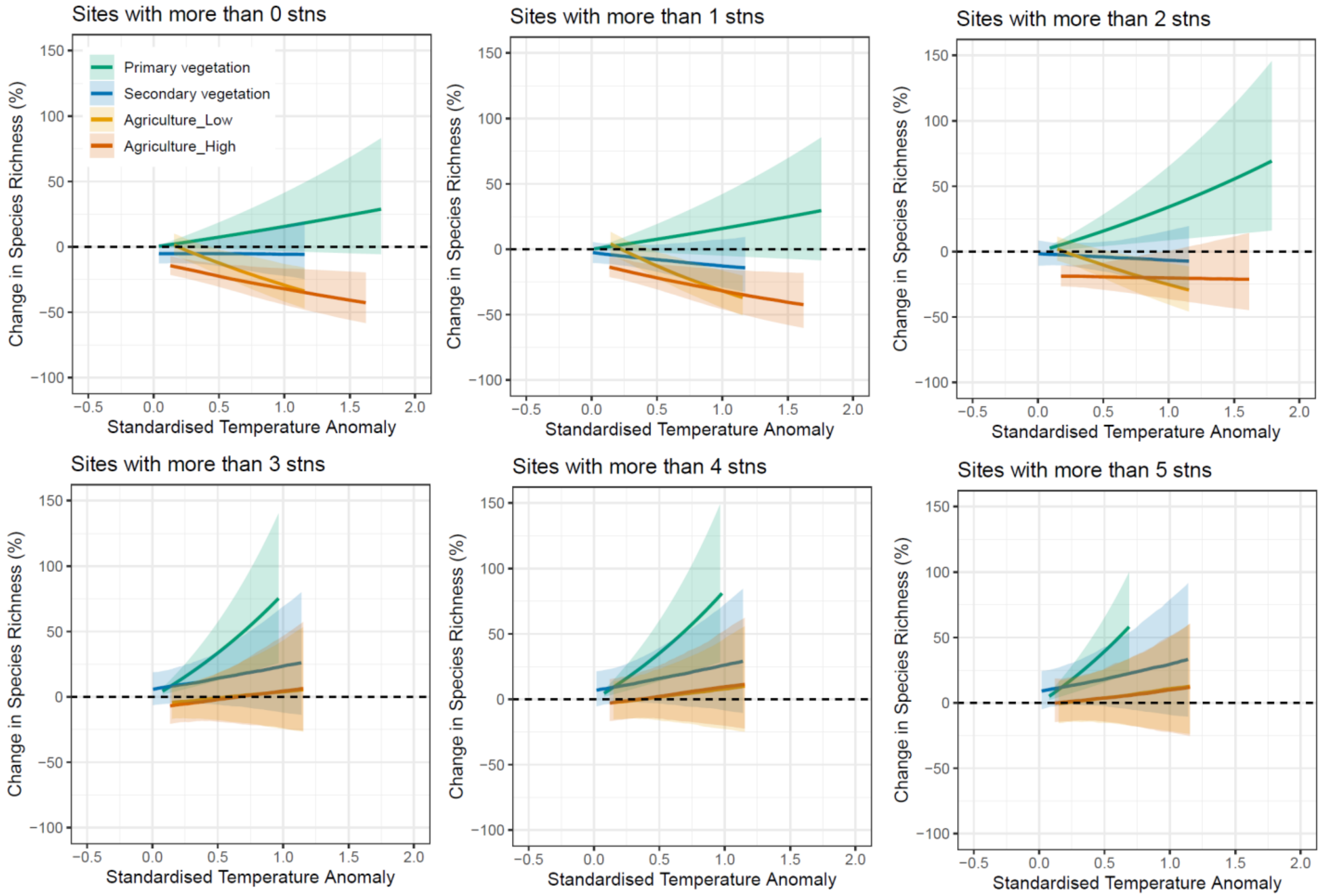


Figure S10: Results from species richness model runs where sites with few observations contributing to the CRU TS temperature data are sequentially removed. First, sites supported by an average of 0 observations are removed and the models run, followed by 1, 2, 3 up to 5. At the point where sites are supported by more than 5 stations, only 243 of the 4,254 sites are from the tropics. Number of sites supported by more than *n* stations 0 = 5,921, more than 1 = 5,743, more than 2 = 5,238, more than 3 = 4,488, more than 4 = 4,341, more than 5 = 4,275. Lines correspond to the median predicted value and shaded area represents the 95% confidence interval.

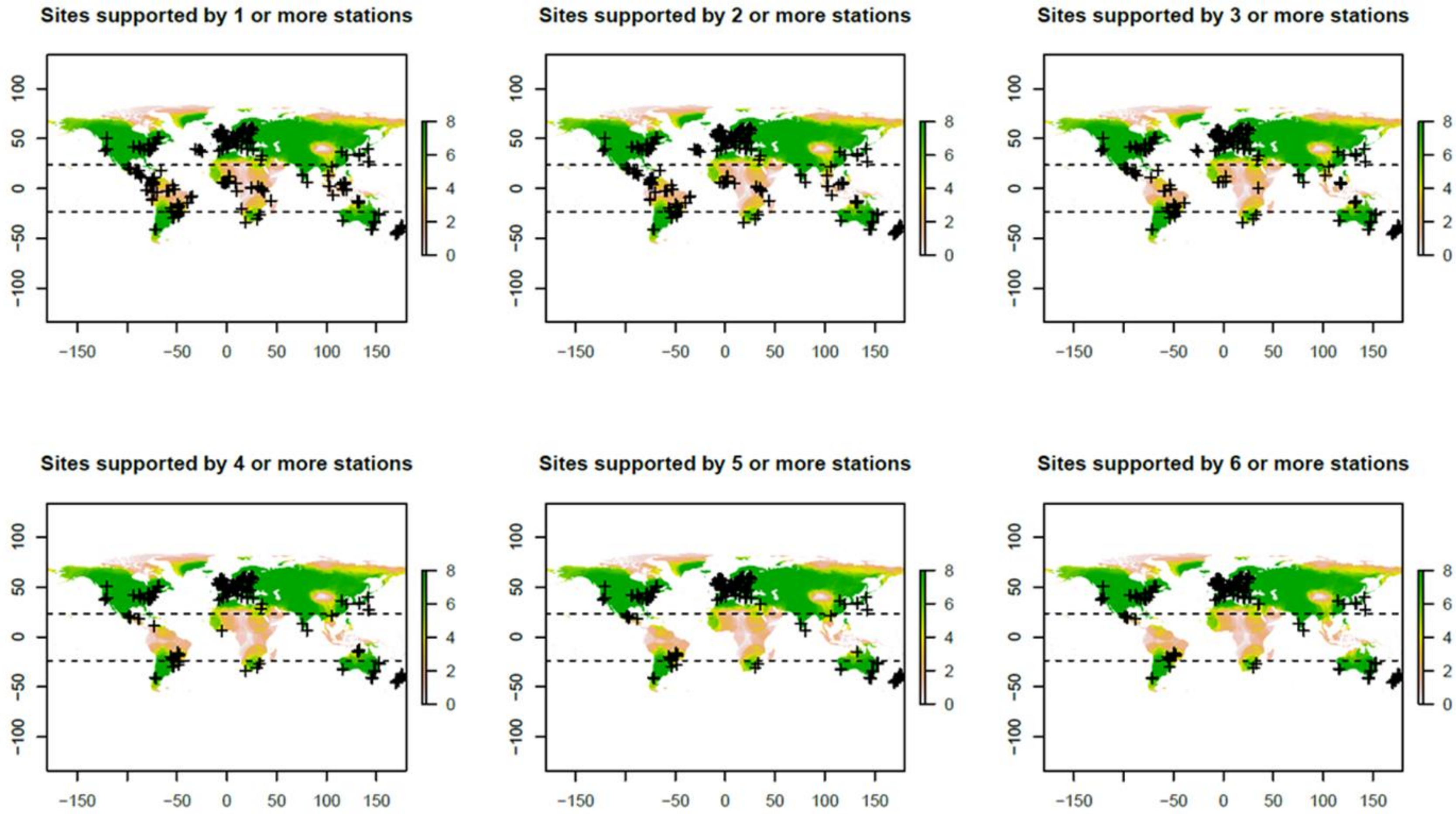


Figure S11: Maps showing the mean number of weather stations across the baseline period 1901-1930 and the PREDICTS sites remaining in the dataset as sites supported by few weather stations are gradually removed. This information is taken from the 'stn' variable supplied alongside the mean temperature data from the CRU TS dataset. Crosses show the locations of the sites sampled in the PREDICTS database and used in this study.

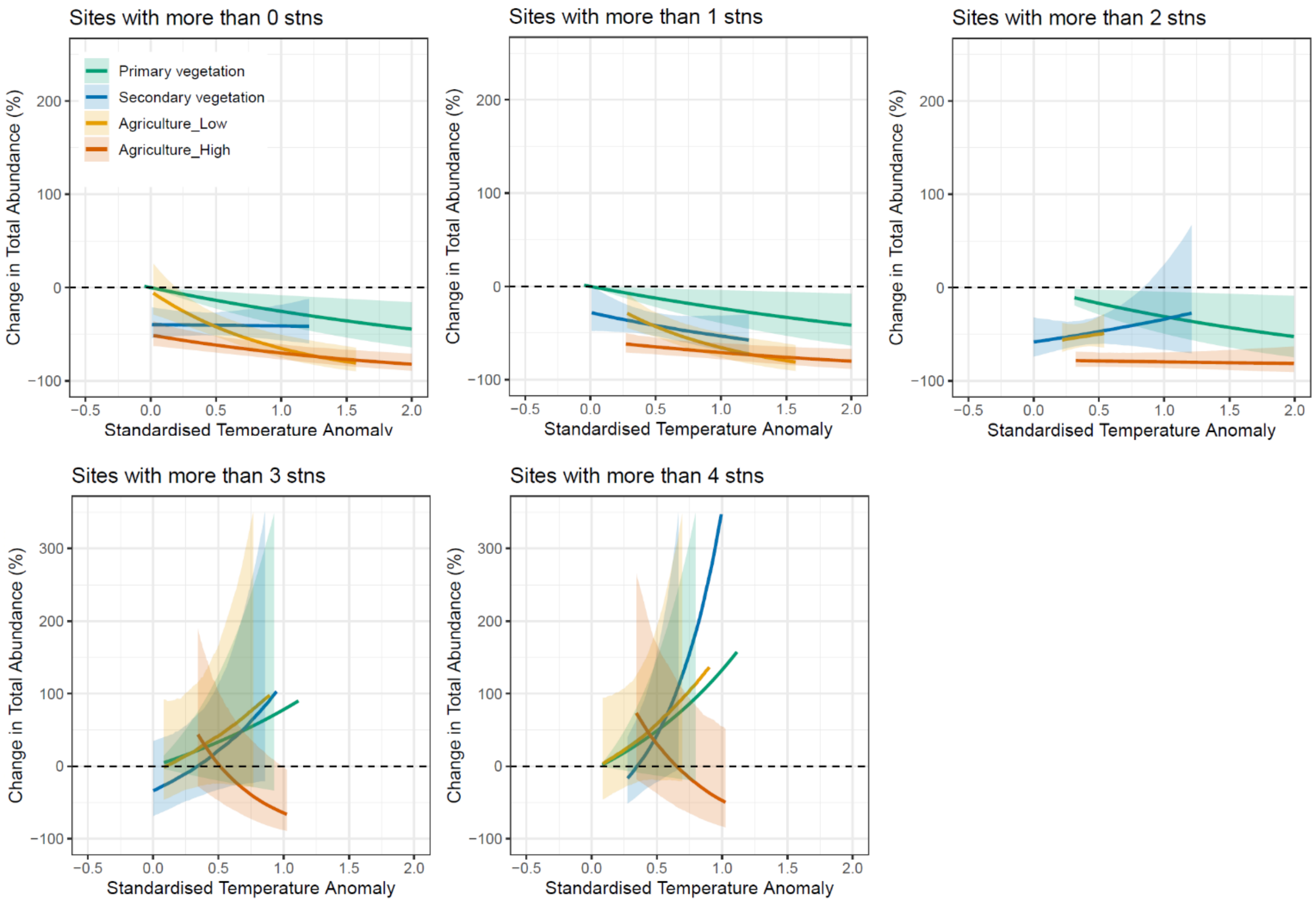


Figure S12: Results from Tropical subset models for total abundance where sites with few observations contributing to the CRU TS temperature data are sequentially removed. First, sites supported by an average of 0 observations are removed and the models run, followed by 1 and 2 etc up to 4. After this point the confidence intervals become very wide (some are cut off here) due to the reduction in the number of sites in the analysis. Number of sites supported by more than *n* stations 0 = 1,462, more than 1 = 1,288, more than 2 = 921, more than 3 = 335, more than 4 = 296.

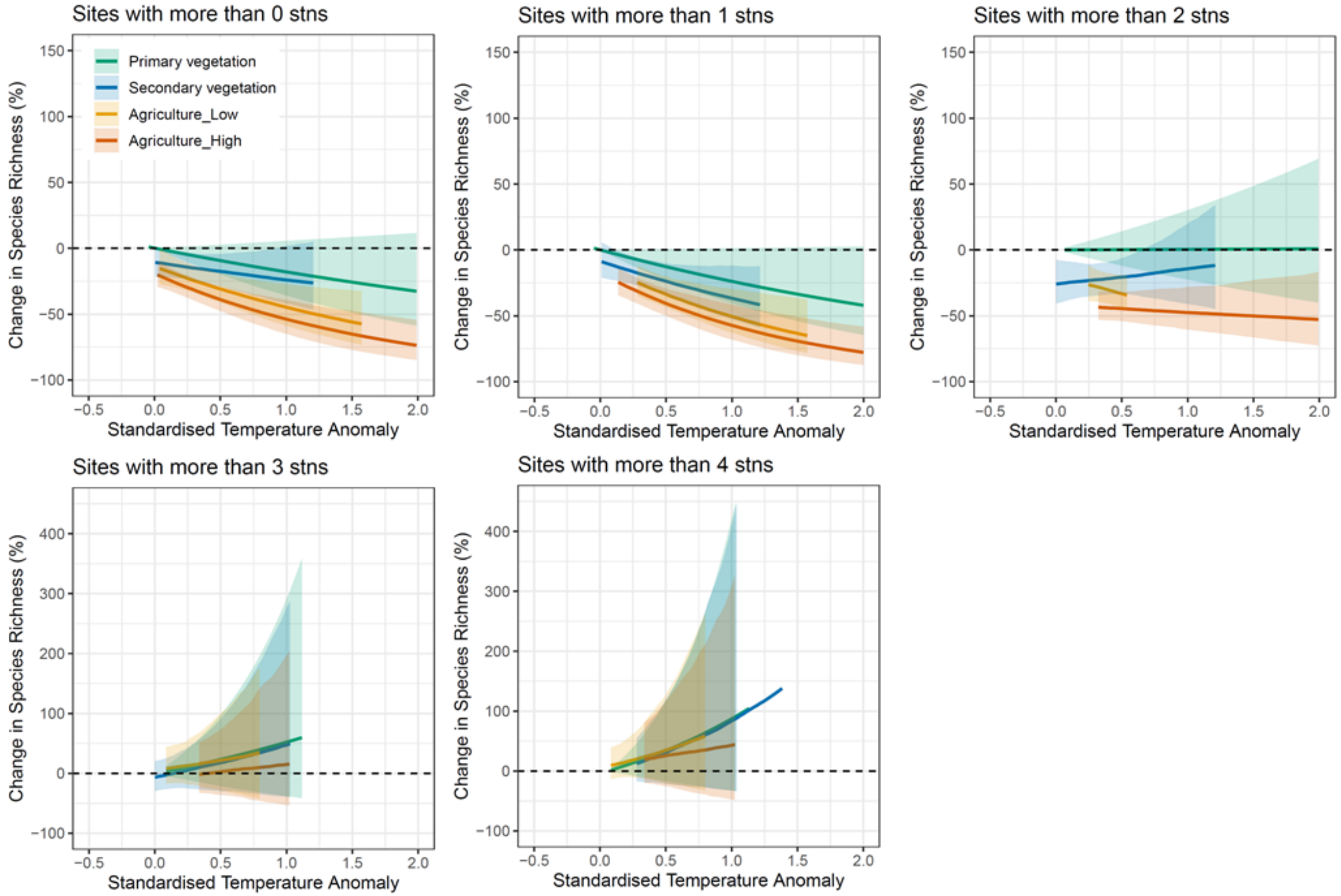


Figure S13: Results from Tropical subset models for species richness where sites with few observations contributing to the CRU TS temperature data are sequentially removed. First, sites supported by an average of 0 observations are removed and the models run, followed by 1 and 2 etc up to 4. After this point the confidence intervals become very wide (some are cut off here) due to the reduction in the number of sites in the analysis. Number of sites supported by more than *n* stations 0 = 1,594, more than 1 = 1,416, more than 2 = 957, more than 3 = 353, more than 4 = 314.

