

Supplementary Materials

Table S1. Effects of tree richness of six neighboring trees and covariates on fungal endophyte diversity and richness.

Response	Intercept	Taxonomic richness	Height	MEM 1	MEM 2	MEM 3
Richness	110.8*** (100.1, 121.6)	-6*** (-9.4, -2.7)	-4.5 (-11.3, 2.2)	2.9 (-3.7, 9.4)	2.4 (-2.1, 6.9)	-6** (-11.1, -0.9)
Shannon's equiv.	12.8*** (10.8, 14.9)	-1.1*** (-1.8, -0.3)	-0.3 (-1.7, 1.1)	0.3 (-1.1, 1.8)	0.8 (-0.2, 1.8)	-1.9*** (-3, -0.8)
Simpson's equiv.	2.3*** (1.6, 2.9)	0.1 (-0.4, 0.6)	0 (-0.6, 0.7)	-0.3 (-0.9, 0.4)	-0.1 (-0.6, 0.5)	0.2 (-0.4, 0.8)

Results shown are from a linear mixed effects model with random effects of plot replicate by host species combinations. Values in cells are beta coefficient estimates, with 95% confidence intervals in parentheses and *p* values denoted by asterisks. All coefficients for the effects of richness treatments are relative to monoculture plots. Height is the total height of the host tree. The effect of spatial autocorrelation was accounted for using Moran's eigenvector mapping (MEM; see main text). We converted all covariates to z scores prior to analysis.*** *p* < 0.01, ** *p* < 0.05, * *p* < 0.1.

Table S2. The effects of tree (plot) richness on fungal endophyte richness among 15 tree species (*N* = 545 focal trees).

Host	Diversity = 1	Diversity = 4	Diversity = 12	<i>p</i> -value (Div4)	<i>p</i> -value (Div12)	Adj. <i>p</i> -value (Div12)
PLOC	60.2	-11.2	-11.0	0.72	0.64	0.74
ACRU	95.5	10.2	19.4	0.59	0.31	0.49
QUPA	250.2	-1.5	-33.9	0.95	0.25	0.49
QUVE	187.9	63.9	-11.3	0.32	0.74	0.80
NYSY	6.9	1.8	25.8	0.95	0.59	0.74
ULAM	31.2	58.4	58.1	0.27	0.09	0.46
CAAL	-4.2	-6.6	-14.5	0.84	0.55	0.74
QUAL	206.2	-6.8	35.7	0.78	0.21	0.49
FAGR	120.8	42.6	35.0	0.37	0.21	0.49
COFL	-26.7	-4.7	-45.8	0.79	0.01	0.10
CACA	130.6	-15.3	-4.1	0.51	0.86	0.86
LIST	23.2	-12.1	-11.4	0.47	0.33	0.49
FRPE	-273.5	3.8	-16.6	0.82	0.24	0.49
QURU	-142.9	-7.9	-101.9	0.81	0.04	0.28
LITU	89.1	-28.6	-37.7	0.22	0.30	0.49

Results shown are from a linear model with random effects of plot replicate by host species combinations. Values in cells are beta coefficient estimates. Coefficients for the effects of richness treatments (e.g., 4-spp. and 12-spp.) are relative to monoculture plots. We corrected for multiple tests with False Discovery Rates (FDR) values for 12-spp plots ("Adj. *p*-value").

Table S3. The effects of tree taxonomic (plot) richness on fungal endophyte Shannon's diversity equivalents among 15 tree species (*N* = 545 focal trees).

Host	Diversity = 1	Diversity = 4	Diversity = 12	<i>p</i> -value (Div4)	<i>p</i> -value (Div12)	Adj. <i>p</i> -value (Div12)
PLOC	16.0	3.3	1.6	0.71	0.80	0.86
ACRU	-3.0	5.0	0.4	0.31	0.94	0.94
QUPA	53.8	-3.6	-6.7	0.52	0.32	0.54

QUVE	25.3	13.7	4.9	0.34	0.53	0.71
NYSY	-3.3	3.4	5.2	0.54	0.57	0.71
ULAM	1.1	13.2	7.8	0.20	0.23	0.44
CAAL	26.7	-3.9	-10.0	0.53	0.04	0.30
QUAL	33.3	-0.8	10.1	0.88	0.14	0.44
FAGR	-1.6	-13.7	-9.0	0.30	0.24	0.44
COFL	-16.0	-0.6	-10.1	0.91	0.02	0.30
CACA	7.8	0.2	2.1	0.97	0.67	0.78
LIST	-0.3	-3.7	-3.4	0.32	0.19	0.44
FRPE	-30.5	-1.3	-2.9	0.79	0.45	0.67
QURU	-53.4	-2.5	-14.8	0.72	0.14	0.44
LITU	-17.1	-11.9	-14.8	0.07	0.16	0.44

