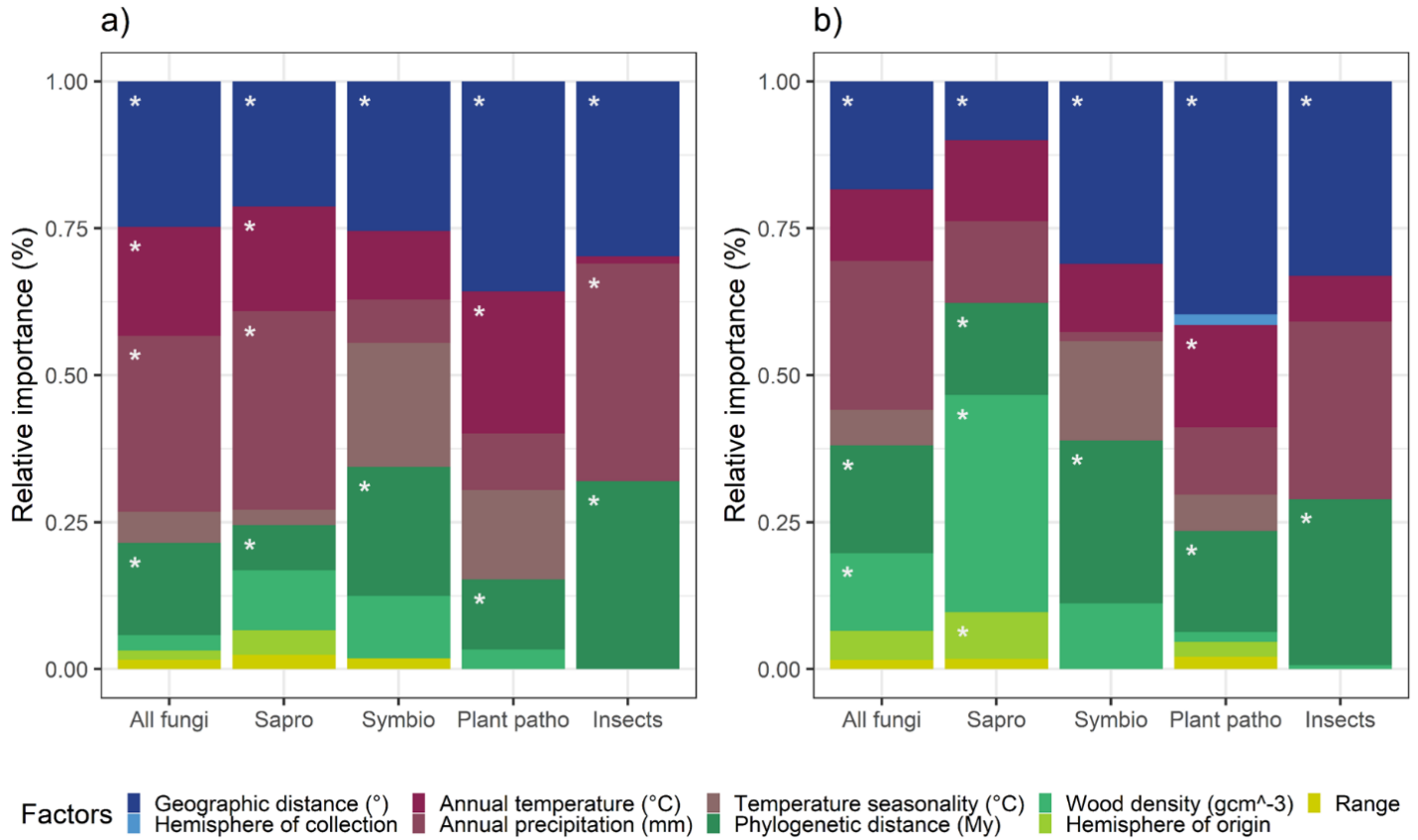
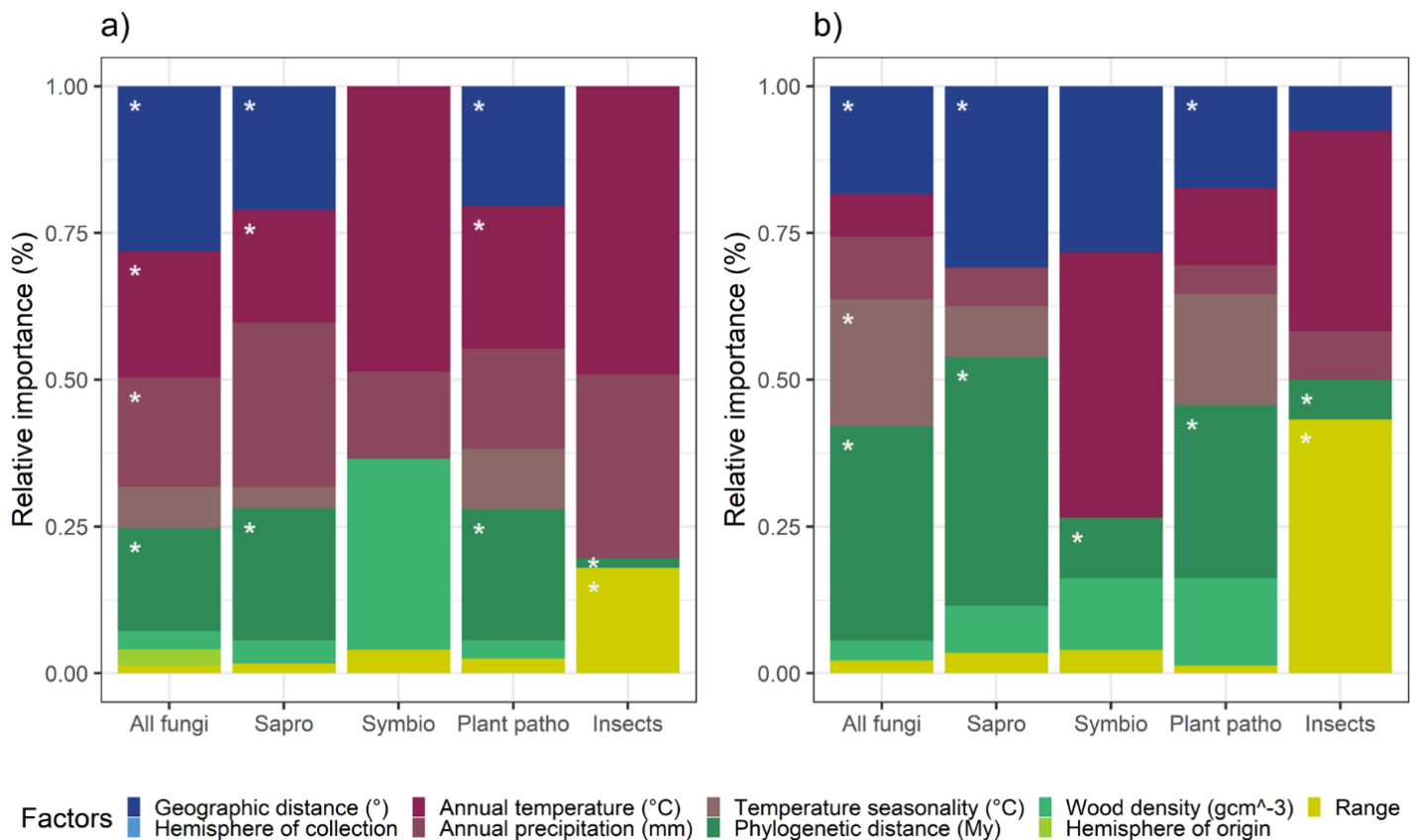