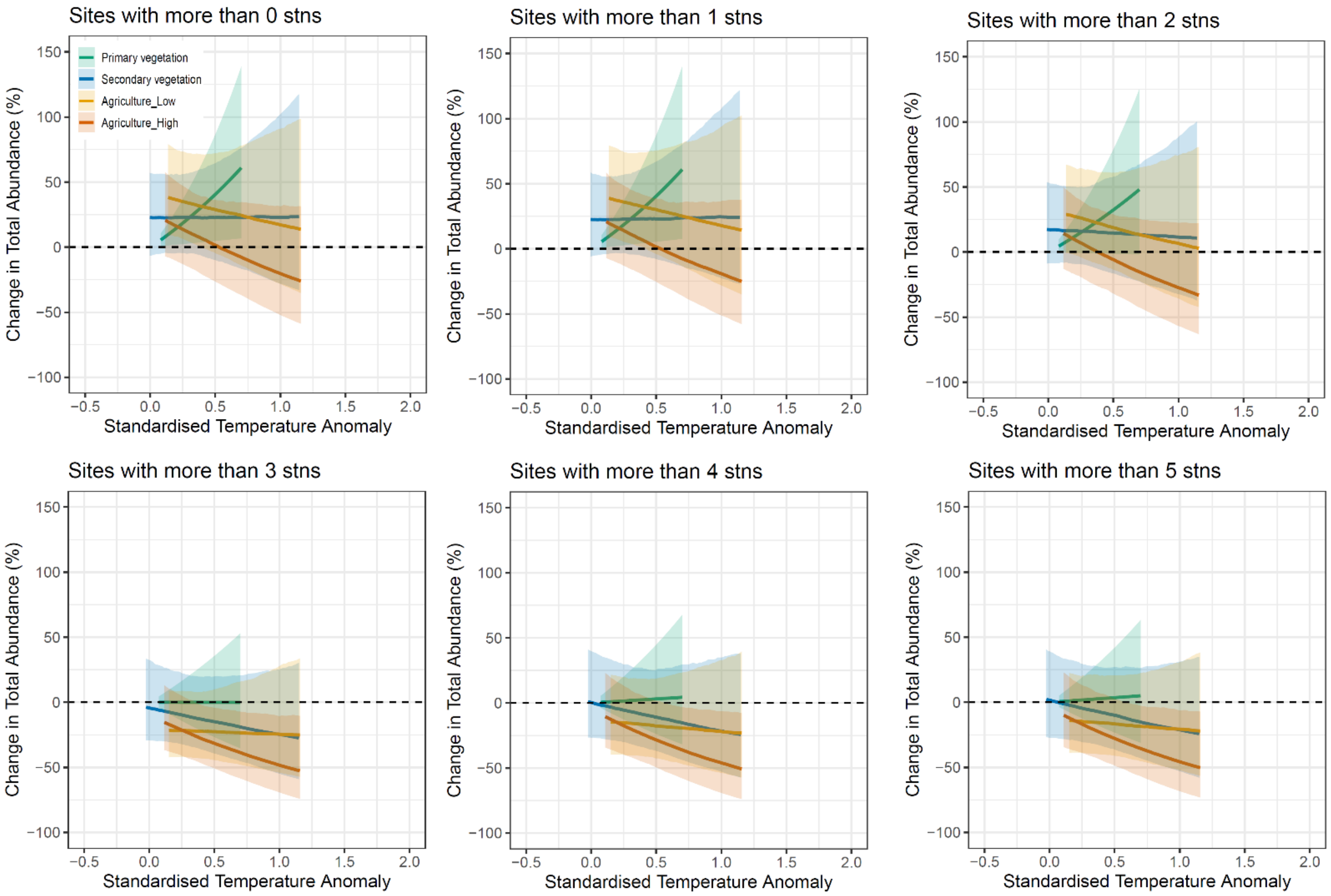


Figure S14: Results from Temperate subset models for total abundance where sites with few observations contributing to the CRU TS temperature data are sequentially removed. First, sites supported by an average of 0 observations are removed and the models run, followed by 1 and 2 etc up to 4. After this point the confidence intervals become very wide (some are cut off here) due to the reduction in the number of sites in the analysis. Number of sites supported by more than *n* stations 0 = 4,146, more than 1 = 4,146, more than 2 = 4,100, more than 3 = 3,954, more than 4 = 3.905, more than 5 = 3,904.

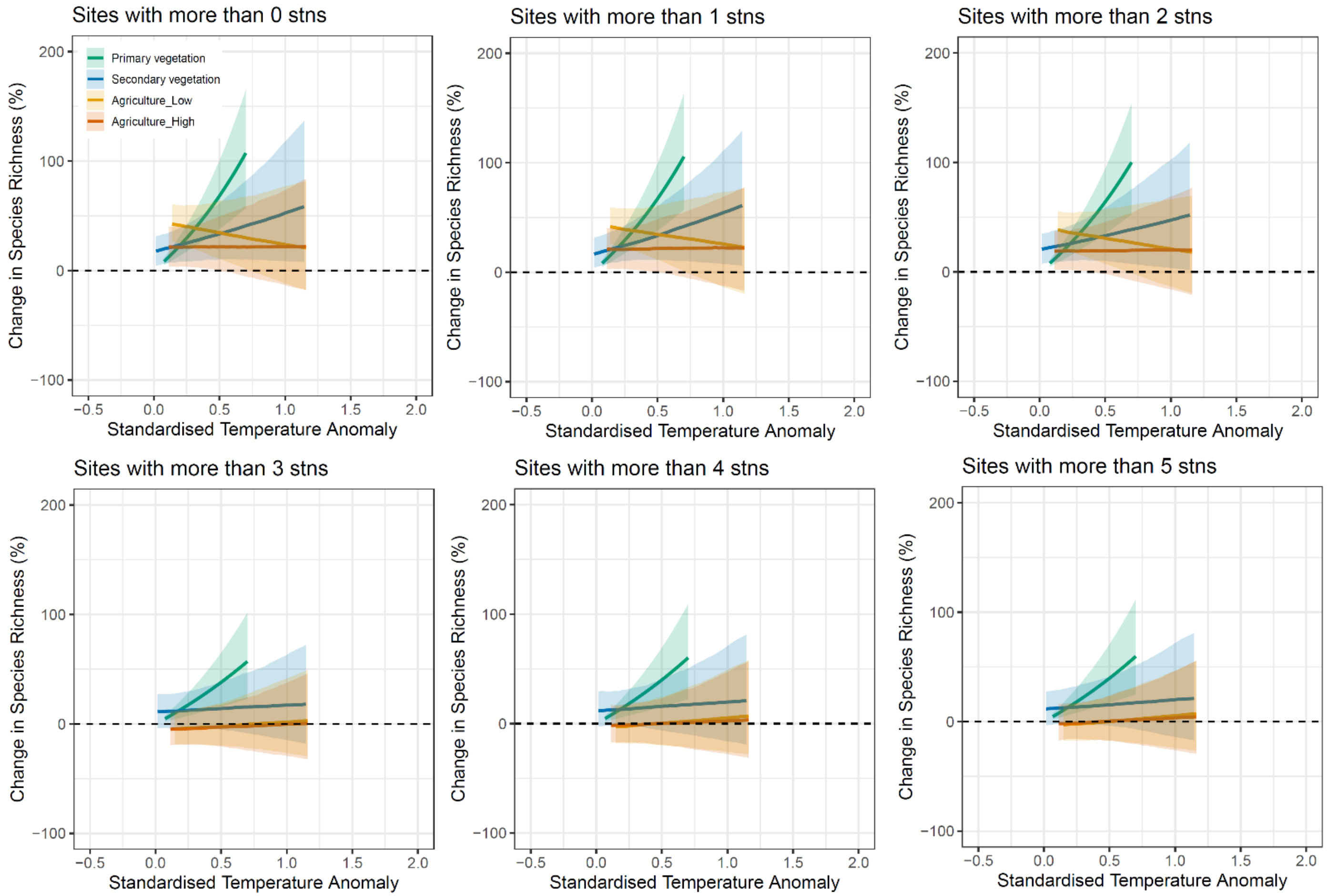


Figure S15: Results from Temperate subset models for species richness where sites with few observations contributing to the CRU TS temperature data are sequentially removed. First, sites supported by an average of 0 observations are removed and the models run, followed by 1 and 2 etc up to 4. After this point the confidence intervals become very wide (some are cut off here) due to the reduction in the number of sites in the analysis. Number of sites supported by more than *n* stations 0 = 4,327, more than 1 = 4,327, more than 2 = 4,281, more than 3 = 4,135, more than 4 = 4,027, more than 5 = 4,026.

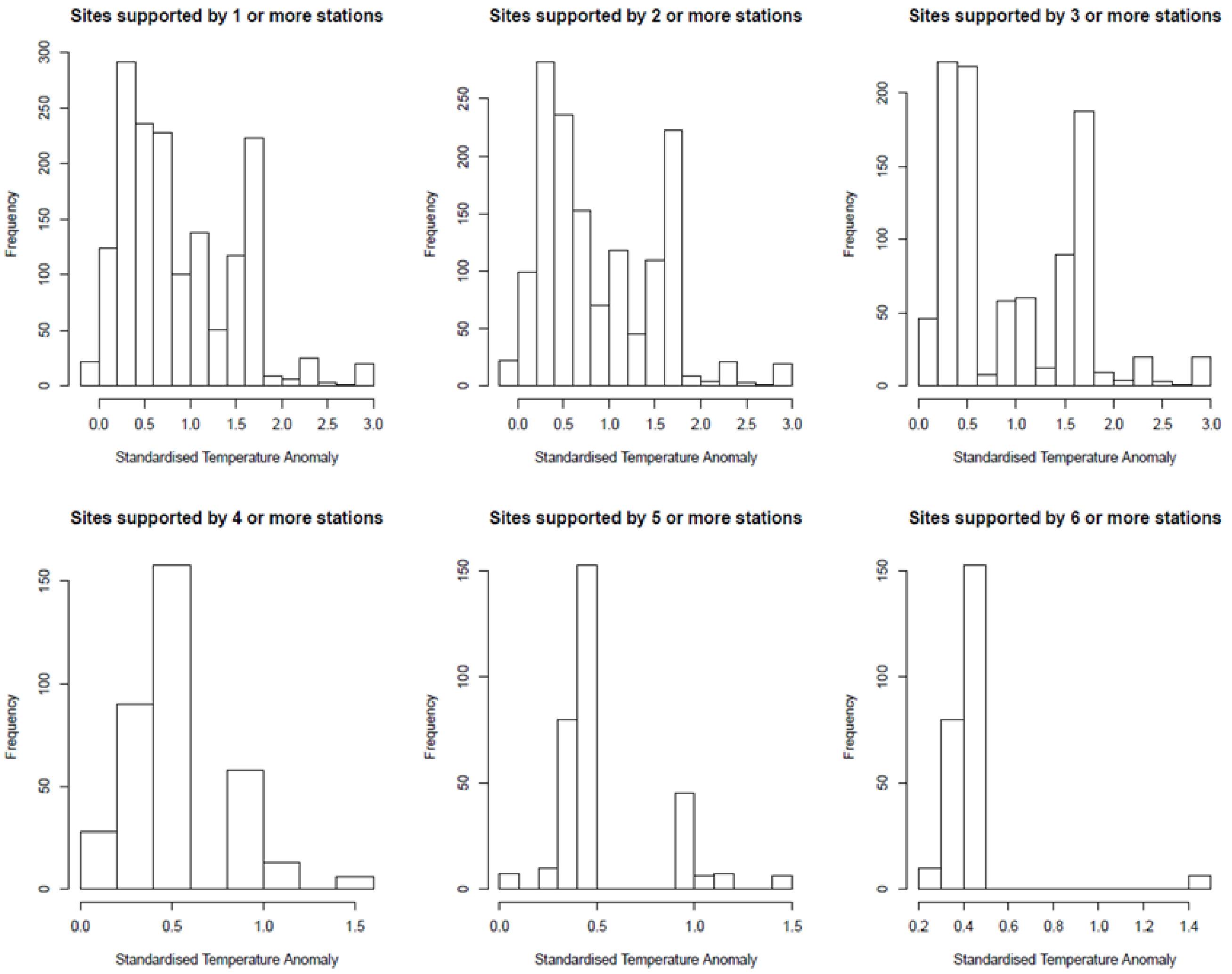


Figure S16: Histograms of the number of sites within the Tropical data subset across the range of the standardised temperature anomaly after sites supported by *n* weather stations are removed.

S4: Models using Chao-estimated species richness

Differences in sampling effort can bias estimates of species richness. Sampling effort in the PREDICTS database is recorded using very different measures and units, and therefore we are unable to account for differences in the main analysis. Instead, we calculate Chao-estimated species richness, which estimates species richness accounting for incomplete sampling[8], for as many sites as possible in the dataset. Chao-estimated species richness can only be calculated for 4,268 of the 6,069 sites in the dataset where species abundances are recorded. Models for Hypothesis 2 were run with Chao-estimated richness as the response variable. The patterns of the results were broadly similar to those presented in the main text, however for both the mean and maximum based anomalies the reductions in richness were not as great as in the original analysis (Figure S17). This however may be because the majority of sites for which Chao-estimated richness could be estimated were non-tropical sites. Of the data subset that could be used for the analysis of Chao-estimated species richness, 3,287 sites were in the non-tropical realm and just 981 in the tropical realm. Our main analysis showed that species richness reductions are not as great in the non-tropics compared to the tropics (Figure 3, main text).

