

SUPPORTING INFORMATION**Logging increases the functional and phylogenetic dispersion of understorey plant communities in tropical lowland rain forest**

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Appendix S1. Supplementary methods describing site selection, vegetation sampling and measurement of predictor variables.

Appendix S1.1 Study sites.

This study was conducted in the Kalabakan Forest Reserve (KFR; 4°70' N, 117°58' E), the Mount Louisa Forest Reserve (MLFR; 4°77' N, 117°68' E) and the Maliau Basin Conservation Area (MBCA; 4°75' N, 116°96' E) in Sabah, Malaysian Borneo, between December 2011 and March 2014 (Fig. S1). The principal 10 000 ha study area in the KFR is part of a one million hectare forest concession managed by the Yayasan Sabah Foundation, which was established in 1966 to promote economic and social development by using sustainable sources of revenue (Marsh & Greer 1992). In this move, the area was first opened for commercial logging activities in the late 1970s, followed by multiple rounds of logging until the early 2000s. Most areas in the reserve that remain under forest cover have been logged at least twice, but approximately half of the reserve is cultivated with oil palm monocultures today (Wearn *et al.* 2013). The other two forest reserve areas are classified as Class I (Protection) reserves (i.e. the highest level of formal protection in Sabah). The MLFR (to the north of the core Stability of Altered Forest Ecosystems (SAFE) project area; Fig. S1) has been logged twice while most parts of the MBCA (to the west of the core SAFE area; Fig. S1) are old-growth forest with no documented record of logging (Reynolds *et al.* 2011). The native vegetation across all sites is tropical lowland rain forest and the canopy is frequently dominated by species in the family Dipterocarpaceae. The climate is aseasonal with an annual rainfall of 2890 mm and a mean annual temperature of 27.8 °C (Luasong Forestry Centre, unpublished data). The acrisolic and

luvisolic soils are derived from an underlying bedrock of predominantly mudstone and sandstone (Wright 1975). The sampling area covers an elevation gradient from 200–700 m above sea level.

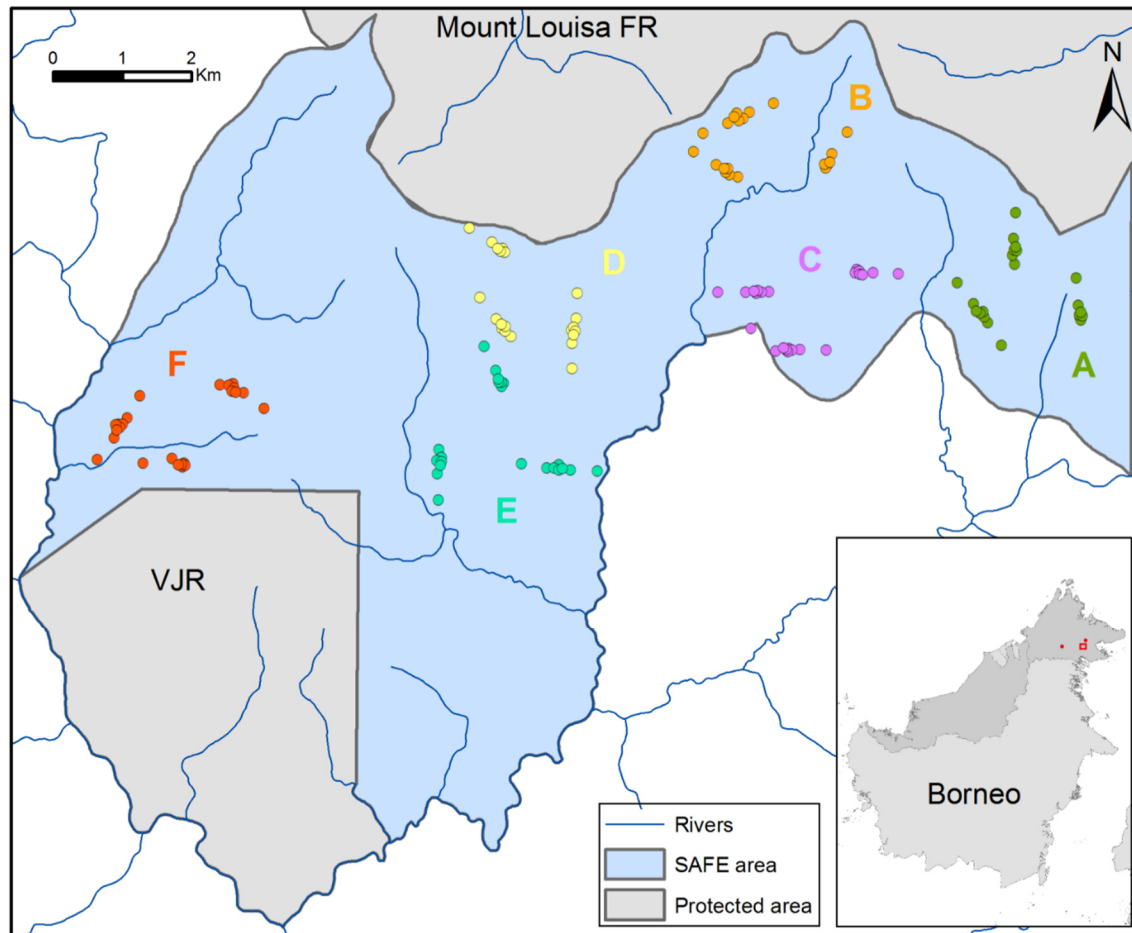


Fig. S1. Map of the Stability of Altered Forest Ecosystems (SAFE) project area, located in Malaysian Borneo (Ewers *et al.* 2011). The study landscape encompasses a logging intensity gradient across an intensively-logged 10 000 ha oil palm concession area (SAFE area; blocks A–F; red square in inset map) to a less-intensively logged local forest control area (LF) to the north and to an intact old-growth forest control area (OG) to the west. Blocks LF and OG are not shown but locations relative to the SAFE area are indicated by red circles in the inset map. Coloured circles illustrate the locations of 2×2 m study plots for blocks A–F (*i.e.* a total of 137 plots across the landscape).

Appendix S1.2. Study design.

We selected eight spatial blocks (A–F, LF and OG), each subdivided into three sub-blocks, across the landscape to reflect the varying logging histories within the region. A total of 33 understorey vegetation plots (2×2 m) were established across the three sub-blocks within each

block (a total of 264 plots). All plots were located at fixed geometric intervals from designated reference points that corresponded with a broader framework of planned landscape fragmentation underpinning the SAFE project (see Ewers *et al.* 2011 for detail; Fig. S1). Plot locations were determined in the geographical information system MapSource (Version 4.0, Garmin, Switzerland) and subsequently ground-truthed. Plot locations were rejected and relocated during ground truthing in cases where a single tree or rock would have occupied more than 10% of the plot surface area, where the slope would have been $>30^\circ$ or where the plot would have been within 5 m of a waterway.

For the purpose of analyses, we systematically excluded plots where two or more plots were less than 37 m apart (the minimum distance at which circular areas of 17.78 m (i.e. $10^{1.25}$ m) radius, centred on the sampling plots, did not overlap). We implemented this by arbitrarily dropping plots in such a way that the maximum number of plots was retained for analysis ($n = 180$ plots after the process was completed). The $10^{1.25}$ m radius was chosen to match the minimum spatial scale of sampling resolution of the wider SAFE project design (Ewers *et al.* 2011). The geographic location and elevation of each plot were recorded with a GPS (Garmin GPSMAP 62s; average accuracy error under mature forest was 5 m; Wing 2011).

Appendix S1.3. Biomass harvest.

In order to assess the floristic composition and structure of the understorey vegetation, we recorded morphospecies identities and quantified their relative contribution to above-ground biomass (AGB) in 2×2 m plots. We destructively harvested AGB up to a height of 2 m, excluding stems greater than 2 cm diameter at breast height (DBH; 1.3 m above ground). We included all plant material rooted outside but growing into the plot and excluded any parts that extended out of the plot from plants rooted within. To avoid observer bias, all biomass removal and sorting was conducted by the same two botanically trained research assistants throughout the study (see Acknowledgements), and regularly cross-checked by TFD. All plant material was rough-sorted into morphospecies on site and subsequently dried (c. 70°C) for a minimum of four days in custom-made field ovens. Due to the lack of a clear annual productivity peak in tropical rain forest, biomass harvest was conducted year-round between December 2011 and March 2014 with plot harvesting randomly stratified across blocks (through time), depending on site access and logistical constraints. The dry biomass was then transferred to the laboratory

where all plant material was again oven-dried (c. 90 °C) for a minimum of 36 h to account for moisture re-absorption over time.

Appendix S1.4. Measurement of predictor variables.

Forest canopy change was manually quantified based on a temporal comparison between high-resolution aerial photographs collected in 1970/71 and high-resolution Worldview 2 satellite imagery taken at the same locations between 2010 and 2014. The aerial photographs were collected at 1:25,000 scale as part of a comprehensive state-wide forest inventory conducted in Sabah in the early 1970s and were manually geo-referenced in ArcGIS for this study. The satellite images had a sensor resolution ground sample distance of 1.84 m. While the exact resolution of the aerial photographs was unknown, individual tree crowns could be depicted at similar spatial grain as in the satellite images, allowing for direct comparisons.

We manually quantified percent forest canopy change at two different spatial extents as a measure of forest canopy loss surrounding a plot, and ground-truthed these measures with plot data at each site. We used a circular buffer area of 17.78 m (i.e. $10^{1.25}$ m) radius to delineate local-scale forest canopy loss and a 562.34 m (i.e. $10^{2.75}$ m) buffer area to capture forest canopy loss at the landscape-scale. A radius of 17.78 m reflects an approximation of a canopy gap that would result from a natural tree fall event or the selective logging of a full-grown canopy tree. The 562.34 m radius accounts for the assumption that dispersal patterns of tropical trees as well as plant invasion dynamics are likely to be most strongly influenced by variation in land cover within the surrounding landscape at this scale (Charbonneau 2003; Seidler & Plotkin 2006; Monteiro *et al.* 2013). Local, landscape and regional scales were pre-defined in accordance with the log₁₀-scale fragment-edge-distance approach used for the broader SAFE project study design (Ewers *et al.* 2011).

We then quantified the density of secondary and primary logging roads (km km^{-2}) as potential vectors for the movement of propagules within circular buffer areas of 1778.28 m (i.e. $10^{3.25}$ m) radius surrounding a plot. Most studies on landscape-scale plant dynamics typically assume, or measure, responses within a range of two kilometres from sampling points (González-Moreno *et al.* 2012). Primary roads were defined as those major roads that have been continuously maintained and used since their establishment including roads within oil palm plantations. Other roads that were only re-opened for new rounds of logging, yet abandoned from use during non-logging periods, were classified as secondary roads. Further, we estimated the shortest distance of each plot to a primary and secondary logging road (m).

Finally, we estimated the distance (m) of plots to rivers (>3 m width) as a natural proxy for propagule pressure. All analyses were conducted in geographic information systems software (ArcGIS version 10.2.1, ESRI 2014, Redlands, CA, USA).

Appendix S1.5. Soil biogeochemistry sampling and analysis.

In order to account for the underlying influence of soil on plant community assembly and heterogeneity, we measured six soil biogeochemical variables, namely pH, humus depth, total nitrogen (N), available phosphorus (P), bulk density and moisture factor. *In situ* measures of pH (accuracy ± 0.2 units) were collected with a Kelway moisture probe and humus depth was measured with a ruler (the dark A-horizon between the leaf litter and lighter more compact soil below). We then collected replicate soil cores of two different dimensions, with 10.1 cm wide \times 7.7 cm deep cores to determine bulk density and 5.5 cm wide \times 10.1 cm deep cores to determine N, P and moisture factor.