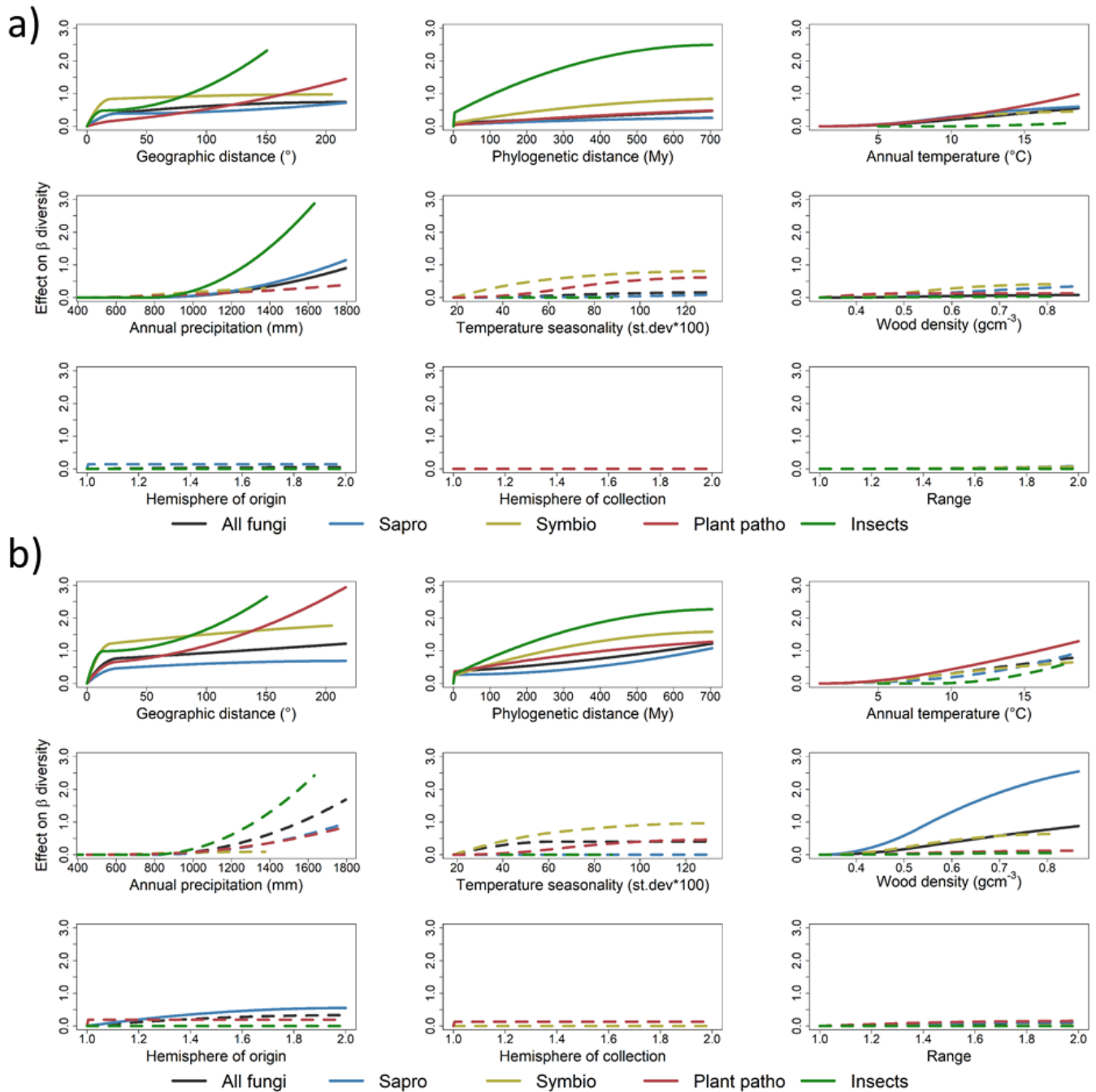
# 1 Supplementary Information



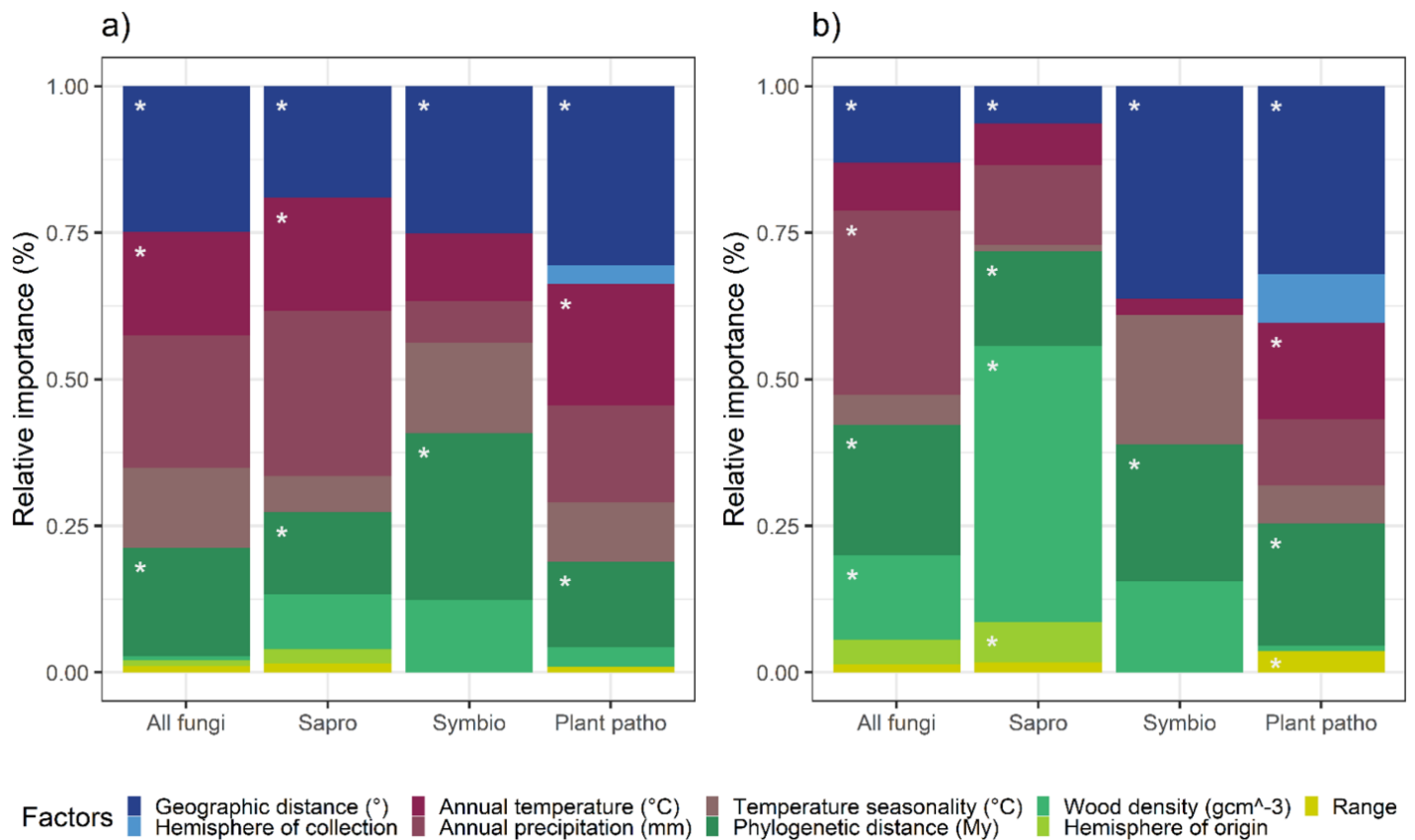
2 Supplementary Figure S1. **The relative importance of different variables for  $\beta$ -diversity of tree-**  
 3 **associated organisms. a, b** the effects of given variables on species turnover component of  $\beta$ -  
 4 diversity (**a**,  $\beta_{sim}$ ) and abundance weighted  $\beta$ -diversity (**b**, Horn  $q=1$ ) as assessed with GDMs.  
 5 Geographic, climatic and host related variables are shown in different shades of blue, red and green,  
 6 respectively. The results are shown for all fungi (“All fungi”), saprotrophs (“Sapro”), symbiotrophs  
 7 (“Symbio”), plant pathogens (“Plant patho”) and herbivorous insects (“Insects”). Significant factors  
 8 are indicated with asterisks. Variable significance testing is done on a basis of 50 permutations. The  
 9 results are shown for the entire data set and samples that contained insect and fungi (“**main**  
 10 **analysis**”).



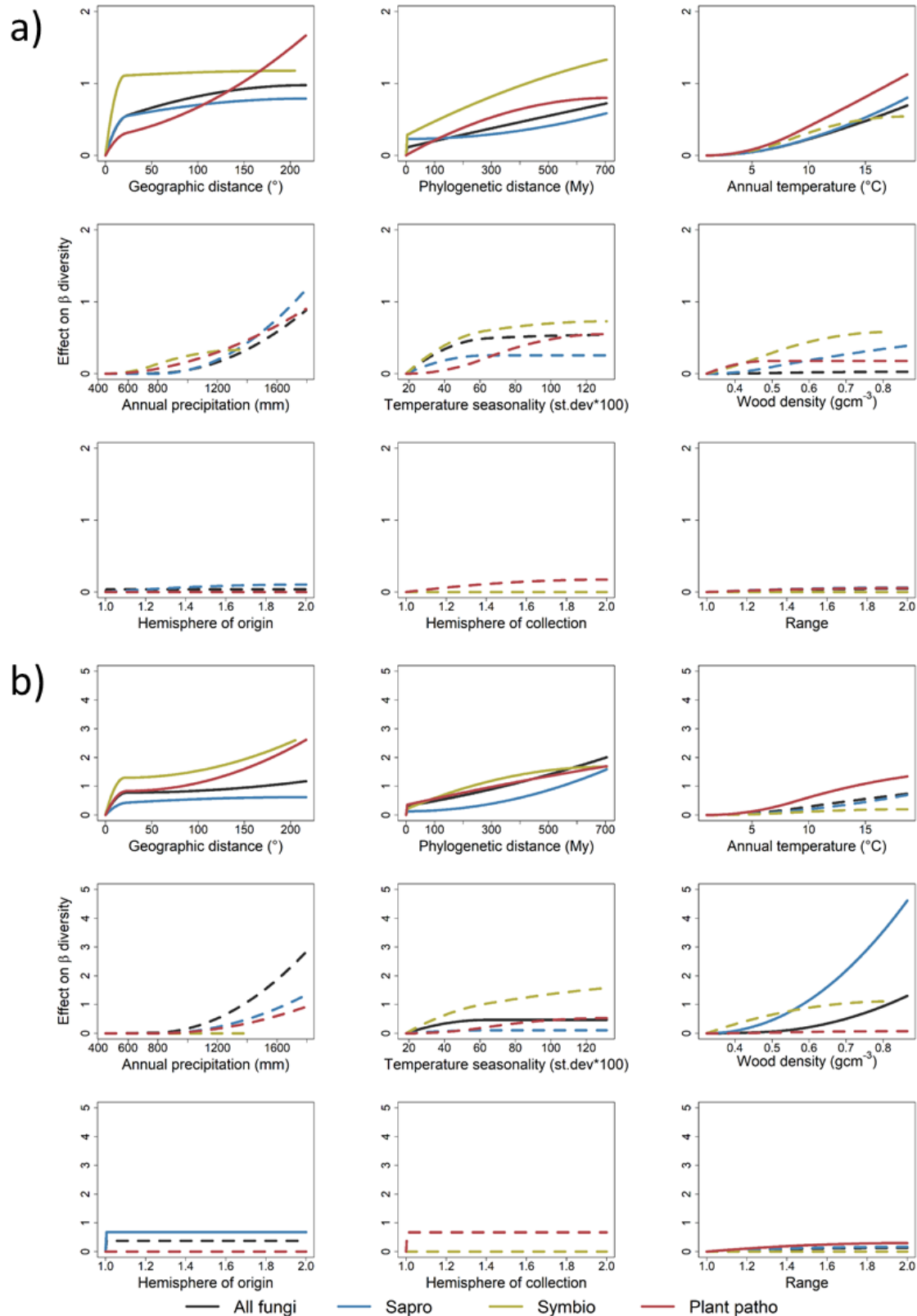
11 **Supplementary Figure S2. The relative importance of different variables for  $\beta$ -diversity of tree-**  
 12 **associated organisms. a, b** the effects of given variables on incidence based  $\beta$ -diversity (Sørensen,  
 13  $q=0$ ) as assessed with GDMs for zero adjusted data for the entire data set (**a**, “zero adjusted  
 14 analysis”) and samples from which both insects and fungi were assessed (**b**, “overlap zero adjusted  
 15 analysis”). Geographic, climatic and host related factors are shown in different shades of blue, red  
 16 and green, respectively. The results are shown for all fungi (“All fungi”), saprotrophs (“Sapro”),  
 17 symbiotrophs (“Symbio”), plant pathogens (“Plant patho”) and herbivorous insects (“Insects”).  
 18 Significant factors are indicated with asterisks. Variable significance testing is done on a basis of 50  
 19 permutations.