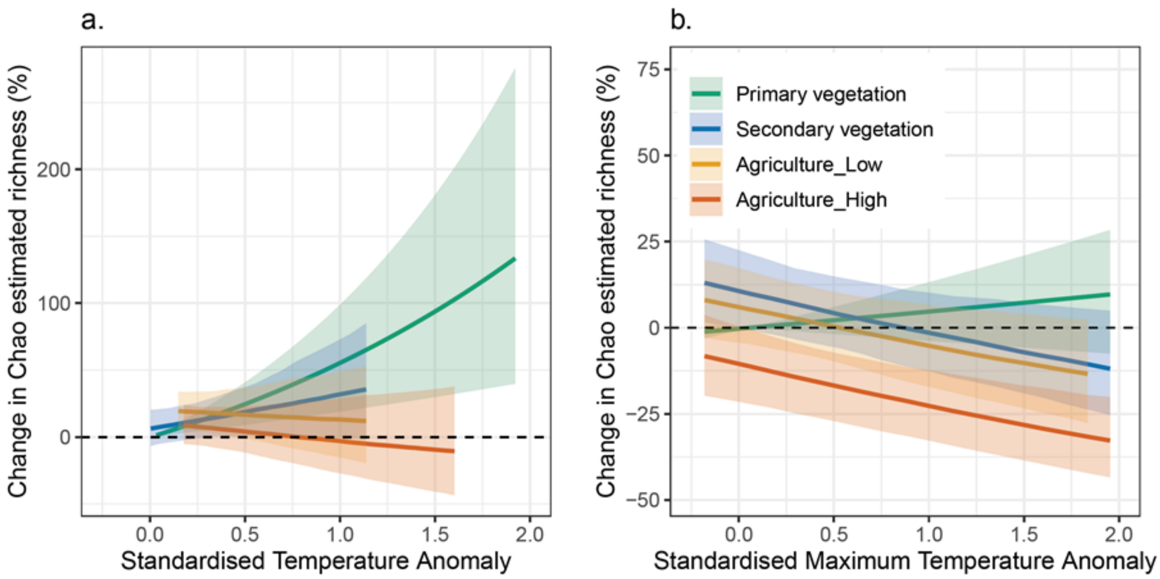


Figure S17: Response of Chao-estimated richness to the interaction between land use and a. the standardised temperature anomaly and b. the standardised maximum temperature anomaly. Values represent the percentage difference compared to primary vegetation with no historical climate warming (a temperature anomaly of 0). Lines correspond to the median predicted value and shaded area represents the 95% confidence interval. Results are plotted for the central 95% of modelled anomaly values for each land use.

S5: Testing alternative distributions and zero-inflated models

To test the robustness of our models, alternative model formulations including zero-inflated models for both total abundance and species richness, and a zero-inflated, negative binomial model for total abundance were carried out.

The zero-inflated models were tested due to the high presence of zero values in the dataset. These models were run using the glmmTMB R package[9] using the same formulation as presented in the main methods, but with the addition of a single zero-inflation parameter applying to all observations. Model families remained as previously specified: Gaussian for scaled, log-transformed total abundance and Poisson for species richness. The coefficients from these models were very similar to those produced using the original model formulations (not zero-inflated; Tables S1 and S2). The zero-inflated models, however, resulted in increased positive skew in the distribution of residuals (Figure S18), and so we do not use them for our main analyses.

As an alternative to the linear mixed effects model for scaled, log-transformed abundance, a zero-inflated negative binomial model was run on the untransformed total abundance data. The coefficients from the zero-inflated, negative binomial model are very similar to those from the original model in most cases (Table S3), however, the associated Q-Q plot and a ballooning of the confidence intervals observed when predictions from the models are plotted indicate that this model is not as robust (Figures S19 and S20).

Table S1: Parameters for the zero-inflated and original mixed effects models of scaled insect total abundance as a function of land use in interaction with the mean temperature anomaly. Output includes estimates and P values for the fixed effects, the variance explained by the random effects (τ00 SS for studies, and τ00 SSB for blocks within studies), residual variance (σ2), and the marginal and conditional R^2 values.

	Zero-inflated model: Dependent variable		**Original model: Dependent variable**	
Predictors	*Fixed effects*	*p*	*Fixed effects*	*p*
Intercept	-0.93	**<0.001**	-0.93	**<0.001**
Agriculture_High	-0.49	**<0.001**	-0.49	**<0.001**
Agriculture_Low	-0.20	**<0.001**	-0.20	**<0.001**
Secondary vegetation	-0.20	**<0.001**	-0.20	**<0.001**
StdTmeanAnomalyRS	2.32	0.506	2.33	0.506
Agriculture_High * StdTmeanAnomalyRS	-17.60	**<0.001**	-17.61	**<0.001**
Agriculture_Low * StdTmeanAnomalyRS	-17.28	**<0.001**	-17.27	**<0.001**
Secondary vegetation * StdTmeanAnomalyRS	-3.42	0.454	-3.41	0.455
Zero-Inflated Model				
(Intercept)	-22.88	0.985		
Random Effects				
σ^2	0.82		0.68	
τ_{00}	0.40 $_{SS}$		0.19 $_{SSB}$	
	0.19 $_{SSB}$		0.41 $_{SS}$	
Marginal R^2 / Conditional R^2	0.034 / 0.440		0.037 / 0.491	

Table S2: Parameters for the zero-inflated and original mixed effects models of species richness as a function of land use in interaction with the mean temperature anomaly. Output includes estimates and p values for the fixed effects, the variance explained by the random effects (τ00 SS for studies, τ00 SSB for blocks within studies and τ00 SSBS for sites within blocks within studies), residual variance (σ2), and the marginal and conditional R^2 values.

	Zero-inflated model: Dependent variable		**Original model: Dependent variable**	
Predictors	*Fixed effects*	*p*	*Fixed effects*	*p*
Intercept	2.72	**<0.001**	2.72	**<0.001**
Agriculture_High	-0.36	**<0.001**	-0.40	**<0.001**
Agriculture_Low	-0.26	**<0.001**	-0.26	**<0.001**
Secondary vegetation	-0.14	**<0.001**	-0.15	**<0.001**
StdTmeanAnomalyRS	6.58	**0.037**	5.63	0.073
Agriculture_High * StdTmeanAnomalyRS	-13.97	**<0.001**	-11.88	**<0.001**
Agriculture_Low * StdTmeanAnomalyRS	-18.91	**<0.001**	-18.02	**<0.001**
Secondary vegetation * StdTmeanAnomalyRS	-5.28	**0.015**	-5.12	**0.027**
Zero-Inflated Model				
(Intercept)	-5.95	**<0.001**		
Random Effects				
σ^2	0.19		0.07	
τ_{00}	1.62 $_{SS}$		0.07 $_{SSBS}$	
	0.04 $_{SSB}$		0.05 $_{SSB}$	
	0.07 $_{SSBS}$		1.58 $_{SS}$	
Marginal R^2 / Conditional R^2	0.016 / 0.898		0.019 / 0.957	

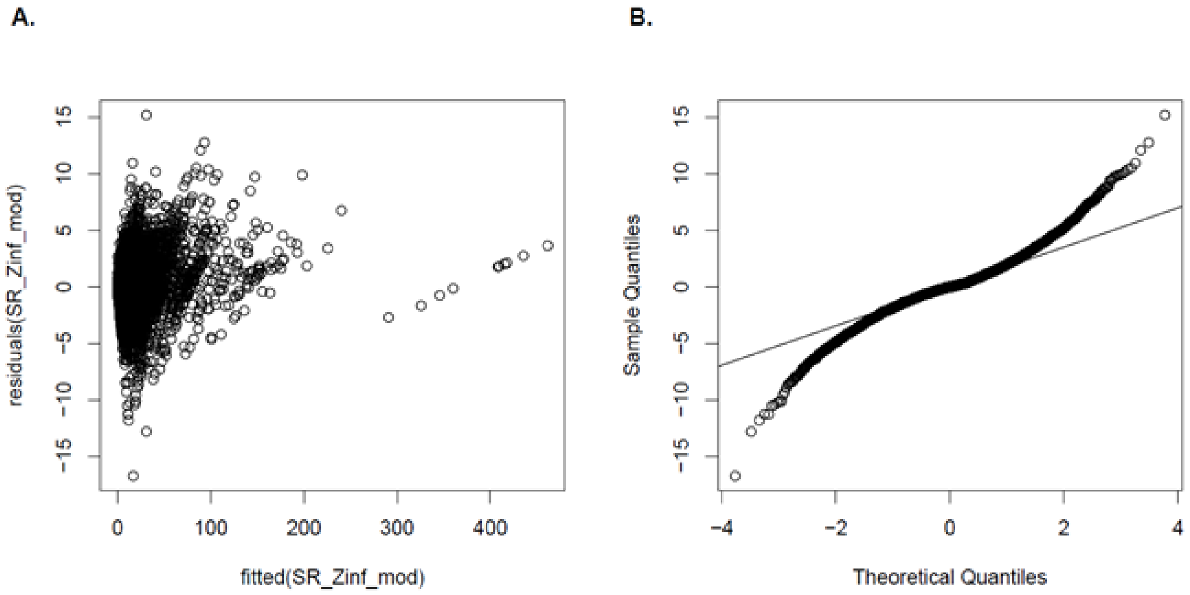


Figure S18: Model checks for the zero-inflated species richness model. a. Fitted vs. residuals plot to check for constant variance across the range of fitted values. b. Normal Q-Q plot to check the normality of the residuals. Note that similar figures for the zero inflated total abundance model could not be produced due to errors applying the same functions.

Table S3: Parameters for the zero-inflated negative binomial mixed effects model of untransformed total abundance and original model of rescaled, log-transformed total abundance as a function of land use in interaction with mean anomaly. Output includes estimates and p values for the fixed effects, the variance explained by the random effects (τ00 SS for studies and τ00 SSB for blocks within studies), residual variance (σ2), and the marginal and conditional R^2 values.

	Zero-inflated negative binomial model: Dependent variable		**Original model: Dependent variable**	
Predictors	*Fixed effects*	*p*	*Fixed effects*	*p*
Intercept	5.17	**<0.001**	-0.93	**<0.001**
Agriculture_High	-0.42	**<0.001**	-0.49	**<0.001**
Agriculture_Low	-0.08	0.110	-0.20	**<0.001**
Secondary vegetation	-0.14	**0.005**	-0.20	**<0.001**
StdTmeanAnomalyRS	8.32	0.160	2.33	0.506
Agriculture_High * StdTmeanAnomalyRS	-18.05	**<0.001**	-17.61	**<0.001**
Agriculture_Low * StdTmeanAnomalyRS	-16.70	**<0.001**	-17.27	**<0.001**
Secondary vegetation * StdTmeanAnomalyRS	-2.13	0.652	-3.41	0.455
Zero-Inflated Model				
(Intercept)	-5.36	**<0.001**		
Random Effects				
σ^2	6.53		0.68	
τ_{00}	4.49 $_{SS}$		0.19 $_{SSB}$	
	0.24 $_{SSB}$		0.41 $_{SS}$	
Marginal R^2 / Conditional R^2	0.004 / 0.422		0.037 / 0.491	

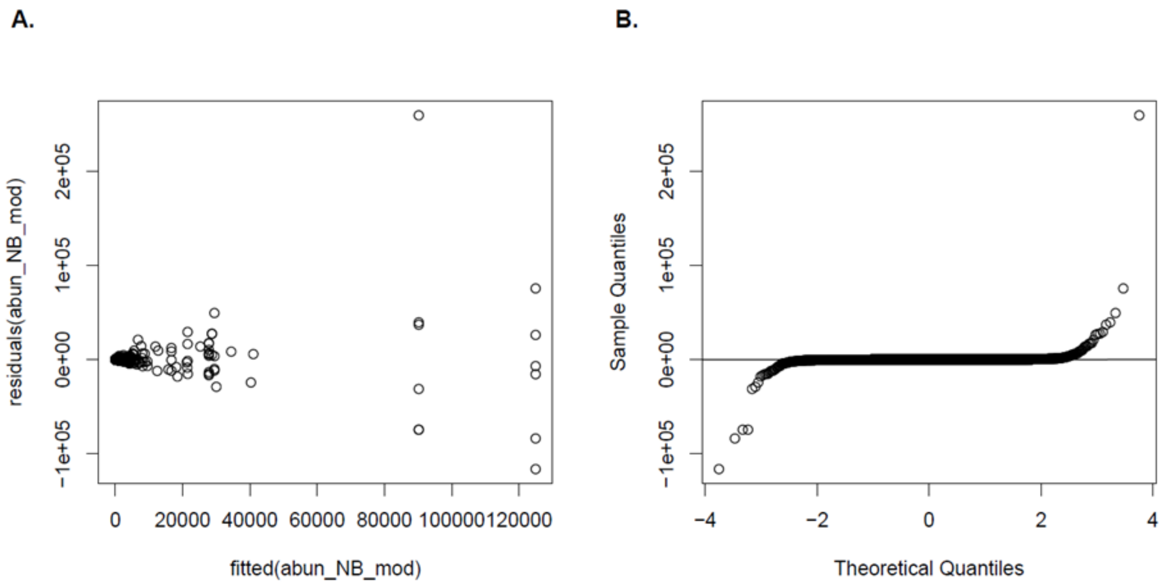


Figure S19: Model checks for the zero-inflated negative binomial model of insect total abundance. a. Fitted vs. residuals plot to check for constant variance across the range of fitted values. b. Normal Q-Q plot to check the normality of the residuals.

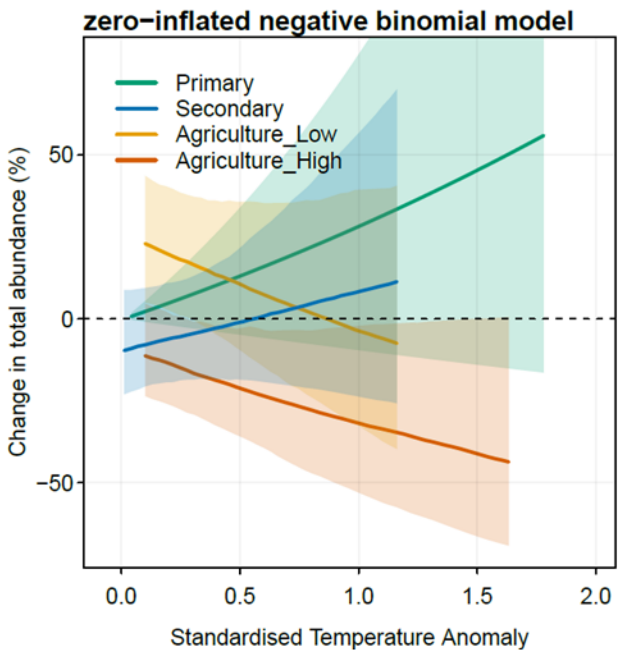


Figure S20: Response of insect total abundance to the interaction between land use and the standardised temperature anomaly, based on a zero-inflated, negative binomial model. Lines correspond to the median predicted value and shaded area represents the 95% confidence interval. Results are plotted for the central 95% of modelled anomaly values for each land use.

S6: Comparisons using average temperature and the unstandardised anomaly

Our main model results could be the outcome of an association between land-use responses and our standardised measure of recent climate change, or alternatively a coincidental correlation caused by confounding effects of current mean climate conditions or absolute recent temperature changes. To test whether the latter was the case, we first assessed the correlations between current mean annual temperature, unstandardised anomaly values and standardised anomaly values, at the sampled sites in the PREDICTS database, all assessed across insect active months. We then ran separate models similar to those for Hypothesis 2, but instead testing for interactions between land use and: 1) mean temperature; or 2) the unstandardised temperature anomaly.

The correlations between mean temperature, the unstandardised anomaly and the standardised anomaly were tested using Pearson correlation coefficients. Correlations at the PREDICTS sites sampled for insect biodiversity were low: between mean temperature and unstandardised anomaly = -0.42, between mean temperature and standardised anomaly = 0.15, and between the unstandardised anomaly and the standardised anomaly = 0.21. When the dataset is split by realm, correlations are generally slightly higher in the non-tropics but generally lower in the tropics (tropics: between mean temperature and unstandardised anomaly = -0.11, between mean temperature and standardised anomaly = 0.005, and between unstandardised and standardised anomaly = 0.33; non-tropics: between mean temperature and unstandardised anomaly = -0.14, between mean temperature and standardised anomaly = -0.66, and between unstandardised and standardised anomaly = 0.62). Including current mean temperature in the main models for Hypothesis 2 did not change the results (results not shown).

