Science Advances

AAAS

advances.sciencemag.org/cgi/content/full/4/3/eaar6603/DC1

Supplementary Materials for

Reconciling biodiversity and carbon stock conservation in an Afrotropical forest landscape

Frederik Van de Perre, Michael R. Willig, Steven J. Presley, Frank Bapeamoni Andemwana, Hans Beeckman, Pascal Boeckx, Stijn Cooleman, Myriam de Haan, André De Kesel, Steven Dessein, Patrick Grootaert, Dries Huygens, Steven B. Janssens, Elizabeth Kearsley, Patrick Mutombo Kabeya, Maurice Leponce, Dries Van den Broeck, Hans Verbeeck, Bart Würsten, Herwig Leirs, Erik Verheyen

Published 28 March 2018, *Sci. Adv.* **4**, eaar6603 (2018)
DOI: 10.1126/sciadv.aar6603

The PDF file includes:

Other Supplementary Material for this manuscript includes the following:
(available at advances.sciencemag.org/cgi/content/full/4/3/eaar6603/DC1)

- Biodiversity data (Microsoft Excel format)

Figures

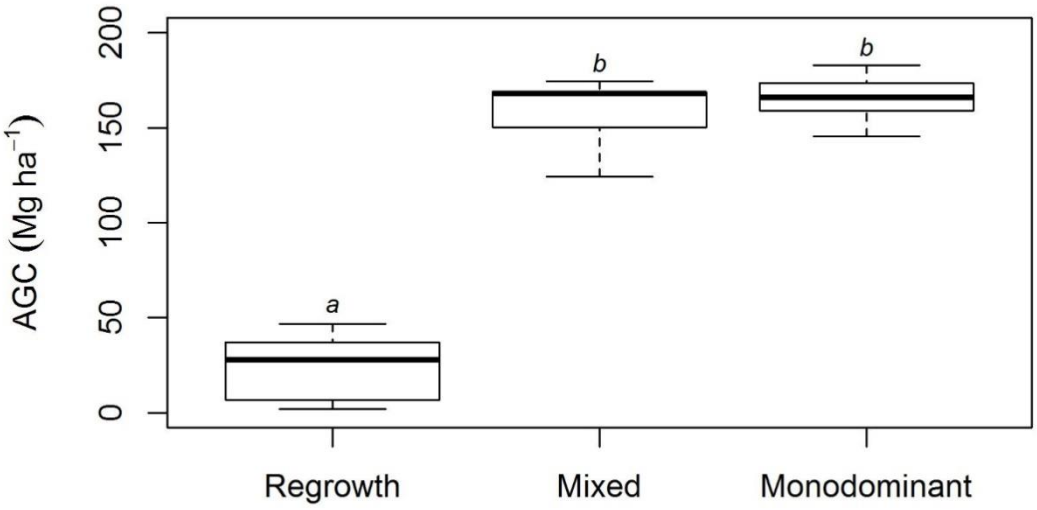
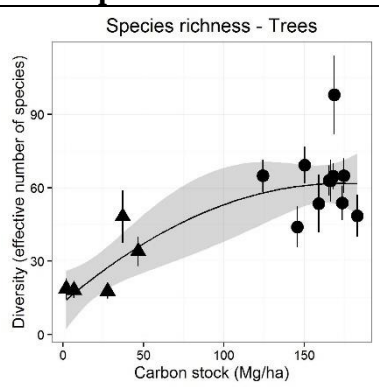
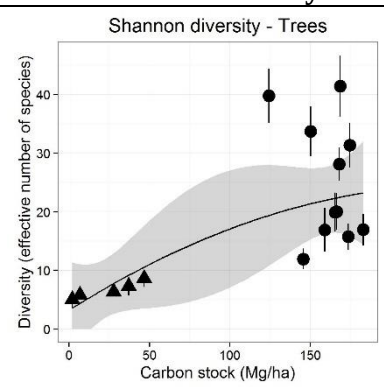
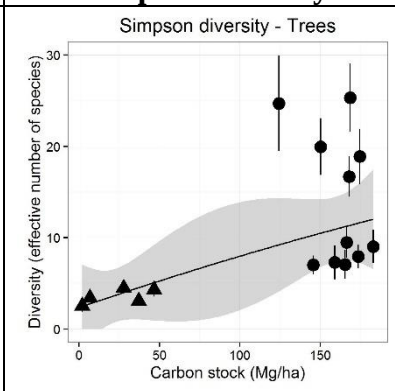
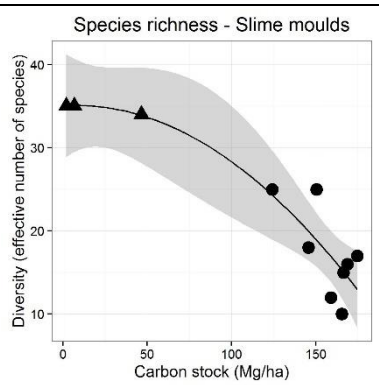
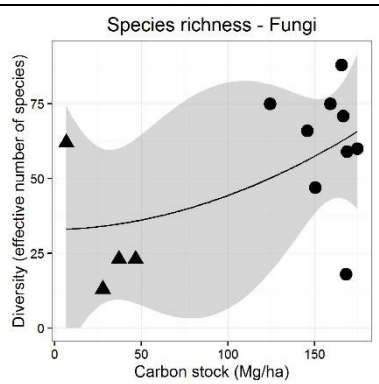
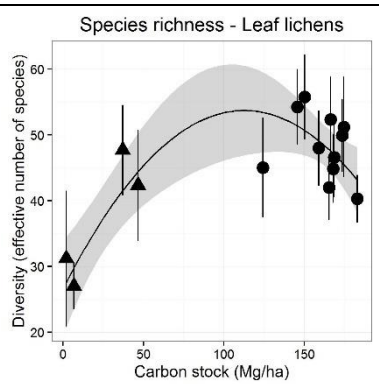
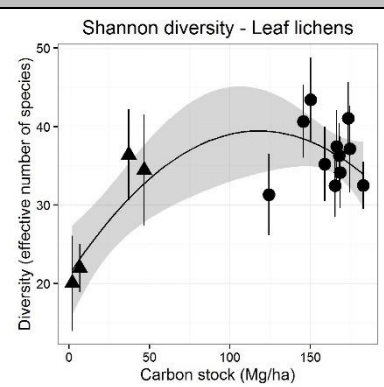
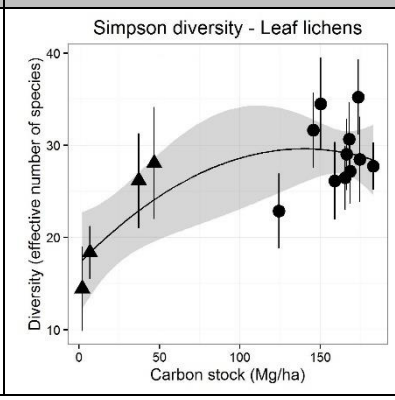
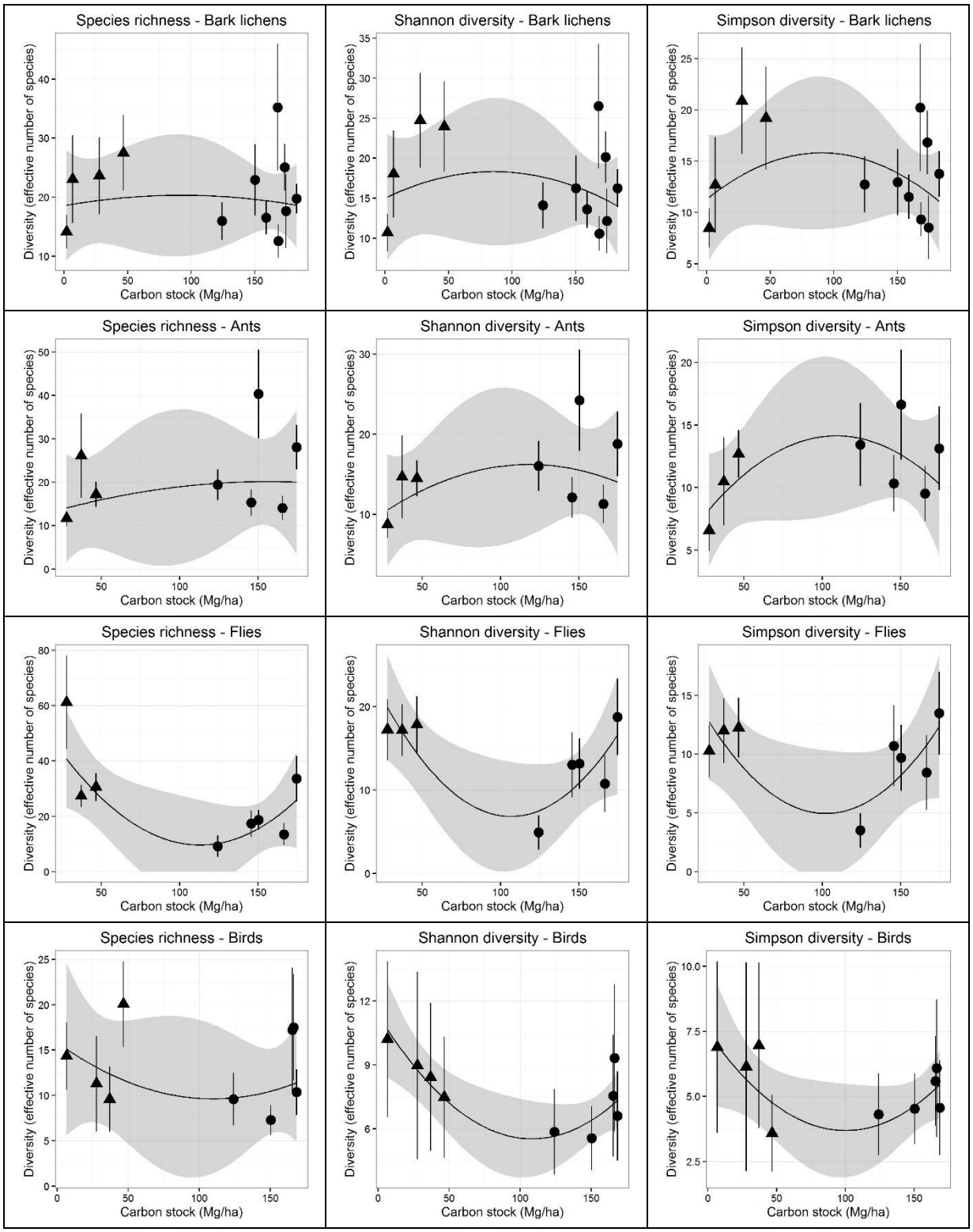


fig. S1. AGC increases from regrowth to old-growth forest (mixed or monodominant). Within boxplots, the solid line shows the median AGC value, whereas the whiskers show minimum and maximum. Forest types with statistically indistinguishable AGC share a common alphabetic designation.