20 Supplementary Figure S3. **Effects of different variables on  $\beta$ -diversity of tree-associated**  
 21 **organisms.** **a, b** The shape of the curve indicates the change in species turnover component of  $\beta$ -  
 22 diversity (**a**,  $\beta_{sim}$ ) and abundance-weighted  $\beta$ -diversity (**b**, Horn  $q=1$ ) along the variable gradient as  
 23 assessed with GDMs. The results are shown for all fungi (“All fungi”), saprotrophs (“Sapro”),  
 24 symbiotrophs (“Symbio”), plant pathogens (“Plant patho”) and herbivorous insects (“Insects”). The  
 25 final height of the curve indicates the relative importance of a variable. Significant factors are indicated  
 26 with solid lines. Variable significance testing is done on a basis of 50 permutations. The results are  
 27 shown for the entire data set and samples that contained insect and fungi (“**main analysis**”).



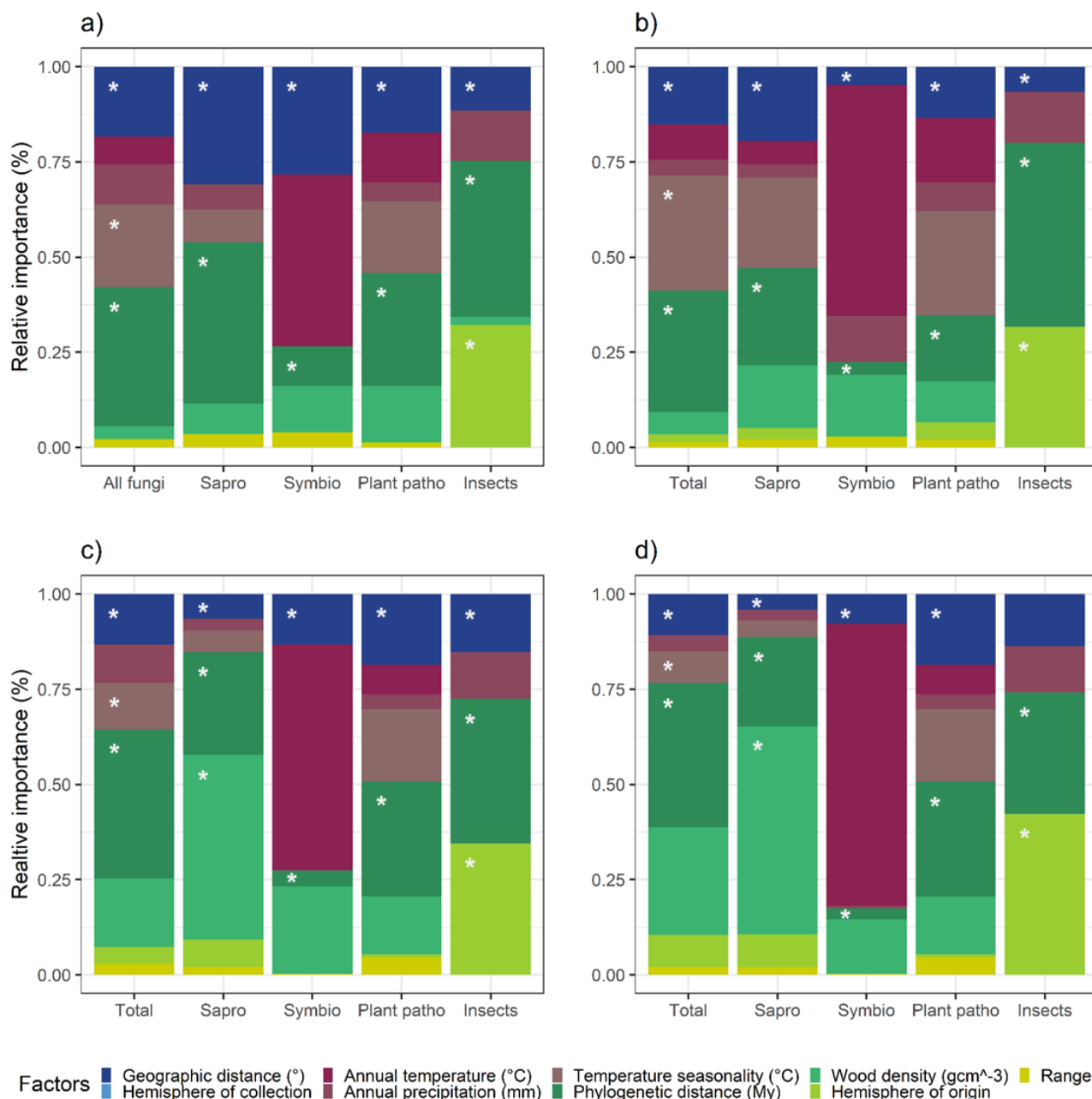
28 **Supplementary Figure S4. The relative importance of different variables for  $\beta$ -diversity of tree-**  
 29 **associated fungi and insects.** The effects of variables on incidence-based (**a**, Sørensen) and  
 30 abundance-weighted (**b**, Morisita Horn)  $\beta$ -diversity as assessed with generalised dissimilarity  
 31 models. Geographic, climatic and host-related variables are shown in different shades of blue, red  
 32 and green, respectively. The results are shown for all fungi together (“All fungi”), and saprotrophs  
 33 (“Sapro”), symbiotrophs (“Symbio”) and plant pathogens (“Plant patho”) separately. Significant  
 34 factors ( $p < 0.05$ ) are indicated with asterisks. Variable significance testing is done using 50  
 35 permutations. The results are shown for the entire data set rarefied to 10,000 reads per sample and  
 36 samples that contained insect and fungi (“rarefied data analysis”).



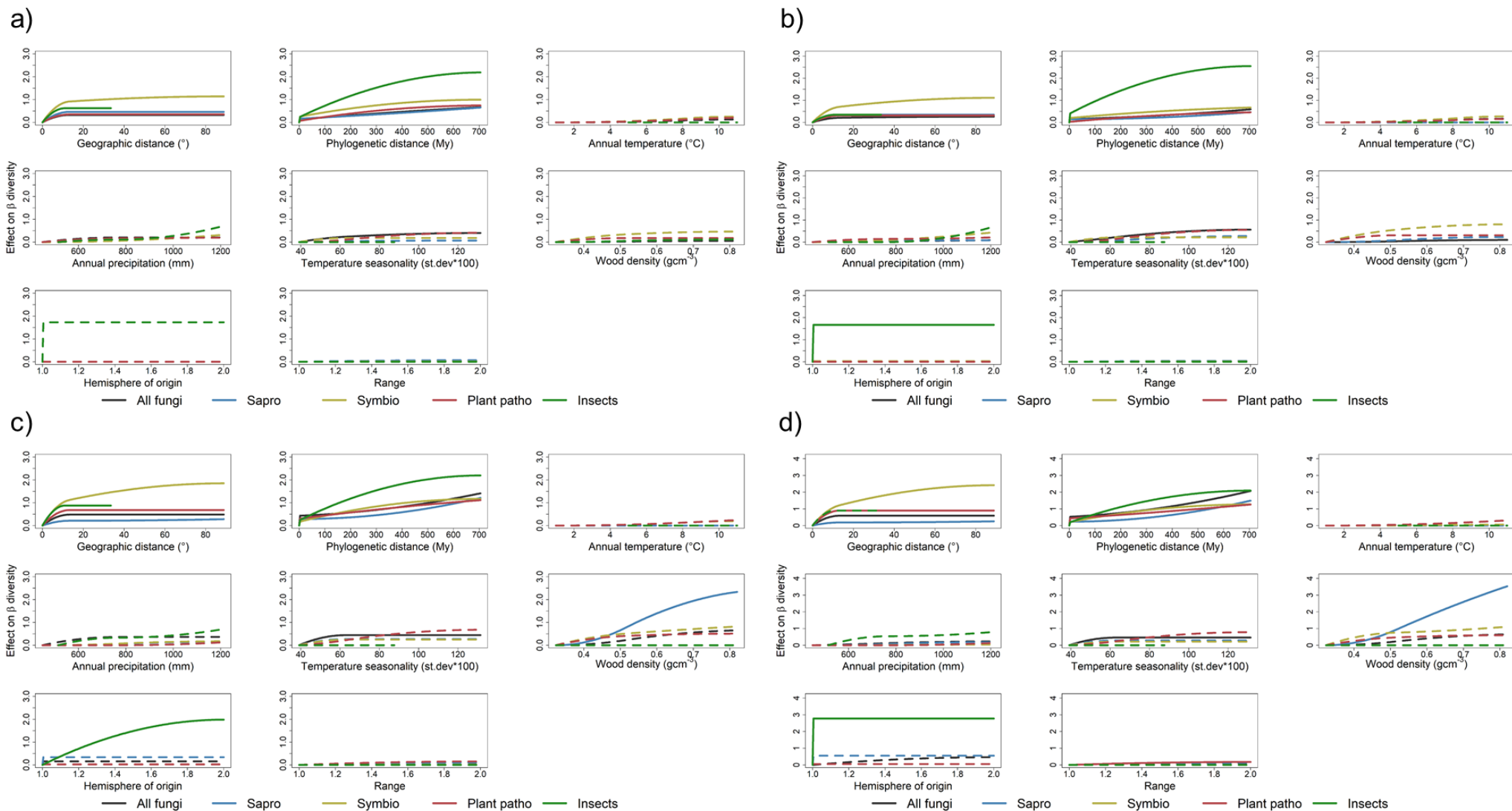
37

38 Supplementary Figure S5. Effects of different variables on  $\beta$ -diversity of tree-associated fungi  
 39 and insects. The shape of the curve indicates the change in the effect of a variable on incidence-  
 40 based (a, Sørensen) and abundance-weighted (b, Morisita Horn)  $\beta$ -diversity, at different points along

41 the gradient of the variable. Generalized dissimilarity models were used to estimate these non-linear  
42 effects of the variables on  $\beta$  diversity. The results are shown for all fungi together (“All fungi”), and  
43 saprotrophs (“Sapro”), symbiotrophs (“Symbio”) and plant pathogens (“Plant patho”) separately. The  
44 final height of the curve indicates the relative importance of a variable in driving  $\beta$ -diversity.  
45 Significant factors ( $p < 0.05$ ) are indicated with solid lines. Variable significance testing is done on a  
46 basis of 50 permutations. The results are shown for the entire data set rarefied to 10,000 reads per  
47 sample and samples that contained insect and fungi (“**rarefied data analysis**”).