Results shown are from a linear model with random effects of plot replicate by host species combinations. Values in cells are beta coefficient estimates. Coefficients for the effects of richness treatments (e.g., 4-spp. and 12-spp.) are relative to monoculture plots. We corrected for multiple tests with False Discovery Rates (FDR) values for 12-spp plots (“Adj. *p*-value”).

Table S4. The effects of tree taxonomic (plot) richness on fungal endophyte Simpson’s effective species number among 15 tree species ($N = 545$ focal trees). .

Host	Diversity = 1	Diversity = 4	Diversity = 12	<i>p</i> -value (Div4)	<i>p</i> -value (Div12)	Adj. <i>p</i> value (Div 12)
PLOC	-0.43	-3.9	-2.3	0.72	0.77	0.84
ACRU	2.8	-0.2	-0.1	0.70	0.73	0.84
QUPA	1.0	0.0	0.0	0.99	0.79	0.84
QUVE	1.1	-0.1	-0.1	0.47	0.21	0.78
NYSY	1.8	-0.2	-0.2	0.26	0.60	0.84
ULAM	0.8	-2.2	-0.4	0.01	0.44	0.84
CAAL	5.8	-1.3	0.3	0.41	0.79	0.84
QUAL	-6.6	2.9	-4.7	0.31	0.18	0.78
FAGR	2.5	1.0	0.2	0.09	0.64	0.84
COFL	-0.3	8.2	9.8	0.27	0.15	0.78
CACA	3.0	-0.1	0.1	0.61	0.68	0.84
LIST	40.4	1.4	-11.5	0.91	0.17	0.78
FRPE	233.2	-6.9	-5.4	0.36	0.39	0.84
QURU	-8.1	5.0	1.2	0.49	0.91	0.91
LITU	2.7	0.2	0.2	0.47	0.75	0.84

Results shown are from a linear model with random effects of plot replicate by host species combinations. Values in cells are beta coefficient estimates. Coefficients for the effects of richness treatments (e.g., 4-spp. and 12-spp.) are relative to monoculture plots. We corrected for multiple tests with False Discovery Rates (FDR) values for 12-spp plots (“Adj. *p*-value”).