Species richness	Shannon diversity	Simpson diversity
		
		
		
		


Species richness - Bark lichens
Shannon diversity - Bark lichens
Simpson diversity - Bark lichens
Species richness - Ants
Shannon diversity - Ants
Simpson diversity - Ants
Species richness - Flies
Shannon diversity - Flies
Simpson diversity - Flies
Species richness - Birds
Shannon diversity - Birds
Simpson diversity - Birds
Diversity (effective number of species)
Carbon stock (Mg/ha)

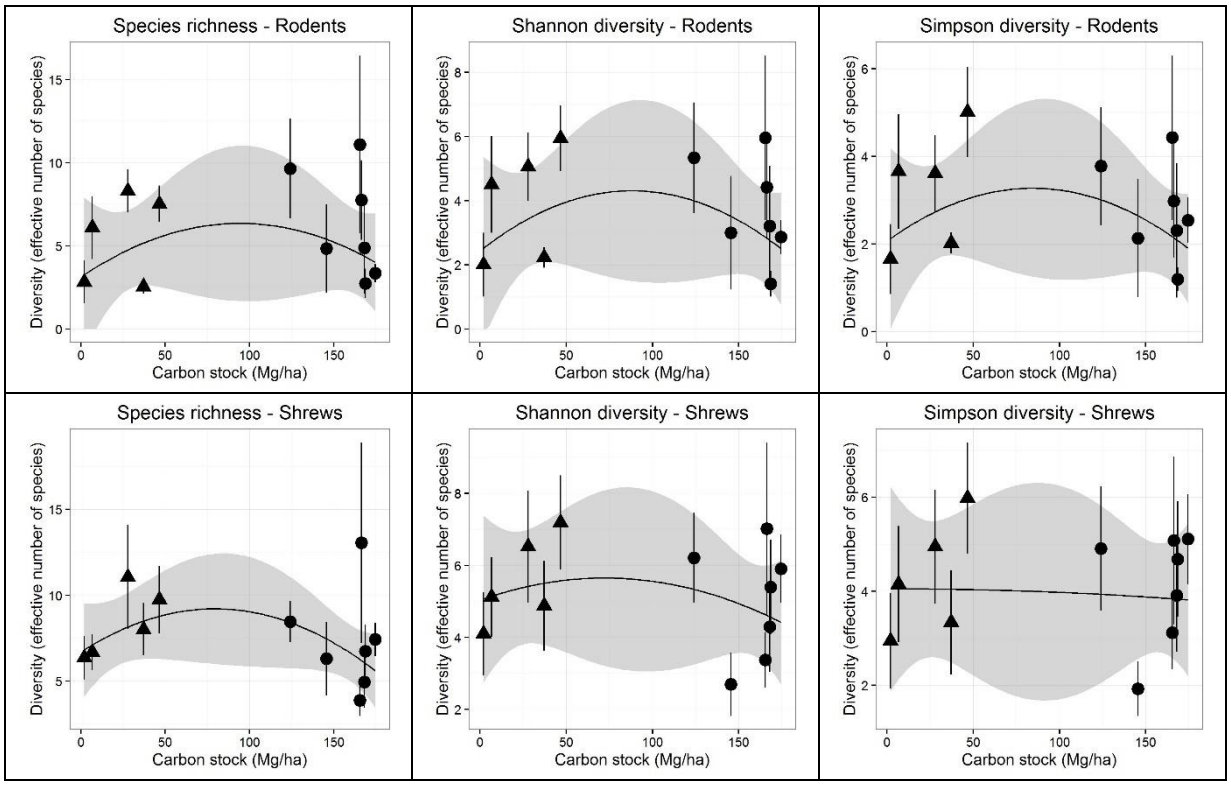
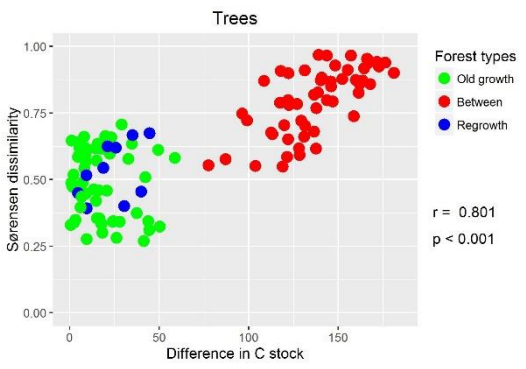
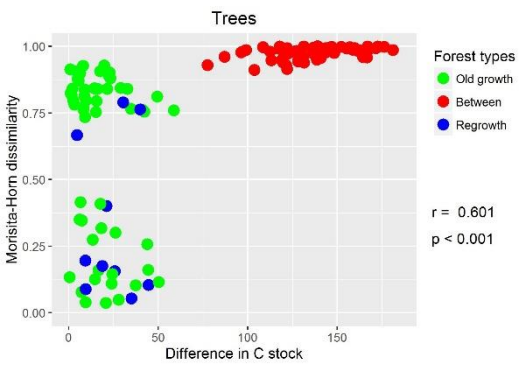
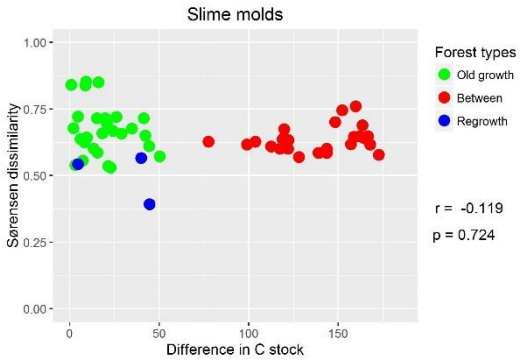
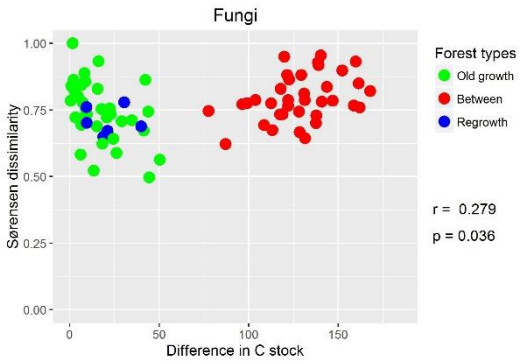
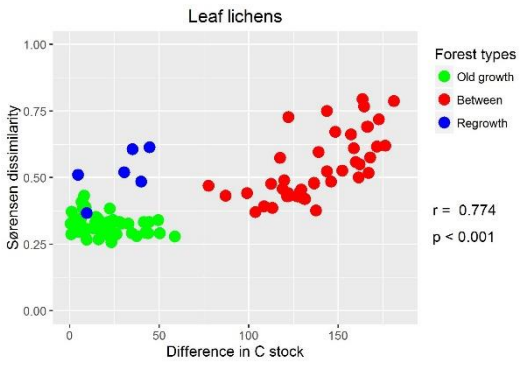
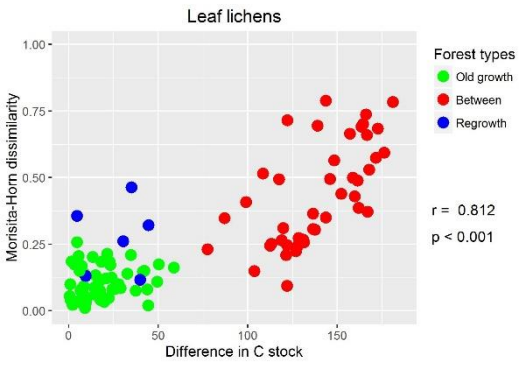
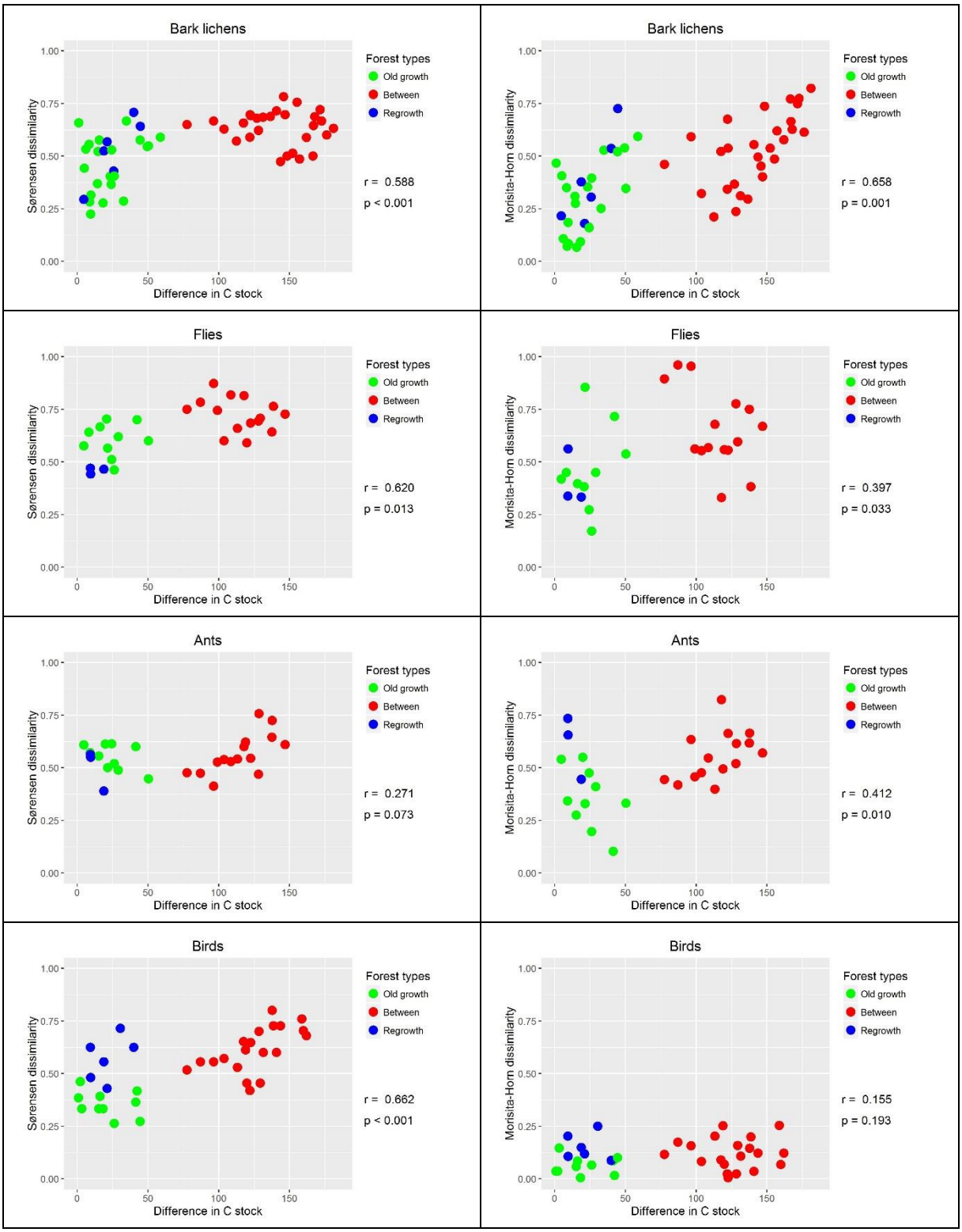