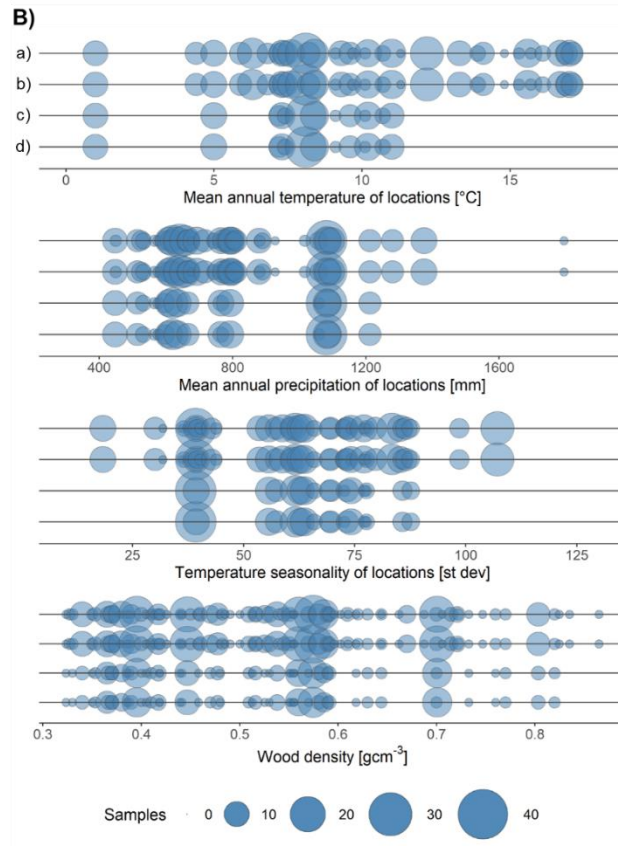
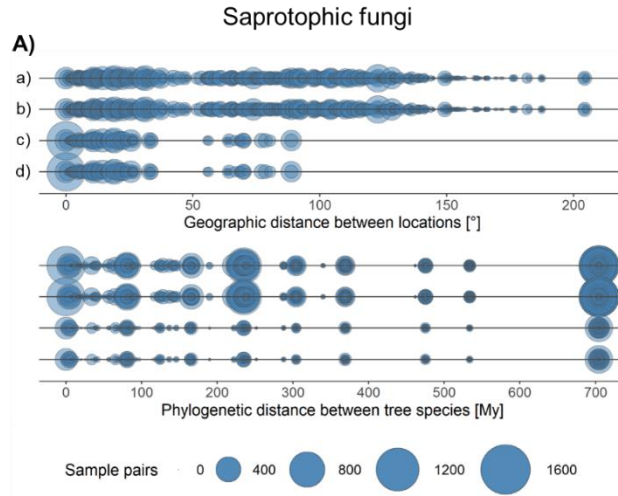
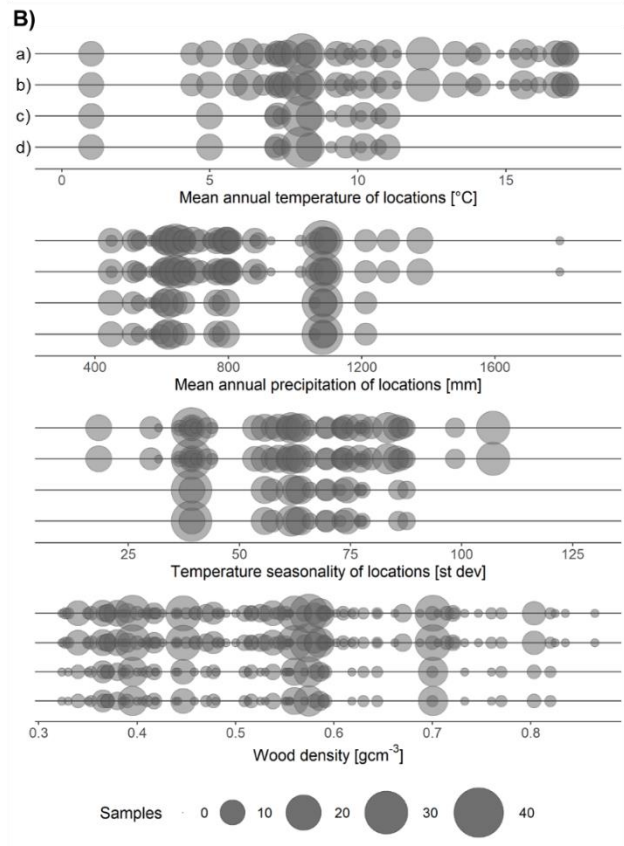
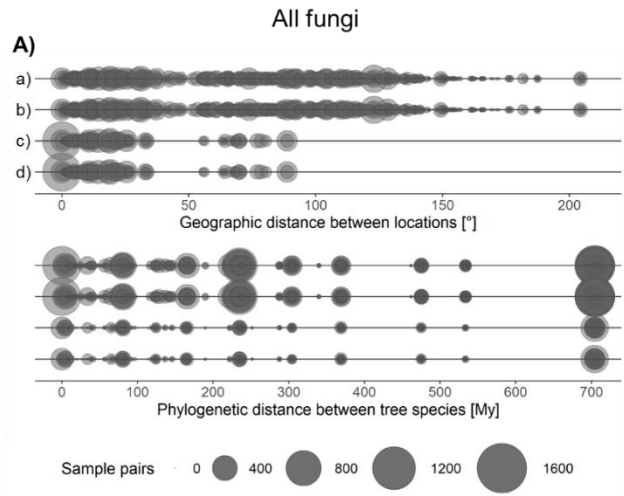