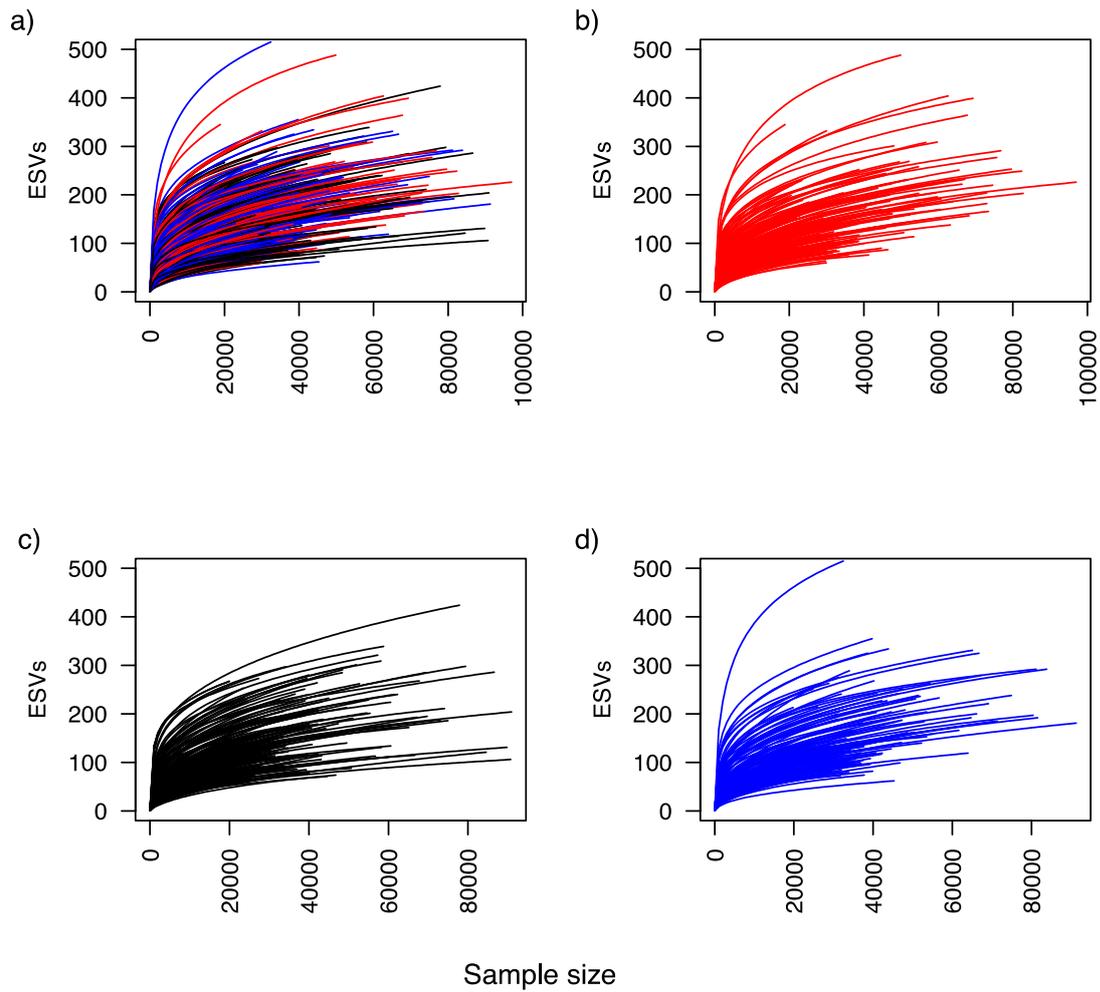


Figure S1. Rarefaction curves for A. all samples, B. 1 sp., C. 4 spp., and D. 12 spp. plot samples compiled together among all host species. For all curves, many samples appear to be somewhat close to approaching an asymptote, suggesting that our sequencing depth is relatively close to encompassing the full extent of endophyte ESV richness in communities among diversity treatments.

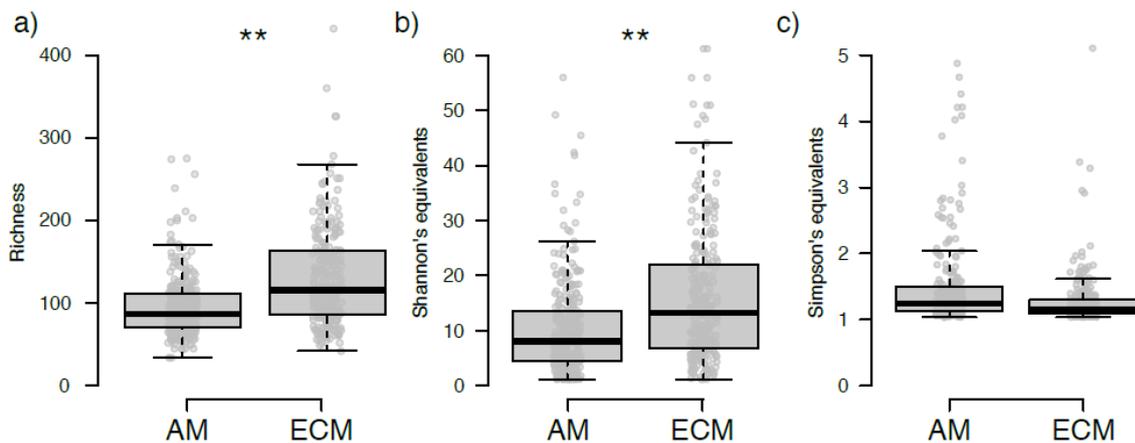


Figure S2. The effects of mycorrhizal association (AM vs. ECM) on A. fungal endophyte richness (0D), B. Shannon's diversity equivalents (1D), and C. Simpson's effective species number (2D) among 15 focal tree species ($N = 545$ focal trees). We used mixed effects models with an interaction term between mycorrhizal associate and richness treatment included. We included each unique combination of plot replicate and host taxon as a random effect, and the reference condition for plot richness was the monoculture treatment.