fig. S2. Orthogonal polynomial regression between each aspect of taxonomic biodiversity at the α level and carbon stock for each group. When abundance data are available (all taxa except slime molds and mushrooms), diversity values are standardized for sample completeness and the 95% confidence intervals are illustrated by vertical lines (in some cases, confidence intervals are smaller than the diameter of the dots that indicate mean values). Regrowth forests are depicted with ▲ and old-growth forests with ●.

Sørensen	Morisita-Horn
	
	
	
	


Bark lichens
Sørensen dissimilarity
Difference in C stock
Forest types
Old growth
Between
Regrowth
r = 0.588
p < 0.001
Bark lichens
Morisita-Horn dissimilarity
Difference in C stock
Forest types
Old growth
Between
Regrowth
r = 0.658
p = 0.001
Flies
Sørensen dissimilarity
Difference in C stock
Forest types
Old growth
Between
Regrowth
r = 0.620
p = 0.013
Flies
Morisita-Horn dissimilarity
Difference in C stock
Forest types
Old growth
Between
Regrowth
r = 0.397
p = 0.033
Ants
Sørensen dissimilarity
Difference in C stock
Forest types
Old growth
Between
Regrowth
r = 0.271
p = 0.073
Ants
Morisita-Horn dissimilarity
Difference in C stock
Forest types
Old growth
Between
Regrowth
r = 0.412
p = 0.010
Birds
Sørensen dissimilarity
Difference in C stock
Forest types
Old growth
Between
Regrowth
r = 0.662
p < 0.001
Birds
Morisita-Horn dissimilarity
Difference in C stock
Forest types
Old growth
Between
Regrowth
r = 0.155
p = 0.193

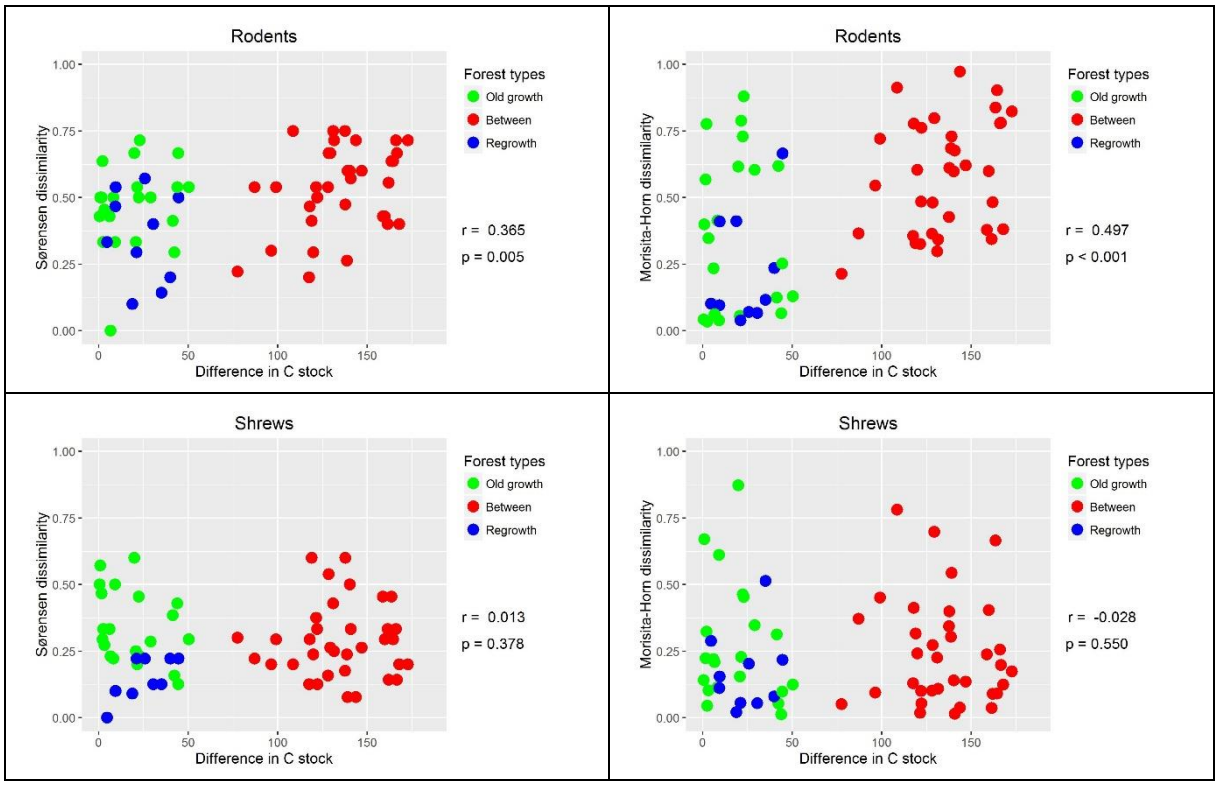
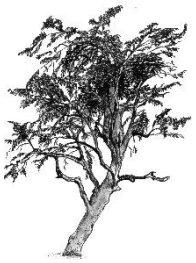
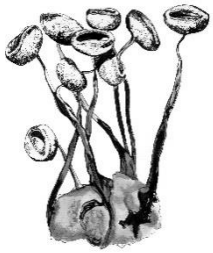