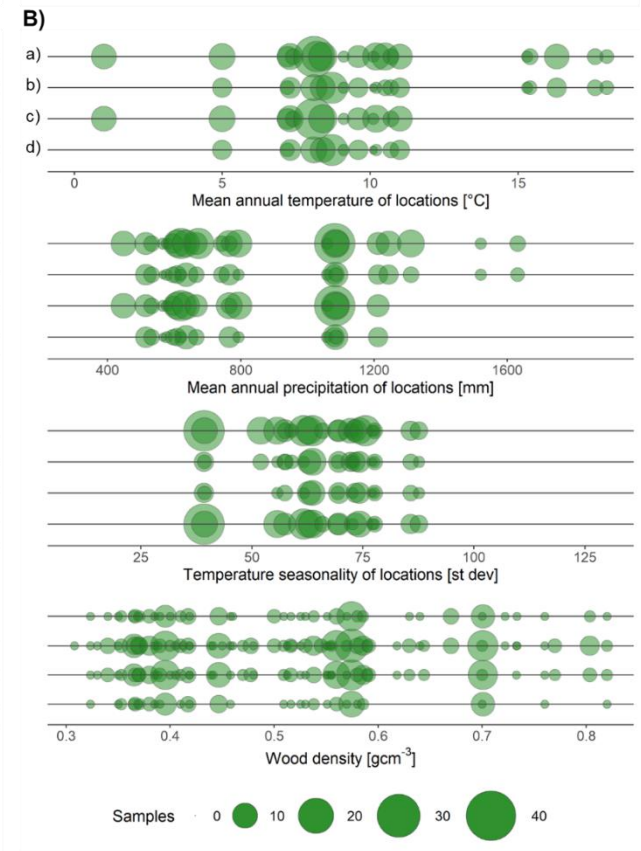
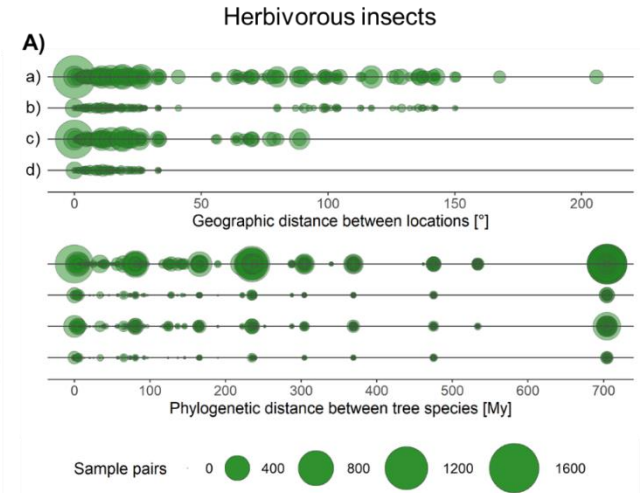
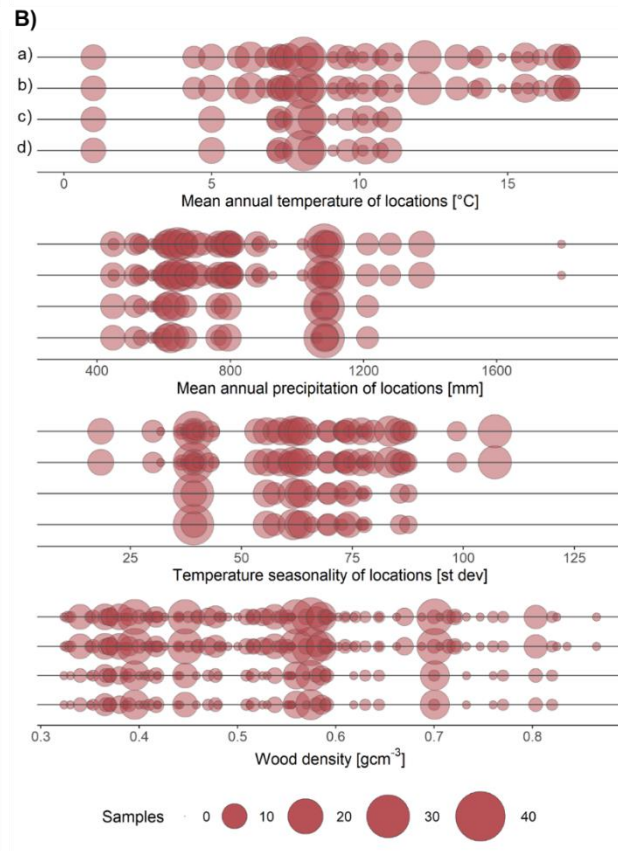
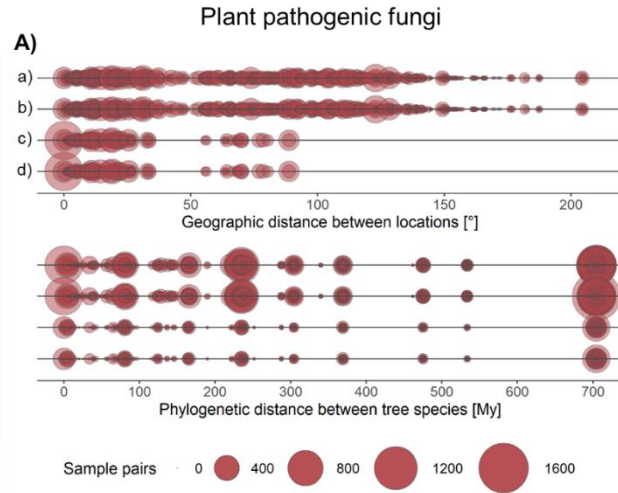
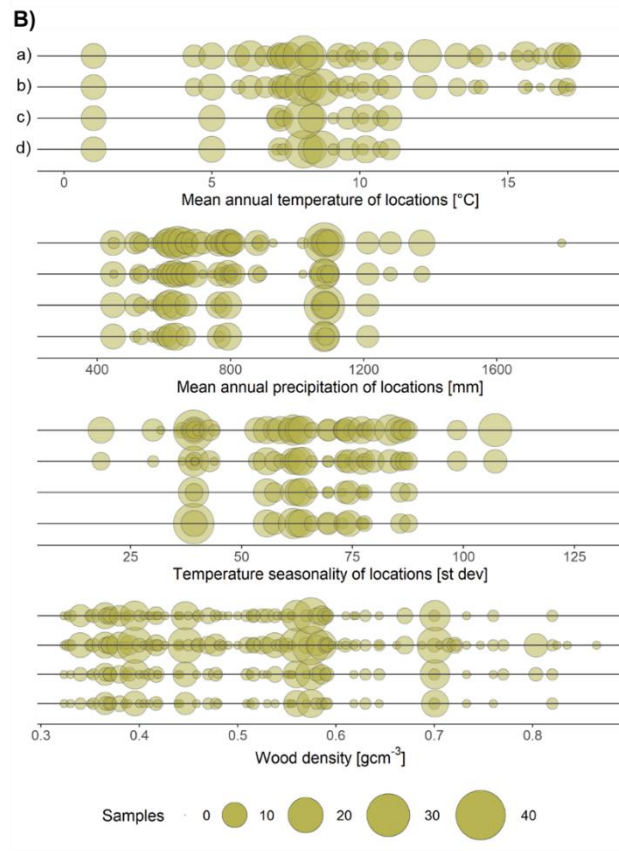
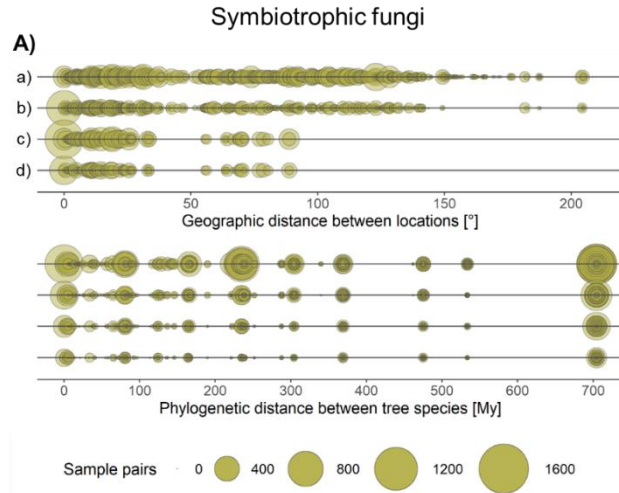
49 Supplementary Figure S6. **The relative importance of different variables for  $\beta$ -diversity of tree-**  
 50 **associated organisms. a, b, c, d** the effects of given variables on incidence based  $\beta$ -diversity (a,  
 51 Sørensen  $q=0$ ), species turnover component of  $\beta$ -diversity (b,  $\beta_{sim}$ ) and abundance weighted  $\beta$ -  
 52 diversity (c, Horn  $q=1$ ; d, Morisita-Horn  $q=2$ ) as assessed with GDMs. Geographic, climatic and host  
 53 related factors are shown in different shades of blue, red and green, respectively. The results are shown  
 54 for all fungi (“All fungi”), saprotrophs (“Sapro”), symbiotrophs (“Symbio”), plant pathogens (“Plant  
 55 patho”) and herbivorous insects (“Insects”). Significant factors are indicated with asterisks. Variable  
 56 significance testing is done on a basis of 50 permutations. The results are shown for the samples from  
 57 which both insects and fungi were assessed and which contained insects and fungi (“**overlap**  
 58 **analysis**”).





60 Supplementary Figure S7. **Effects of different variables on  $\beta$ -diversity of tree-associated organisms.** **a, b, c, d** The shape of the curve indicates the  
61 change in incidence based  $\beta$ -diversity (**a**, Sørensen  $q=0$ ), species turnover component of  $\beta$ -diversity (**b**,  $\beta_{sim}$ ) and abundance weighted  $\beta$ -diversity (**c**,  
62 Morisita  $q=1$ ; **d**, Morisita-Horn  $q=2$ ) along the variable gradient as assessed with GDMs. The results are shown for all fungi (“All fungi”), saprotrophs  
63 (“Sapro”), symbiotrophs (“Symbio”), plant pathogens (“Plant patho”) and herbivorous insects (“Insects”). The final height of the curve indicates the  
64 relative importance of a variable. Significant factors are indicated with solid lines. Variable significance testing is done on a basis of 50 permutations.  
65 The results are shown for the samples from which both insects and fungi were assessed and which contained insects and fungi (“**overlap analysis**”).





Supplementary Figure S8. **Distribution of collected samples along gradients of different variables. A, B** Frequency of values for pairwise comparisons of host geographic origin (geographic distance) and host species (phylogenetic distance) (**A**) and frequency distribution of climate variables for sites (i.e. mean annual temperature, temperature seasonality and mean annual precipitation) and wood density for tree species (**B**). **a, b, c, d** Distribution of collected samples along gradients of different variables is shown for analysis considering all samples from which organisms were assessed, including blank samples (**a**, “zero adjusted analysis”), all samples from which organisms were assessed and in which they were detected (**b**; “main analysis”), samples from which both insects and fungi were assessed, including blank samples (**c**, “overlap zero adjusted analysis”) and samples from which both insects and fungi were assessed and in which they were detected (**d**, “overlap analysis”). The size of the circles indicates the number of sample pairs (A) or samples (B). Colors indicate different groups (all fungi = grey, saprotrophic fungi = blue, symbiotrophic fungi = yellow, plant pathogenic fungi = red, herbivorous insects = green).

Table S1 **Statistical details on the Generalized Dissimilarity Models (GDMs) in the “main analysis”**. The numbers show model deviance, percent deviance explained by the full model, the p-value of the full model, and the number of permutations used to calculate the statistics for each fitted model (n=50). Numbers are shown for different measures of  $\beta$ -diversity (i.e., Sørensen  $q=0$ , Morisita  $q=1$ , Morisita-Horn  $q=2$ ) and species turnover component (i.e., species turnover) and for different functional groups of organisms (i.e., herbivorous insects and all, saprotrophic, symbiotrophic, and plant pathogenic fungi). Numbers in brackets indicate number of samples that were included in the analysis. The percentage of unique variance explained by each variable (i.e., %devexp), the coefficients (i.e., coef; the maximum height of the spline for that variable), the relative value of the coefficients and the p-values (p) are also shown. Bold numbers indicate significant variables.

Herbivorous insects (n=96)																
	q=0				q=1				q=2				species turnover			
Model deviance	457				364				318				987			
Percent deviance explained	18				18				17				17			
Fitted permutations	50				50				50				50			
Model p value	0				0				0				0			
	%devexp	coef	%coef	p-value	%devexp	coef	%coef	p-value	%devexp	coef	%coef	p-value	%devexp	coef	%coef	p-value
Geographic distance	9.74	2.95	36	<b>0.00</b>	9.89	2.65	33	<b>0.00</b>	9.83	2.44	30	<b>0.00</b>	5.45	2.31	30	<b>0.00</b>
Ann. Temp	0.48	0.30	4	0.56	1.54	0.63	8	0.52	5.43	1.44	18	0.36	0.06	0.10	1	0.70
Ann. Prec	12.19	2.63	32	0.06	8.60	2.43	30	0.08	4.61	1.96	24	0.40	15.11	2.88	37	<b>0.00</b>
Temp. Seasonality	0.00	0.00	0	0.92	0.00	0.00	0	0.94	0.00	0.00	0	1.00	0.00	0.00	0	0.96
Wood.denisty	0.00	0.00	0	0.96	0.01	0.05	1	0.86	0.00	0.03	0	0.88	0.00	0.00	0	0.86
Hem.of.colection	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Hem.of.origin	0.00	0.00	0	0.98	0.00	0.00	0	0.90	0.00	0.00	0	0.92	0.00	0.00	0	0.92
Range	0.00	0.00	0	0.94	0.00	0.00	0	0.90	0.00	0.00	0	0.94	0.00	0.00	0	0.94
Phylogenetic distance	25.19	2.26	28	<b>0.00</b>	26.85	2.27	28	<b>0.00</b>	26.04	2.22	27	<b>0.00</b>	32.42	2.49	32	<b>0.00</b>