Soil bulk density is a measure of soil compaction and an indicator of soil permeability and potential root growth (McKenzie *et al.* 2004). We collected two replicate soil cores at randomly-selected points within 2 m outside a plot. Leaf litter and loose organic matter were first scraped off the surface. The corer was initially pressed and then hammered vertically down into the ground until level with the soil surface. It was then carefully dug out to prevent soil from falling out and the soil on both sides was levelled to the surface of the corer. Samples were then transferred into ziplock plastic bags which were temporarily sealed during transport to reduce the risk of biological and chemical changes. The soil bulk density samples were dried (c. 70 °C) for a minimum of four days in custom-made field ovens. Prior to lab processing, all samples were re-dried under the same conditions to a constant weight, to account for moisture re-absorption over time. The accurate determination of soil bulk density requires the removal of the coarse stone fraction as well as roots (Mehler, Schöning & Berli 2014). We removed those stones and roots that were retained in sieves of 10 mm mesh size and measured their volume using displacement of water. We then recorded the dry weight for each soil sample and related the weight to the adjusted corer volume for a measure of bulk density.

Soil nutrient samples were collected in five replicate soil cores at randomly-selected points within 2 m outside of the plot boundary. These soil samples were used to determine N and P, which are often limiting resources for plants and have been shown to play important roles in the invasibility of habitats (Davis, Grime & Thompson 2000). The field sampling

procedures followed the bulk density sampling protocol. The five samples were pooled to account for local spatial heterogeneity as well as the constraint of analytical costs. Upon return to the field camp, the samples were immediately sieved through a 0.5 cm mesh size sieve and transferred into aluminium trays for air-drying. All samples were air-dried for a minimum of four weeks and subsequently divided into two fractions. Approximately 100 g of soil was separated for the nutrient analysis, while a small fraction of each sample was used for determining a soil moisture factor, calculated as the difference between air-dry and oven-dry weight. The remainder was archived and all samples were kept in tightly sealed ziplock bags for storage and transport at all times.

Soil nutrient samples were analysed for N and P at the Sandakan Forestry Department chemical laboratory. For the analysis of N, a portion of each sample was further ground to pass through a 212- μ m sieve. To determine N, the soil was digested following the Kjeldahl digestion method described by Bremner (1965) on a Labconco Rapidigest block digester and the digest measured for N content on a Burkard SFA2 auto-analyser (UK). Extraction of P followed the method of Bray & Kurtz (1945) and the P contents in the extract were determined using the molybdenum-blue method described in Anderson & Ingram (1993) and read at 880 nm on the Hitachi UV-VIS spectrophotometer (Japan).

In order to quantify N and P mass per volume, we first corrected for the moisture content and then for bulk density to account for varying compaction and clay content as well as differences in soil moisture-holding capacity. At the laboratory in Maliau Basin, we quantified a moisture factor for each sample to account for the differences in soil moisture retention capacity and variation in soil moisture content of air-dried soil with time and storage conditions (Blakemore, Searle & Daly 1987). Exactly 10 g of each air-dried sample was oven-dried at 105 °C until a constant weight was reached and then re-weighed. The soil moisture factor was calculated as the air-dried weight divided by the oven-dried weight.

Prior to statistical analyses, a correlation-based principal component analysis (PCA) was conducted to test for collinearity among the six soil variables (Fig. S2). Soil variables were first standardised to a mean of zero and a standard deviation of one to account for the different unit scales of measure. With the exception of pH and bulk density, soil variables were transformed to minimise the influence of outliers and to approximate the assumption of normality. Both N and P were \log_e -transformed, humus depth was square-root-transformed and moisture factor was double \log_e -transformed. None of the soil variables showed correlation above a 0.6 threshold and thus all six soil variables were retained for further analyses.

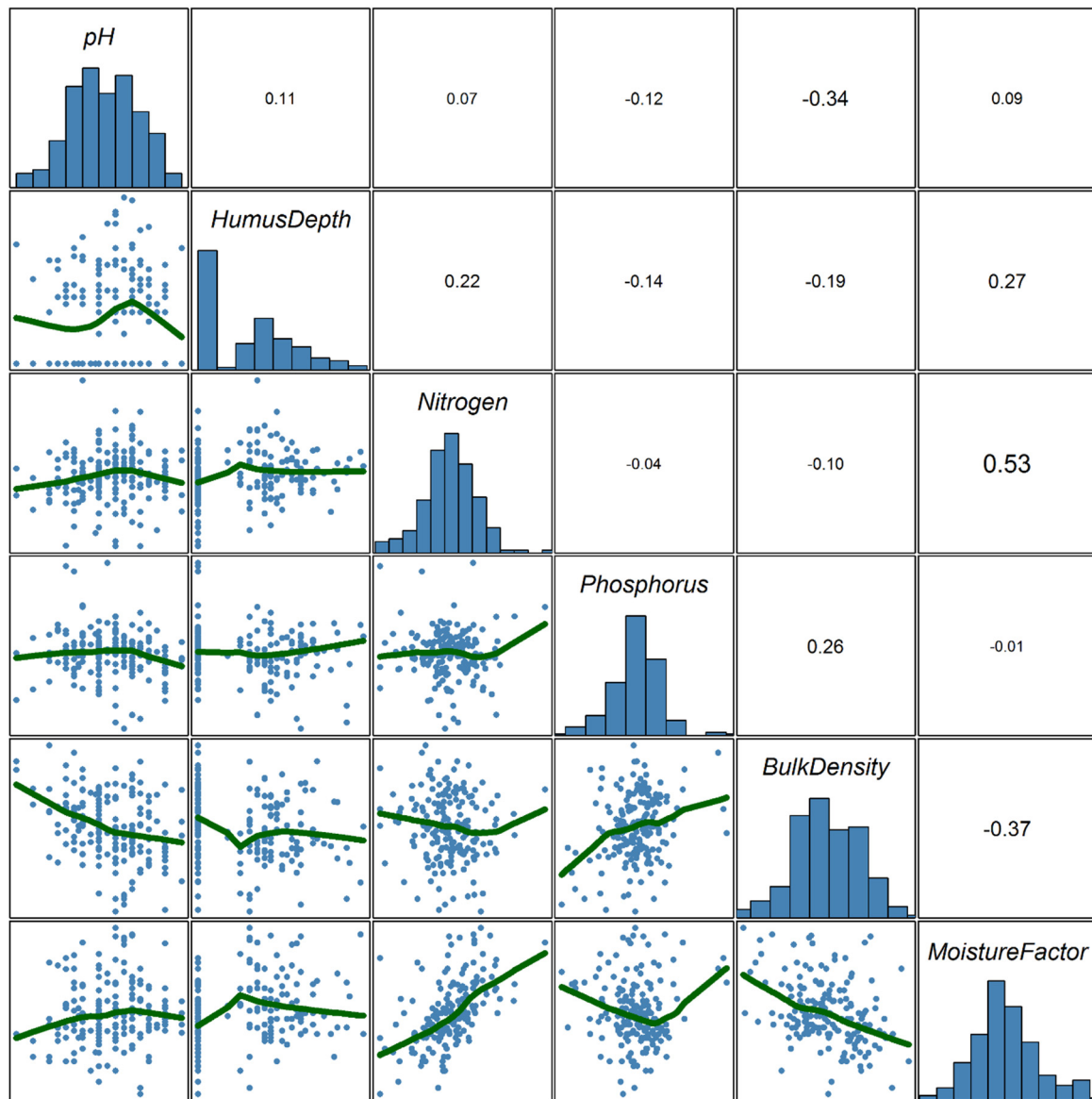


Fig. S2. A correlation matrix assessing collinearity among six transformed soil variables: pH, humus depth (cm), total nitrogen (mg cm^{-3}), available phosphorus ($\mu\text{ cm}^{-3}$), bulk density (g cm^{-3}) and moisture factor across the 180 plots. Green lines illustrate average trends. The diagonal shows histograms of each variable. Correlation coefficients (Pearson) shown in the upper right half.

We then created composite variables that reflected orthogonal gradients in soil conditions. The selection of retained principal component axes was based on visual interpretation of a scree plot and Kaiser's criterion (Kaiser 1960). Cumulatively, the first two axes accounted for approximately 55% of the total variation in soil characteristics. PCA axis 1 characterised a gradient in soil types from soils with higher moisture-holding capacity, high depth and N content at lower axis 1 scores, to soils with higher bulk density at higher axis 1 scores (hereafter referred to as 'soil-compaction gradient'). PCA axis 2 indicated a gradient

from P and N rich soils at lower axis 2 scores, to soils with high pH at higher axis 2 scores (hereafter referred to as ‘soil-fertility gradient’; Table S1).

Table S1. PCA loadings based on principal component analysis on six soil biogeochemical variables measured across 180 plots: pH, humus depth (cm), total nitrogen (N; mg cm⁻³), available phosphorus (P; µ cm⁻³), bulk density (g cm⁻³) and moisture factor

	pH	Humus depth	Total N	Available P	Bulk density	Moisture factor
PCA1	-0.30	-0.40	-0.44	0.24	0.47	-0.53
PCA2	0.47	-0.06	-0.50	-0.50	-0.38	-0.37

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Appendix S2. Supplementary methods describing the measurement of functional traits and phylogenetic structure.

Appendix S2.1. Measurement of plant functional traits.

Plant functional traits are increasingly used for assessing changes in community composition and ecosystem functioning following disturbance (Diaz & Cabido 2001; McIntyre & Lavorel 2001; Laliberté *et al.* 2010). For each plant species, we recorded whether they were native or exotic (i.e. where presence in the study area could only be attributed to human actions; Webber & Scott 2012) and then recorded 10 ‘core’ plant traits considered to be crucial for plant resource use, dispersal, persistence and re-establishment in response to disturbance (Westoby 1998; Weiher *et al.* 1999; McIntyre *et al.* 1999; Lavorel & Garnier 2002; Kleyer *et al.* 2008). The 10 plant traits are known to either respond to disturbance (hereafter referred to as ‘response traits’: dispersal mode, fruit type, life-history mode, pollination syndrome, reproduction strategy and seed number) or influence ecosystem function (hereafter referred to as ‘effect traits’: plant growth form, plant height, specific leaf area (SLA) and wood density; Lavorel & Garnier 2002; Suding *et al.* 2008; Laliberté *et al.* 2010). These traits have previously been used to explore the response-effect trait framework as well as to determine functional and phylogenetic community assembly patterns following land use change (e.g. Ding *et al.* 2012; Bässler *et al.* 2014; Rader *et al.* 2014). To maximise predictability of community functional responses to logging disturbance, the selected traits ranged across a wide spectrum of functional dimensionality without exceeding a recommended maximum number of eight traits for either the response or the effect group (Laughlin 2014).

The availability of trait data for the diverse flora of Borneo is sparse, but we ensured that at least half of the taxa had measurements for each trait (Table S2), corresponding to the 50-percent threshold suggested by Laliberté *et al.* (2010). Trait data were derived from different sources including compilations of the ‘Floras’ on Southeast Asian plants, published databases of specific traits, compilations of plant family and genus characteristics, and direct measurements of herbarium specimens or field-sampled plant material (Table S2). We did not consider analyses of intraspecific trait variability due to logistical reasons and a lack of such information for the majority of tropical rain forest understorey species in Borneo. Moreover, the magnitude of within-species variation relative to among-species variation is likely to be lower for broader clades (i.e. all angiosperms; Garnier *et al.* 2001).

