



Supplementary Materials for

Functional traits—not nativeness—shape the effects of large mammalian herbivores on plant communities

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1 **Materials and Methods**

2 **Literature screening and digitization**

3 This meta-analysis was part of a larger effort to understand megafauna impacts on multiple facets
4 of ecosystems [e.g. including soil nutrients, invertebrates, etc, see (43)]. This ensured that the
5 dataset included plant responses that were also measured in studies focused on other response
6 variables (e.g., spider diversity). We searched Web of Science with a string of search terms that
7 included the common names and Latin genera of all terrestrial mammalian megafauna species
8 [common names from HerbiTraits v1.2 (54)] separated with an ‘OR’ operand, along with the
9 following search terms: “disturb*, graz*, brows*, impact*, effect, affect, disrupt, facilitate,
10 invasi*, ecosystem*, vegetat*, plant*, fauna*, reptil*, amphib*, bird*, rodent*, fish*, invertebrat*,
11 insect*, soil*, carbon, climate, albedo, river*, riparian, desert*, forest*, tundra, decomposition,
12 grassland*, savanna*, chaparral, scrub, shrub, diversity, heterogeneity, extinction, richness,
13 environment, reptile*, ecolog*, hydrolog*, disturbance, density, biodiversity, response*,
14 ecosystem, herbaceous, canopy, germination, cover, pollinator*, tree, nutrient*, understorey,
15 erosion, grass*, vegetation, community, exclosure, competition, effect*, abundance, productivity”.
16 To reduce unrelated results we also included a Web of Science category filter (“WC”) of
17 “ECOLOGY OR ZOOLOGY OR ENVIRONMENTAL SCIENCES OR BIODIVERSITY
18 CONSERVATION OR EVOLUTIONARY BIOLOGY OR GEOGRAPHY PHYSICAL OR
19 REMOTE SENSING OR PLANT SCIENCES OR MULTIDISCIPLINARY SCIENCE OR
20 FORESTRY OR ENTOMOLOGY OR MARINE & FRESHWATER BIOLOGY OR
21 MYCOLOGY OR BIOLOGY OR OCEANOGRAPHY OR ORNITHOLOGY OR
22 BEHAVIORAL SCIENCES OR FISHERIES”.

23 The Web of Science review was concluded on the 18th of February 2021 and returned
24 60,537 studies. We removed duplicate studies using the fuzzy matching algorithm with the
25 function ‘find_duplicates’ in the R package ‘revtools’ (version 0.4.1) (55). After removing
26 duplicates, our final search returned 46,825 studies. Title screening reduced the number of studies
27 to 2,369.

28 We screened the full text of these studies to only include studies focused on wild
29 megafauna (≥ 45 kg) and that compared areas with low versus high megafauna densities due to
30 exclosures, policy-driven differences (hunting versus no-hunting in adjacent properties), and
31 differences in introduction or eradication histories (adjacent islands with and without megafauna).
32 Some studies compared areas with and without focal megafauna populations for unknown reasons
33 [e.g., a site with and without horses with no indication of why horses might be absent (56)], which
34 were excluded due to low confidence in the ultimate drivers of observed differences. We excluded
35 all before-after comparisons (e.g., a plot measured prior to exclosure construction and then
36 afterwards) because of the high rates of change in many systems through time (via afforestation,
37 shifts in climate, succession, etc.). Studies that excluded megafauna but also all vertebrates were
38 excluded. Two additional studies reported data from extremely limiting resources (i.e., wetlands
39 in deserts). These were excluded given that such scenarios should be analyzed separately, for
40 which we did not have sufficient sample size. Studies that evaluated the effects of megafauna on
41 transplants or agricultural crops (including plantations) were not digitized. Studies that included
42 an appropriate comparison and reported a central tendency (mean or median), a measurement of
43 error (standard deviation, standard error, variance, etc), and sample size were digitized (n=154).

44 This literature list was supplemented by the literature contained in other relevant meta-
45 analyses (47, 57) and those encountered in the bibliographies of the studies we digitized. Given

1 the limited number of studies from oceanic islands and regarding widely distributed introduced
2 species (feral pigs, goats) in our initial Web of Science search, we conducted focused Google
3 Scholar searches on July 15th, 2022 with the following terms: “ungulate impacts island*”,
4 “introduced goat impact island*”, “introduced deer impact*”, “feral camel impact*”, “wild OR
5 feral boar OR hog OR swine impact*”, “feral cattle impact*”, “invasive ungulate hawaii OR guam
6 OR new zealand OR pacific island OR new caledonia OR galapagos OR caribbean OR oceanic
7 island” and a Web of Science search on the 22nd of December 2022 using the search string
8 “herbivore* AND plant* AND response*”. This uncovered an additional 482 studies of which 66
9 studies were fit for inclusion, leading to a total of 221 studies in our final dataset [see Fig. S11 for
10 PRISMA diagram, (58)].