Of the three models, the model using the standardised anomaly had the lowest AIC; abundance models: Standardised anomaly model AIC = 15092.59, unstandardised anomaly model AIC =

15122.35 and mean temperature model AIC = 15107.56, species richness models: Standardised anomaly model AIC = 33277.79, unstandardised anomaly model AIC = 33364.64 and mean temperature model AIC = 33352.27.

S7: Testing the influence of outliers

We checked for the potential influence of outliers on our analysis by identifying studies that had a disproportionate influence on the model results. Cook's distances were calculated at the Study level using the *influence* function from the *influence.ME* R package[10]. We re-ran the models for Hypothesis 2 removing influential Studies from the dataset. For the abundance models, Cook's distances were relatively low so Studies with a distance greater than 0.4 were removed, whereas for the richness models Studies with distances greater than 1 were removed. In each case, this incorporated all Studies with much higher Cook's distances than the rest of the Studies in the dataset. Most results were the same after outliers were removed (Figure S21 and S22). The only result that differed slightly was for species richness in response to land use and the standardised temperature anomaly, where the reduction in richness in agricultural sites as the mean temperature anomaly increased was not present (Figure S21b). Although only 3 studies were removed as potential outliers in this case, these studies contributed 650 sites to the analysis.

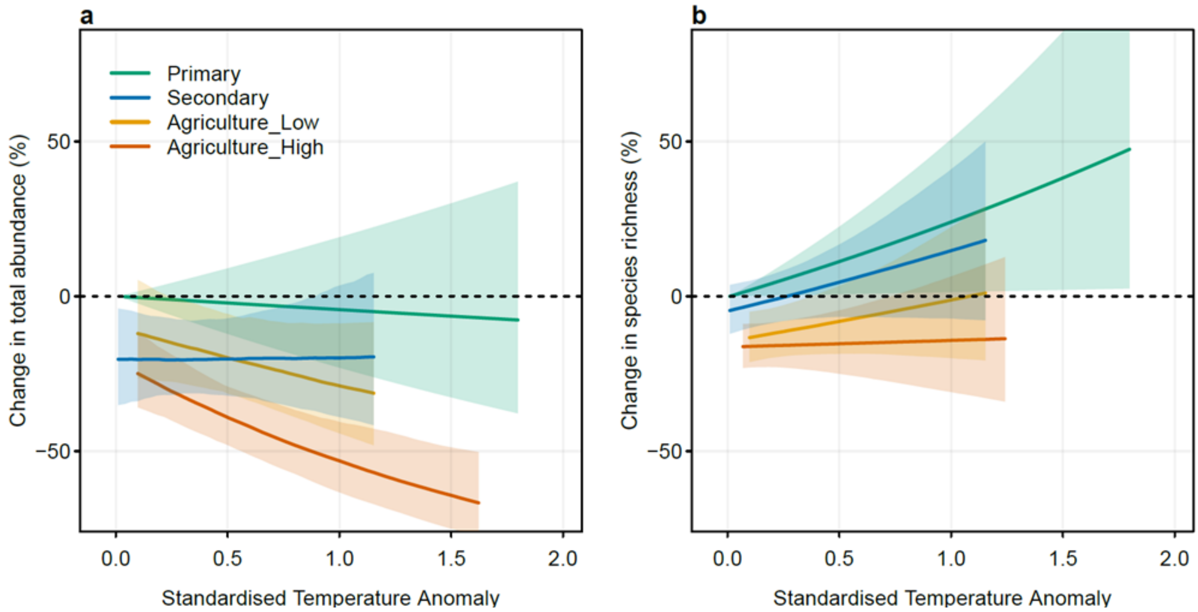


Figure S21: Response of total abundance (a) and species richness (b) to the interaction between land use and the standardised mean temperature anomaly when influential outlier studies were removed from the dataset (abundance: 2 studies removed including 385 sites, richness: 3 studies removed including 650 sites). Values represent the percentage difference compared to primary vegetation with no recent climate warming (a standardised temperature anomaly of 0). Standardised temperature anomaly is the difference in mean monthly temperatures between the baseline of 1901-1930 and the year preceding biodiversity sampling, divided by the standard deviation of baseline temperatures across months in which insects are assumed to be active (i.e., monthly average daily-mean temperature > 10°C). Lines correspond to the median predicted value and shaded area represents the 95% confidence interval. Results are plotted for the central 95% of modelled anomaly values for each land use

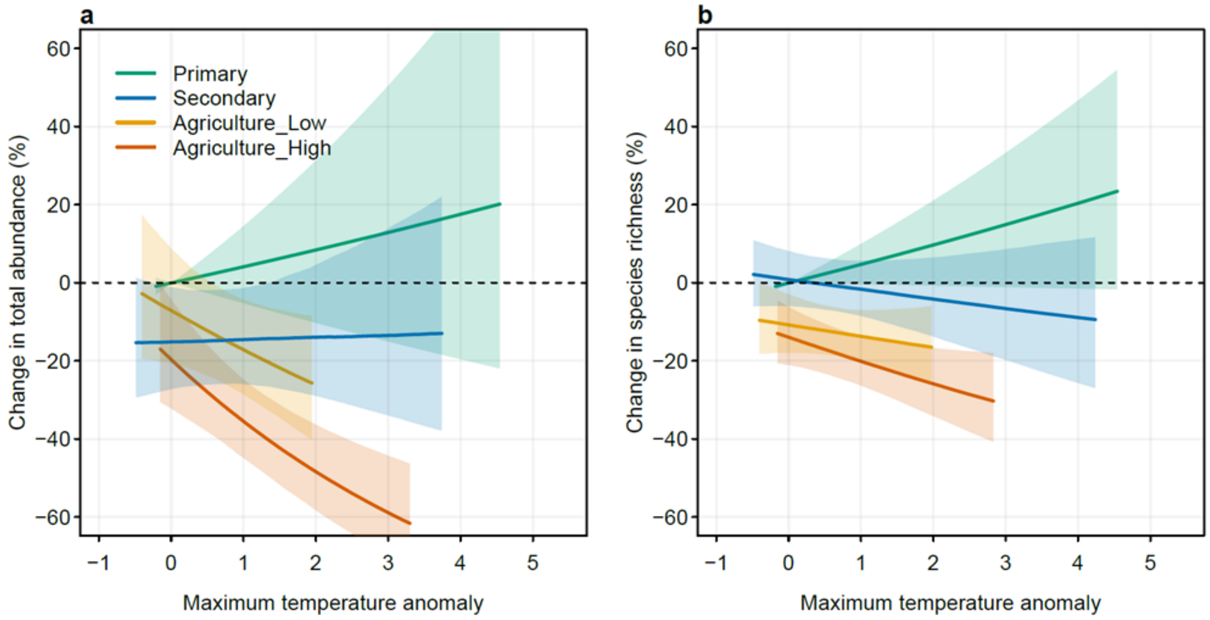


Figure S22: Response of total abundance (a) and species richness (b) to the interaction between land use and the standardised maximum temperature anomaly when influential outlier studies were removed from the dataset (abundance: 3 studies removed including 433 sites, richness: 4 studies removed including 698 sites). Values represent the percentage difference compared to primary vegetation with no historical climate warming (a maximum temperature anomaly of 0). Maximum temperature anomaly is the difference in the average of the maximum temperatures in the three hottest months each year between the baseline of 1901-1930 and the year of biodiversity sampling, divided by the standard deviation of the baseline maximum temperatures (for the same three hottest months in all baseline years). Lines correspond to the median predicted value and shaded area represents the 95% confidence interval. Results are plotted for the central 95% of modelled anomaly values for each land use.

S8: Model Diagnostic Plots

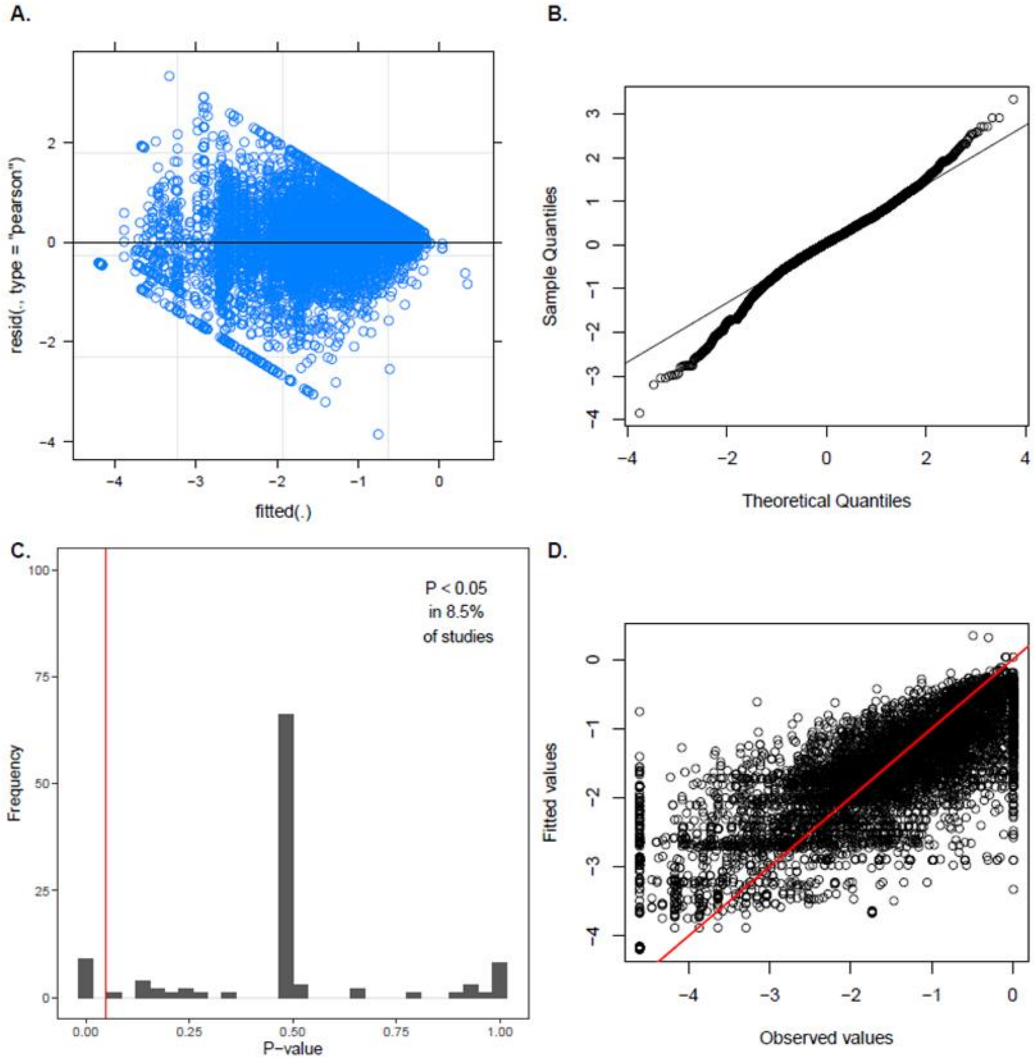


Figure S23: Model checks for the model of rescaled total abundance as a function of land use and the standardised temperature anomaly. a. Fitted values versus residuals to check for constant variance across the range of fitted values. b. Normal Q-Q plot to check the normality of the residuals. c. Histograms of P values from sets of Moran's tests for spatial autocorrelation in the residuals of the best models for each Study. The red line represents P = 0.05. By chance, we expect to detect significant spatial autocorrelation in the residuals associated with 5% of studies. d. Observed versus fitted values.

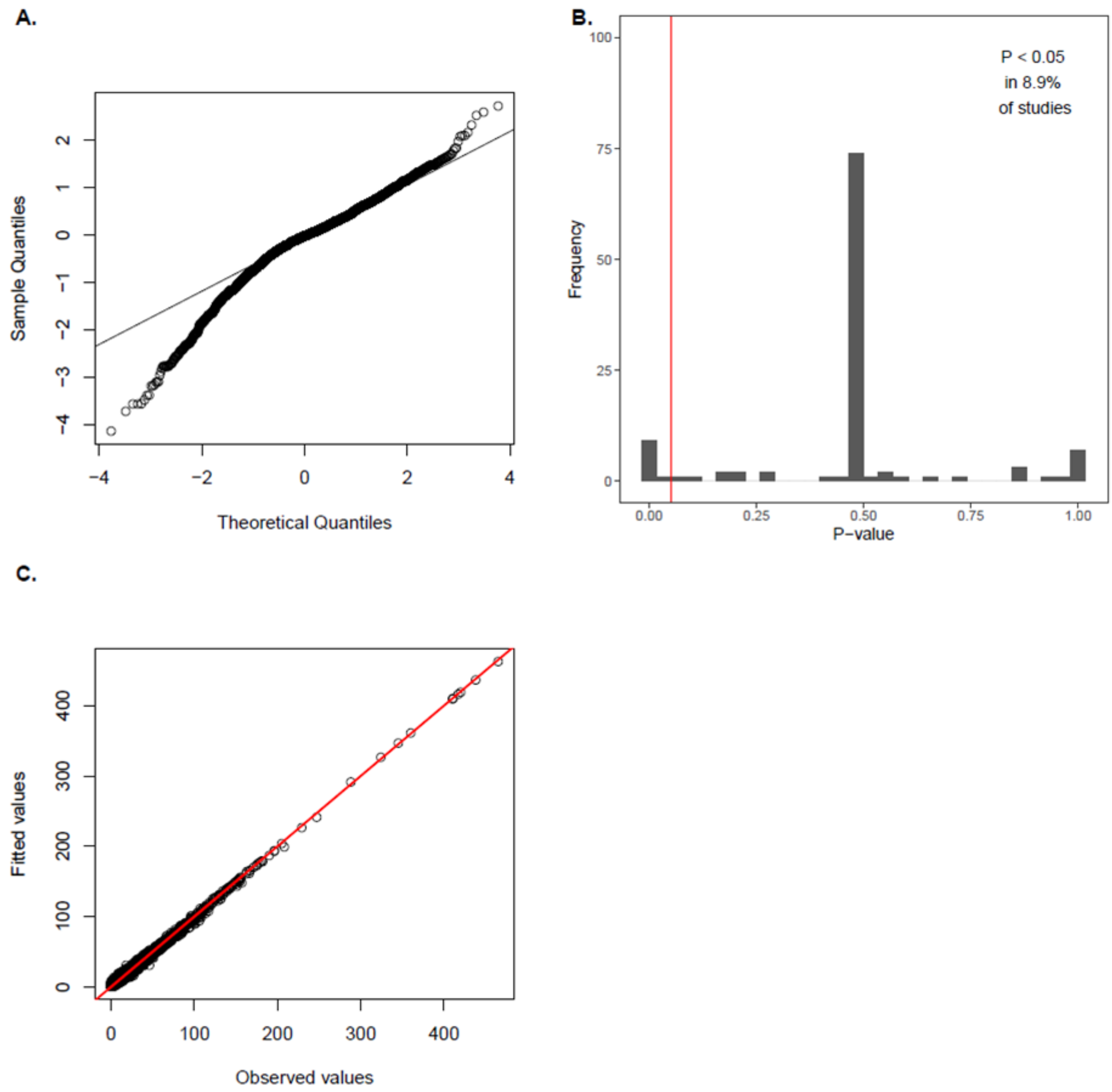


Figure S24: Model checks for species richness model as a function of land use and the standardised temperature anomaly. a. Normal Q-Q plot to check the normality of the residuals. b. Histograms of P values from sets of Moran's tests for spatial autocorrelation in the residuals of the best models for each Study. The red line represents P = 0.05. By chance, we expect to detect significant spatial autocorrelation in the residuals associated with 5% of studies. c. Observed values versus fitted values.