Table S2. Number of species or morphospecies (out of 691 taxa) with recorded trait data derived from different sources including compiled ‘Floras’ of Southeast Asian plants, published databases on specific traits, compilations of plant family and genus characteristics, and direct measurements of herbarium specimens or field-sampled plant material

Functional trait	Measured	Genus inferred	Assumed	Not found	Not possible
Dispersal mode**	402 (58%)	58 (8%)	95 (14%)	121 (18%)	15 (2%)*
Fruit type	589 (85%)	22 (3%)	na	10 (1%)	70 (10%)*,§
Life-history mode	632 (91%)	na	na	52 (8%)	7 (1%)*
Pollination syndrome††	311 (45%)	298 (43%)	3 (<1%)	66 (10%)	15 (2%)*
Reproduction strategy	685 (99%)	na	na	1 (<1%)	5 (<1%)*
Seed number‡‡	552 (80%)	1 (<1%)	7 (1%)	58 (8%)	73 (11%)*,§
Plant growth form	681 (99%)	na	na	3 (<1%)	7 (1%)*
Plant height§§	375 (54%)	1 (<1%)	4 (<1%)	34 (5%)	277 (40%)*,†
Specific leaf area¶¶	691 (100%)	na	na	na	na
Wood density***	150 (22%)	248 (36%)^	na	128 (19%)‡	165 (24%)¶

*Genus indeterminate. †Height only for self-supporting species. ‡Includes woody climbers. ¶Includes all herbaceous species (Pérez-Harguindeguy *et al.* 2013). §Fern n.a. ^Based on Southeast Asian species (233) and based on global averages (15). **Plant species for which the specific animal disperser was unknown were classed as ‘animal dispersed’. ††Beetles and weevils were grouped as ‘beetle’ both belonging to the insect order Coleoptera. In those cases where the insect order was not known or where two insect orders contributed to pollination of the same species they were grouped as ‘entomophilous.narrow’. More than two orders were grouped as ‘entomophilous.broad’. ‡‡In those cases where the range of the potential number of seeds was across more than one class, allocation to a class was based on the median of that range. ¶¶For a detailed description of specific leaf area calculation see Appendix S2.2. §§Recorded as maximum plant height. ***Estimates of wood density based on genus level inference are considered a valid approach in ecosystem studies according to studies conducted in both Neotropical (Baker *et al.* 2004) as well as Paleotropical forests (Slik 2006).

Data on plant growth form, plant height, dispersal mode, life-history, reproduction strategy and seed number were primarily obtained from the Tree Flora of Sabah and Sarawak Vol. 1–8 (1995–2014)^I, the Families and Genera of Vascular Plants Vol. 1–10 (1990 onward)^{II}, the Flora of China (English edition: www.efloras.org), the Tree and Shrub Genera of Borneo database (<http://phylodiversity.net/borneo/delta>), the Families of Flowering Plants database (<http://delta-intkey.com/angio>) and the Plants of Southeast Asia database (www.asianplant.net). Data on wood density came from the Global Wood Density database (Chave *et al.* 2009; Zanne *et al.* 2009). Data on pollination syndromes were primarily sourced from (Momose *et al.* 1998; Sakai *et al.* 1999; the Families and Genera of Vascular Plants Vol. 1–10 (1990 onward)^{II}). Information on plant native status was obtained from (Barnes & Chan 1990) and the Global Invasive Species Database (<http://www.issg.org/database/welcome>).

^ISoepadmo, E., Saw, L.G., Chung, R.C.K. & Kiew, R. (eds; 1995–2014), Tree Flora of Sabah and Sarawak Vol. 1–8, Forest Research Institute Malaysia.

^{II}Kubitzki, K. (ed; 1990 onward) The Families and Genera of Vascular Plants, Springer-Verlag: Berlin, Germany.

Appendix S2.2. Measurement of specific leaf area.

Calculation of specific leaf area (SLA) should be based on the ratio of the one-sided area of a fresh leaf divided by its oven-dry mass, expressed in $\text{m}^2 \text{kg}^{-1}$ (Cornelissen *et al.* 2003). The standard SLA of fresh leaves ($\text{SLA}_{\text{fresh}}$) has not previously been measured for the majority of tropical rain forest understorey species in Borneo. To address this constraint we combined limited field measurements of $\text{SLA}_{\text{fresh}}$ with more extensive measurements of SLA_{dry} values of herbarium specimens, using the approach of Queenborough & Porras (2014) to back-calculate unknown $\text{SLA}_{\text{fresh}}$ values from measured family-level shrinkage estimates.

We therefore estimated SLA_{dry} of 186 species (and 52 variants and subspecies therein) using identified specimens lodged at the Sandakan Herbarium, calculated as the dry area to dry weight ratio of between one and eight undamaged leaves obtained from a maximum of three independent specimens. All leaves were re-dried (c. 40 °C) for 18 h to remove excess moisture. The leaves (including petioles) were then weighed to 0.01 g and scanned with a flatbed scanner (Epson GT-15000; 300dpi, 24-bit jpeg format) for subsequent leaf area analysis using the open-source software Easy Leaf Area (Easlon 2014). In those cases where field-collected specimens in the survey plots could only be identified to genus or family level, SLA_{dry} was extrapolated based on phylogenetic relationships (Angiosperm Phylogeny Group 2009). Overall, SLA_{dry} was measured directly (at the species level) for 28% of plant specimen records, and a further 23% were extrapolated measures at the genus level (i.e. extrapolating the average of SLA_{dry} from known species within the genus to an unknown species in the same genus), while the remainder were estimated at a coarser phylogenetic level.

To calculate family-level shrinkage estimates, fresh leaf samples for a subset of 32 species across 23 families were collected from rain forest and oil palm plantation sites in the vicinity of the Sandakan Herbarium. Leaves across the spectrum of leaf sizes and shapes were selected, including common forbs, shrubs and trees of native species and dominant forbs of exotic species that could be positively identified in the field. Sampling and processing procedures followed the protocol described in Pérez-Harguindeguy *et al.* (2013). Mature and fully expanded leaves (including petiole) without obvious signs of damage were sampled during standard light conditions between 9 am and 2 pm. Up to five individual plants were sampled for a maximum of 10 leaves per species (range: 2–10 leaves per species). During fieldwork, leaves were kept in CO_2 -enriched sealed plastic bags in an ice box to avoid folding and prevent dehydration. Leaves were immediately refrigerated (c. 8 °C) upon return to the herbarium and processed within 24 h.

The fresh mass of each leaf was recorded (± 0.01 g), including its petiole and rachis (in the case of compound leaves). Leaves were then scanned with a flatbed scanner (Epson GT-15000; 300dpi, 24-bit jpeg format). Leaves were placed underside down on the scanner glass with lobes spread out to avoid overlap. Each leaf was then dried (c. 40 °C) for a minimum of one week or until dry and re-scanned following the same procedure as for the fresh leaves. SLA_{fresh} was calculated as the fresh area of a leaf divided by its dry weight, while SLA_{dry} was calculated as the dry area of a leaf divided by its dry weight. The ratio between SLA_{dry} and SLA_{fresh} gave the shrinkage factor. The shrinkage ratio for individual leaves was averaged to get a family-based shrinkage factor. Measured shrinkage factors were complemented with published shrinkage values for 20 additional families from a tropical rain forest site in Amazonian Ecuador (Queenborough & Porras 2014) and eight additional families from tropical rain forest sites in Costa Rica (Blonder *et al.* 2012), giving a total of 51 families recorded. Approximately 70% of all species were directly accounted for by family-level shrinkage estimates. The shrinkage factor for the remaining species was either assigned based on phylogenetic extrapolation (as described above) or by growth form extrapolation in the case of mosses and ferns.

Appendix S2.3. Functional richness and dispersion.

Functional richness (FRic) measures the volume of niche trait space occupied by a community (Cornwell, Schwilk & Ackerly 2006; Villegér, Mason & Mouillot 2008; Mouchet *et al.* 2010); that is, community functional richness should increase with an increasing range of traits among species (Mason *et al.* 2012). Under circumstances in which none of the traits within an effect group are continuous, FRic provides a measure of the number of unique trait combinations within a community (Cornwell, Schwilk & Ackerly 2006).

Functional dispersion (FDis) is a distance-based metric that measures the mean distance of species to the centroid of the whole community in multidimensional trait space (Laliberté & Legendre 2010). Among the various metrics of functional diversity available, FDis is considered to be the most suitable for the purposes of this study, as it is independent of species richness, considers species' relative biomass, can tolerate missing data and can be measured for continuously-varying traits as well as categorical trait types (Laliberté & Legendre 2010). As such, it provides a weighted measure of trait variation or complementarity among individual species within a community.

To calculate FRic and FDis (Table S3), we first compiled a multivariate species-by-trait matrix upon which we calculated Gower dissimilarity coefficients between species trait complexes using the *gowdis* function in the ‘FD’ package (Laliberté & Legendre 2010). Gower’s distance allows the use of continuous, nominal and ordinal trait data as well as missing values (Laliberté & Legendre 2010; Pavoine *et al.* 2009). We then determined multivariate trait richness and dispersion for each community using the Gower dissimilarity coefficients weighted by log-transformed species’ relative biomass values across all sites. A square-root correction was applied to the species \times trait matrix to ensure representation in Euclidean space.

We compared observed FRic and FDis values to those expected under a null model of random community assembly (Mason *et al.* 2013). To preserve species richness patterns and relative biomass within the random communities, we applied an ‘independent swap’ algorithm using 999 randomisations for each community (Gotelli & Graves 1996; Gotelli & Rohde 2002). Biomass-weighted standardised effect sizes (SES) for each plot were calculated as:

$$\text{SES} = -1 \times ((y_{\text{obs}} - \bar{y}_{\text{exp}}) / \text{SD}_{\text{exp}}),$$

where ‘ y_{obs} ’ is the observed value, ‘ \bar{y}_{exp} ’ the mean value of the random draw and ‘ SD_{exp} ’ the standard deviation of the mean. Observed values of functional richness and dispersion that are significantly different from those expected by chance alone can suggest patterns of functional trait divergence (negative SES values) or convergence (positive SES values). For example, a negative SES-FDis value might suggest that competitive structuring of community assembly is driving greater trait divergence than expected by chance alone. In contrast, a positive SES-FDis implies underdispersion of trait complexes in response to strong environmental structuring of community assembly. In general, the use of SES values for functional diversity metrics provides a more powerful approach than the use of raw observed values *per se* for detecting differences in community assembly processes (Mason *et al.* 2013). All functional trait metrics were calculated using the *dbFD* function in the ‘FD’ package (Laliberté & Legendre 2010) in R 3.1.0 (R Core Team 2013).