11 We digitized central tendencies (mean, median), error (standard deviation, standard error,
12 interquartile ranges) and sample sizes for each response (diversity, richness, and abundance) in
13 each study [final studies: (8, 50, 52, 53, 59–264)]. We used ImageJ to extract data from figures
14 (265). Interquartile ranges and medians (e.g., as extracted from boxplots) were converted to means
15 and standard deviation using the function `qe.mean.sd` in the package ‘`estmeansd`’ version 1.0.0
16 (266). Means and SD/SE were reported by 213 studies (3,846 observations) while 11 studies (149
17 observations) reported medians and interquartile ranges.

18 We also digitized relevant covariates from the text, which included time since treatment
19 (e.g., exclosure construction, introduction, eradication, etc), study coordinates (latitude,
20 longitude), megafauna density (standardized to kg per hectare), relative abundance of megafauna
21 (in the case of multispecies megafauna communities and if density was not provided), and the scale
22 of measurement (treated both as area, m², and maximum measurement length, m, to allow the
23 comparison of transects to plots).

24 If study coordinates were not exactly provided, we extracted latitude and longitude from
25 the approximate center of each study location in Google Maps. Maximum measurement length
26 was calculated as either the hypotenuse of square/rectangular plots, the length of transects, or the
27 diameter of circular plots. Distributions of megafauna traits, environmental variables (see below),
28 and methodological variables were similar between native and introduced megafauna communities
29 in our final dataset [Fig. S12-S13, (25)].

30 We treated measurements of species richness and species diversity (e.g., Shannon Weiner
31 index) as ‘diversity’ responses and density estimates (individual plants per plot), % cover, and
32 biomass as measurements of abundance. Analyzing these responses alone led to similar results.
33 We excluded seed abundance and diversity responses, given that seedbanks can be at
34 disequilibrium from realized plant communities. We included all true plant species, excluding
35 multicellular algae and lichen.
36

37 **Effect sizes**

38 Given the presence of negative values and zeros in our dataset, we calculated effect sizes using
39 Hedges’ *g*, a unitless measure of standardized mean difference between groups. Each effect size
40 was associated with sampling variance calculated from the sample size and standard deviation of
41 each observation. Effect sizes and sampling variances were calculated with the function ‘`escale`’
42 in the R package ‘`metafor`’ (version 3.5-12) (267).
43

1 **Model specification**

2 Random-effect meta-analytic models were constructed with the function ‘rma.mv’ (‘metafor’
3 version 3.9-14) (267). These models weight each observation (e.g. effect size) by the inverse of
4 their sampling variance. Studies with larger sample sizes and/or lower variance thus have higher
5 weight in models.

6 Several models involved interactions between multiple categorical variables (i.e.,
7 megafauna nativeness, plant nativeness, landform coevolutionary history, etc). Given the
8 challenges of interpreting three and four-way interaction terms between categorical variables, and
9 in conducting contrast tests, we elected to concatenate combinations of factors into distinct levels
10 of a single variable. For example, the three-level variable for landform evolutionary history with
11 megafauna (continent, offshore island, and oceanic island) was produced from the concatenation
12 of megafauna evolutionary history (present or absent) and landform (continent or island).
13 Concatenating variables produced identical predictions as models with interaction terms between
14 each categorical variable but was more tractable to interpretation and reporting. We removed
15 intercepts from all models containing categorical predictors [following (47)]. Planned contrast
16 tests were conducted with the R function ‘glht’ (‘multcomp’, version 1.4-20) (268) with function
17 default p-value adjustments (single-step adjustment).

18 We included a random effect term for study citation, with the individual plant
19 species/group as a nested effect to capture multiple measurements of these groups within a study
20 (e.g., at different plots). Since the data included time series, we included an ordered time series
21 variable for each individual experiment (e.g., a specific plant species/group, response, and
22 sampling block) as a random effect. Likelihood ratio tests and BIC indicated that the inclusion of
23 this time series variable significantly improved model quality across all models (LR=[22.7,
24 1,043.1]; $p < 0.0001$, $\Delta \text{BIC} = [-12.5, -1,027.1]$). We did not include individual response IDs as
25 an inner random effect [e.g., following (267)] because doing so produced σ^2 values of 0.