All fungi (n=352)																
	q=0				q=1				q=2				species turnover			
Model deviance	1,377				3,145				3,675				2,302			
Percent deviance explained	49				33				24				40			
Fitted permutations	50				50				50				50			
Model p value	0				0				0				0			
	%devexp coef	%coef	p-value		%devexp coef	%coef	p-value		%devexp coef	%coef	p-value		%devexp coef	%coef	p-value	
Geographic distance	11.38	0.94	28	<b>0.00</b>	7.50	1.22	18	<b>0.00</b>	5.10	1.30	15	<b>0.00</b>	11.77	0.74	25	<b>0.00</b>
Ann. Temp	7.66	0.73	22	<b>0.00</b>	3.39	0.81	12	0.06	1.99	0.84	10	0.22	7.44	0.55	19	<b>0.00</b>
Ann. Prec	1.43	0.63	19	0.14	3.01	1.68	25	0.10	3.07	2.20	25	0.14	4.53	0.90	30	<b>0.00</b>
Temp. Seasonality	0.55	0.24	7	0.46	0.60	0.40	6	0.52	0.25	0.35	4	0.80	0.44	0.16	5	0.56
Wood.denisty	0.21	0.11	3	0.50	3.47	0.88	13	<b>0.04</b>	5.51	1.63	18	<b>0.00</b>	0.16	0.08	3	0.70
Hem.of.colection	0.00	0.01	0	0.66	0.00	0.00	0	1.00	0.00	0.00	0	0.98	0.00	0.00	0	0.98
Hem.of.origin	0.64	0.10	3	0.08	2.06	0.33	5	0.06	3.55	0.64	7	<b>0.00</b>	0.23	0.05	2	0.26
Range	0.20	0.04	1	0.36	0.42	0.10	2	0.22	0.47	0.14	2	0.30	0.40	0.05	2	0.14
Phylogenetic distance	8.73	0.57	17	<b>0.00</b>	13.54	1.22	18	<b>0.00</b>	16.38	1.73	20	<b>0.00</b>	10.16	0.47	16	<b>0.00</b>

Saprotrophic fungi (n=352)																
	q=0				q=1				q=2				species turnover			
Model deviance	4,609				8,352				8,231				9,944			
Percent deviance explained	17				26				25				11			
Fitted permutations	50				50				50				50			
Model p value	0				0				0				0			
	%devexp coef	%coef	p-value		%devexp coef	%coef	p-value		%devexp coef	%coef	p-value		%devexp coef	%coef	p-value	
Geographic distance	10.35	0.77	23	<b>0.00</b>	2.49	0.69	10	<b>0.00</b>	1.46	0.60	7	<b>0.00</b>	8.17	0.72	21	<b>0.00</b>
Ann. Temp	11.59	0.76	23	<b>0.00</b>	3.36	0.95	14	0.06	2.03	0.89	10	0.06	11.76	0.60	18	<b>0.00</b>
Ann. Prec	2.71	0.74	23	0.10	0.78	0.96	14	0.40	0.48	0.91	11	0.50	8.72	1.14	34	<b>0.00</b>
Temp. Seasonality	0.39	0.15	5	0.60	0.00	0.00	0	0.98	0.00	0.00	0	0.98	0.13	0.09	3	0.84
Wood.denisty	0.80	0.19	6	0.56	18.28	2.55	37	<b>0.00</b>	23.49	4.02	47	<b>0.00</b>	3.30	0.35	10	0.24
Hem.of.colection	0.00	0.00	0	1.00	0.00	0.00	0	0.94	0.00	0.00	0	1.00	0.00	0.00	0	0.88
Hem.of.origin	0.74	0.09	3	0.14	3.60	0.55	8	<b>0.00</b>	4.31	0.80	9	<b>0.00</b>	2.16	0.14	4	0.08
Range	0.72	0.07	2	0.18	0.41	0.12	2	0.12	0.39	0.14	2	0.16	1.48	0.08	2	0.08
Phylogenetic distance	7.96	0.50	15	<b>0.00</b>	7.72	1.08	16	<b>0.00</b>	6.59	1.21	14	<b>0.00</b>	2.89	0.26	8	<b>0.00</b>

	Symbiotrophic fungi (n=223)															
	q=0				q=1				q=2				species turnover			
Model deviance	4,786				2,902				2,241				11,070			
Percent deviance explained	11				17				17				8			
Fitted permutations	50				50				50				50			
Model p value	0				0				0				0			
	%devexp	coef	%coef	p-value	%devexp	coef	%coef	p-value	%devexp	coef	%coef	p-value	%devexp	coef	%coef	p-value
Geographic distance	12.27	1.04	24	<b>0.00</b>	10.80	1.77	31	<b>0.00</b>	10.22	2.00	31	<b>0.00</b>	11.77	0.98	25	<b>0.00</b>
Ann. Temp	2.27	0.62	15	0.26	1.02	0.66	12	0.62	0.52	0.50	8	0.48	1.61	0.45	12	0.40
Ann. Prec	1.64	0.44	10	0.40	0.06	0.09	2	0.84	0.00	0.00	0	0.98	1.23	0.28	7	0.34
Temp. Seasonality	1.21	0.65	15	0.54	1.14	0.96	17	0.52	1.19	1.12	18	0.48	2.48	0.81	21	0.28
Wood.denisty	0.60	0.30	7	0.64	1.20	0.64	11	0.44	1.85	0.97	15	0.42	1.40	0.41	11	0.36
Hem.of.colection	0.00	0.00	0	0.94	0.00	0.00	0	1.00	0.00	0.00	0	0.94	0.00	0.00	0	1.00
Hem.of.origin	0.00	0.00	0	1.00	0.00	0.00	0	0.92	0.01	0.03	0	0.52	0.00	0.00	0	0.96
Range	0.28	0.07	2	0.38	0.00	0.00	0	0.98	0.00	0.00	0	1.00	0.33	0.07	2	0.24
Phylogenetic distance	16.86	1.14	27	<b>0.00</b>	17.12	1.58	28	<b>0.00</b>	16.70	1.73	27	<b>0.00</b>	13.10	0.84	22	<b>0.00</b>

	Plant pathogenic fungi (n=347)															
	q=0				q=1				q=2				species turnover			
Model deviance	5,491				5,525				4,899				12,606			
Percent deviance explained	24				21				17				17			
Fitted permutations	50				50				50				50			
Model p value	0				0				0				0			
	%devexp	coef	%coef	p-value	%devexp	coef	%coef	p-value	%devexp	coef	%coef	p-value	%devexp	coef	%coef	p-value
Geographic distance	8.31	1.36	33	<b>0.00</b>	7.75	2.94	40	<b>0.00</b>	8.11	3.65	43	<b>0.00</b>	8.30	1.45	36	<b>0.00</b>
Ann. Temp	8.48	0.96	23	<b>0.00</b>	6.21	1.29	17	<b>0.02</b>	4.98	1.36	16	<b>0.04</b>	12.25	0.98	24	<b>0.00</b>
Ann. Prec	0.70	0.42	10	0.58	0.75	0.85	11	0.58	0.35	0.65	8	0.80	0.87	0.39	10	0.56
Temp. Seasonality	1.01	0.39	9	0.34	0.60	0.46	6	0.54	0.26	0.36	4	0.68	3.63	0.62	15	0.08
Wood.denisty	0.04	0.06	1	0.80	0.08	0.12	2	0.74	0.16	0.20	2	0.84	0.30	0.13	3	0.76
Hem.of.colection	0.22	0.13	3	0.36	0.09	0.13	2	0.34	0.27	0.28	3	0.26	0.00	0.00	0	0.96
Hem.of.origin	0.06	0.04	1	0.44	0.65	0.19	3	0.16	0.65	0.22	3	0.20	0.00	0.00	0	1.00
Range	0.00	0.00	0	1.00	0.86	0.16	2	0.16	1.59	0.25	3	<b>0.00</b>	0.00	0.00	0	0.56
Phylogenetic distance	9.35	0.74	18	<b>0.00</b>	11.96	1.27	17	<b>0.00</b>	14.01	1.54	18	<b>0.00</b>	6.83	0.48	12	<b>0.00</b>

Table S2 **Statistical details on the Generalized Dissimilarity Models (GDMs) in the “zero-adjusted analysis”**. The numbers show model deviance, percent deviance explained by the full model, the p-value of the full model, and the number of permutations used to calculate the statistics for each fitted model (n=50). Numbers are shown for Sørensen (q=0)  $\beta$ -diversity and for different functional groups of organisms (i.e., herbivorous insects and all, saprotrophic, symbiotrophic, and plant pathogenic fungi). Numbers in brackets indicate number of samples that were included in the analysis. The percentage of unique variance explained by each variable (i.e., %devexp), the coefficients (i.e., coef; the maximum height of the spline for that variable), the relative value of the coefficients and the p-values (p) are also shown. Bold numbers indicate significant variables.