Table S3. Summary table of species richness, functional diversity metrics and phylogenetic diversity for each of 180 plots. Bolded values indicate coefficients significantly different from zero ($p < 0.05$). No. = Number of taxa per plot; FRic = Functional richness; FDis = Functional dispersion; FDisR = Functional dispersion for response traits only; FDisE = Functional dispersion for effect traits only; NRI = net relatedness index; and P = p-value

Plot	No.	FRic	P	FDis	P	FDisR	P	FDisE	P	NRI	P
a100f177r	11	0.39	0.01	0.94	0.19	1.20	0.12	−0.74	0.25	0.81	0.20
a100f562r	7	0.39	0.01	−0.26	0.41	0.12	0.44	−1.05	0.12	0.62	0.28
a100f56r	13	0.54	0.00	1.13	0.12	1.59	0.05	0.56	0.28	0.49	0.36

a100f5r	11	0.63	0.00	0.25	0.38	0.31	0.35	0.40	0.34	0.71	0.23
a100m177r	5	0.05	0.02	0.39	0.34	0.55	0.29	0.10	0.38	-0.16	0.57
a100m17r	13	0.51	0.00	-0.54	0.32	-0.97	0.17	-0.18	0.50	-1.19	0.89
a100m562r	22	0.49	0.01	0.52	0.29	0.52	0.29	0.59	0.28	0.71	0.25
a100m56r	9	0.26	0.02	1.12	0.14	0.61	0.28	0.47	0.30	-0.20	0.60
a100m5r	14	0.42	0.01	0.10	0.45	0.45	0.31	0.10	0.43	0.45	0.35
a10f177r	14	0.58	0.00	-1.18	0.12	-1.31	0.08	-0.16	0.48	-1.28	0.89
a10f56r	9	0.25	0.02	0.07	0.45	0.21	0.40	0.36	0.33	0.01	0.54
a10m177r	13	0.78	0.00	1.56	0.05	1.68	0.04	0.53	0.30	0.46	0.34
a10m17r	6	0.45	0.01	-0.19	0.46	0.29	0.38	-0.21	0.49	0.30	0.40
a10m562r	21	0.55	0.00	0.39	0.34	0.68	0.24	-0.02	0.47	0.30	0.42
a10m56r	7	0.51	0.00	1.25	0.12	1.54	0.06	-1.01	0.13	1.86	0.02
a10m5r	13	0.38	0.01	1.23	0.11	1.28	0.11	-0.96	0.15	0.63	0.27
a1f17r	10	0.33	0.01	0.56	0.28	-0.75	0.27	-0.22	0.47	-0.72	0.75
a1f56r	10	0.54	0.01	0.38	0.33	0.22	0.41	0.81	0.19	-0.54	0.68
a1m177r	9	0.41	0.01	0.02	0.46	-0.93	0.19	0.25	0.36	-0.73	0.70
a1m17r	23	0.22	0.02	0.65	0.26	0.74	0.23	-0.69	0.26	0.13	0.47
a1m562r	18	0.58	0.00	0.92	0.19	1.08	0.15	1.26	0.11	0.95	0.18
a1m56r	15	0.51	0.00	-0.16	0.44	-0.07	0.48	0.83	0.20	0.83	0.21
a1m5r	13	0.57	0.01	0.50	0.32	0.60	0.28	-0.67	0.26	0.35	0.37
b100f177r	11	0.58	0.00	0.06	0.45	-0.64	0.26	-0.47	0.37	0.46	0.33
b100f17r	15	0.38	0.01	0.88	0.19	0.93	0.19	0.85	0.19	-0.12	0.61
b100f562r	11	0.21	0.02	0.91	0.19	0.84	0.21	0.52	0.27	0.27	0.43
b100f56r	12	0.54	0.01	-0.44	0.34	-0.25	0.40	-0.45	0.35	0.12	0.49
b100m177r	17	0.27	0.01	-0.09	0.50	-0.68	0.25	-0.65	0.27	-0.36	0.64
b100m17r	15	0.17	0.02	-0.42	0.35	-0.47	0.35	0.13	0.40	-0.67	0.73
b100m562r	17	0.27	0.01	1.75	0.04	1.89	0.03	-0.08	0.50	-0.28	0.64
b100m56r	15	0.29	0.01	0.35	0.34	0.18	0.44	-0.16	0.48	0.31	0.40
b100m5r	13	0.23	0.01	0.63	0.26	0.22	0.40	-0.29	0.42	-0.20	0.61
b10f177r	15	0.43	0.01	2.17	0.01	1.50	0.06	0.05	0.44	0.03	0.50
b10f56r	9	0.62	0.01	0.14	0.44	0.62	0.25	0.33	0.35	0.46	0.32
b10m177r	13	0.33	0.01	0.42	0.32	0.63	0.26	0.20	0.38	1.45	0.05
b10m1r	6	0.32	0.01	0.29	0.36	-0.20	0.44	0.43	0.29	0.60	0.26
b10m562r	7	0.43	0.01	0.30	0.35	0.29	0.38	-0.78	0.23	0.48	0.33
b10m56r	17	0.47	0.01	0.97	0.17	0.76	0.22	-0.04	0.46	0.98	0.15
b10m5r	16	0.70	0.00	1.52	0.07	1.67	0.04	0.56	0.27	0.64	0.28
b1f1r	12	0.56	0.01	-0.33	0.40	-0.76	0.24	-0.20	0.46	-1.04	0.85
b1f56r	18	0.49	0.01	0.76	0.23	0.71	0.23	-0.04	0.50	1.75	0.02
b1m177r	14	0.38	0.01	0.00	0.47	-0.74	0.23	0.21	0.36	-0.47	0.67
b1m1r	17	0.38	0.01	-0.61	0.28	-1.11	0.13	0.90	0.20	-0.32	0.61
b1m562r	17	0.48	0.00	1.02	0.16	0.98	0.17	-0.32	0.42	0.42	0.35
b1m56r	15	0.32	0.01	0.21	0.40	-0.52	0.33	0.79	0.20	-0.33	0.64
c100f177r	13	0.37	0.01	0.72	0.22	-0.34	0.40	0.36	0.31	-0.20	0.57
c100f17r	12	0.43	0.01	0.00	0.49	0.22	0.42	0.06	0.43	0.06	0.50
c100f562r	18	0.40	0.01	-0.99	0.16	-1.25	0.10	0.03	0.44	-0.76	0.76
c100f56r	12	0.50	0.01	-0.93	0.18	-1.21	0.10	0.96	0.17	-0.89	0.81
c100f5r	6	0.47	0.00	-1.05	0.15	-1.02	0.20	0.46	0.32	0.73	0.19
c100m177r	15	0.50	0.01	0.36	0.35	0.77	0.22	-0.36	0.40	0.60	0.31
c100m17r	13	0.41	0.01	1.38	0.09	1.40	0.08	-0.75	0.23	0.21	0.46
c100m562r	8	0.46	0.00	1.64	0.06	0.10	0.45	-0.77	0.19	0.29	0.35
c100m56r	10	0.49	0.01	0.78	0.23	1.10	0.11	-0.13	0.50	0.31	0.41
c10f177r	12	0.52	0.00	-0.05	0.50	-1.33	0.06	1.01	0.16	-0.30	0.59
c10f56r	14	0.78	0.00	1.27	0.10	-0.14	0.45	0.06	0.44	-0.34	0.64
c10m177r	10	0.38	0.01	0.19	0.40	-0.10	0.46	-0.89	0.19	0.16	0.46
c10m17r	23	0.44	0.01	-0.90	0.20	-0.73	0.24	-0.52	0.33	-0.02	0.55
c10m562r	14	0.16	0.02	1.46	0.08	1.09	0.14	-0.16	0.48	-0.86	0.81
c10m56r	9	0.52	0.01	0.25	0.40	0.11	0.47	-0.62	0.29	0.40	0.36
c10m5r	14	0.55	0.00	0.36	0.33	-0.80	0.21	-0.24	0.45	0.46	0.34
c1f56r	13	0.44	0.01	0.80	0.21	-0.02	0.50	1.37	0.09	-0.95	0.83
c1f5r	18	0.29	0.01	-0.26	0.40	-0.83	0.22	-0.98	0.15	0.22	0.44

c1m177r	10	0.56	0.00	-0.39	0.36	-0.13	0.44	-0.30	0.43	0.76	0.23
c1m1r	18	0.22	0.02	1.17	0.13	1.52	0.07	-0.62	0.31	0.54	0.31
c1m562r	8	0.24	0.01	-1.05	0.15	-1.13	0.13	0.40	0.30	-0.57	0.64
c1m56r	13	0.45	0.01	-0.67	0.25	-0.44	0.34	0.41	0.33	-0.29	0.63
c1m5r	10	0.59	0.00	0.90	0.18	0.65	0.28	-0.76	0.23	-0.08	0.58
d100f177r	9	0.42	0.01	0.02	0.45	0.02	0.50	0.14	0.39	0.15	0.47
d100f562r	11	0.36	0.01	-0.28	0.41	-0.49	0.32	0.99	0.16	-0.54	0.69
d100f56r	13	0.62	0.00	-0.35	0.39	-0.79	0.23	-0.03	0.45	0.70	0.25
d100f5r	12	0.38	0.01	0.04	0.48	-0.34	0.36	-0.11	0.49	0.16	0.48
d100m177r	14	0.56	0.01	0.14	0.41	0.12	0.42	-0.24	0.43	0.07	0.51
d100m562r	10	0.43	0.01	0.25	0.40	0.43	0.31	-0.65	0.27	-0.33	0.61
d100m56r	15	0.36	0.01	0.44	0.32	0.06	0.48	-0.95	0.17	-0.04	0.55
d100m5r	13	0.55	0.00	0.88	0.19	0.75	0.23	-0.04	0.47	1.22	0.08
d10f177r	14	0.20	0.01	-0.45	0.33	-1.36	0.08	0.14	0.40	-0.82	0.80
d10f56r	19	0.45	0.01	0.58	0.27	0.81	0.21	-0.01	0.46	0.14	0.46
d10f5r	19	0.42	0.01	0.09	0.46	-1.02	0.16	-0.87	0.19	0.73	0.23
d10m177r	9	0.41	0.01	0.37	0.34	-0.72	0.27	-0.23	0.47	0.31	0.41
d10m562r	14	0.34	0.01	-0.87	0.19	-1.20	0.11	-0.70	0.26	-0.98	0.83
d10m56r	23	0.37	0.01	-1.78	0.03	-0.94	0.18	-0.60	0.31	-1.18	0.88
d10m5r	14	0.34	0.01	-0.08	0.48	-0.72	0.23	-0.41	0.38	1.03	0.14
d1f1r	18	0.60	0.00	-0.17	0.45	-1.11	0.12	0.77	0.22	-0.27	0.61
d1f56r	19	0.45	0.01	-0.28	0.40	-0.65	0.26	0.18	0.40	0.57	0.32
d1m177r	15	0.19	0.02	-0.39	0.40	-0.74	0.25	-1.07	0.13	-1.00	0.83
d1m17r	22	0.37	0.01	0.88	0.19	1.11	0.13	-0.57	0.31	0.42	0.35
d1m562r	15	0.23	0.01	-0.19	0.44	0.07	0.47	-0.13	0.49	0.00	0.54
d1m56r	18	0.21	0.02	0.60	0.26	0.56	0.28	0.08	0.45	0.26	0.41
e100f177r	7	0.41	0.01	0.12	0.41	0.27	0.36	0.26	0.35	0.26	0.45
e100f1r	12	0.42	0.01	-0.96	0.17	-1.07	0.14	-0.53	0.32	-0.41	0.67
e100f562r	13	0.44	0.01	-0.48	0.31	-0.66	0.26	-0.40	0.37	-0.67	0.73
e100f56r	18	0.30	0.01	-0.39	0.35	0.38	0.34	0.23	0.38	0.55	0.31
e100f5r	13	0.29	0.01	-0.37	0.39	-0.46	0.34	-0.36	0.38	-0.36	0.62
e100m177r	12	0.54	0.00	1.31	0.09	1.52	0.06	-1.30	0.06	1.18	0.10
e100m1r	16	0.57	0.01	-0.32	0.38	-0.49	0.30	-0.18	0.48	0.33	0.41
e100m562r	10	0.54	0.00	0.09	0.45	0.30	0.39	0.49	0.29	0.09	0.49
e100m56r	13	0.57	0.00	0.72	0.23	0.67	0.25	-0.56	0.31	1.03	0.14
e10f177r	12	0.43	0.01	-0.77	0.21	-1.18	0.11	1.10	0.14	-1.13	0.86
e10f56r	12	0.60	0.00	0.17	0.41	-0.33	0.39	-0.86	0.19	-0.64	0.72
e10f5r	7	0.53	0.01	0.19	0.41	0.64	0.26	-0.81	0.19	1.08	0.11
e10m177r	10	0.37	0.01	0.20	0.41	0.39	0.35	-0.58	0.32	1.68	0.02
e10m1r	18	0.59	0.00	-1.09	0.14	-1.38	0.07	0.06	0.46	0.18	0.45
e10m562r	7	0.56	0.00	1.15	0.12	0.97	0.18	-0.02	0.47	1.22	0.10
e10m56r	14	0.56	0.00	-0.67	0.27	-0.90	0.21	-0.20	0.47	-1.10	0.86
e10m5r	5	0.67	0.00	1.25	0.10	1.44	0.07	0.19	0.36	0.95	0.16
e1f56r	11	0.35	0.01	-1.57	0.04	-0.92	0.19	-0.50	0.34	-0.37	0.60
e1f5r	18	0.27	0.01	-0.04	0.50	-0.38	0.39	0.15	0.40	-0.81	0.78
e1m177r	13	0.50	0.01	0.02	0.50	0.24	0.40	-0.64	0.29	0.17	0.47
e1m17r	18	0.24	0.02	-0.71	0.24	-0.64	0.27	-1.24	0.09	-0.47	0.69
e1m1r	19	0.60	0.00	-0.41	0.37	-0.74	0.25	-0.85	0.19	-1.16	0.87
e1m562r	10	0.60	0.00	-0.10	0.47	-0.15	0.46	-0.97	0.17	-1.10	0.84
e1m56r	15	0.47	0.00	-0.91	0.16	-1.00	0.17	-1.03	0.15	-1.13	0.87
f100f177r	26	0.38	0.01	0.64	0.26	0.67	0.26	-0.60	0.30	-0.62	0.74
f100f17r	16	0.21	0.01	0.46	0.31	0.27	0.40	-1.58	0.03	-0.53	0.72
f100f562r	12	0.25	0.02	-0.49	0.33	-0.40	0.34	1.09	0.14	0.16	0.47
f100f56r	10	0.47	0.01	-0.36	0.38	-0.69	0.25	-1.26	0.06	-0.66	0.78
f100m177r	14	0.30	0.01	0.52	0.29	0.44	0.31	-0.42	0.37	-0.78	0.78
f100m1r	16	0.37	0.01	-0.70	0.26	-1.28	0.09	0.31	0.37	-0.56	0.69
f100m562r	19	0.21	0.02	0.00	0.49	0.29	0.37	-0.28	0.42	-0.39	0.67
f100m56r	17	0.40	0.01	0.31	0.37	0.77	0.22	-0.53	0.31	0.22	0.47
f100m5r	15	0.45	0.01	-0.54	0.31	-1.46	0.06	-0.12	0.50	-1.29	0.91
f10f177r	18	0.49	0.00	1.23	0.11	0.40	0.34	0.86	0.20	-0.77	0.77