26 Similar to the inclusion of multiple results from the same experiment over time, which we
27 controlled for by the time series random effect, eight studies (94 responses) reported data at
28 different measurement scales from the same experiment (3.6% of all studies, 2.35% of all
29 responses). We therefore ran all models with only the largest measurement scale, or the final time
30 point from each experiment, which produced similar results as our main analyses (Fig. S14).

31 Given that data came from single-species as well as mixed-species megafauna
32 communities, we could not control for megafauna species identity as a random effect in our
33 models. We instead captured this by explicitly analyzing megafauna functional traits (see below)
34 and by controlling for study site location as a random effect, which would capture a significant
35 deal of shared species identities between studies. Study site location IDs were assigned for all sites
36 within 100 km of each other. Because some studies occurred in multiple study locations, we treated
37 this as a crossed random effect instead of nesting citation ID within it. Models were estimated with
38 maximum likelihood given our interest in model comparison. See R scripts for exact model
39 specifications (25).

40 Some studies reported plant responses at the species level, some at broad functional levels
41 (e.g., grasses, trees, etc), and some for all plants combined. For abundance analyses, we conducted
42 analyses with all data (Fig. 1, Fig. 2) and conducted additional sensitivity analyses including only
43 species-level data (Fig. S15). We also analyzed the effect of native versus introduced megafauna
44 on total native plant abundance responses, for which we had sufficient data, which confirmed our
45 primary results (introduced $g = -0.66$ [-0.98, -0.34], native $g = -0.62$ [-0.99, -0.34], contrast: $z = 0.20$,
46 $p\text{-value} = 0.84$, likelihood ratio test compared to intercept-only model: LR=0.04, $p\text{-value} = 0.85$).

1 For diversity analyses, which by definition consist of collective plant responses, we analyzed
2 whether there were significant differences between native and introduced megafauna for the 367
3 plant responses (49 studies) that were described for total plant diversity, and not a subset, which
4 supported our primary results (introduced $g=-0.14$ [-0.47, 0.18], native $g=0.22$ [-0.06, 0.49],
5 contrast: $z=1.9$, $p\text{-value}=0.06$, likelihood ratio test: $LR=3.14$, $p\text{-value}=0.08$). Furthermore,
6 explicitly modeling megafauna impacts on plant diversity by plant functional group (Fig. S6) while
7 controlling for megafauna dietary preferences (see below), which thus excluded total plant
8 responses, also confirmed no difference between native and introduced megafauna (contrast: $z=-$
9 0.39 , $p\text{-value}=0.70$).

10 Meta-analyses can be prone to misleading results due to small sample size publication bias,
11 wherein low power studies (high sampling variance due to low sample size or high error) are not
12 published due to non-significant results, especially if those results conflict with prevailing notions
13 (269). This can be assessed with funnel plots, which plot the sampling variance by effect size. An
14 asymmetrical distribution of high sampling variance data around the overall estimated effect is an
15 indication of small sample publication bias. We plotted funnel plots for our primary analyses,
16 which suggested some degree of publication bias towards negative effects for introduced
17 megafauna (Fig. S16-17). However, given that there is no clear way to correct for this type of
18 publication bias in multilevel random-effect meta-analytic models (267), we elected to report
19 results as-is. Other types of publication bias, e.g., from authors not publishing high sample size,
20 low-variance results that contradict their beliefs, cannot be accounted for.

22 **Megafauna and plant nativeness**

23 Megafauna nativeness was based on study author designations or IUCN range maps (17), if
24 unreported. While many communities had both native and introduced megafauna present, most
25 studies only manipulated (excluded) the introduced megafauna, which was possible because of
26 body size differences or through eradication. Only one study manipulated both native and
27 introduced megafauna (158). Given that the majority of megafauna biomass in this study consisted
28 of introduced megafauna, we classified this study as introduced. Excluding it (only relevant for
29 abundance analyses) led to similar results (Fig. S18, $z=[-0.84, 1.65]$, $p=[0.44, 1.0]$).