	Herbivorous insects (n=217)				All fungi (n=352)				Saprotrophic fungi (n=352)				Symbiotrophic fungi (n=352)				Plant pathogenic fungi (n=352)			
	q=0				q=0				q=0				q=0				q=0			
Model deviance	11,125				1,295				2,528				21,791				3,224			
Percent deviance explained	6				48				17				4				17			
Fitted permutations	50				50				50				50				50			
Model p value	0.46				0				0				0.3				0			
	%devexp	coef	%coef	p-value	%devexp	coef	%coef	p-value	%devexp	coef	%coef	p-value	%devexp	coef	%coef	p-value	%devexp	coef	%coef	p-value
Geographic distance	0.00	0.00	0	0.50	11.73	0.89	28	<b>0.00</b>	11.84	0.37	21	<b>0.00</b>	0.00	0.00	0	0.34	8.95	0.38	20	<b>0.00</b>
Ann. Temp	49.91	0.42	49	0.16	7.61	0.68	21	<b>0.00</b>	9.51	0.34	19	<b>0.00</b>	17.09	0.41	49	0.32	12.29	0.46	24	<b>0.00</b>
Ann. Prec	5.67	0.26	31	0.46	1.50	0.59	19	<b>0.04</b>	4.62	0.49	28	0.06	3.14	0.13	15	0.62	2.22	0.32	17	0.24
Temp. Seasonality	0.00	0.00	0	0.94	0.54	0.22	7	0.32	0.23	0.06	4	0.70	0.00	0.00	0	1.00	1.66	0.19	10	0.26
Wood.denisty	0.00	0.00	0	0.96	0.19	0.10	3	0.62	0.36	0.07	4	0.70	27.08	0.28	33	0.28	0.20	0.06	3	0.84
Hem.of.colection	NA	NA	NA	NA	0.00	0.00	0	0.96	0.00	0.00	0.00	1.00	0.00	0.00	0	0.98	0.00	0.00	0	1.00
Hem.of.origin	0.00	0.00	0	1.00	0.53	0.09	3	0.08	0.00	0.00	0	1.00	0.00	0.00	0	0.98	0.00	0.00	0	1.00
Range	27.65	0.15	18	<b>0.02</b>	0.22	0.04	1	0.26	0.39	0.03	2	0.34	1.77	0.03	4	0.42	0.80	0.05	2	0.18
Phylogenetic distance	0.23	0.01	2	<b>0.00</b>	9.20	0.55	18	<b>0.00</b>	16.99	0.39	22	<b>0.00</b>	0.00	0.00	0	1.00	11.15	0.42	22	<b>0.00</b>



Table S3 **Statistical details on the Generalized Dissimilarity Models (GDMs) in the “rarefied data analysis”**. The numbers show model deviance, percent deviance explained by the full model, the p-value of the full model, and the number of permutations used to calculate the statistics for each fitted model (n=50). Numbers are shown for different measures of  $\beta$ -diversity (i.e., Sørensen  $q=0$  and Morisita-Horn  $q=2$ ) and for different functional groups of organisms (i.e., all, saprotrophic, symbiotrophic, and plant pathogenic fungi). Numbers in brackets indicate number of samples that were included in the analysis. The percentage of unique variance explained by each variable (i.e., %devexp), the coefficients (i.e., coef; the maximum height of the spline for that variable), the relative value of the coefficients and the p-values (p) are also shown. Bold numbers indicate significant variables.

	All fungi (n=302)							
	q=0				q=2			
Model deviance	1,111				3,210			
Percent deviance explained	48				24			
Fitted permutations	50				50			
Model p value	0				0			
	%devexp	coef	%coef	p-value	%devexp	coef	%coef	p-value
Geographic distance	10.37	0.98	25	<b>0.00</b>	4.79	1.18	13	<b>0.00</b>
Ann. Temp	5.56	0.69	18	<b>0.00</b>	1.80	0.74	8	0.22
Ann. Prec	2.20	0.88	23	0.12	4.66	2.83	31	<b>0.02</b>
Temp. Seasonality	2.06	0.54	14	0.08	0.48	0.47	5	0.60
Wood.denisty	0.01	0.03	1	0.90	3.44	1.30	14	<b>0.02</b>
Hem.of.colection	0.00	0.00	0	0.98	0.00	0.00	0	0.96
Hem.of.origin	0.06	0.04	1	0.44	1.32	0.38	4	0.08
Range	0.19	0.05	1	0.26	0.41	0.13	1	0.20
Phylogenetic distance	13.29	0.72	18	<b>0.00</b>	22.70	2.00	22	<b>0.00</b>

	Saprotrophic fungi (n=301)							
	q=0				q=2			
Model deviance	4,046				6,897			
Percent deviance explained	17				25			
Fitted permutations	50				50			
Model p value	0				0			
	%devexp	coef	%coef	p-value	%devexp	coef	%coef	p-value
Geographic distance	9.99	0.79	19	<b>0.00</b>	1.55	0.62	6	<b>0.00</b>
Ann. Temp	8.93	0.80	19	<b>0.02</b>	1.36	0.70	7	0.12
Ann. Prec	4.26	1.17	28	0.06	1.00	1.33	14	0.40
Temp. Seasonality	0.71	0.25	6	0.44	0.03	0.10	1	0.90
Wood.denisty	1.97	0.39	9	0.24	21.66	4.62	47	<b>0.00</b>
Hem.of.colection	0.00	0.00	0	1.00	0.00	0.00	0	0.96
Hem.of.origin	0.56	0.10	2	0.22	2.98	0.68	7	<b>0.00</b>
Range	0.41	0.06	1	0.18	0.61	0.17	2	0.06
Phylogenetic distance	6.25	0.59	14	<b>0.00</b>	11.92	1.59	16	<b>0.00</b>

	Symbiotrophic fungi (n=187)							
	q=0				q=2			
Model deviance	3,393				1,888			
Percent deviance explained	13				17			
Fitted permutations	50				50			
Model p value	0				0			
	%devexp	coef	%coef	p-value	%devexp	coef	%coef	p-value
Geographic distance	11.53	1.18	25	<b>0.00</b>	10.30	2.60	36	<b>0.00</b>
Ann. Temp	1.23	0.54	12	0.32	0.09	0.20	3	0.78
Ann. Prec	1.14	0.33	7	0.50	0.00	0.00	0	1.00
Temp. Seasonality	1.16	0.73	16	0.42	1.91	1.58	22	0.26
Wood.denisty	1.11	0.58	12	0.44	1.81	1.11	15	0.32
Hem.of.colection	0.00	0.00	0	0.92	0.00	0.00	0	0.98
Hem.of.origin	0.00	0.00	0	0.96	0.00	0.00	0	1.00
Range	0.00	0.00	0	0.98	0.00	0.00	0	0.98
Phylogenetic distance	15.66	1.33	28	<b>0.00</b>	18.54	1.68	23	<b>0.00</b>

	Plant pathogenic fungi (n=296)							
	q=0				q=2			
Model deviance	4,278				3,982			
Percent deviance explained	24				18			
Fitted permutations	50				50			
Model p value	0				0			
	%devexp	coef	%coef	p-value	%devexp	coef	%coef	p-value
Geographic distance	4.76	1.67	31	<b>0.00</b>	5.12	2.61	32	<b>0.00</b>
Ann. Temp	8.41	1.13	21	<b>0.00</b>	5.00	1.34	16	<b>0.02</b>
Ann. Prec	2.41	0.90	17	0.26	0.49	0.92	11	0.66
Temp. Seasonality	1.54	0.55	10	0.26	0.59	0.53	7	0.60
Wood.denisty	0.34	0.18	3	0.70	0.02	0.07	1	0.94
Hem.of.colection	0.27	0.17	3	0.32	1.05	0.67	8	0.06
Hem.of.origin	0.00	0.00	0	0.98	0.00	0.00	0	0.92
Range	0.18	0.05	1	0.28	2.18	0.30	4	<b>0.04</b>
Phylogenetic distance	13.16	0.80	15	<b>0.00</b>	17.30	1.70	21	<b>0.00</b>

Table S4 **Statistical details on the Generalized Dissimilarity Models (GDMs) in the “overlap analysis”**. The numbers show model deviance, percent deviance explained by the full model, the p-value of the full model, and the number of permutations used to calculate the statistics for each fitted model (n=50). Numbers are shown for different measures of  $\beta$ -diversity (i.e., Sørensen q=0, Morisita q=1, Morisita-Horn q=2) and species turnover component (i.e., betasim) and for different functional groups of organisms (i.e., herbivorous insects and all, saprotrophic, symbiotrophic, and plant pathogenic fungi). Numbers in brackets indicate number of samples that were included in the analysis. The percentage of unique variance explained by each variable (i.e., %devexp), the coefficients (i.e., coef; the maximum height of the spline for that variable), the relative value of the coefficients and the p-values (p) are also shown. Bold numbers indicate significant variables.

<b>Herbivorous insects (n=74)</b>																
	q=0				q=1				q=2				species turnover			
Model deviance	343				292				267				733			
Percent deviance explained	14				14				12				15			
Fitted permutations	50				50				50				50			
Model p value	0				0.02				0.14				0			
	%devexp	coef	%coef	p-value	%devexp	coef	%coef	p-value	%devexp	coef	%coef	p-value	%devexp	coef	%coef	p-value
Geographic distance	3.47	0.62	12	<b>0.02</b>	8.36	0.88	15	<b>0.04</b>	9.57	0.90	14	0.18	0.93	0.35	7	<b>0.00</b>
Ann. Temp	0.00	0.00	0	1.00	0.00	0.00	0	1.00	0.00	0.00	0	1.00	0.00	0.00	0	0.96
Ann. Prec	4.05	0.71	13	0.48	2.74	0.71	12	0.68	3.71	0.80	12	0.70	4.88	0.70	13	0.28
Temp. Seasonality	0.00	0.00	0	0.98	0.00	0.00	0	0.94	0.00	0.00	0	0.94	0.00	0.00	0	1.00
Wood.denisty	0.03	0.12	2	0.88	0.00	0.00	0	1.00	0.00	0.00	0	0.98	0.00	0.00	0	0.84
Hem.of.colection	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Hem.of.origin	2.51	1.73	32	<b>0.00</b>	2.66	1.98	34	<b>0.00</b>	3.55	2.78	42	<b>0.00</b>	2.04	1.67	32	<b>0.00</b>
Range	0.00	0.00	0	1.00	0.00	0.00	0	1.00	0.00	0.00	0	0.96	0.00	0.00	0	0.92
Phylogenetic distance	37.03	2.19	41	<b>0.00</b>	37.81	2.19	38	<b>0.00</b>	39.29	2.09	32	<b>0.00</b>	37.90	2.55	48	<b>0.00</b>