fl0f56r	22	0.27	0.02	-0.80	0.21	-0.71	0.24	0.35	0.35	-0.58	0.72
fl0f5r	16	0.33	0.01	-0.23	0.44	-0.04	0.50	-0.30	0.40	-1.04	0.85
fl0m177r	16	0.24	0.02	1.07	0.16	0.47	0.30	0.68	0.24	-0.16	0.55
fl0m17r	16	0.45	0.01	1.27	0.11	1.05	0.17	1.68	0.05	-0.03	0.51
fl0m562r	16	0.48	0.00	2.16	0.01	1.99	0.02	0.34	0.32	1.01	0.14
fl0m56r	18	0.32	0.01	0.21	0.41	0.36	0.36	0.38	0.32	-0.34	0.63
fl0m5r	14	0.47	0.00	1.20	0.12	1.20	0.11	-0.19	0.45	0.95	0.17
fl1f17r	18	0.21	0.02	0.02	0.48	-0.28	0.40	0.27	0.37	0.27	0.41
fl1f56r	10	0.26	0.02	0.86	0.20	1.33	0.10	0.53	0.26	0.10	0.45
fl1f5r	10	0.20	0.02	-1.29	0.07	-1.21	0.11	-0.41	0.39	-1.08	0.84
fl1m177r	10	0.42	0.01	0.58	0.28	0.77	0.23	-0.14	0.48	0.51	0.34
fl1m17r	11	0.23	0.02	0.72	0.24	1.30	0.09	-0.86	0.18	0.25	0.42
fl1m562r	17	0.57	0.00	0.09	0.44	-1.19	0.12	-0.45	0.36	-0.84	0.79
fl1m56r	15	0.28	0.02	0.47	0.34	-0.17	0.45	0.37	0.34	-0.17	0.58
lf100f177r	17	0.55	0.00	1.35	0.09	0.92	0.19	-0.82	0.21	1.16	0.10
lf100f17r	16	0.28	0.02	0.23	0.40	0.44	0.32	-0.01	0.44	0.05	0.50
lf100f562r	7	0.23	0.02	-0.35	0.39	0.07	0.44	0.13	0.41	0.30	0.40
lf100f56r	13	0.37	0.01	-0.18	0.44	-0.09	0.49	0.18	0.38	-0.38	0.62
lf100f5r	10	0.35	0.01	0.91	0.18	0.47	0.32	0.05	0.46	0.06	0.49
lf100m177r	17	0.60	0.00	1.21	0.12	1.34	0.09	-0.01	0.48	0.62	0.27
lf100m17r	14	0.45	0.01	0.03	0.47	-0.21	0.43	0.21	0.38	0.03	0.52
lf100m562r	15	0.17	0.01	0.25	0.40	0.27	0.41	-0.08	0.49	-0.52	0.69
lf100m56r	10	0.51	0.01	0.82	0.21	0.19	0.42	1.08	0.14	0.42	0.30
lf10f177r	26	0.29	0.01	0.55	0.30	0.76	0.22	0.69	0.23	0.38	0.35
lf10f56r	19	0.45	0.01	0.90	0.19	0.55	0.30	0.14	0.40	-0.04	0.56
lf10f5r	13	0.35	0.01	0.02	0.48	0.47	0.32	-0.02	0.47	0.07	0.49
lf10m177r	22	0.55	0.01	1.18	0.13	1.02	0.16	-0.74	0.24	-0.28	0.61
lf10m562r	18	-0.11	0.02	-0.01	0.48	-0.32	0.38	0.16	0.40	-0.47	0.70
lf10m56r	15	0.47	0.00	1.54	0.07	1.32	0.09	-0.52	0.32	0.10	0.50
lf10m5r	21	0.56	0.00	0.57	0.28	1.10	0.13	1.29	0.09	0.39	0.38
lf1f17r	9	0.49	0.01	0.78	0.22	1.25	0.11	-1.56	0.03	0.12	0.47
lf1f56r	19	0.17	0.02	0.27	0.38	0.87	0.19	-1.42	0.06	0.25	0.44
lf1m177r	10	0.64	0.01	1.23	0.10	1.07	0.14	-0.19	0.46	-0.04	0.55
lf1m17r	17	0.67	0.00	1.29	0.09	1.27	0.10	0.63	0.24	1.00	0.15
lf1m562r	12	0.45	0.01	0.99	0.16	0.69	0.25	0.52	0.27	0.34	0.39
lf1m56r	22	0.11	0.02	0.32	0.38	0.53	0.30	0.11	0.40	0.14	0.45
og100f177r	12	0.50	0.01	0.68	0.24	0.80	0.21	-0.64	0.28	0.21	0.47
og100f562r	11	0.39	0.01	1.66	0.05	1.09	0.14	0.14	0.43	-0.51	0.70
og100f56r	12	0.35	0.01	1.27	0.10	1.45	0.06	0.51	0.28	0.72	0.24
og100f5r	15	0.68	0.00	2.08	0.02	1.89	0.02	-0.23	0.48	1.23	0.10
og100m177r	13	0.66	0.00	0.81	0.20	0.60	0.28	0.13	0.43	0.99	0.15
og100m562r	14	0.44	0.01	0.49	0.31	0.46	0.32	0.31	0.34	0.74	0.24
og100m56r	15	0.38	0.01	1.01	0.15	0.44	0.32	1.12	0.13	0.36	0.37
og100m5r	10	0.39	0.01	1.81	0.03	1.68	0.04	-0.56	0.33	0.90	0.16
og10f177r	6	0.07	0.02	1.47	0.08	1.38	0.08	-0.97	0.15	0.24	0.42
og10f56r	10	0.51	0.01	1.79	0.04	1.52	0.05	-0.77	0.22	1.49	0.05
og10m177r	10	0.44	0.01	1.40	0.08	1.35	0.08	-0.67	0.27	1.16	0.10
og10m17r	21	0.57	0.00	1.44	0.08	1.41	0.08	0.52	0.29	0.61	0.27
og10m1r	15	0.40	0.01	0.33	0.36	0.38	0.35	-0.89	0.18	0.25	0.41
og10m562r	8	0.46	0.00	1.41	0.08	1.93	0.03	0.62	0.27	2.22	0.02
og10m56r	6	0.40	0.01	1.56	0.07	1.27	0.09	-0.77	0.22	1.64	0.05
og1f56r	6	0.53	0.01	0.35	0.36	0.40	0.34	-1.02	0.11	0.51	0.31
og1m177r	7	0.35	0.01	-0.41	0.38	-0.82	0.22	0.60	0.25	1.23	0.10
og1m1r	13	0.42	0.01	1.11	0.13	1.21	0.11	0.25	0.38	0.51	0.32
og1m562r	10	0.61	0.00	1.33	0.09	0.76	0.22	-0.72	0.24	0.07	0.48
og1m56r	14	0.63	0.00	1.99	0.03	1.51	0.08	-0.64	0.29	1.16	0.11
og1m5r	10	0.67	0.00	1.24	0.09	1.42	0.07	-0.45	0.37	-0.38	0.69

Appendix S2.4. Phylogenetic structure.

A phylogenetic tree was constructed using the plant phylogeny database Phylomatic 4.1 (Webb & Donoghue 2005), on the basis of the Angiosperm Phylogeny Group III (2009) classification (supertree R20120829; Fig. S3, Table S4).