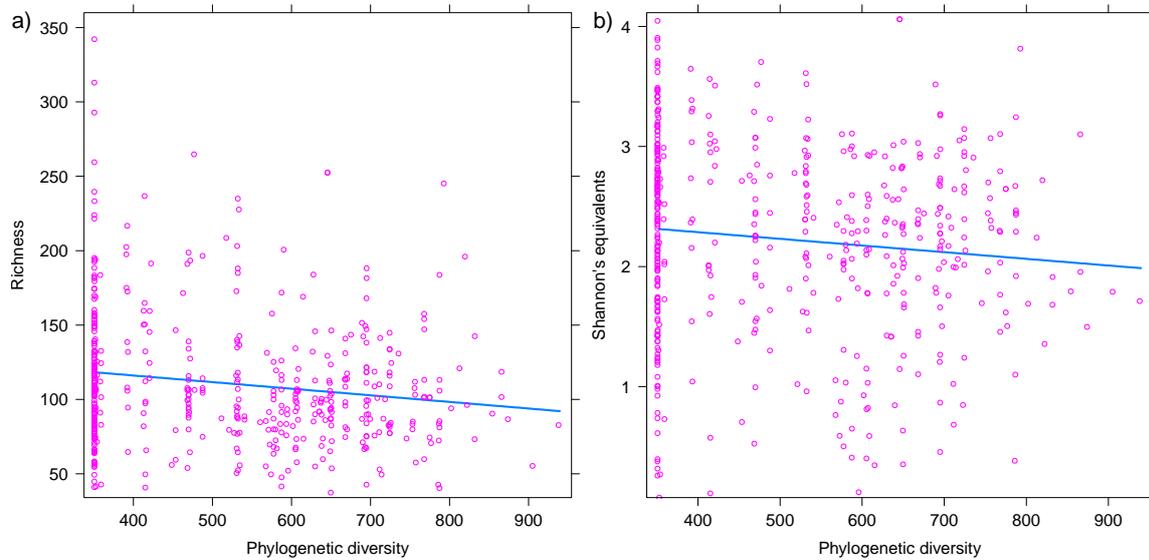


Figure S3. Partial regression plots from a mixed effects model examining the effects of tree neighborhood phylogenetic diversity on fungal endophyte A. richness and B. Shannon's diversity equivalents. Models also included fixed effects of plant height and three MEMs to account for spatial autocorrelation and random effects of plot replicate and host taxon.

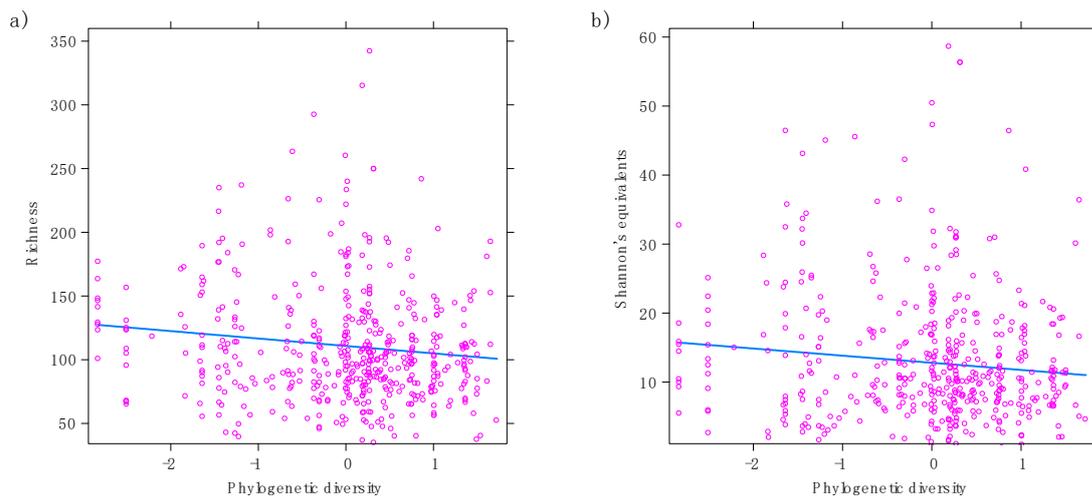


Figure S4. Partial regression plots from a mixed effects model examining the effects of plot-level tree phylogenetic diversity on fungal endophyte A. richness and B. Shannon's diversity equivalents. Models also included fixed effects of plant height and three MEMs to account for spatial autocorrelation and random effects of plot replicate and host taxon.