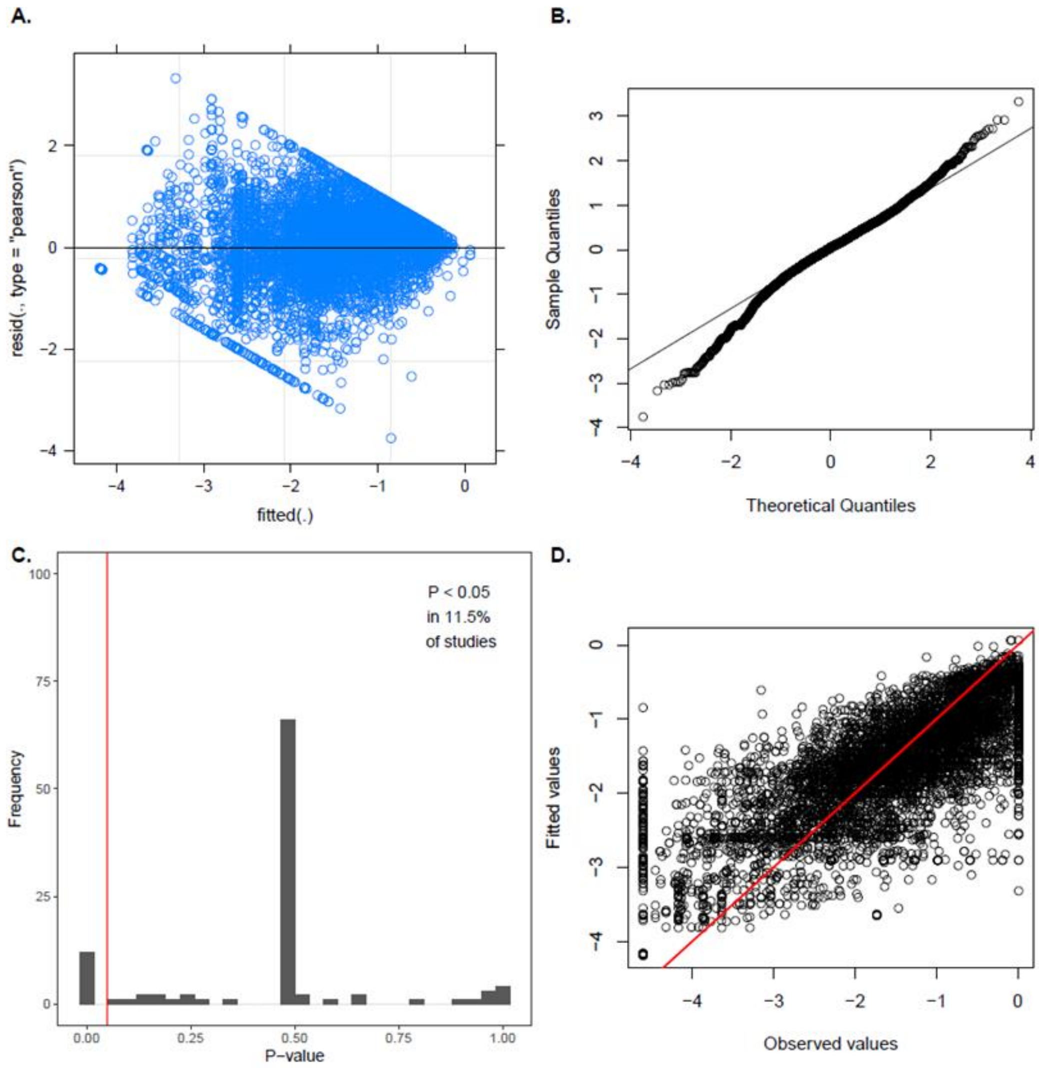


Figure S25: Model checks for the model of rescaled total abundance as a function of land use and the standardised maximum temperature anomaly. a. Fitted values versus residuals plot to check for constant variance across the range of fitted values. b. Normal Q-Q plot to check the normality of the residuals. c. Histograms of P values from sets of Moran's tests for spatial autocorrelation in the residuals of the best models for each Study. The red line represents P = 0.05. By chance, we expect to detect significant spatial autocorrelation in the residuals associated with 5% of studies. d. Observed values versus fitted values.

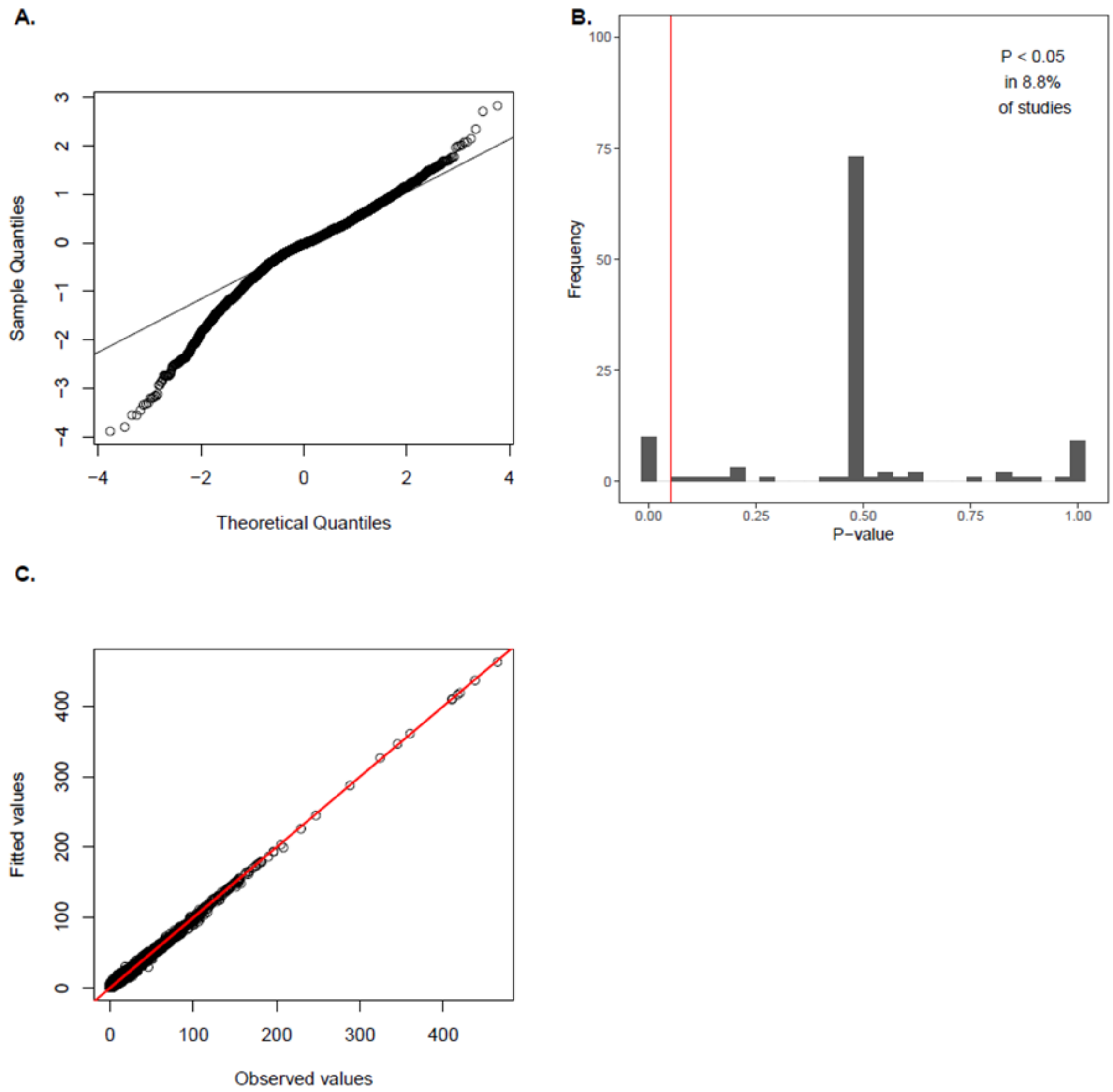


Figure S26: Model checks for the model of species richness as a function of land use and the standardised maximum temperature anomaly. a. Normal Q-Q plot to check the normality of the residuals. b. Histograms of P values from sets of Moran's tests for spatial autocorrelation in the residuals of the best models for each Study. The red line represents P = 0.05. By chance, we expect to detect significant spatial autocorrelation in the residuals associated with 5% of studies. c. Observed values versus fitted values.

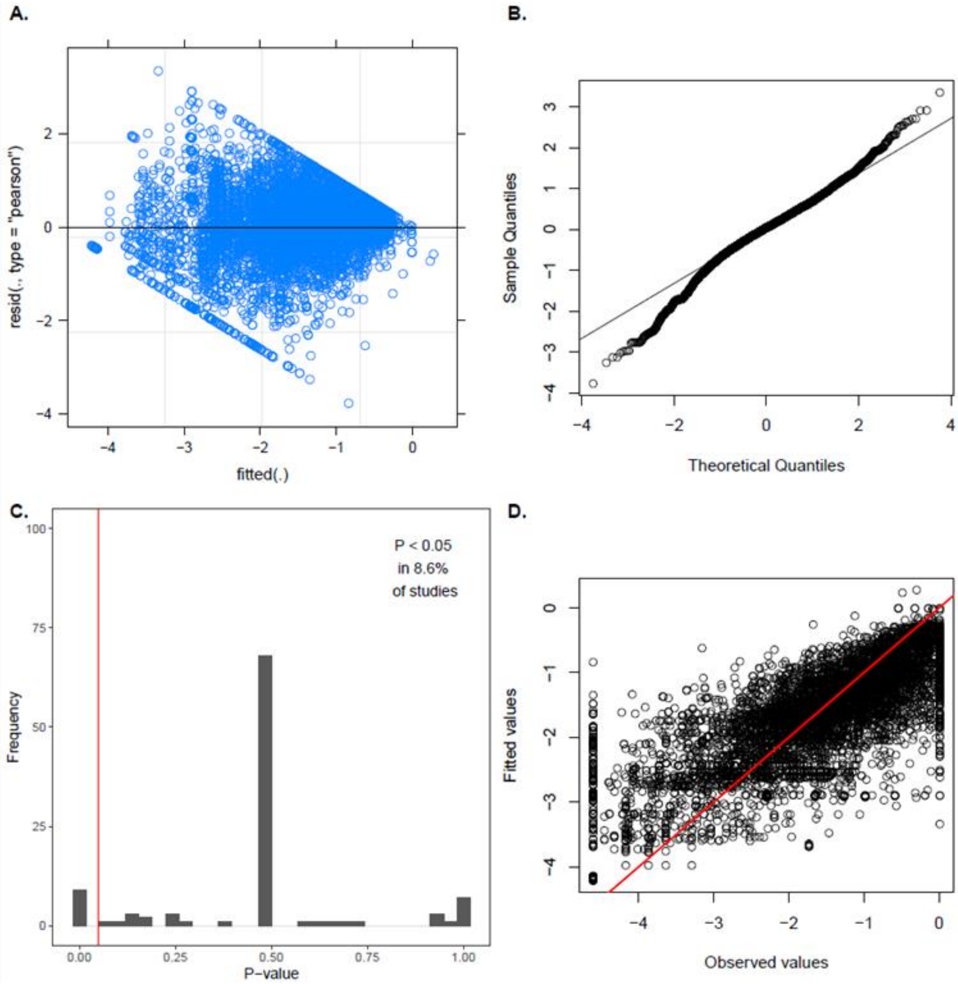


Figure S27: Model checks for the model of rescaled total abundance as a function of land use, the standardised temperature anomaly and natural habitat availability. a. Fitted values versus residuals plot to check for constant variance across the range of fitted values. b. Normal Q-Q plot to check the normality of the residuals. c. Histograms of P values from sets of Moran's tests for spatial autocorrelation in the residuals of the best models for each Study. The red line represents P = 0.05. By chance, we expect to detect significant spatial autocorrelation in the residuals associated with 5% of studies. d. Observed values versus fitted values.

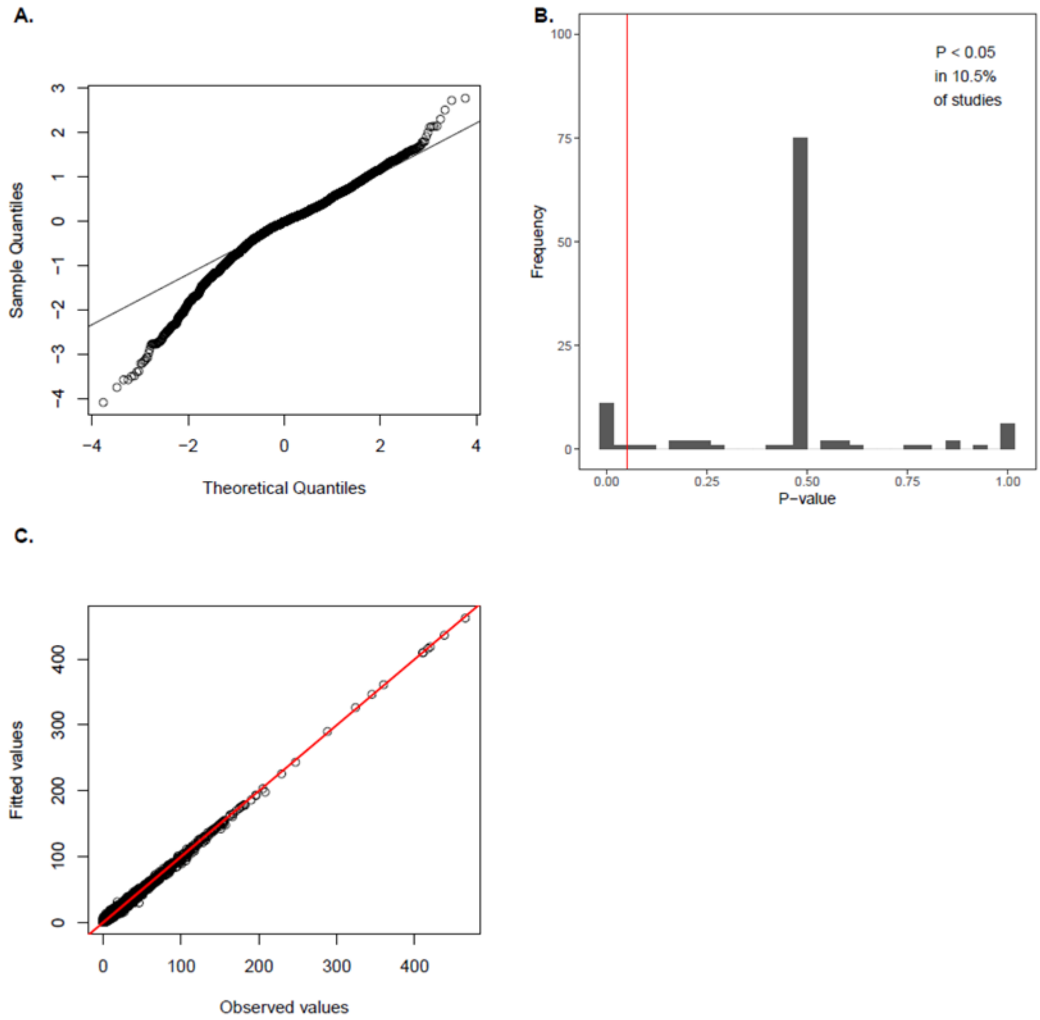


Figure S28: Model checks for the model of species richness as a function of land use, standardised temperature anomaly and natural habitat availability. a. Normal Q-Q plot to check the normality of the residuals. b. Histograms of P values from sets of Moran's tests for spatial autocorrelation in the residuals of the best models for each Study. The red line represents P = 0.05. By chance, we expect to detect significant spatial autocorrelation in the residuals associated with 5% of studies. c. Observed values versus fitted values.