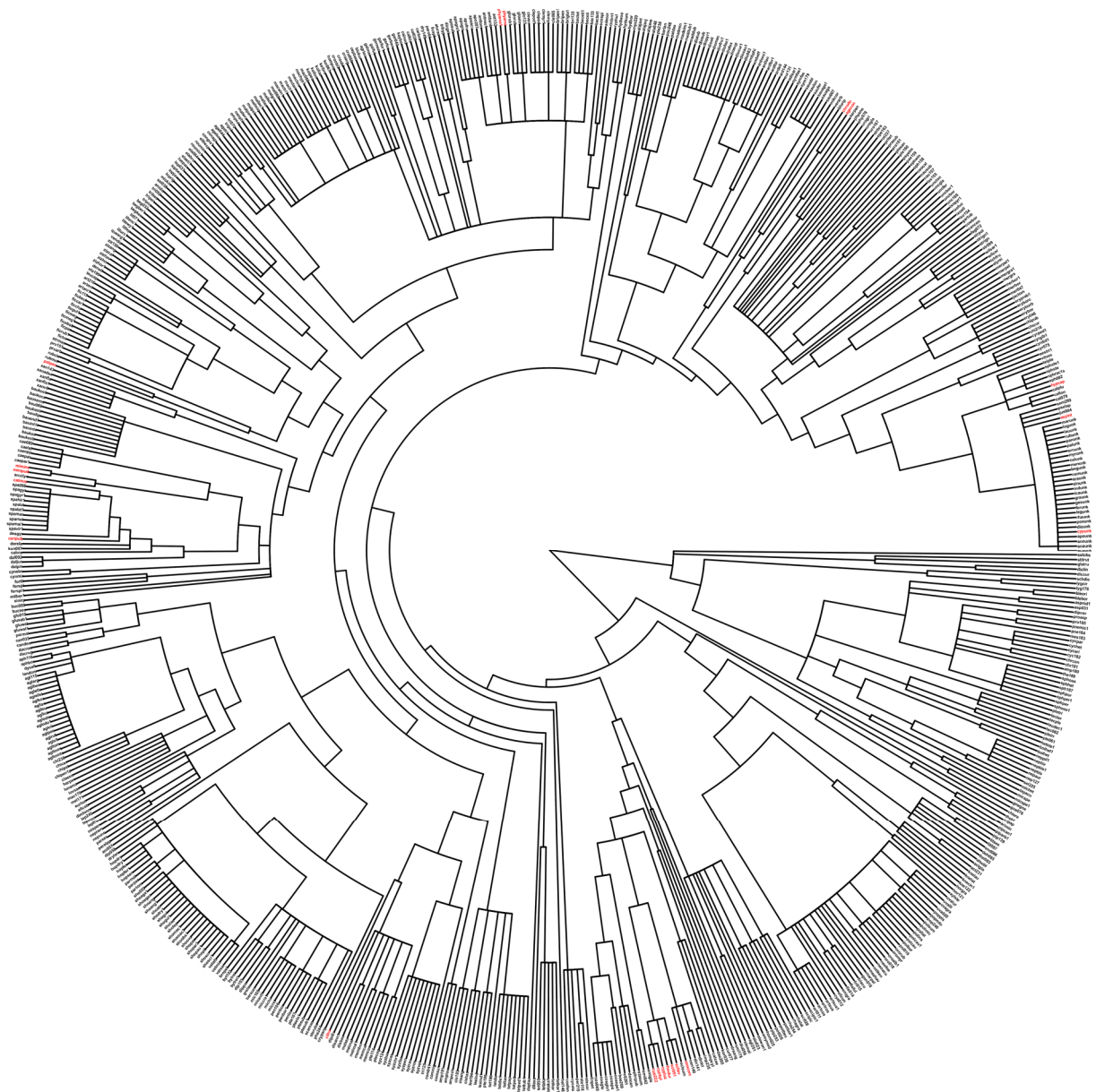


Fig. S3. The phylogenetic relationship of the 679 taxa across the sampling gradient from intact to repeatedly logged forest in Sabah, Malaysian Borneo. Tip labels of exotic plant taxa are indicated in red.

The phylogenetic dispersion of plant communities in each plot was calculated as the net relatedness index (NRI). This diversity measure is equivalent to the SES of the mean pairwise phylogenetic distance (MPD) for all individuals in each community (Webb 2000) and is based on the average branch length between each pair of taxa in a plot. We used a cophenetic distance matrix because our main interest was in the relative variation in ancestral relationships. First, an ‘independent swap’ null model was implemented to determine whether the observed phylogenetic diversity differed from that expected by chance. As such, tip labels were randomly shuffled across the tips of the phylogeny (with 999 repeats) to randomise phylogenetic relationships among species. This method maintains species occurrence frequency as well as relative abundance structure (i.e. in this case biomass-weighted) and only randomises relatedness (Swenson 2014). Measures of relative biomass hold important ecological information and their use is advisable for analyses of community structure and diversity (Swenson 2014).

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Biomass-weighted NRI (Table S3) was then calculated with the following equation:

$$\text{NRI} = -1 \times ((\text{MPD}_{\text{obs}} - \text{MPD}_{\text{exp}}) / \text{sdMPD}_{\text{exp}}),$$

where ‘MPD_{obs}’ is the observed values, ‘MPD_{exp}’ the mean value of the random draw and ‘sdMPD_{exp}’ the standard deviation of the expected mean. A negative NRI indicated that a community was phylogenetically overdispersed, whereas a positive NRI indicated that a community was phylogenetically clustered (Table S3; Webb *et al.* 2002; Kraft & Ackerly 2010). Computation of MPD was conducted using the ‘ape’ (Paradis, Claude & Strimmer 2004) and ‘picante’ (Kembel *et al.* 2010) packages in R.

As a sensitivity test of whether any observed relationship between logging and phylogenetic dispersion was driven solely by a shift from woody to non-woody vegetation, we also quantified NRI values based on independent phylogenies for tree saplings only, for the wider woody plant fraction (that also included woody shrubs and vines), and for the non-woody plant fraction only. We used a cophenetic distance matrix and the ‘independent swap’ null model to quantify NRI following the methods described above (phylogenies not shown here).

To test whether closely related species resembled each other more in trait space than species drawn at random from the phylogenetic tree, we quantified the phylogenetic signal for continuous traits according to Blomberg’s *K* (Blomberg, Garland & Ives 2003) using the ‘picante’ (Kembel *et al.* 2010) and ‘phytools’ packages (Revell 2012) in R. For each trait, we constructed a separate Newick tree including only those species for which a particular trait was available (Table S2). A Blomberg’s *K* value of 0 implied that the distribution of trait values among species was independent of phylogenetic relatedness. We tested for significant deviation from null expectation using 999 randomisations implemented in the function *phylosig* in ‘phytools’ (Revell 2012). We used the *fitDiscrete* function implemented in the R package ‘Geiger’ (Harmon *et al.* 2008) to test for phylogenetic signal in the discrete traits (Pagel 1999). The function uses continuous-time Markov models to fit trait values to different models of evolution. A value of $\lambda = 0$ suggests that a polytomy best represents the trait relationships among species (i.e. a complete lack of phylogenetic structure), whereas a value of $\lambda = 1$ suggests that the actual phylogeny best represents the trait relationships. We used a likelihood ratio test to compare the likelihood of the original model to that of a model where λ was set to zero (no phylogenetic signal).

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Appendix S3. Supplementary methods and results for statistical analyses.

Appendix S3.1. Statistical analyses.

Investigating the drivers of plant community diversity

We tested the effects of historical logging intensity on taxonomic, phylogenetic and functional dispersion using generalised linear mixed effects models (GLMMs) in the ‘lme4’ (Bates *et al.* 2015) package in R version 3.1.0 (R Core Team 2013). Fixed predictor variables in the GLMMs were ‘local-scale forest canopy loss’, ‘landscape-scale forest canopy loss’, ‘regional-scale density of secondary roads’ and ‘distance to nearest primary road’, and their interaction effects (Table S5). Of the original predictor variables, we excluded ‘density of primary roads’ and ‘distance to the nearest secondary road’ due to strong collinearity with logging variables ($r > 0.65$), and ‘shortest distance to river’ due to moderate collinearity ($r > 0.4$) with elevation (Figure S4). Collinearity amongst predictors can present a problem in best fit model selection and therefore the recommendation is to reduce the complexity of the model in these situations (Freckleton 2010).

The distribution of some predictor variables was moderately skewed (Fig. S4), so we also conducted a PCA on all predictor variables to ensure that there were no outlier plots that might have undue leverage on the models (Fig. S5). In the PCA, predictor variables were first standardised to a mean of zero and a standard deviation of one to account for the different unit scales of measure. The selection of retained principal component axes was based on visual interpretation of a scree plot and Kaiser’s criterion (Kaiser 1960). Cumulatively, the first two axes accounted for approximately 62% of the total variation in predictor variables. No substantial outlier points were detected in the reduced ordination space (Fig. S5), therefore data from all 180 vegetation plots were retained in the GLMM analyses.

In the GLMM, we first specified a full model for each response variable, testing the four predictor variables, and their potential interaction effects (i.e. one 4-way, four 3-way, six 2-way). Plot elevation, soil PC1 and soil PC2 were used as covariate effects across all models (Table S5). Random intercepts were specified for ‘block’ (total eight blocks) and ‘sub-block’ nested within block (three sub-areas per block for a total of 24). The fixed covariate terms were not included in any interaction effects. For species richness, we specified a Poisson distribution (log-link function) and tested the full model for overdispersion of model residuals. For functional and phylogenetic diversity metrics, we specified a Gaussian distribution (identity

link function), and tested the residuals of the full models for normality and homogeneity of variances. All response variables met model assumptions.