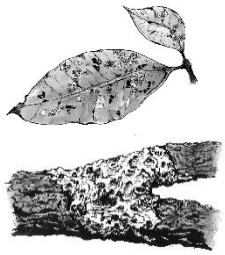
fig. S3. Relationships between compositional dissimilarity (Sørensen and Morisita-Horn indices) and difference in carbon stocks (in Mg ha^{-1}) between plots. P-values of Mantel tests and Pearson coefficients (r) are indicated. The color indicates whether the dissimilarity is calculated between two old-growth forests (green dots), two regrowth forests (blue), or between an old-growth and a regrowth forest (red).

Tables

table S1. Overview of the sampled groups. For each species group, we indicate the number of research plots that were surveyed and summarize the sampling methodology. Initials of responsible authors are indicated below the drawings. Sample storage locations include BGM (Botanic Garden Meise, Belgium), RBINS (Royal Belgian Institute for Natural Sciences), RMCA (Royal Museum for Central Africa, Belgium), UA (University of Antwerp, Belgium), and CSB (Centre de Surveillance de la Biodiversité, DR Congo).

Group	# plots	Summary sampling methodology
 (B.W., S.J.)	16	**Trees** are primary producers that represent the structural and energetic foundation of forest ecosystems for all other taxa. October 2012, July 2013. All trees with a DBH ≥ 10 cm were identified to species level. For individuals that could not be identified to species level in the field, botanical specimens were collected and identified based on a comparison with herbarium material and DNA sequencing. Vouchers are stored at the BGM and RMCA. Wood samples have been added to the Tervuren xylarium (RMCA).
 (M.d.H.)	11	**Plasmodial slime molds** or Myxomycetes are bacterivorous amoebozoans that live in plant necromass and are arguably the most important group of amoebae in the soil (*61*). They contribute to biogeochechemical dynamics by unlocking nutrients from microbial biomass. October 2013. The total sampling time per plot was 6 hours (except for GIL5 and BRA1, which were sampled for 4 hours). Sampling was done by walking through a plot and searching through substrates. We collected field specimens and various aerial and ground substrates for moist chamber cultures to obtain as much species as possible. Vouchers and photographs are stored at the BGM.
 (A.D.K)	14	**Fungi** are important actors in the carbon cycle and co-drivers of ecosystem function in forests. They are highly diverse, belong to various functional groups (ecto- and endomycorrhizal, saprotrophic or parasitic) and are significantly affected by qualitative and quantitative environmental changes. Edible species are an important food source for local communities (*62*). October 2012 and 2013. Each plot was searched for 3 days, recording species' presence. Vouchers and photographs are stored at the BGM.

16

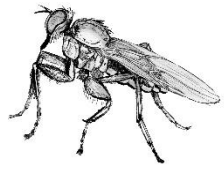


(D.V.d.B.)

Lichens are long-lived organisms with a high sensitivity to environmental variation. Many species that persist in old-growth forests are different from those in disturbed forests, making them good indicators of historical disturbance (*63*). Leaf lichens have a particularly short life cycle and respond rapidly to changes in environmental conditions (*64*).

October-November 2012 and October-November 2013. Bark-inhabiting (corticolous) and leaf-inhabiting (foliicolous) lichens were collected. For the sampling of bark lichens, 12 trees were selected in each plot in a standardized way (*42*). Depending on the DBH of trees, lichen species were collected in 4 frequency ladders of 10 x 50 cm (trees with DBH > 36 cm) or between 100 and 150 cm above the ground (DBH ≤ 36 cm).
In each plot, 18 leaves were examined for leaf lichens: six leaves of *Scaphopetalum thonneri*, six of *Marantaceae* sp., and six of other trees and shrubs. To compare biodiversity data, a similar sample size was chosen. An ellipsoid grid of 16 x 6.4 cm, covering an area of ca. 100.5 cm^2, was placed on the upper and under sides of the leaf with one edge of the grid touching one of the margins of the leaf. Vouchers are stored at the BGM.

9



(P.G.)

Empidoid flies (Diptera, Empidoidea) are important invertebrate predators in tropical ecosystems.

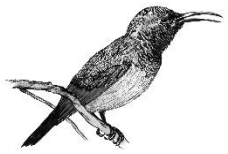
June 2013. Flies were collected via standardized net sweeping. At least two 20-min periods of net sweeping was performed per plot. Samples are stored at the RBINS.

8

(M.L.)

Ants are important components of food webs (*65*) because they comprise a large quantity of animal biomass and interact with many species (e.g., plants [mutualism, seed dispersion, pollination] and other arthropods [mutualism, predation]). Furthermore, ants are ecosystem engineers that create habitat for other species by concentrating nutrients in a localized area around their nests (*66*). Our study focused on tree-dwelling ants.

June 2012 and July 2013. Arboreal-dwelling ants were collected according to standardized protocol (*43*) using baits spread every 5 m along a rope. One end of the rope is tied around the trunk and the other is positioned over a branch in the canopy, forming a loop. Baits comprised a mixture of proteins and carbohydrates, and were left for about 4 hours before collection. Samples are stored at the RBINS.