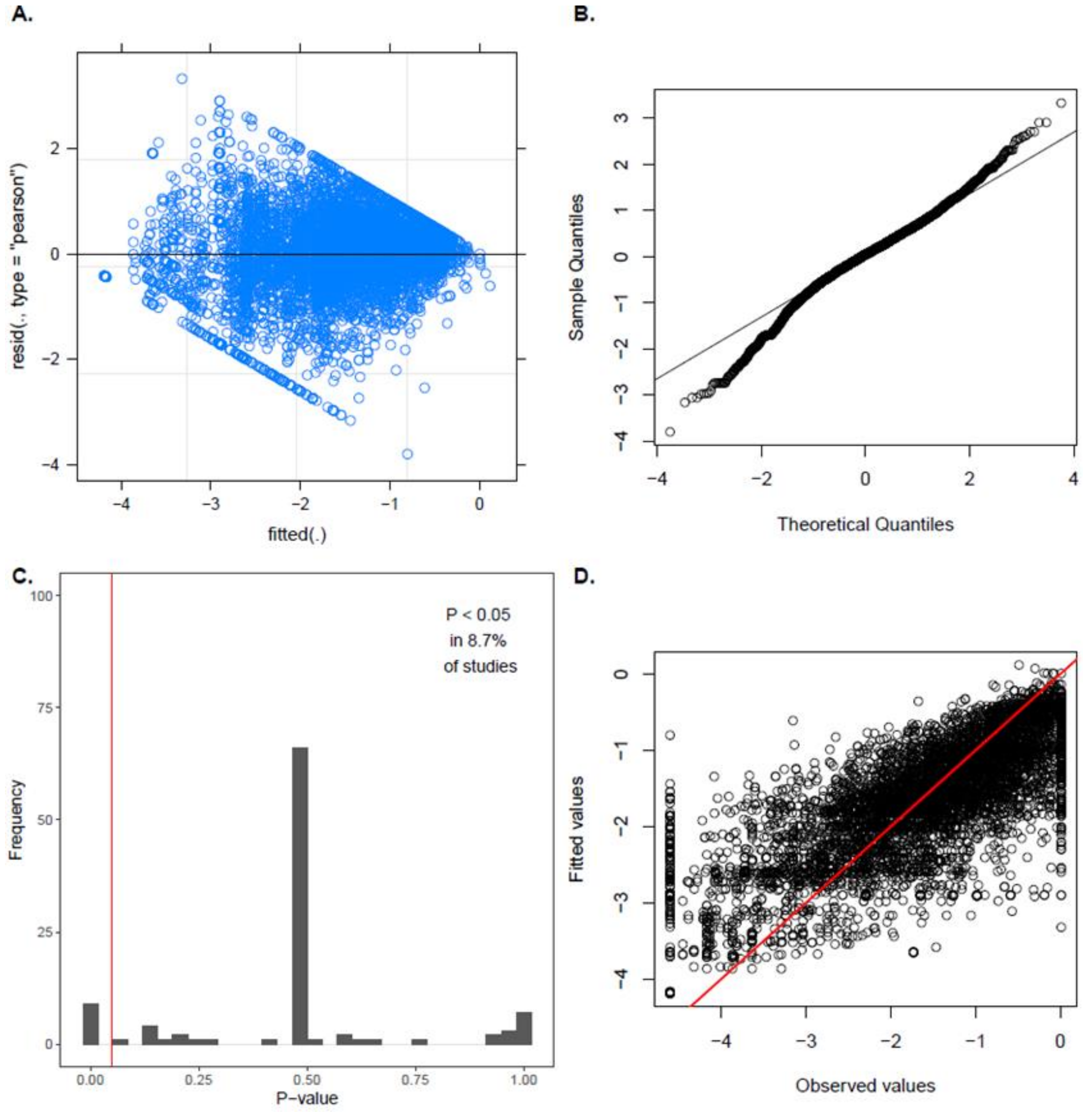


Figure S29: Model checks for the model of rescaled abundance as a function of land use, standardised temperature anomaly and natural habitat availability. a. Fitted versus residuals plot to check for constant variance across the range of fitted values. b. Normal Q-Q plot to check the normality of the residuals. c. Histograms of P values from sets of Moran's tests for spatial autocorrelation in the residuals of the best models for each Study. The red line represents P = 0.05. By chance, we expect to detect significant spatial autocorrelation in the residuals associated with 5% of studies. d. Observed values versus fitted values.

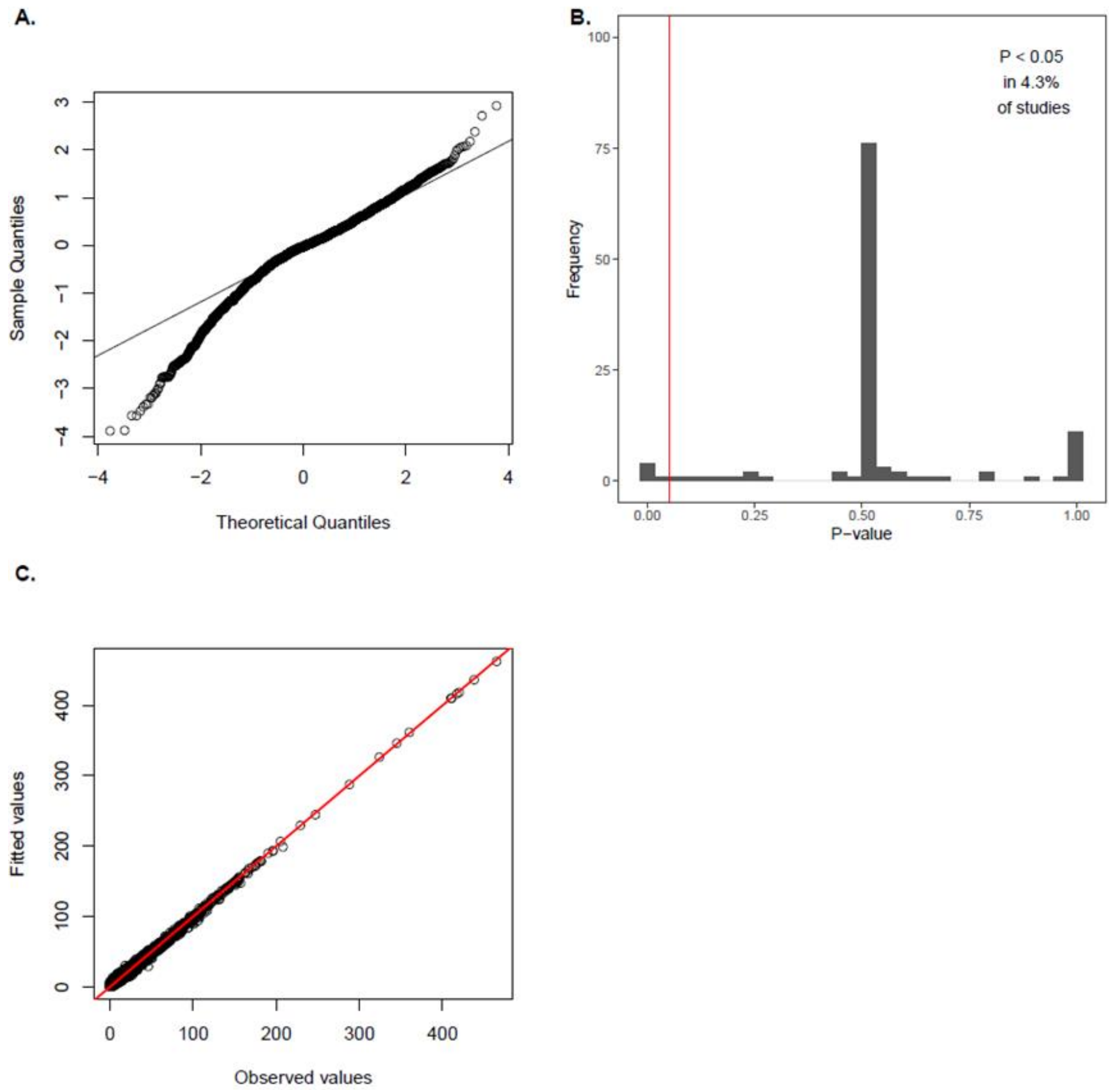


Figure S30: Model checks for the model of species richness as a function of land use, standardised maximum temperature anomaly and natural habitat availability. a. Normal Q-Q plot to check the normality of the residuals. b. Histograms of P values from sets of Moran's tests for spatial autocorrelation in the residuals of the best models for each Study. The red line represents P = 0.05. By chance, we expect to detect significant spatial autocorrelation in the residuals associated with 5% of studies. c. Observed values versus fitted values.

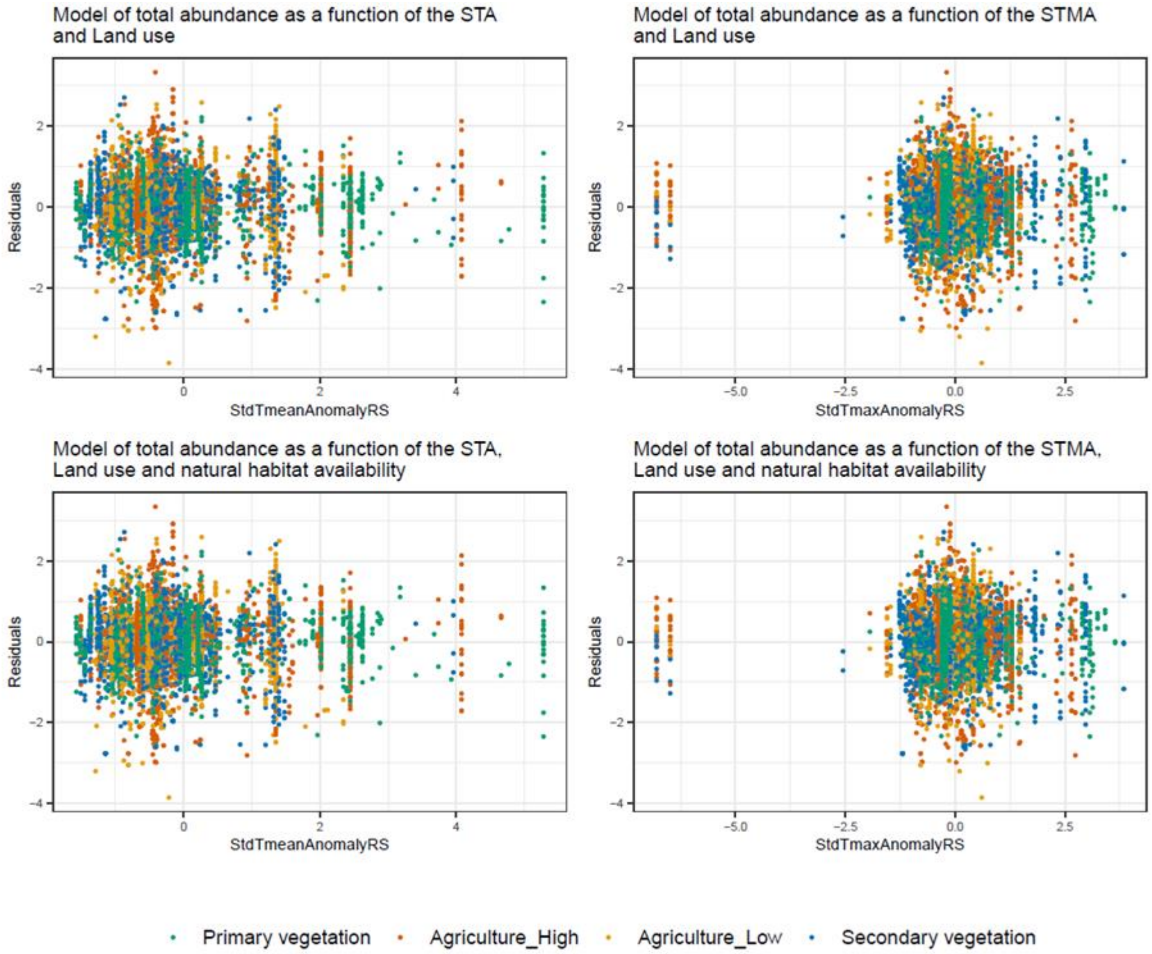


Figure S31: Plots of the model residuals for each model of total abundance plotted against the associated standardised temperature anomaly value where points are coloured by land use classification.

Supplementary Tables

Table S4: Land-use classifications for agricultural sites in PREDICTS, and assignments to the pooled classification used in this study. Classifications are based on two important determinants of insect biodiversity: pesticide application and presence of monoculture. For the purposes of this study, owing to our focus on insects, land-use classes in PREDICTS with high inputs of pesticides are classified as high-intensity agriculture. For classes where pesticide input is uncertain based on the given definition, classes identified as consisting of monoculture are classified as high-intensity agriculture. If both pesticide input is low/uncertain and site is not in monoculture/uncertain, then the site is considered to be low-intensity agriculture. For the case of high use-intensity pasture, high stock density or high fertiliser use justifies inclusion in high-intensity agriculture.

PREDICTS Land Use Class	PREDICTS definition	Assignment	Justification
Plantation forest – Minimal Use	Extensively managed or mixed timber, fruit/coffee, oil-palm or rubber plantations in which native understorey and/or other native tree species are tolerated, which are not treated with pesticide or fertiliser, and which have not been recently (< 20 years) clear-felled	Low-intensity agriculture	No pesticides and not in monoculture
Plantation forest – Light Use	Monoculture fruit/coffee/rubber plantations with limited pesticide input, or mixed species plantations with significant inputs. Monoculture timber plantations of mixed age with no recent (< 20 years) clear-felling. Monoculture oil-palm plantations with no recent (< 20 years) clear-felling.	High-Intensity agriculture	Significant input of pesticide or monoculture still with pesticides
Plantation forest – Intense Use	Monoculture fruit/coffee/rubber plantations with significant pesticide input. Monoculture timber plantations with similarly aged trees or timber/oil-palm plantations with extensive recent (< 20 years) clear-felling.	High-intensity agriculture	Significant input of pesticides and Monoculture
Pasture – Minimal Use	Pasture with minimal input of fertiliser and pesticide, and with low stock density (not high enough to cause significant disturbance or to stop regeneration of vegetation).	Low-intensity agriculture	Minimal inputs and low stock density, not in monoculture.

Pasture – Light Use	Pasture either with significant input of fertiliser or pesticide, or with high stock density (high enough to cause significant disturbance or to stop regeneration of vegetation).	Low-intensity agriculture	Level of pesticide application uncertain based on PREDICTS definition but not in monoculture.
Pasture – Intense Use	Pasture with significant input of fertiliser or pesticide, and with high stock density (high enough to cause significant disturbance or to stop regeneration of vegetation).	High-intensity agriculture	Pesticide input uncertain but high stock density and high fertilizer usage justify inclusion in high-intensity agriculture
Cropland – Minimal Use	Low-intensity farms, typically with small fields, mixed crops, crop rotation, little or no inorganic fertiliser use, little or no pesticide use, little or no ploughing, little or no irrigation, little or no mechanisation	Low-intensity agriculture	No pesticide use and not in monoculture
Cropland –Light Use	Medium intensity farming, typically showing some but not many of the following: large fields, annual ploughing, inorganic fertiliser application, pesticide application, irrigation, no crop rotation, mechanisation, monoculture crop. Organic farms in developed countries often fall within this category, as may high-intensity farming in developing countries.	Low-intensity agriculture	Low or no input of pesticides and not guaranteed to be in monoculture (organic farms fall in this category)
Cropland Intense Use	High-intensity monoculture farming, typically showing many of the following features: large fields, annual ploughing, inorganic fertiliser application, pesticide application, irrigation, mechanisation, no crop rotation.	High-intensity agriculture	High pesticide use, and monoculture

Table S5: Spread of data across land uses and realms, for the dataset used in the species richness model. Apart from the number of studies, all values are the number of sites within each category. Number of sites within each land use-use intensity class are also presented for each biome.