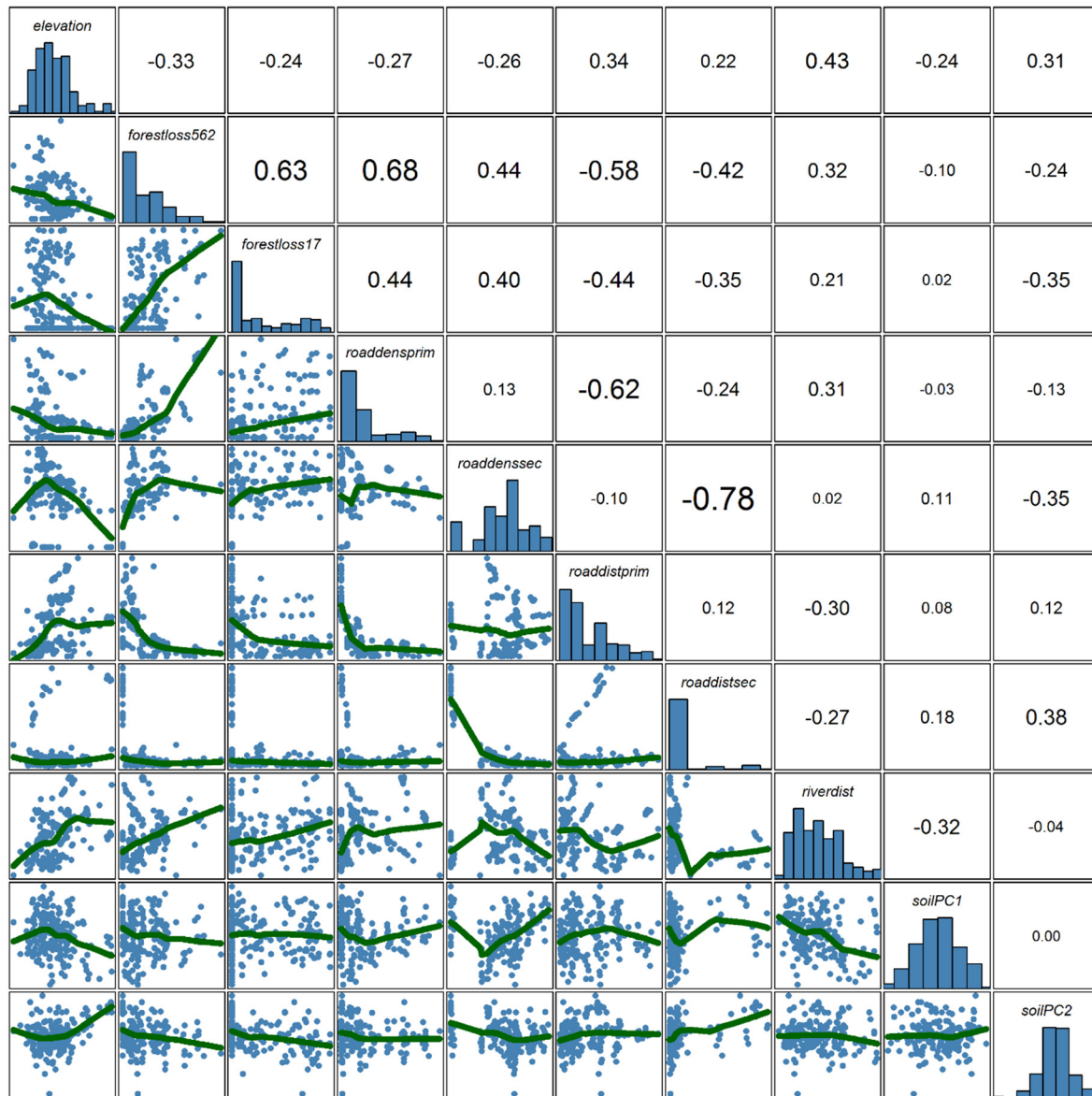


Fig. S4. A correlation matrix assessing collinearity among predictor variables and covariates: elevation (m), landscape-scale forest canopy loss (forestloss562; %), local-scale forest canopy loss (forestloss17; %), density of primary roads (roaddensprim; km km⁻²), density of secondary roads (roaddenssec; km km⁻²), distance to nearest primary road (roaddistprim; m), distance to nearest secondary road (roaddistsec; m), distance to river (riverdist; m), soil PC1 scores (soilPC1) and soil PC2 scores (soilPC2). Green lines illustrate average trends. The diagonal shows histograms of each variable. Correlation coefficients (Pearson) shown in the upper right.

GLMM model simplification

Model simplification was performed using a multi-model inference approach (Burnham & Anderson 2002) and model averaging procedures based on the Akaike information criterion

(AIC) in the ‘MuMIn’ package (Bartón 2015) in R 3.1.0 (R Core Team 2013). This model selection method compares and ranks multiple competing models (including model selection uncertainty) and orders predictor variables according to their influence on dependent variables (Burnham, Anderson & Huyvaert 2011).

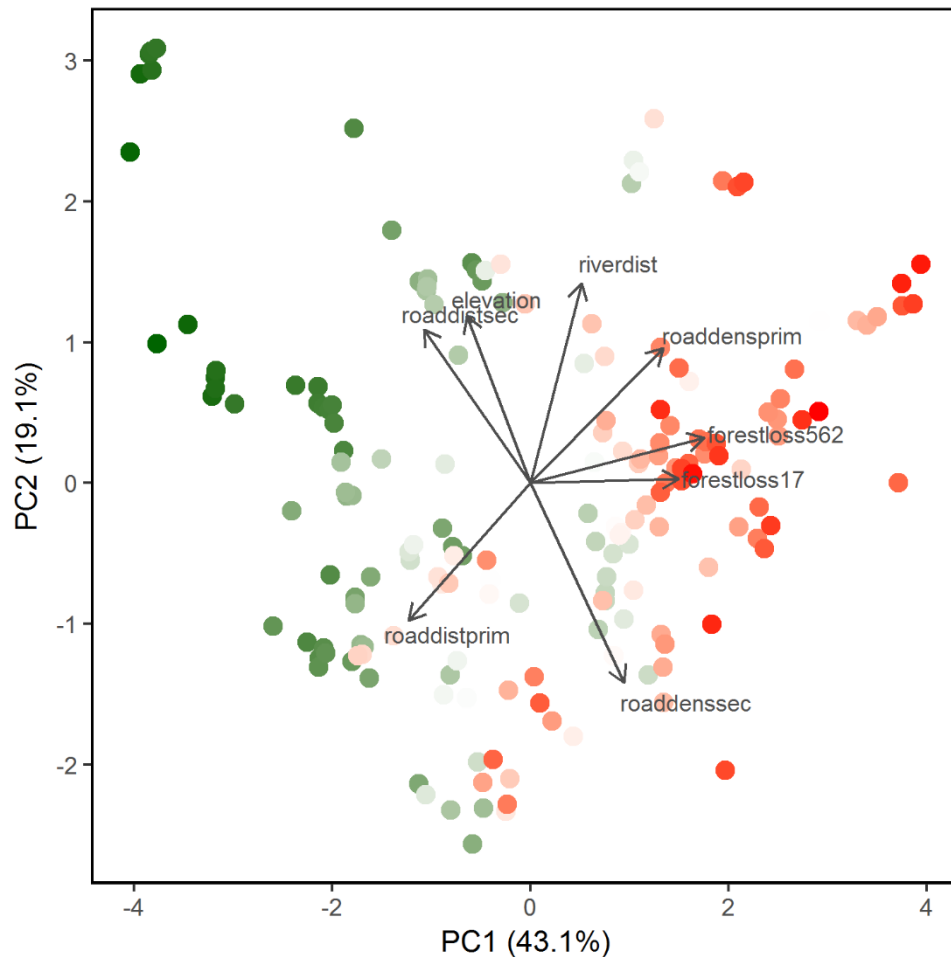


Fig. S5. Distribution of the 180 study plots (symbols) in two-dimensional ordination space based on a principal component analysis (PCA) of variation in logging predictors and key environmental covariates (red arrows; standardised to a mean of zero and a standard deviation of one). For illustrative purposes, plot symbols are colour-coded on a gradient from low (green) to high (red) local forest loss due to logging.

We centred and standardised all predictor variables by two standard deviations (SD) to a mean of 0 and a SD of 0.5. This standardisation of continuous predictor variables to a common scale is required for interpreting the direction and magnitude of parameter estimates (effect sizes) during model selection (Gelman 2008). We applied the *dredge* function to generate a full set of submodels (including the null model; Bartón 2015), and used maximum likelihood estimation and AIC_c to determine the top models within 2 AIC_c units of the best-fit model with

the function *get.models*. The AIC_c is a frequently used form of the AIC that corrects for small sample size or a large number of predictors (Hurvich & Tsai 1989), while 2 AIC units is a commonly used cut-off criterion (Burnham & Anderson 2002). AIC_c thus gives lower weight to those models that have less influence on the variance of a response (Grueber *et al.* 2011).

In a final step, we used model averaging and restricted maximum likelihood (REML) estimation based on the function *model.avg* to calculate the final model coefficients from the candidate sets of top models (Grueber *et al.* 2011). We used the so-called zero method (or shrinkage method) which adds a zero to those models where a parameter is absent prior to top model averaging, thus reducing the influence of predictors with weak effects (Lukacs, Burnham & Anderson 2010). The model output also provided adjusted standard errors that we used to calculate unconditional confidence intervals for the model-averaged effect size of each predictor variable. In addition, relative importance values were calculated that indicate the probability of a variable being present in the best-performing model based on Akaike weights (Burnham & Anderson 2002).

Following model averaging, we tested for potential confounding spatial autocorrelation of the residuals of the single best fit model for each of the original response variables (i.e. species richness, FDis, NRI, FRic, FDisR and FDisE) using plot northings and eastings. We plotted a spline correlogram using the *spline.correlog* function in the ‘ncf’ package (Bjørnstad & Falck 2001). None of the GLMMs showed spatial autocorrelation in the residuals (i.e. confidence intervals overlapped zero at any given spatial scale).

For the final model-averaged solution, in each case, model fit was calculated as the marginal R^2_{GLMM} (variance explained by fixed effects only) and conditional R^2_{GLMM} (variance explained by both fixed and random effects; Nakagawa & Schielzeth 2013). This approach quantifies how the inclusion of the fixed effects in a model changed variance components at different levels of the mixed-effect model by calculating the percent change in variance (PCV) based on a comparison of the final model vs. a null (intercept-only) model that contained the same random effects (Nakagawa & Schielzeth 2013).

Finally, for any significant relationships with logging we tested whether there was evidence for a nonlinear ‘threshold’ effect of logging on understorey plant communities using a segmented mixed models approach (Muggeo *et al.* 2014). We applied the *segmented.lme* function (Muggeo 2016) to quantify slope-differences and changepoint estimates along the logging intensity gradient. Input to the *segmented.lme* function required a mixed model object returned by the function *lme* in the ‘nlme’ package (Pinheiro *et al.* 2015).

Table S5. List of four predictor variables (local-scale forest canopy loss, landscape-scale forest canopy loss, secondary road density and primary road distance) and three covariates (elevation, soil PC1 and soil PC2) with values averaged across sub-blocks (SE provided in brackets)

Block	Sub-block	Plot	Elevation	Local-scale loss	Landscape-scale loss	Density sec. road	Distance prim. road	Soil PC1	Soil PC2
A	1	7	520.4 (10.8)	41.1 (14.4)	16.7 (1.0)	2.5 (0.04)	487.0 (77.34)	0.86 (0.43)	−0.56 (0.45)
	10	7	457.1 (28.0)	3.6 (1.8)	6.4 (0.8)	2.9 (0.07)	1453.3 (39.96)	0.49 (0.32)	−0.41 (0.18)
	100	9	332.8 (15.4)	6.9 (2.9)	25.2 (1.5)	3.6 (0.03)	501.8 (12.82)	1.10 (0.27)	0.17 (0.28)
B	1	6	420.7 (19.7)	36.0 (15.4)	5.6 (0.5)	3.5 (0.12)	2508.6 (57.11)	1.07 (0.27)	−0.64 (0.35)
	10	7	342.1 (9.7)	19.0 (8.2)	9.7 (1.1)	3.9 (0.16)	1759.7 (14.36)	1.19 (0.09)	−0.27 (0.24)
	100	9	481.4 (8.1)	21.1 (6.7)	6.6 (0.2)	2.8 (0.04)	2474.0 (82.24)	1.20 (0.34)	0.15 (0.33)
C	1	7	323.1 (13.0)	59.1 (10.4)	24.7 (1.1)	4.2 (0.03)	811.2 (39.37)	1.47 (0.40)	0.20 (0.37)
	10	7	341.4 (14.0)	59.2 (11.6)	31.8 (0.5)	3.5 (0.02)	577.1 (15.51)	0.01 (0.21)	−0.45 (0.29)
	100	9	352.4 (17.7)	67.7 (9.5)	58.4 (2.0)	2.6 (0.06)	290.0 (54.44)	0.17 (0.33)	−0.43 (0.28)
D	1	6	517.3 (21.4)	42.1 (10.8)	25.4 (2.1)	2.3 (0.09)	282.4 (33.26)	−0.11 (0.67)	0.39 (0.33)
	10	7	409.1 (15.5)	73.4 (4.0)	31.8 (0.5)	2.9 (0.04)	231.9 (51.22)	−0.52 (0.33)	−0.76 (0.51)
	100	8	315.9 (5.4)	67.7 (8.5)	44.6 (1.8)	2.6 (0.05)	136.6 (21.99)	−1.40 (0.15)	−0.68 (0.39)
E	1	7	442.0 (5.7)	69.0 (11.3)	26.9 (0.7)	3.0 (0.03)	691.9 (32.70)	−0.84 (0.40)	−0.28 (0.18)
	10	8	359.9 (16.5)	29.5 (11.7)	10.9 (0.2)	2.9 (0.02)	1802.7 (35.54)	−0.95 (0.75)	−1.51 (0.60)
	100	9	298.8 (23.6)	48.8 (6.7)	16.6 (2.9)	1.9 (0.09)	77.6 (65.10)	−0.07 (0.34)	0.64 (0.34)
F	1	7	428.3 (26.6)	17.5 (12.4)	5.3 (1.7)	1.4 (0.01)	445.8 (69.80)	−1.92 (0.45)	−0.61 (0.12)
	10	8	616.1 (25.5)	0.0	8.4 (1.3)	1.7 (0.02)	1230.6 (76.79)	−2.21 (0.22)	1.36 (0.36)
	100	9	283.1 (11.4)	23.6 (6.0)	22.7 (0.6)	2.2 (0.04)	115.7 (56.12)	−0.87 (0.23)	−0.16 (0.23)
LF	1	6	494.7 (11.43)	0.0 (0.0)	10.5 (2.53)	1.8 (0.00)	3832.9 (66.50)	−0.90(0.39)	0.24 (0.10)
	10	7	428.4 (8.75)	3.6 (3.59)	7.2 (0.36)	2.1 (0.00)	2570.9 (87.83)	−0.21 (0.31)	0.67 (0.16)
	100	9	422.4 (9.23)	6.5 (4.31)	2.0 (0.22)	1.9 (0.01)	3309.7 (79.43)	−0.24 (0.20)	0.07 (0.08)
OG	1	6	718.8 (18.9)	0.0	0.0	0.0 (0.05)	1697.4 (83.97)	−0.62 (0.18)	1.98 (0.26)
	10	7	372.6 (12.4)	0.0	0.0	0.0 (0.05)	1775.7 (12.78)	2.05 (0.33)	1.04 (0.51)
	100	8	284.0 (2.5)	0.0	0.0	0.1 (0.05)	703.0 (144.25)	1.27 (0.25)	0.14 (0.35)