30 The evolutionary exposure of study sites to megafauna (i.e., oceanic islands versus
31 continents and offshore islands) was determined using PHYLACINE v1.2 range maps (33). We
32 considered New Zealand, which possessed avian megafauna, an oceanic island without
33 coevolutionary history with mammalian megafauna (due to distinctive foraging strategies of avian
34 versus mammalian herbivores). However, counting New Zealand as an offshore island led to
35 similar results.

36 The nativeness of collective plant responses was assigned as reported by the authors (1,864
37 observations from 104 studies). In cases where plant nativeness was unspecified (2,136
38 observations from 155 studies) we evaluated nativeness based on author-provided flora
39 descriptions of the study site by referring to the Plants of the World Online (32) and the study site
40 location. If introduced plants were described in the study system, we described the study as mixed
41 (and thus excluded it) unless the introduced plants collectively constituted $<5\%$ relative abundance
42 (cover, biomass, density), as reported by authors, in which case we counted these systems as
43 'native'. From this we were able to classify an additional 1,718 observations from 113 studies as
44 native (1,499 observations, 97 studies), mixed (218 observations, 15 studies), and introduced (1
45 observation, 1 study). A final portion of studies did not provide site flora descriptions (418

1 observations, 42 studies). These studies generally came from large, well-protected landscapes
2 (e.g., Kruger National Park, Arctic tundra). We treated these ‘unspecified’ responses as native.

3 The nativeness of individual plant species, relevant only to plant abundance responses, was
4 extracted from the Plants of the World Online (32), as above. Plant taxonomy was standardized
5 with the Taxonomic Name Resolution Service (TNRS) (270). To test the influence of plant
6 nativeness designations, we report on plant diversity effects excluding unspecified results (Fig.
7 S19) and for each plant nativeness designation (i.e., native, unspecified, mixed, and introduced,
8 Fig. S20). For plant abundance, we report species-level plant abundance results (Fig. S15). Across
9 all these sensitivity analyses, there was no significant difference between native and introduced
10 megafauna (see Table S2)

12 **Coevolutionary history and coevolutionary novelty**

13 The coevolutionary history between megafauna and the biomes to which they have been
14 introduced was determined using biome maps from Olson et al. 2001 (271). Introduced megafauna
15 were considered ‘coevolved’ with the biome if they would have occurred in the absence of human-
16 caused extinctions and range contractions (e.g., *Equus ferus caballus* in North America), based on
17 PHYLACINE v1.2’s (33) megafauna distributions in the absence of extinctions and range
18 contractions, or if the megafauna species was native elsewhere within the focal biome, as in the
19 case of megafauna introduced to offshore islands within their native continent. Species-level
20 coevolutionary history between megafauna and individual plant species was determined by
21 comparing plant distributions (32) to PHYLACINE range maps (33). In cases of multiple
22 introduced megafauna, we based this on the dominant megafauna species, with dominance
23 determined by relative biomass.

24 Functional and phylogenetic novelty were calculated by identifying coevolved megafauna
25 communities, in the absence of Late Pleistocene extinctions and range contractions, for each study
26 location from PHYLACINE v1.2 range maps (33). Functional novelty was calculated as the Gower
27 distance to the most functionally similar ‘coevolved’ megafauna. Gower distances were calculated
28 using the function ‘gowdis’ (R package ‘FD’, version 1.0-12.1) (272) from key megafauna
29 functional traits that determine their effect on the environment [provided by HerbiTraits (54)].
30 These included body mass (log₁₀ scale), two ordinal dietary traits (graminoid consumption, browse
31 consumption), fermentation type (converted to an ordinal variable describing fermentation
32 efficiency), three non-exclusive binary habitat use variables (aquatic, terrestrial, arboreal), three
33 exclusive binary variables describing limb morphology (plantigrade, digitigrade, unguligrade).
34 Variable weightings followed (5). To visualize megafauna functional space (Fig. S21), we
35 conducted a principal coordinates analysis on the Gower distance matrix using the R function
36 ‘cmdscale’ (R package ‘stats’ v4.2.1) with a maximum of 4 dimensions (k=4). Phylogenetic
37 novelty was defined as the cophenetic distance between the introduced megafauna and the most
38 closely related megafauna in the absence of human-caused extinctions and range contractions
39 using the function ‘pd’ [R package ‘ape’ version 5.6-2, (273), with the phylogeny provided by
40 PHYLACINE v1.2 (33)].