SPECIES RICHNESS	**Studies**	**Sites**		
	264	6095		
Realm	**Non-Tropical**	**Tropical**		
	4334	1742		
Land Use/intensity classes	**Primary vegetation**	**Secondary vegetation**	**Agriculture_Low**	**Agriculture_High**
Global	1516	1483	1317	1779
Boreal Forests/Taiga	172	13	6	2
Temperate Conifer Forests	10	88	103	4
Temperate Broadleaf & Mixed Forests	315	787	671	1308
Montane Grasslands & Shrublands	247	33	200	2
Temperate Grasslands, Savannas & Shrublands	15	27	11	15
Mediterranean Forests, Woodlands & Scrub	96	58	32	21
Deserts & Xeric Shrublands	16	16	30	0
Tropical & Subtropical Grasslands, Savannas & Shrublands	175	78	47	56
Tropical & Subtropical Coniferous Forests	32	43	26	2
Flooded Grasslands & Savannas	0	0	6	6
Tropical & Subtropical Dry Broadleaf Forests	13	50	66	62
Tropical & Subtropical Moist Broadleaf Forests	420	283	119	293
Mangroves	5	7	0	8

Table S6: Spread of data across land uses and realms, for the dataset used in the total abundance model. Apart from the number of studies, all values are the number of sites within each category. Number of sites within each land use-use intensity class are also presented for each biome.

ABUNDANCE	**Studies**	**Sites**		
	244	5759		
Realm	**Non-tropical**	**Tropical**		
	4170	1589		
Land Use/intensity classes	**Primary vegetation**	**Secondary vegetation**	**Agriculture_Low**	**Agriculture_High**
Global	1410	1338	1294	1717
Boreal Forests/Taiga	172	13	6	2
Temperate Conifer Forests	10	88	103	4
Temperate Broadleaf & Mixed Forests	289	729	669	1280
Montane Grasslands & Shrublands	247	33	200	2
Temperate Grasslands, Savannas & Shrublands	15	27	11	15
Mediterranean Forests, Woodlands & Scrub	92	58	26	21
Deserts & Xeric Shrublands	16	16	30	0
Tropical & Subtropical Grasslands, Savannas & Shrublands	165	70	47	56
Tropical & Subtropical Coniferous Forests	32	43	26	2
Flooded Grasslands & Savannas	0	0	0	0
Tropical & Subtropical Dry Broadleaf Forests	13	50	66	62
Tropical & Subtropical Moist Broadleaf Forests	354	204	110	265
Mangroves	5	7	0	8

Table S7: Spread of data across land uses, separately for the non-tropical and tropical realms, for the dataset used in the species richness model.

NON-TROPICAL	**Studies**	**Sites**		
	161	4327		
Land Use/intensity classes	**Primary vegetation**	**Secondary vegetation**	**Agriculture_Low**	**Agriculture_High**
	902	1034	1047	1344
TROPICAL	**Studies**	**Sites**		
	102	1742		
Land Use/intensity classes	**Primary vegetation**	**Secondary vegetation**	**Agriculture_Low**	**Agriculture_High**
	613	435	265	429

Table S8: Spread of data across land uses, separately for the non-tropical and tropical realms, for the dataset used in the total abundance model.

NON-TROPICAL	**Studies**	**Sites**		
	152	4146		
Land Use/intensity classes	**Primary vegetation**	**Secondary vegetation**	**Agriculture_Low**	**Agriculture_High**
	857	941	1031	1317
TROPICAL	**Studies**	**Sites**		
	91	1589		
Land Use/intensity classes	**Primary vegetation**	**Secondary vegetation**	**Agriculture_Low**	**Agriculture_High**
	552	384	258	395

Table S9: Parameters for the mixed effects model of total abundance as a function of only land use. Output includes estimates, confidence intervals and p values for the fixed effects, the variance explained by the random effects ($\tau_{00\ SS}$ for studies and $\tau_{00\ SSB}$ for blocks within studies), the residual variance (σ^2), the number of observations in total and for each random effect (N_{SS} for studies and N_{SSB} for blocks within studies), and the marginal and conditional R^2 values.

	LogAbund		
Predictors	*Estimates*	*CI*	*p*
(Intercept)	4.48	4.21 – 4.75	**<0.001**
Agriculture_Low	0.38	0.28 – 0.48	**<0.001**
Primary vegetation	0.59	0.49 – 0.69	**<0.001**
Secondary vegetation	0.34	0.23 – 0.44	**<0.001**
Random Effects			
σ^2	0.64		
$\tau_{00\ SSB}$	0.25		
$\tau_{00\ SS}$	4.03		
N_{SS}	244		
N_{SSB}	906		
Observations	5759		
Marginal R^2 / Conditional R^2	0.010 / 0.871		

Table S10: Parameters for the mixed effects model of species richness as a function of only land use. Output includes estimates, confidence intervals and p values for the fixed effects, the variance explained by the random effects ($\tau_{00\ SS}$ for studies and $\tau_{00\ SSB}$ for blocks within studies), the residual variance (σ^2), the number of observations in total and for each random effect (N_{SS} for studies and N_{SSB} for blocks within studies), and the marginal and conditional R^2 values.

	Species_richness		
Predictors	*Log-Mean*	*CI*	*p*
(Intercept)	2.34	2.17 – 2.50	**<0.001**
Agriculture_Low	0.16	0.10 – 0.21	**<0.001**
Primary vegetation	0.41	0.35 – 0.46	**<0.001**
Secondary vegetation	0.27	0.21 – 0.33	**<0.001**
Random Effects			
σ^2	0.07		
$\tau_{00\ SSBS}$	0.07		
$\tau_{00\ SSB}$	0.05		
$\tau_{00\ SS}$	1.60		
N_{SS}	264		
N_{SSB}	945		
N_{SSBS}	6095		
Observations	6095		
Marginal R^2 / Conditional R^2	0.01 / 0.637		

Table S11: Parameters for the mixed effects model of total abundance as a function of land use in interaction with the mean temperature anomaly. Output includes estimates, confidence intervals and p values for the fixed effects, the variance explained by the random effects ($\tau_{00\ SS}$ for studies and $\tau_{00\ SSB}$ for blocks within studies), the residual variance (σ^2), the number of observations in total and for each random effect (N_{SS} for studies and N_{SSB} for blocks within studies), and the marginal and conditional R^2 values.

	LogAbund		
Predictors	*Estimates*	*CI*	*p*
Intercept	-0.93	-1.05 – -0.82	**<0.001**
Agriculture_High	-0.49	-0.59 – -0.39	**<0.001**
Agriculture_Low	-0.20	-0.29 – -0.11	**<0.001**
Secondary vegetation	-0.20	-0.30 – -0.10	**<0.001**
StdTmeanAnomalyRS	2.33	-4.52 – 9.18	0.506
Agriculture_High * StdTmeanAnomalyRS	-17.61	-23.16 – -12.06	**<0.001**
Agriculture_Low * StdTmeanAnomalyRS	-17.27	-25.22 – -9.32	**<0.001**
Secondary vegetation * StdTmeanAnomalyRS	-3.41	-12.36 – 5.54	0.455
Random Effects			
σ^2	0.68		
$\tau_{00\ SSB}$	0.19		
$\tau_{00\ SS}$	0.41		
N_{SS}	243		
N_{SSB}	905		
Observations	5735		
Marginal R^2 / Conditional R^2	0.037 / 0.491		

Table S12: Parameters for the mixed effects model of species richness as a function of land use in interaction with the mean temperature anomaly. Output includes estimates, confidence intervals and p values for the fixed effects, the variance explained by the random effects ($\tau_{00\ SS}$ for studies and $\tau_{00\ SSB}$ for blocks within studies), the residual variance (σ^2), the number of observations in total and for each random effect (N_{SS} for studies and N_{SSB} for blocks within studies), and the marginal and conditional R^2 values.

	Species_richness		
Predictors	*Log-Mean*	*CI*	*p*
Intercept	2.71	2.55 – 2.87	**<0.001**
Agriculture_High	-0.35	-0.41 – -0.30	**<0.001**
Agriculture_Low	-0.25	-0.30 – -0.21	**<0.001**
Secondary vegetation	-0.14	-0.18 – -0.09	**<0.001**
StdTmeanAnomalyRS	7.25	1.42 – 13.08	**0.015**
Agriculture_High * StdTmeanAnomalyRS	-14.10	-17.04 – -11.17	**<0.001**
Agriculture_Low * StdTmeanAnomalyRS	-18.50	-22.71 – -14.29	**<0.001**
Secondary vegetation * StdTmeanAnomalyRS	-5.65	-9.82 – -1.47	**0.008**
Random Effects			
σ^2	0.07		
$\tau_{00\ SSBS}$	0.07		
$\tau_{00\ SSB}$	0.04		
$\tau_{00\ SS}$	1.62		
N_{SS}	263		
N_{SSB}	944		
N_{SSBS}	6069		
Observations	6069		
Marginal R^2 / Conditional R^2	0.01 / 0.64		

Table S13: Parameters for the mixed effects model of total abundance as a function of land use in interaction with the maximum temperature anomaly. Output includes estimates, confidence intervals and p values for the fixed effects, the variance explained by the random effects ($\tau_{00\ SS}$ for studies and $\tau_{00\ SSB}$ for blocks within studies), the residual variance (σ^2), the number of observations in total and for each random effect (N_{SS} for studies and N_{SSB} for blocks within studies), and the marginal and conditional R^2 values.

		LogAbund	
Predictors	*Estimates*	*CI*	*p*
Intercept	-0.91	-1.03 – -0.80	**<0.001**
Agriculture_High	-0.51	-0.61 – -0.41	**<0.001**
Agriculture_Low	-0.21	-0.31 – -0.12	**<0.001**
Secondary vegetation	-0.21	-0.30 – -0.11	**<0.001**
StdTmaxAnomalyRS	0.85	-6.58 – 8.28	0.822
Agriculture_High * StdTmaxAnomalyRS	-13.97	-21.08 – -6.85	**<0.001**
Agriculture_Low * StdTmaxAnomalyRS	-11.25	-19.18 – -3.32	**0.005**
Secondary vegetation * StdTmaxAnomalyRS	-1.47	-9.28 – 6.33	0.711
Random Effects			
σ^2	0.68		
$\tau_{00\ SSB}$	0.20		
$\tau_{00\ SS}$	0.41		
N_{SS}	243		
N_{SSB}	905		
Observations	5735		
Marginal R^2 / Conditional R^2	0.037 / 0.492		

Table S14: Parameters for the mixed effects model of species richness as a function of land use in interaction with the maximum temperature anomaly. Output includes estimates, confidence intervals and p values for the fixed effects, the variance explained by the random effects ($\tau_{00\ SS}$ for studies and $\tau_{00\ SSB}$ for blocks within studies), the residual variance (σ^2), the number of observations in total and for each random effect (N_{SS} for studies and N_{SSB} for blocks within studies), and the marginal and conditional R^2 values.

	Species_richness		
Predictors	*Log-Mean*	*CI*	*p*
Intercept	2.73	2.57 – 2.89	**<0.001**
Agriculture_High	-0.39	-0.45 – -0.34	**<0.001**
Agriculture_Low	-0.24	-0.29 – -0.20	**<0.001**
Secondary vegetation	-0.13	-0.17 – -0.08	**<0.001**
StdTmaxAnomalyRS	0.33	-3.72 – 4.37	0.874
Agriculture_High * StdTmaxAnomalyRS	-7.28	-10.64 – -3.92	**<0.001**
Agriculture_Low * StdTmaxAnomalyRS	-2.80	-6.51 – 0.91	0.139
Secondary vegetation * StdTmaxAnomalyRS	-4.61	-8.17 – -1.05	**0.011**
Random Effects			
σ^2	0.07		
$\tau_{00\ SSBS}$	0.07		
$\tau_{00\ SSB}$	0.05		
$\tau_{00\ SS}$	1.60		
N_{SS}	263		
N_{SSB}	944		
N_{SSBS}	6069		
Observations	6069		
Marginal R^2 / Conditional R^2	0.01 / 0.64		

Table S15: Parameters for the mixed effects model of total abundance as a function of the interactions between land use, the mean temperature anomaly, and the amount of surrounding natural habitat. Output includes estimates, confidence intervals and p values for the fixed effects, the variance explained by the random effects ($\tau_{00\ SS}$ for studies and $\tau_{00\ SSB}$ for blocks within studies), residual variance (σ^2), the number of observations in total and for each random effect (N_{SS} for studies and N_{SSB} for blocks within studies), and the marginal and conditional R^2 values.

	LogAbund		
Predictors	*Estimates*	*CI*	*p*
Intercept	-0.91	-1.03 – -0.79	**<0.001**
Agriculture_High	-0.49	-0.61 – -0.37	**<0.001**
Agriculture_Low	-0.20	-0.30 – -0.11	**<0.001**
Secondary vegetation	-0.23	-0.33 – -0.12	**<0.001**
StdTmeanAnomalyRS	0.10	-0.02 – 0.21	0.114
NH_5000.rs	-0.03	-0.13 – 0.06	0.499
Agriculture_High * StdTmeanAnomalyRS	-0.37	-0.50 – -0.25	**<0.001**
Agriculture_Low * StdTmeanAnomalyRS	-0.30	-0.42 – -0.19	**<0.001**
Secondary vegetation * StdTmeanAnomalyRS	-0.13	-0.27 – 0.00	0.057
Agriculture_High * NH_5000.rs	0.15	0.03 – 0.26	**0.011**
Agriculture_Low] * NH_5000.rs	0.07	-0.02 – 0.16	0.134
Secondary vegetation * NH_5000.rs	0.14	0.03 – 0.24	**0.010**
StdTmeanAnomalyRS * NH_5000.rs	-0.07	-0.15 – 0.02	0.118
Agriculture_High * StdTmeanAnomalyRS * NH_5000.rs	0.09	-0.01 – 0.20	0.088
Agriculture_Low] * StdTmeanAnomalyRS * NH_5000.rs	0.30	0.17 – 0.43	**<0.001**
Secondary vegetation *StdTmeanAnomalyRS * NH_5000.rs	0.14	0.01 – 0.27	**0.040**
Random Effects			
σ^2	0.68		
$\tau_{00\ SSB}$	0.19		
$\tau_{00\ SS}$	0.42		
N_{SS}	243		
N_{SSB}	905		
Observations	5735		
Marginal R^2 / Conditional R^2	0.045 / 0.495		

Table S16: Parameters for the mixed effects model of species richness as a function of interactions between land use, the mean temperature anomaly, and the amount of surrounding natural habitat. Output includes estimates, confidence intervals and p values for the fixed effects, the variance explained by the random effects ($\tau_{00\ SS}$ for studies and $\tau_{00\ SSB}$ for blocks within studies), the residual variance (σ^2), the number of observations in total and for each random effect (N_{SS} for studies and N_{SSB} for blocks within studies), and the marginal and conditional R^2 values.