Local-scale loss = the amount of forest canopy cover loss at local scale (*i.e.* 17.78 m radius); Landscape-scale loss = the amount of forest canopy cover loss at landscape scale (*i.e.* 562.34 m radius); Density secondary roads = the density of secondary roads at landscape scale (*i.e.* 1778.23 m radius); Distance primary roads = the distance of primary roads at landscape scale (*i.e.* 1778.23 m radius); Soil PC1 = the first principal component axis based on soil variables; and Soil PC2 = the second principal component axis based on soil variables.

Appendix S3.2. Supplementary results.

Across the 180 plots we identified 691 plant taxa (species or morphospecies), 400 of which were identified to species level, from 289 known genera and 101 families. Only a low proportion (15%) of the total specimens recorded could not be identified below the family level, predominantly within the Zingiberaceae (27% of specimens unidentified), graminoids (15%) and in cases of tiny seedlings (*i.e.* <5 cm in height) or where specimens had insufficiently distinct features for identification (25%). Twenty exotic plant taxa in total were recorded across the 180 plots (Table S6).

Table S6. List of exotic plant taxa sampled across 180 vegetation plots

Family	Species	Growth form	No. plots
Acanthaceae	<i>Asystasia intrusa</i>	Herbaceous climber	1
Compositae	<i>Ageratum conyzoides</i>	Forb	5
	<i>Chromolaena odorata</i>	Herbaceous climber	27
Cyperaceae	<i>Cyperus kyllingia</i>	Graminoid	1
	<i>Cyperus luzulae</i>	Graminoid	1
	<i>Cyperus</i> sp.	Graminoid	2
	<i>Fimbristylis dura</i>	Graminoid	4
	<i>Scleria levis</i>	Graminoid	2
	<i>Scleria</i> sp.	Graminoid	1
	Indeterminate	Graminoid	1
Lamiaceae	<i>Hyptis capitata</i>	Forb	13
Leguminosae	<i>Calopogonium mucunoides</i>	Herbaceous climber	6
	<i>Centrosema pubescens</i>	Herbaceous climber	1
	<i>Mimosa invisa</i>	Herbaceous climber	1
	<i>Mimosa pudica</i>	Herbaceous climber	3
Melastomataceae	<i>Clidemia hirta</i>	Herbaceous shrub	94
Phyllanthaceae	<i>Phyllanthus amarus</i>	Forb	4
	<i>Phyllanthus</i> cf. <i>amarus</i>	Forb	1
Poaceae	<i>Axonopus compressus</i>	Graminoid	3
Polygalaceae	<i>Polygala paniculata</i>	Forb	2

No. plots = The total number of plots in which a taxa was recorded.

GLMM-predicted effects of local-scale forest canopy loss due to logging on functional richness (FRic), functional dispersion for response traits only (FDisR), and functional dispersion for effect traits only (FDisE), are presented in Fig. S6a-c and Table S7, respectively.

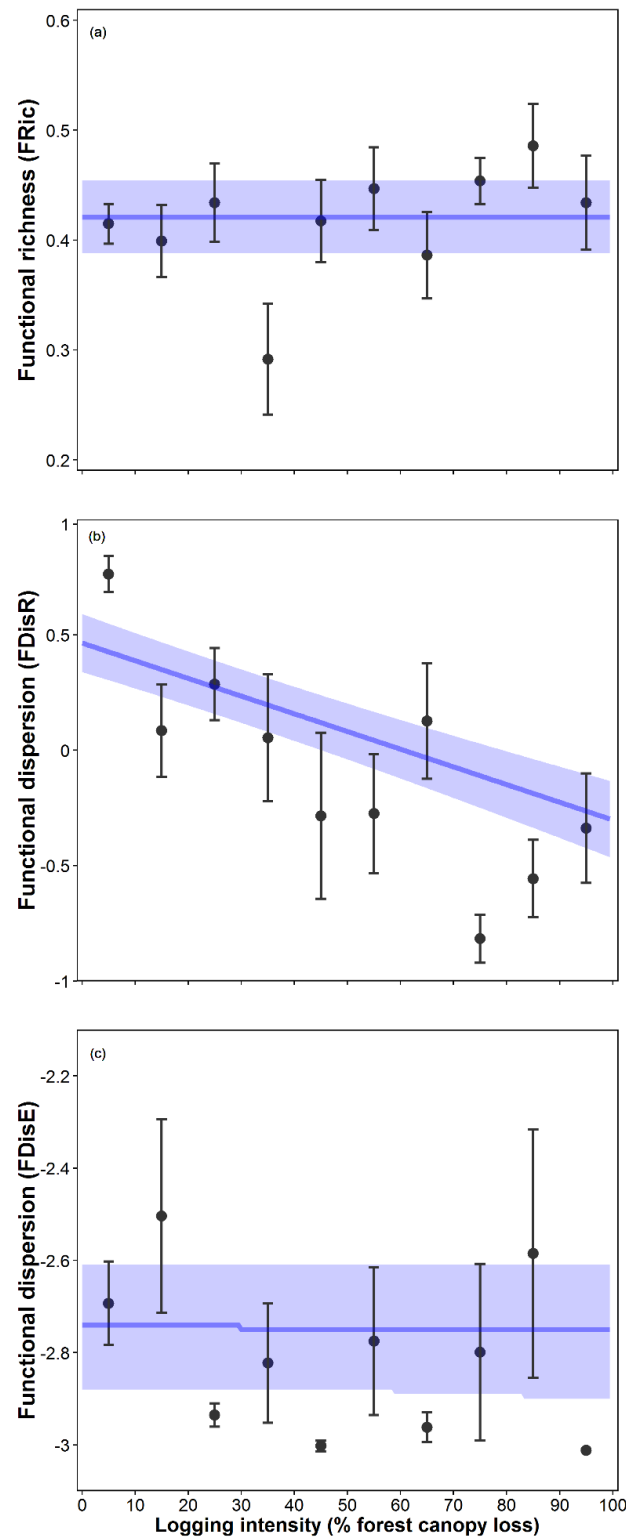


Fig. S6. GLMM model-predicted relationships between percent local forest canopy loss and functional richness (FRic; ± 1 S.E.), functional dispersion of response traits (FDisR; ± 1 S.E.), and functional dispersion of effect traits (FDisE; ± 1 S.E.). The mean fitted relationships were generated using the *predict* function from the GLMM analyses, with blue shaded areas indicating the confidence intervals around estimates. Symbols represent the raw means (± 1 SE). Logging intensity represents forest canopy loss from 1970 to 2010 at the local scale (i.e. 17.78 m radius buffers).

Table S7. Results of mixed-effect modelling of the effects of local- and landscape-scale logging intensity on functional richness (FRic), functional dispersion in response traits (FDisR) and functional dispersion in effect traits (FDisE).

Response variable:	FRic	FDis (response)		FDis (effect)
	Null model	Null model	Full model	Null model
Fixed effects	$b (\pm 1 \text{ SE})$	$b (\pm 1 \text{ SE})$	$b (\pm 1 \text{ SE})$	$b (\pm 1 \text{ SE})$
Intercept	0.421 (0.016)	0.247 (0.158)	0.243 (0.072)	-2.746 (0.069)
Local-scale forest canopy loss	–	–	-0.532 (0.060)	–
VC for random effects	VC	VC	VC	VC
Block	0.034	0.410	0.140	0.070
Sub-block	0.011	0.150	–	0.191
VC for fixed effects	–	–	–	–
PCV _(Block)	–	–	65.85%	–
PCV _(Sub-block)	–	–	100.00%	–
$R^2_{GLMM(m)}$	–	–	36.45%	–
$R^2_{GLMM(c)}$	–	–	38.95%	–
AIC	-171.96	449.10	397.11	402.92

AIC = Akaike information criterion; PCV = percent change in variance between the null and full models; VC = variance components. Model parameters were calculated using restricted maximum likelihood (REML) estimation, and a weighted model averaging approach. Marginal R^2 (variance explained by just the fixed effects) and conditional R^2 (variance explained by both fixed and random effects) were calculated for the top models after Nakagawa & Schielzeth (2013). To account for model selection uncertainty we report unconditional SE. Bolded coefficients are significantly different from zero ($p < 0.05$).

Table S8. Output parameters of the function *segmented.lme* for phylogenetic dispersion (NRI), based on standardised and centered predictor variables. U = slope difference; G0 = changepoint estimate. The confidence interval for the slope difference overlaps zero, so there is no evidence to support a segmented model for these data

NRI:				
CI	(Intercept)	Forestloss17	U	G0
2.5%	-0.4599	0.6572	-2.4292	-0.1114
97.5%	0.2615	-0.0126	0.2200	2.2829
Fixed	-0.0992	-0.3349	-1.1047	1.0854
Block StdDev	0.2592	0.0008	0.0043	0.0022
Fragment/Block StdDev	0.0019	0.0002	0.0004	0.0003

CI = Confidence interval; Forestloss17 = local-scale forest canopy loss.

Table S9. Output parameters of the function *segmented.lme* for functional dispersion (FDis) based on standardised and centered predictor variables. U = slope difference; G0 = changepoint estimate. The confidence interval for the slope difference does not overlap zero, so there is strong evidence to support a segmented model for these data

FDis:				
CI	(Intercept)	Forestloss17	U	G0
2.5%	−0.3371	−1.3090	0.3171	−0.0403
97.5%	0.4475	−0.2975	1.6723	1.1171
Fixed	0.0552	−0.8033	0.9947	0.5384
Block StdDev	0.1728	0.0006	0.2471	0.0077
Fragment/Block StdDev	0.0000	0.0000	0.0000	0.0000

CI = Confidence interval; Forestloss17 = local-scale forest canopy loss.

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