41 For both phylogenetic and functional novelty, we identified the distances between the
42 introduced megafauna and the most similar prehistoric ‘coevolved’ megafauna. This value was
43 relativized by the introduced species’ relative biomass in their community and then averaged
44 across all introduced megafauna (Eq. 1). Relative biomass estimates were calculated from relative
45 abundance or absolute density estimates per species, which were reported for 78.4% of data points.

$$\text{Mean community weighted novelty} = \frac{\sum NN \text{ distance} * \text{rel.biomass}}{N \text{ megafauna species}}$$

Equation 1. Calculation of community weighted functional and phylogenetic novelty per introduced megafauna community. Functional and phylogenetic novelty was calculated from Gower distance and cophenetic distance, respectively, to the most similar coevolved species. NN distance = Nearest neighbor distance; rel. biomass = relative biomass in megafauna community (0-1).

Environmental covariates

Environmental covariates were extracted for each study location by buffering each study location by 5 km and using the function ‘extract’ from the R package ‘terra’ (version 1.7-6) (274). Values were averaged across the 5 km buffer. Specifically, we extracted values of net primary productivity (275), maximum annual temperature and precipitation (276), and the human footprint index (277). The human footprint index was available for both 1993 and 2009. We thus used values closest to the year the data was collected or, if unreported, the year the study was published (n=78 studies). For studies reporting data over multiple years, the year was adjusted for the time when the individual response was collected based on commencement of study and collection interval.

Megafauna community functional traits

To understand how megafauna functional traits influence their effects on plants, we evaluated key megafauna functional traits for all species in our dataset. Given that 80 studies (1,433 observations) manipulated multiple species of megafauna, we analyzed megafauna functional trait summaries at a community level. We did this by multiplying species trait values by their relative biomass in their community (0-1) and then calculating the maximum and mean of these traits (henceforth ‘community-weighted’). Mean trait values reflect overall community tendencies, while the possibility that ecological outcomes may be shaped more by extremes (while accounting for relative biomass) is captured by maximum trait values.

Traits were extracted from HerbiTraits (54) and included body mass, proportion of megafauna biomass with hindgut fermentation [which has distinct effects on ecosystems relative to foregut fermentation, (278)], and dietary preference for graminoids (grasses and allies). Note that while our meta-analysis focused on megafauna ≥ 45 kg, some studies excluded smaller herbivores as well. These herbivores were included in trait summaries if ≥ 10 kg in mass, for which trait data was available.

Browse and graminoid (grass and allies) consumption are the two primary axes of dietary differentiation in herbivores. Browse and graminoid consumption were available from HerbiTraits as two non-exclusive variables ranging from 0 (avoided) to 3 (highly preferred). To synthesize these variables into a single measure, we relativized each species’ graminoid consumption value by multiplying it by their relative biomass (0-1) within their community. We then divided this value by the sum of relativized browse and graminoid consumption (Eq. 2). This variable was used in conjunction with the plant growth form of each response, categorized as forb, woody, or

1 graminoid. Species-level plant growth forms were derived from the World Checklist of Vascular
2 Plants and from the ‘growthform’ package (279).

$$CW \text{ species level graminoid preference} = \frac{Gr * rel.biomass}{(Gr * rel.biomass) + (Br * rel.biomass)}$$
$$Mean CW \text{ community level graminoid preference} = \frac{\sum CW \text{ species level gram. pref.}}{N \text{ megafauna species}}$$

7 **Equation 2.** Calculation of community weighted (CW) graminoid preference to synthesize
8 graminoid (‘Gr’) and browse consumption (‘Br.’) values into a single value across a community
9 (see Fig. S6), while accounting for relative biomass (‘rel. biomass’) per species. Relative biomass
10 ranged from 0-1 and graminoid and browse consumption were 0-3 ordinal variables respectively.

11
12 Muzzle widths were extracted from (280, 281). Species-level muzzle widths were absent
13 for 42 species of 114 herbivore species in our dataset (36.8%). We used genus-level averages for
14 the 25 of these species for which genus-level data was available. A remaining 17 species without
15 genus-level estimates were minor members (median 13% relative biomass) of speciose herbivore
16 communities in 40 observations (4 studies). For these observations, we excluded these particular
17 species, calculating muzzle width summaries with the other species present only. Elephants
18 (*Loxodonta africana* and *Elephas maximus*), on the other hand, were important components (by
19 biomass) of 154 data points (10 studies). Muzzle width is a poor proxy for dietary selectivity in
20 elephants since these animals use their trunk to forage and can both be selective and consume large
21 quantities of biomass. We thus assigned elephants the same muzzle width as black rhinos (*Diceros*
22 *bicornis*) because of their similar body mass and diet. All muzzle width analyses were conducted
23 with and without data containing elephants, producing similar results (without elephants,
24 maximum muzzle width slope=0.27 [0.10, 0.45], p=0.002, Table S1). The final dataset included
25 community weighted muzzle width estimates for all but 56 abundance responses (1.7%) and 13
26 diversity responses (1.7%), which were excluded from analysis.