	Species_richness		
Predictors	*Log-Mean*	*CI*	*p*
Intercept	2.70	2.54 – 2.86	**<0.001**
Agriculture_High	-0.35	-0.41 – -0.29	**<0.001**
Agriculture_Low	-0.24	-0.28 – -0.19	**<0.001**
Secondary vegetation	-0.12	-0.18 – -0.07	**<0.001**
StdTmeanAnomalyRS	0.09	-0.00 – 0.19	0.061
NH_5000.rs	0.02	-0.04 – 0.08	0.530
Agriculture_High * StdTmeanAnomalyRS	-0.24	-0.30 – -0.17	**<0.001**
Agriculture_Low * StdTmeanAnomalyRS	-0.27	-0.34 – -0.21	**<0.001**
Secondary vegetation * StdTmeanAnomalyRS	-0.08	-0.15 – -0.02	**0.010**
Agriculture_High * NH_5000.rs	0.07	0.01 – 0.13	**0.016**
Agriculture_Low *NH_5000.rs	0.10	0.05 – 0.14	**<0.001**
Secondary vegetation * NH_5000.rs	0.04	-0.01 – 0.09	0.130
StdTmeanAnomalyRS * NH_5000.rs	-0.01	-0.06 – 0.04	0.711
Agriculture_High * StdTmeanAnomalyRS * NH_5000.rs	0.04	-0.02 – 0.10	0.159
Agriculture_Low * StdTmeanAnomalyRS * NH_5000.rs	0.20	0.13 – 0.27	**<0.001**
Secondary vegetation * StdTmeanAnomalyRS * NH_5000.rs	0.06	0.00 – 0.12	**0.049**
Random Effects			
σ^2	0.07		
$\tau_{00\ SSBS}$	0.07		
$\tau_{00\ SSB}$	0.04		
$\tau_{00\ SS}$	1.62		
N_{SS}	263		
N_{SSB}	944		
N_{SSBS}	6069		
Observations	6069		

Marginal R^2 / Conditional R^2	0.013 / 0.638

Table S17: Parameters for the mixed effects model of total abundance as a function of interactions between land use, the maximum temperature anomaly, and the amount of surrounding natural habitat. Output includes estimates, confidence intervals and p values for the fixed effects, the variance explained by the random effects ($\tau_{00\ SS}$ for studies and $\tau_{00\ SSB}$ for blocks within studies), the residual variance (σ^2), the number of observations in total and for each random effect (N_{SS} for studies and N_{SSB} for blocks within studies), and the marginal and conditional R^2 values.

	LogAbund		
Predictors	*Estimates*	*CI*	*p*
Intercept	-0.92	-1.03 – -0.80	**<0.001**
Agriculture_High	-0.47	-0.58 – -0.36	**<0.001**
Agriculture_Low	-0.20	-0.29 – -0.10	**<0.001**
Secondary vegetation	-0.19	-0.29 – -0.09	**<0.001**
StdTmaxAnomalyRS	-0.01	-0.11 – 0.10	0.903
NH_5000.rs	-0.03	-0.12 – 0.07	0.600
Agriculture_High * StdTmaxAnomalyRS	-0.17	-0.28 – -0.07	**0.001**
Agriculture_Low * StdTmaxAnomalyRS	-0.14	-0.25 – -0.02	**0.019**
Secondary vegetation * StdTmaxAnomalyRS	0.00	-0.11 – 0.12	0.962
Agriculture_High * NH_5000.rs	0.07	-0.03 – 0.18	0.167
Agriculture_Low * NH_5000.rs	0.08	-0.02 – 0.18	0.135
Secondary vegetation * NH_5000.rs	0.10	0.00 – 0.20	**0.050**
StdTmaxAnomalyRS *NH_5000.rs	0.07	-0.02 – 0.15	0.137
Agriculture_High * StdTmaxAnomalyRS *NH_5000.rs	-0.14	-0.25 – -0.03	**0.014**
Agriculture_Low * StdTmaxAnomalyRS * NH_5000.rs	-0.02	-0.16 – 0.11	0.758
Secondary vegetation * StdTmaxAnomalyRS * NH_5000.rs	-0.10	-0.22 – 0.01	0.077
Random Effects			
σ^2	0.68		
$\tau_{00\ SSB}$	0.20		
$\tau_{00\ SS}$	0.42		
N_{SS}	243		
N_{SSB}	905		

Observations	5735
Marginal R^2 / Conditional R^2	0.040 / 0.498

Table S18: Parameters for the mixed effects model of species richness as a function of interactions between land use, the maximum temperature anomaly, and the amount of surrounding natural habitat. Output includes estimates, confidence intervals and p values for the fixed effects, the variance explained by the random effects ($\tau_{00\ SS}$ for studies and $\tau_{00\ SSB}$ for blocks within studies), the residual variance (σ^2), the number of observations in total and for each random effect (N_{SS} for studies and N_{SSB} for blocks within studies), and the marginal and conditional R^2 values.

	Species_richness		
Predictors	*Log-Mean*	*CI*	*p*
Intercept	2.69	2.53 – 2.85	**<0.001**
Agriculture_High	-0.34	-0.40 – -0.28	**<0.001**
Agriculture_Low	-0.17	-0.22 – -0.12	**<0.001**
Secondary vegetation	-0.07	-0.12 – -0.03	**0.002**
StdTmaxAnomalyRS	-0.06	-0.12 – -0.00	**0.040**
NH_5000.rs	0.01	-0.04 – 0.07	0.638
Agriculture_High * StdTmaxAnomalyRS	-0.05	-0.10 – -0.00	**0.041**
Agriculture_Low * StdTmaxAnomalyRS	-0.01	-0.06 – 0.05	0.738
Secondary vegetation *StdTmaxAnomalyRS	-0.03	-0.08 – 0.02	0.299
Agriculture_High * NH_5000.rs	0.03	-0.03 – 0.08	0.366
Agriculture_Low * NH_5000.rs	0.05	0.00 – 0.10	**0.044**
Secondary vegetation * NH_5000.rs	0.00	-0.05 – 0.05	0.976
StdTmaxAnomalyRS *NH_5000.rs	0.13	0.08 – 0.17	**<0.001**
Agriculture_High *StdTmaxAnomalyRS *NH_5000.rs	-0.15	-0.21 – -0.10	**<0.001**
Agriculture_Low *StdTmaxAnomalyRS * NH_5000.rs	-0.20	-0.27 – -0.14	**<0.001**
Secondary vegetation * StdTmaxAnomalyRS * NH_5000.rs	-0.08	-0.13 – -0.02	**0.004**
Random Effects			
σ^2	0.07		
$\tau_{00\ SSBS}$	0.07		
$\tau_{00\ SSB}$	0.04		
$\tau_{00\ SS}$	1.60		
N_{SS}	263		
N_{SSB}	944		

N $_{SSBS}$	6069
Observations	6069
Marginal R^2 / Conditional R^2	0.012 / 0.636

Table S19: Parameters for the mixed effects models of total abundance as a function of interactions between land use and the mean temperature anomaly, separated by non-tropical and tropical realms. Output includes estimates, confidence intervals and p values for the fixed effects, the variance explained by the random effects ($\tau_{00\ SS}$ for studies and $\tau_{00\ SSB}$ for blocks within studies), the residual variance (σ^2), the number of observations in total and for each random effect (N $_{SS}$ for studies and N $_{SSB}$ for blocks within studies), and the marginal and conditional R^2 values.

	NON_TROPICAL: LogAbund			**TROPICAL LogAbund**		
Predictors	*Estimates*	*CI*	*p*	*Estimates*	*CI*	*p*
Intercept	-1.06	-1.23 – -0.90	**<0.001**	-0.74	-0.88 – -0.59	**<0.001**
Secondary vegetation	-0.13	-0.26 – 0.01	0.066	-0.25	-0.42 – -0.07	**0.006**
Agriculture_Low	-0.08	-0.20 – 0.05	0.223	-0.56	-0.75 – -0.37	**<0.001**
Agriculture_High	-0.31	-0.46 – -0.16	**<0.001**	-0.79	-0.92 – -0.65	**<0.001**
StdTmeanAnomalyRS	11.74	1.99 – 21.48	**0.018**	-6.47	-11.51 – -1.42	**0.012**
Secondary vegetation * StdTmeanAnomalyRS	-11.68	-20.55 – -2.81	**0.010**	7.71	-1.19 – 16.61	0.089
Agriculture_Low * StdTmeanAnomalyRS	-15.03	-23.29 – -6.77	**<0.001**	-13.88	-23.31 – -4.45	**0.004**
Agriculture_High * StdTmeanAnomalyRS	-19.53	-28.84 – -10.22	**<0.001**	-6.70	-11.77 – -1.62	**0.010**
Random Effects						
σ^2	0.69			0.61		
τ_{00}	0.18 $_{SSB}$			0.31 $_{SSB}$		
	0.50 $_{SS}$			0.11 $_{SS}$		
N	152 $_{SS}$			91 $_{SS}$		
	625 $_{SSB}$			280 $_{SSB}$		
Observations	4146			1589		
Marginal R^2 / Conditional R^2	0.013 / 0.501			0.134 / 0.485		

Table S20: Parameters for the mixed effects models of species richness as a function of land use and the mean temperature anomaly, separated by non-tropical and tropical realms. Output includes estimates, confidence intervals and p values for the fixed effects, the variance explained by the random effects ($\tau_{00\ SS}$ for studies and $\tau_{00\ SSB}$ for blocks within studies), the residual variance (σ^2), the number of observations in total and for each random effect (N_{SS} for studies and N_{SSB} for blocks within studies), and the marginal and conditional R^2 values.

	NON_TROPICAL: Species_richness			**TROPICAL: Species_richness**		
Predictors	*Log-Mean*	*CI*	*p*	*Log-Mean*	*CI*	*p*
Intercept	2.57	2.34 – 2.79	**<0.001**	3.05	2.82 – 3.27	**<0.001**
Secondary vegetation	-0.22	-0.29 – -0.16	**<0.001**	-0.11	-0.20 – -0.01	**0.024**
Agriculture_Low	-0.20	-0.26 – -0.14	**<0.001**	-0.38	-0.49 – -0.26	**<0.001**
Agriculture_High	-0.31	-0.40 – -0.22	**<0.001**	-0.58	-0.66 – -0.51	**<0.001**
StdTmeanAnomalyRS	17.71	11.51 – 23.91	**<0.001**	-3.20	-8.79 – 2.38	0.261
Secondary vegetation * StdTmeanAnomalyRS	-13.42	-17.61 – -9.23	**<0.001**	1.93	-2.82 – 6.67	0.426
Agriculture_Low * StdTmeanAnomalyRS	-20.47	-24.44 – -16.50	**<0.001**	-4.37	-10.16 – 1.42	0.139
Agriculture_High * StdTmeanAnomalyRS	-17.38	-22.66 – -12.10	**<0.001**	-6.25	-9.00 – -3.50	**<0.001**
Random Effects						
σ^2	0.07			0.08		
τ_{00}	0.07_{SSBS}			0.08_{SSBS}		
	0.04_{SSB}			0.05_{SSB}		
	1.85_{SS}			1.06_{SS}		
N	152_{SS}			91_{SS}		
	625_{SSB}			280_{SSB}		
	4146_{SSBS}			1589_{SSBS}		
Observations	4146			1589		
Marginal R^2 / Conditional R^2	0.008 / 0.665			0.036 / 0.56		

Table S21: Parameters for the mixed effects models of total abundance as a function of land use and the maximum temperature anomaly, separated by non-tropical and tropical realms. Output includes estimates, confidence intervals and p values for the fixed effects, the variance explained by the random effects ($\tau_{00\ SS}$ for studies and $\tau_{00\ SSB}$ for blocks within studies), the residual variance (σ^2), the number of observations in total and for each random effect (N_{SS} for studies and N_{SSB} for blocks within studies), and the marginal and conditional R^2 values.

	NON_TROPICAL: LogAbund			**TROPICAL: LogAbund**		
Predictors	*Estimates*	*CI*	*p*	*Estimates*	*CI*	*p*
Intercept	-1.12	-1.28 – -0.96	**<0.001**	-0.70	-0.85 – -0.54	**<0.001**
Secondary vegetation	-0.05	-0.18 – 0.08	0.433	-0.31	-0.45 – -0.17	**<0.001**
Agriculture_Low	-0.03	-0.15 – 0.09	0.621	-0.47	-0.63 – -0.32	**<0.001**
Agriculture_High	-0.24	-0.38 – -0.10	**0.001**	-0.80	-0.94 – -0.66	**<0.001**
Intercept	-1.12	-1.28 – -0.96	**<0.001**	-0.70	-0.85 – -0.54	**<0.001**
StdTmaxAnomalyRS				-5.68	-12.88 – 1.52	0.122
Secondary vegetation * StdTmaxAnomalyRS				3.40	-4.37 – 11.16	0.391
Agriculture_Low * StdTmaxAnomalyRS				-8.25	-16.39 – -0.10	**0.047**
Agriculture_High * StdTmaxAnomalyRS				-6.77	-13.87 – 0.33	0.062
Random Effects						
σ^2	0.70			0.61		
τ_{00}	0.17 $_{SSB}$			0.31 $_{SSB}$		
	0.49 $_{SS}$			0.17 $_{SS}$		
N	152 $_{SS}$			91 $_{SS}$		
	625 $_{SSB}$			280 $_{SSB}$		
Observations	4146			1589		
Marginal R^2 / Conditional R^2	0.007 / 0.493			0.124 / 0.510		

Table S22: Parameters for the mixed effects models of species richness as a function of land use and the maximum temperature anomaly, separated by non-tropical and tropical realms. Output includes estimates, confidence intervals and p values for the fixed effects, the variance explained by the random effects ($\tau_{00\ SS}$ studies and $\tau_{00\ SSB}$ for blocks within studies), the residual variance (σ^2), the number of observations in total and for each random effect (N_{SS} for studies and N_{SSB} for blocks within studies), and the marginal and conditional R^2 values.

	NON_TROPICAL Species_richness			**TROPICAL: Species_richness**		
Predictors	*Log-Mean*	*CI*	*p*	*Log-Mean*	*CI*	*p*
Intercept	2.45	2.23 – 2.68	**<0.001**	3.06	2.84 – 3.28	**<0.001**
Secondary vegetation	-0.06	-0.13 – 0.00	0.068	-0.16	-0.24 – -0.09	**<0.001**
Agriculture_Low	-0.13	-0.19 – -0.08	**<0.001**	-0.37	-0.46 – -0.28	**<0.001**
Agriculture_High	-0.19	-0.28 – -0.10	**<0.001**	-0.57	-0.65 – -0.49	**<0.001**
StdTmaxAnomalyRS	-10.36	-13.97 – -6.75	**<0.001**	1.60	-3.05 – 6.25	0.499
Secondary vegetation *StdTmaxAnomalyRS	8.56	4.92 – 12.20	**<0.001**	-3.69	-7.77 – 0.38	0.076
Agriculture_Low * StdTmaxAnomalyRS	15.22	11.60 – 18.83	**<0.001**	-5.06	-9.39 – -0.73	**0.022**
Agriculture_High * StdTmaxAnomalyRS	7.83	1.51 – 14.14	**0.015**	-5.36	-9.13 – -1.58	**0.005**
Random Effects						
σ^2	0.07			0.08		
τ_{00}	0.07 $_{SSBS}$			0.08 $_{SSBS}$		
	0.04 $_{SSB}$			0.06 $_{SSB}$		
	1.81 $_{SS}$			1.04 $_{SS}$		
N	152 $_{SS}$			91 $_{SS}$		
	625 $_{SSB}$			280 $_{SSB}$		
	4146 $_{SSBS}$			1589 $_{SSBS}$		
Observations	4146			1589		
Marginal R^2 / Conditional R^2	0.005 / 0.66			0.026 / 0.553		

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