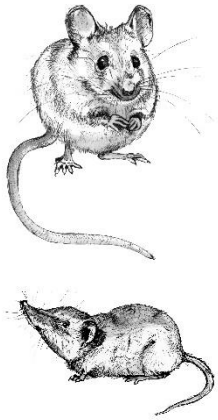
(S.C.)

9 Although **birds** are highly mobile, they are relatively easy to detect and identify, and represent a vertebrate group with considerable taxonomic and functional diversity. 39 out of 44 species are considered forest-dependent (*67*). The five open-habitat species were found in low abundances in regrowth forest (n=2), old-growth forest (n=1), or both (n=2).

September 2012. Twenty ground-level mist-nets were erected in up to 3 adjacent plots simultaneously. Opened nets were checked regularly during daytime. Nets were deployed for 2–5 days in each plot. Mist-nets were set for a total of 22,717 meter-net-hours (mnh). Sampling effort ranged from 1272 to 3828 mnh.

12 **Rodents** (Muridae) and **shrews** (Soricidae) both roam the forest floor, but represent different functional groups. Murids have a broad diet, whereas soricids are strictly insectivorous.

June-July 2013-2016. Rodents and shrews were collected using the Paceline Method, which consists of placing traps at 5 m intervals on transects (*44*). On each trap line, three types of traps were used: Sherman LFA traps, Victor snap traps and Pitfall traps. Trap lines were monitored for 21 nights in each plot. Species were identified using DNA barcoding. Tissue samples are stored at the UA, carcasses at the CSB.



(F.V.d.P)

table S2. Parameter estimates for orthogonal polynomial regression between each of three measures of taxonomic biodiversity at the α-level and carbon storage, separately for each organismal group. The last two columns contain p-values of the Mitchell-Olds & Shaw (MOS) test (*56*) and the form of the relation resulting from the orthogonal polynomial regression and MOS test. We only consider a correlation to be significant if both the model and at least one of the regression coefficients (b_1* and b_2*) are significant ($p \leq 0.05$). Only regressions with significant quadratic terms are evaluated with the MOS test for modality (NA = MOS test not applicable).

Group	Metric	p(model)	R^2	b^*_0	b^*_1	p(b^*_1)	b^*_2	p(b^*_2)	p(MOS)	Relation
Trees	Species richness	**< 0.001**	0.780	49.904	68.168	**< 0.001**	-13.535	0.216	NA	Linear increasing
	Shannon diversity	**0.003**	0.540	17.348	28.439	**0.001**	-2.940	0.682	NA	Linear increasing
	Simpson diversity	**0.013**	0.407	8.754	13.881	**0.004**	-0.344	0.935	NA	Linear increasing
Mushrooms	Species richness	0.204	0.127	52.308	44.776	0.084	6.306	0.793	NA	Random
Slime molds	Species richness	**< 0.001**	0.839	22.000	-26.981	**< 0.001**	-5.480	0.181	NA	Linear decreasing
Leaf lichens	Species richness	**< 0.001**	0.692	44.788	20.590	**0.001**	-17.692	**0.003**	**0.045**	Nonlinear increasing
	Shannon diversity	**0.001**	0.630	34.073	16.191	**0.001**	-10.887	**0.018**	0.091	Nonlinear increasing
	Simpson diversity	**0.003**	0.552	26.897	14.643	**0.002**	-5.276	0.172	NA	Linear increasing
Bark lichens	Species richness	0.963	-0.212	19.228	-0.005	0.999	-1.589	0.931	NA	Random
	Shannon diversity	0.776	-0.155	15.751	-1.515	0.784	-3.504	0.726	NA	Random
	Simpson diversity	0.601	-0.091	12.822	-0.593	0.891	-4.272	0.535	NA	Random
Flies	Species richness	0.069	0.519	23.920	-20.249	0.072	19.082	0.080	NA	Random
	Shannon diversity	0.050	0.576	13.839	-5.488	0.180	9.370	**0.035**	NA	Random
	Simpson diversity	0.124	0.393	9.693	-1.687	0.589	6.274	0.062	NA	Random
Ants	Species richness	0.657	-0.184	18.092	6.924	0.413	-1.619	0.846	NA	Random
	Shannon diversity	0.462	-0.028	13.865	4.503	0.336	-3.062	0.518	NA	Random
	Simpson diversity	0.265	0.177	11.183	3.097	0.297	-3.954	0.227	NA	Random
Birds	Species richness	0.634	-0.145	11.815	-3.367	0.508	2.913	0.546	NA	Random

	Shannon diversity	**0.023**	0.623	7.631	-2.942	**0.032**	2.802	**0.030**	0.079	Nonlinear decreasing
	Simpson diversity	0.159	0.278	5.243	-1.036	0.370	2.122	0.076	NA	Random
Rodents	Species richness	0.663	-0.116	4.615	0.469	0.871	-2.649	0.383	NA	Random
	Shannon diversity	0.546	-0.069	3.120	-0.395	0.819	-1.759	0.346	NA	Random
	Simpson diversity	0.495	-0.046	2.422	-0.567	0.647	-1.229	0.365	NA	Random
Shrews	Species richness	0.222	0.125	7.113	-2.303	0.258	-2.907	0.155	NA	Random
	Shannon diversity	0.691	-0.126	4.988	-1.074	0.503	-0.856	0.590	NA	Random
	Simpson diversity	0.973	-0.215	3.934	-0.332	0.821	-0.059	0.968	NA	Random

table S3. For most groups, community composition differs more between forests with larger differences in carbon stock. Estimated parameters of Mantel correlations between species dissimilarity (Sørensen and Morisita-Horn) and difference in carbon stock (no abundances were available for fungi and slime molds). For each index, the Pearson correlation coefficient (r) illustrates the strength of association. When monodominant forests were excluded from analyses, the pattern of significance were similar except for flies and ants.