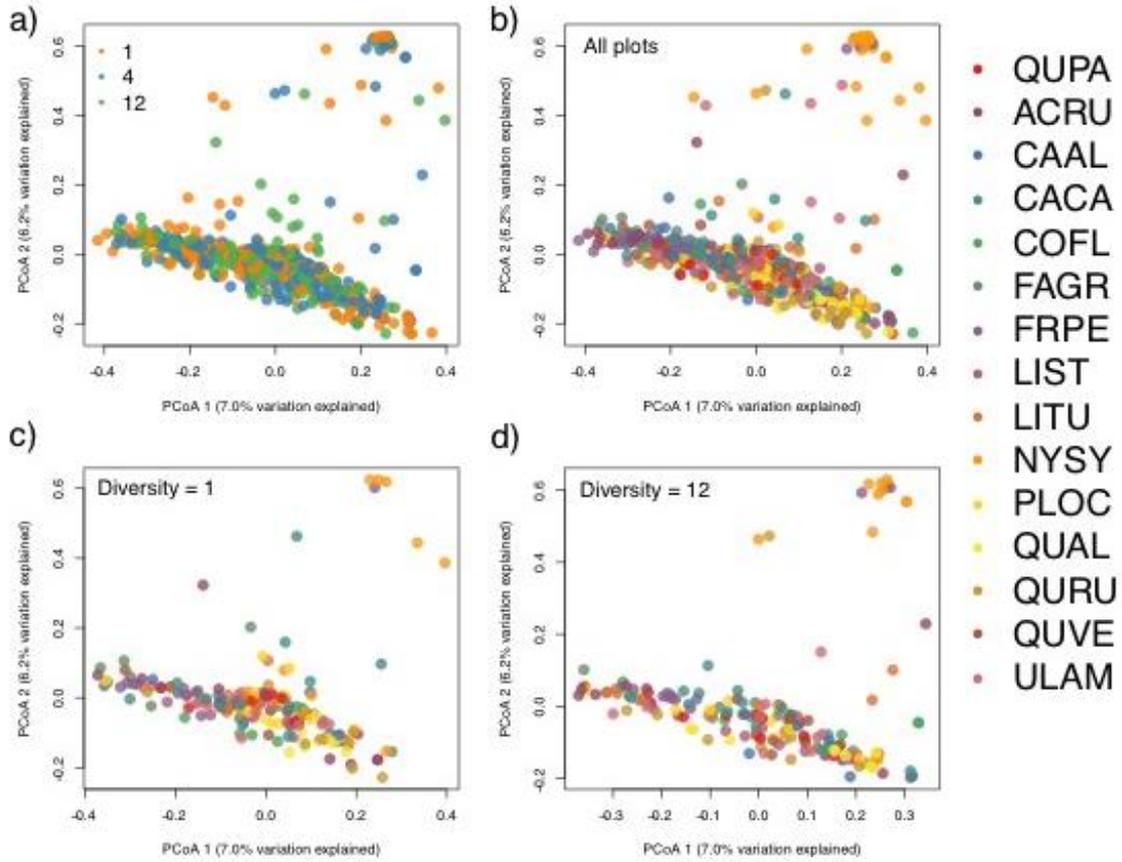


Figure S5. The effects of A. tree richness and B. 15 focal tree species on fungal endophyte community composition ($N = 545$ focal trees). We conducted permutational multivariate analysis of variance (PERMANOVA) to test whether fungal community composition (Bray-Curtis dissimilarity) differed among tree richness treatments and host species. A. Ordination and the partial regression plots for phylogenetic diversity vs fungi with captions. Plot richness was a significant predictor of variation in community composition, but explained little variation ($< 1\%$). B. Endophyte community composition did not vary significantly among tree species, but surprisingly explained $\sim 9\%$ of the overall variation in endophyte communities. C and D. Though tree species richness was a significant predictor of endophyte community composition ($P < 0.05$), it explains $< 1\%$ of the overall variation in endophyte community composition. .