All fungi (n=167)																
	q=0				q=1				q=2				species turnover			
Model deviance	297				821				1,103				439			
Percent deviance explained	44				34				26				44			
Fitted permutations	50				50				50				50			
Model p value	0				0				0				0			
	%devexp	coef	%coef	p-value	%devexp	coef	%coef	p-value	%devexp	coef	%coef	p-value	%devexp	coef	p-value	
Geographic distance	6.39	0.33	18	<b>0.00</b>	3.98	0.48	13	<b>0.00</b>	3.78	0.59	11	<b>0.00</b>	2.82	0.26	14	<b>0.00</b>
Ann. Temp	0.30	0.13	7	0.74	0.00	0.00	0	1.00	0.00	0.00	0	1.00	0.52	0.17	9	0.64
Ann. Prec	1.36	0.20	11	0.22	1.28	0.36	10	0.32	0.35	0.23	4	0.74	0.20	0.09	5	0.72
Temp. Seasonality	5.27	0.40	22	<b>0.04</b>	5.09	0.44	12	<b>0.04</b>	2.63	0.46	8	0.26	3.57	0.57	31	<b>0.04</b>
Wood.denisty	0.09	0.05	3	0.84	2.72	0.65	18	0.08	5.86	1.54	28	<b>0.04</b>	0.31	0.10	5	0.74
Hem.of.colection	0.00	0.00	0	1.00	0.00	0.00	0	1.00	0.00	0.00	0	1.00	0.00	0.00	0	1.00
Hem.of.origin	0.00	0.00	0	1.00	0.59	0.16	4	0.08	1.85	0.46	8	0.10	0.12	0.03	2	0.52
Range	0.28	0.04	2	0.44	0.52	0.10	3	0.20	0.28	0.11	2	0.42	0.15	0.03	1	0.44
Phylogenetic distance	20.68	0.67	37	<b>0.00</b>	21.42	1.41	39	<b>0.00</b>	20.19	2.07	38	<b>0.00</b>	15.75	0.59	32	<b>0.00</b>

Saprotrophic fungi (n=167)																
	q=0				q=1				q=2				species turnover			
Model deviance	913				2,370				2,416				1,789			
Percent deviance explained	17				27				26				12			
Fitted permutations	50				50				50				50			
Model p value	0				0				0				0			
	%devexp	coef	%coef	p-value	%devexp	coef	%coef	p-value	%devexp	coef	%coef	p-value	%devexp	coef	p-value	
Geographic distance	15.15	0.46	30	<b>0.00</b>	0.64	0.28	6	<b>0.00</b>	0.37	0.25	4	<b>0.00</b>	10.49	0.35	24	<b>0.00</b>
Ann. Temp	0.00	0.00	0	1.00	0.00	0.00	0	1.00	0.00	0.00	0	1.00	0.00	0.00	0	1.00
Ann. Prec	1.46	0.19	12	0.58	0.29	0.15	3	0.56	0.32	0.19	3	0.60	0.45	0.08	6	0.62
Temp. Seasonality	0.22	0.07	5	0.76	1.47	0.27	6	0.34	1.15	0.29	4	0.44	1.78	0.27	19	0.40
Wood.denisty	0.50	0.12	8	0.66	19.05	2.34	50	<b>0.00</b>	23.21	3.53	55	<b>0.00</b>	2.49	0.23	16	0.40
Hem.of.colection	0.00	0.00	0	1.00	0.00	0.00	0	1.00	0.00	0.00	0	1.00	0.00	0.00	0	1.00
Hem.of.origin	0.00	0.00	0	0.94	1.53	0.34	7	0.18	2.29	0.55	9	0.10	0.00	0.00	0	0.52
Range	1.03	0.07	4	0.26	0.34	0.10	2	0.38	0.35	0.13	2	0.38	0.54	0.04	3	0.34
Phylogenetic distance	21.71	0.65	42	<b>0.00</b>	9.11	1.21	26	<b>0.00</b>	8.30	1.49	23	<b>0.00</b>	13.95	0.47	32	<b>0.00</b>

	Symbiotrophic fungi (n=127)															
	q=0				q=1				q=2				species turnover			
Model deviance	1,687				1,177				971				3,894			
Percent deviance explained	13				16				15				11			
Fitted permutations	50				50				50				50			
Model p value	0				0				0				0			
	%dev	exp	coef	p-value	%dev	exp	coef	p-value	%dev	exp	coef	p-value	%dev	exp	coef	p-value
Geographic distance	14.12	1.14	33	<b>0.00</b>	12.77	1.85	41	<b>0.00</b>	12.65	2.41	46	<b>0.00</b>	9.74	1.11	31	<b>0.00</b>
Ann. Temp	0.35	0.26	7	0.72	0.11	0.19	4	0.78	0.01	0.06	1	0.90	0.44	0.27	8	0.72
Ann. Prec	1.72	0.32	9	0.34	0.32	0.17	4	0.72	0.01	0.04	1	0.90	3.60	0.44	12	<b>0.04</b>
Temp. Seasonality	0.69	0.18	5	0.46	0.65	0.25	5	0.68	0.43	0.22	4	0.68	1.05	0.21	6	0.56
Wood.denisty	1.05	0.46	13	0.38	1.65	0.82	18	0.56	2.22	1.11	21	0.52	2.94	0.80	23	<b>0.04</b>
Hem.of.colection	0.00	0.00	0	1.00	0.00	0.00	0	1.00	0.00	0.00	0	1.00	0.00	0.00	0	1.00
Hem.of.origin	0.05	0.04	1	0.50	0.04	0.05	1	0.46	0.28	0.16	3	0.44	0.03	0.03	1	0.58
Range	0.02	0.02	1	0.60	0.01	0.01	0	0.60	0.00	0.00	0	1.00	0.02	0.02	0	0.60
Phylogenetic distance	11.86	0.99	29	<b>0.00</b>	10.86	1.17	26	<b>0.00</b>	10.07	1.27	24	<b>0.00</b>	5.44	0.67	19	<b>0.00</b>

	Plant pathogenic fungi (n=167)															
	q=0				q=1				q=2				species turnover			
Model deviance	1,180				1,758				1,731				2,263			
Percent deviance explained	21				16				13				17			
Fitted permutations	50				50				50				50			
Model p value	0				0				0				0			
	%dev	exp	coef	p-value	%dev	exp	coef	p-value	%dev	exp	coef	p-value	%dev	exp	coef	p-value
Geographic distance	5.27	0.35	17	<b>0.00</b>	8.43	0.68	19	<b>0.00</b>	10.21	0.90	21	<b>0.00</b>	5.63	0.31	16	<b>0.00</b>
Ann. Temp	0.71	0.21	10	0.60	0.33	0.24	7	0.80	0.37	0.31	7	0.88	0.48	0.15	8	0.78
Ann. Prec	0.88	0.19	9	0.58	0.32	0.13	4	0.84	0.25	0.14	3	0.90	1.02	0.21	11	0.72
Temp. Seasonality	1.72	0.41	20	0.50	2.06	0.68	19	0.54	1.63	0.78	19	0.56	4.17	0.55	28	0.34
Wood.denisty	0.59	0.18	9	0.56	1.11	0.51	14	0.56	1.03	0.60	14	0.66	2.31	0.31	16	0.30
Hem.of.colection	0.00	0.00	0	1.00	0.00	0.00	0	1.00	0.00	0.00	0	1.00	0.00	0.00	0	1.00
Hem.of.origin	0.00	0.00	0	1.00	0.01	0.02	1	0.58	0.07	0.06	1	0.58	0.00	0.00	0	1.00
Range	0.00	0.00	0	1.00	1.27	0.15	4	0.34	1.18	0.18	4	0.36	0.00	0.00	0	0.98
Phylogenetic distance	21.53	0.74	36	<b>0.00</b>	12.93	1.11	32	<b>0.00</b>	10.26	1.26	30	<b>0.00</b>	12.01	0.46	23	<b>0.00</b>

Table S5 **Statistical details on the Generalized Dissimilarity Models (GDMs) in the “zero-adjusted overlap analysis”**. The numbers show model deviance, percent deviance explained by the full model, the p-value of the full model, and the number of permutations used to calculate the statistics for each fitted model (n=50). Numbers are shown for Sørensen (q=0)  $\beta$ -diversity and for different functional groups of organisms (i.e., herbivorous insects and all, saprotrophic, symbiotrophic, and plant pathogenic fungi). Numbers in brackets indicate number of samples that were included in the analysis. The percentage of unique variance explained by each variable (i.e., %devexp), the coefficients (i.e., coef; the maximum height of the spline for that variable), the relative value of the coefficients and the p-values (p) are also shown. Bold numbers indicate significant variables.

	Herbivorous insects (n=167)				All fungi (n=167)				Saprotrophic fungi (n=167)				Symbiotrophic fungi (n=167)				Plant pathogenic fungi (n=167)			
	q=0				q=0				q=0				q=0				q=0			
Model deviance	6,787				284				534				3210				663			
Percent deviance explained	4				44				21				6				25			
Fitted permutations	50				50				50				50				50			
Model p value	0.8				0				0				0.64				0			
	%devexp	coef	%coef	p-value	%devexp	coef	%coef	p-value	%devexp	coef	%coef	p-value	%devexp	coef	%coef	p-value	%devexp	coef	%coef	p-value
Geographic distance	0.86	0.04	8	0.80	6.82	0.33	18	<b>0.00</b>	15.81	0.35	31	<b>0.00</b>	23.37	0.25	28	0.52	6.55	0.28	17	<b>0.00</b>
Ann. Temp	21.20	0.16	34	0.54	0.30	0.13	7	0.74	0.00	0.00	0	0.98	1.22	0.40	45	0.70	1.58	0.21	13	0.48
Ann. Prec	0.47	0.04	8	0.78	1.26	0.19	11	0.42	0.97	0.07	7	0.46	0.00	0.00	0	0.74	0.41	0.08	5	0.74
Temp. Seasonality	0.00	0.00	0	1.00	4.97	0.38	22	<b>0.00</b>	0.34	0.10	9	0.62	0.00	0.00	0	0.96	1.85	0.30	19	0.42
Wood.denisty	0.00	0.00	0	0.84	0.11	0.06	3	0.88	0.54	0.09	8	0.56	1.77	0.11	12	0.56	2.67	0.24	15	0.24
Hem.of.colection	NA	NA	NA	NA	0.00	0.00	0	1.00	0.00	0.00	0	1.00	0.00	0.00	0	1.00	0.00	0.00	0	1.00
Hem.of.origin	0.00	0.00	0	0.98	0.00	0.00	0	1.00	0.00	0.00	0	0.94	0.00	0.00	0	1.00	0.00	0.00	0	1.00
Range	70.00	0.20	43	<b>0.02</b>	0.10	0.04	2	0.40	0.63	0.04	4	0.30	1.11	0.04	4	0.32	0.13	0.02	1	0.44
Phylogenetic distance	1.31	0.03	7	<b>0.00</b>	20.28	0.64	37	<b>0.00</b>	21.23	0.48	42	<b>0.00</b>	0.78	0.09	10	<b>0.00</b>	15.45	0.47	30	<b>0.00</b>