	Between all plots				**Excluding monodominant plots**			
	Sørensen		**Morisita-Horn**		**Sørensen**		**Morisita-Horn**	
	r	**p**	**r**	**p**	**r**	**p**	**r**	**p**
Trees	**0.801**	**< 0.001**	**0.601**	**< 0.001**	**0.850**	**< 0.001**	**0.855**	**0.003**
Slime molds	-0.119	0.721			0.119	0.319		
Fungi	**0.279**	**0.037**			**0.434**	**0.009**		
Leaf lichens	**0.774**	**< 0.001**	**0.812**	**< 0.001**	**0.586**	**0.001**	**0.692**	**< 0.001**
Bark lichens	**0.588**	**< 0.001**	**0.658**	**0.002**	**0.515**	**0.009**	**0.661**	**0.005**
Flies	**0.620**	**0.012**	**0.397**	**0.037**	0.747	0.061	0.644	0.088
Ants	0.271	0.071	**0.412**	**0.012**	0.209	0.181	0.161	0.226
Birds	**0.662**	**< 0.001**	0.155	0.190	**0.463**	**0.037**	-0.211	0.836
Rodents	**0.365**	**0.005**	**0.497**	**< 0.001**	**0.519**	**0.005**	**0.725**	**0.005**
Shrews	0.013	0.564	-0.028	0.719	0.190	0.103	-0.089	0.717

table S4. Compositional dissimilarity (Sørensen and Morisita-Horn) is unrelated to geographic distance between pairs of plots, except for trees based on Sørensen dissimilarity in old-growth forests. We show the Pearson correlation coefficient (r) and p-value (p) of the Mantel tests.

	Between all plots				**Within regrowth**				**Within old-growth**			
	Sørensen		**Morisita-Horn**		**Sørensen**		**Morisita-Horn**		**Sørensen**		**Morisita-Horn**	
	r	**p**	**r**	**p**	**r**	**p**	**r**	**p**	**r**	**p**	**r**	**p**
Trees	0.082	0.247	0.025	0.322	-0.208	0.565	-0.195	0.496	**0.314**	**0.005**	0.017	0.324
Slime molds	0.013	0.386			-0.232	0.667			-0.140	0.634		
Fungi	-0.055	0.548			0.226	0.463			-0.152	0.700		
Leaf lichens	-0.172	0.870	-0.138	0.784	-0.487	1.000	-0.739	0.961	0.125	0.305	0.071	0.312
Bark lichens	-0.104	0.680	-0.225	0.904	0.631	0.255	0.740	0.249	0.056	0.381	-0.294	0.849
Flies	-0.034	0.510	-0.090	0.632	-0.832	1.000	0.441	0.667	-0.022	0.577	0.123	0.301
Ants	-0.198	0.875	-0.158	0.818	-0.509	1.000	-0.669	1.000	-0.593	1.000	0.025	0.487
Birds	-0.350	0.980	-0.292	0.948	-0.178	0.627	-0.616	0.792	-0.390	0.845	-0.254	0.764
Rodents	0.217	0.150	0.077	0.297	-0.895	1.000	0.916	0.334	0.134	0.326	0.067	0.319
Shrews	-0.024	0.470	0.146	0.282	-0.566	1.000	-0.187	0.668	0.028	0.459	0.124	0.391

table S5. Number of observed individuals and species in regrowth and old-growth forests for each organismal group. When abundances are available, we determine specialization using the classification method of Chazdon *et al*. (*18*).

Group:	**Trees**	**Slime molds**	**Fungi**	**Bark lichens**	**Leaf lichens**	**Flies**	**Ants**	**Birds**	**Rodents**	**Shrews**
Number of encountered individuals in regrowth	1527	104	121	194	424	471	201	129	235	282
Number of encountered individuals in old-growth	4001	138	559	555	1789	270	296	202	180	258
Number of encountered species in regrowth	66	64	82	49	79	60	34	28	11	12
Number of encountered species in old-growth	157	67	275	63	118	50	55	23	14	11
Number of encountered shared species	50	35	57	29	66	23	24	12	10	10
Number of encountered total species	173	96	300	83	131	87	65	39	15	13
% old-growth species in regrowth	75.8	54.7	69.5	59.2	83.5	38.3	70.6	42.9	90.9	83.3
Too rare to classify (#species)	119			60	83	61	42	34	8	4
Regrowth specialists (#species)	10			8	11	10	4	0	3	1
Old-growth specialists (#species)	36			4	13	10	3	1	2	1
Generalists (#species)	8			11	24	6	16	4	2	7
Too rare to classify (%)	68.79			72.29	63.36	70.11	64.62	87.18	53.33	30.77
Regrowth specialists (%)	5.78			9.64	8.4	11.49	6.15	0	20	7.69
Old-growth specialists (%)	20.81			4.82	9.92	11.49	4.62	2.56	13.33	7.69
Generalists (%)	4.62			13.25	18.32	6.9	24.62	10.26	13.33	53.85