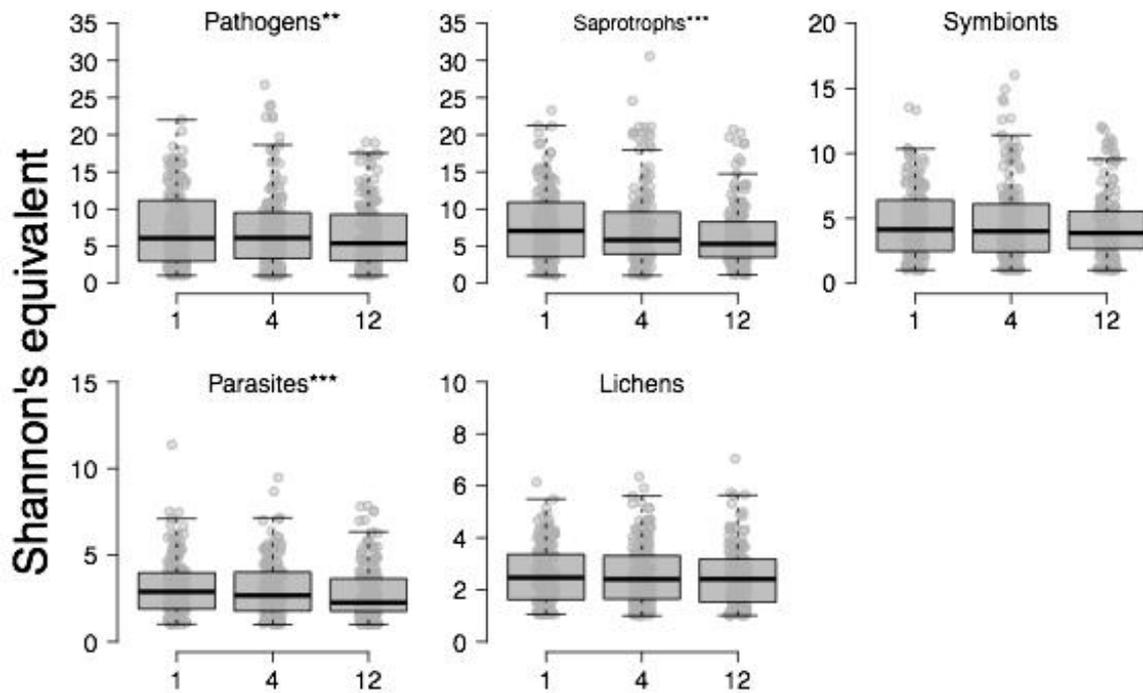


Figure S6. The effects of tree richness on fungal ESV diversity (Shannon's diversity equivalents) of the most common functional guilds among 15 focal tree species ($N = 545$ focal trees). We used linear mixed effects models with a random intercept for each unique combination of plot replicate and host taxon. The reference condition for plot richness was the monoculture treatment. Increases in tree richness decreased ESV richness within all guilds as well as guild diversity. *** $p < 0.001$, ** $p < 0.01$, * $p < 0.05$.

Supplemental Results

The Diversity Begets Diversity Hypothesis (H1): Tree Taxonomic and Phylogenetic Diversity Decreased Fungal Richness and Diversity

Fungal richness. Overall, fungal richness decreased as tree richness increased (Table 1, Figure 2, $p < 0.01$). Specifically, fungal richness decreased by 5% from one-species to four-species plots, and by 10% from one-species plots to 12-species plots. Some of the individual tree taxa showed significant effects of tree diversity on fungal richness (e.g., *Cornus florida*, *Fraxinus pennsylvanica*, *Quercus rubra*); however, after correcting for multiple tests with False Discovery Rates (FDR) values, the effects of tree diversity on fungal richness did not differ among tree species (Supplementary Table S2).

Shannon's fungal diversity. As tree richness increased, Shannon's diversity equivalents decreased (Table 1, Figure 2, $p < 0.01$). Specifically, Shannon's diversity decreased by 6% from one-species plots to four-species plots, and by 8% from one-species plots to 12-species plots. Some of the individual tree taxa showed significant effects of tree diversity on fungal diversity (e.g., *Carya alba*, *C. florida*, *Liquidambar styraciflua*, *Quercus rubra*); however, after correcting for multiple tests with FDR values, the effects of tree diversity on fungal diversity did not differ among tree species (Table S3).

Simpson's fungal diversity. Conversely, increases in one to four-species plots increased fungal Simpson's effective species number by 4%; however, increases in one- to 12-species plots had no effect on Simpson's diversity (Table 1, Figure 2, 1-4sp: $p < 0.05$; 1-12sp: $p > 0.10$). *Nyssa sylvatica* showed significant effects of tree diversity on Simpson's diversity; however, after correcting for multiple tests with FDR values, the effects of tree diversity on Simpson's did not differ among tree species (Supplementary Table S4).