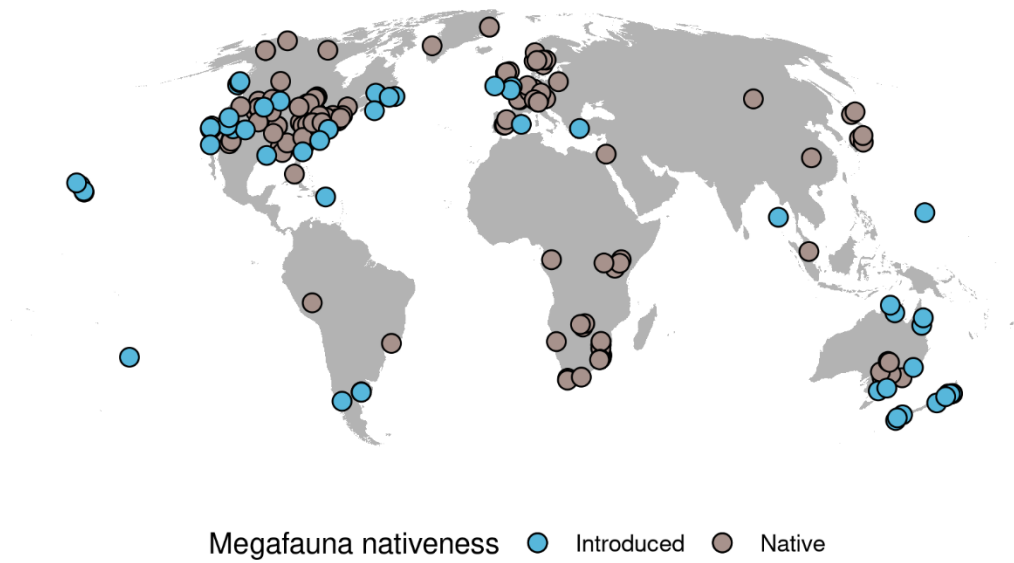
27 Finally, we assigned each megafauna into functional groups to evaluate whether functional
28 group richness shaped megafauna impacts. Functional groups were based on combinations of body
29 mass bins (10-45 kg, 45-100 kg, 100-1,000 kg, ≥1,000 kg), dietary guilds (browser, mixed feeder,
30 grazer), and fermentation type (foregut, hindgut, and simple gut).

32 **Influence of functional traits and environmental and methodological variables**

33 We formulated 24 hypotheses regarding environmental and functional variables that could explain
34 megafauna impacts on plant diversity and abundance. These variables included community-
35 weighted megafauna functional traits (body mass, muzzle width, the interaction of plant growth
36 form with graminoid consumption, proportion of megafauna that were hindgut fermenters,
37 megafauna biomass per hectare), environmental variables (maximum annual temperature and
38 precipitation, net primary productivity, absolute latitude, the human footprint index, and landform
39 type), as well as methodological variables (treatment duration, scale of measurement). Some
40 variables were treated with interaction terms (e.g., treatment duration with net primary
41 productivity, Table S2). All continuous variables were scaled prior to analysis. See Table S2 for a
42 full list of model formulas and model comparisons.

1 While we suspected that predator presence/protection status would influence megafauna
2 impacts, we lacked confidence in reconstructing predator communities from IUCN distribution
3 data (282) given the broad temporal range of studies and because of significant heterogeneity (e.g.,
4 landscape of fear) within the range of a predator-prey pair [e.g., (44)].

5 For each variable we constructed three models: an intercept-only null model, a model
6 containing the factor(s) of interest, and a model containing the factor of interest(s) as well as
7 megafauna nativeness (Table S2). We used likelihood ratio tests to compare the factors of interest
8 to the null model, and to test if adding megafauna nativeness improved model quality. We also
9 tested for significant differences between native and introduced megafauna within each of these
10 final candidate models with planned contrast tests with the function ‘glht’ in the package
11 ‘multcomp’ (version 1.4-20). Each model and model comparison, and corresponding sample size
12 of the dataset, is presented in Table S2.



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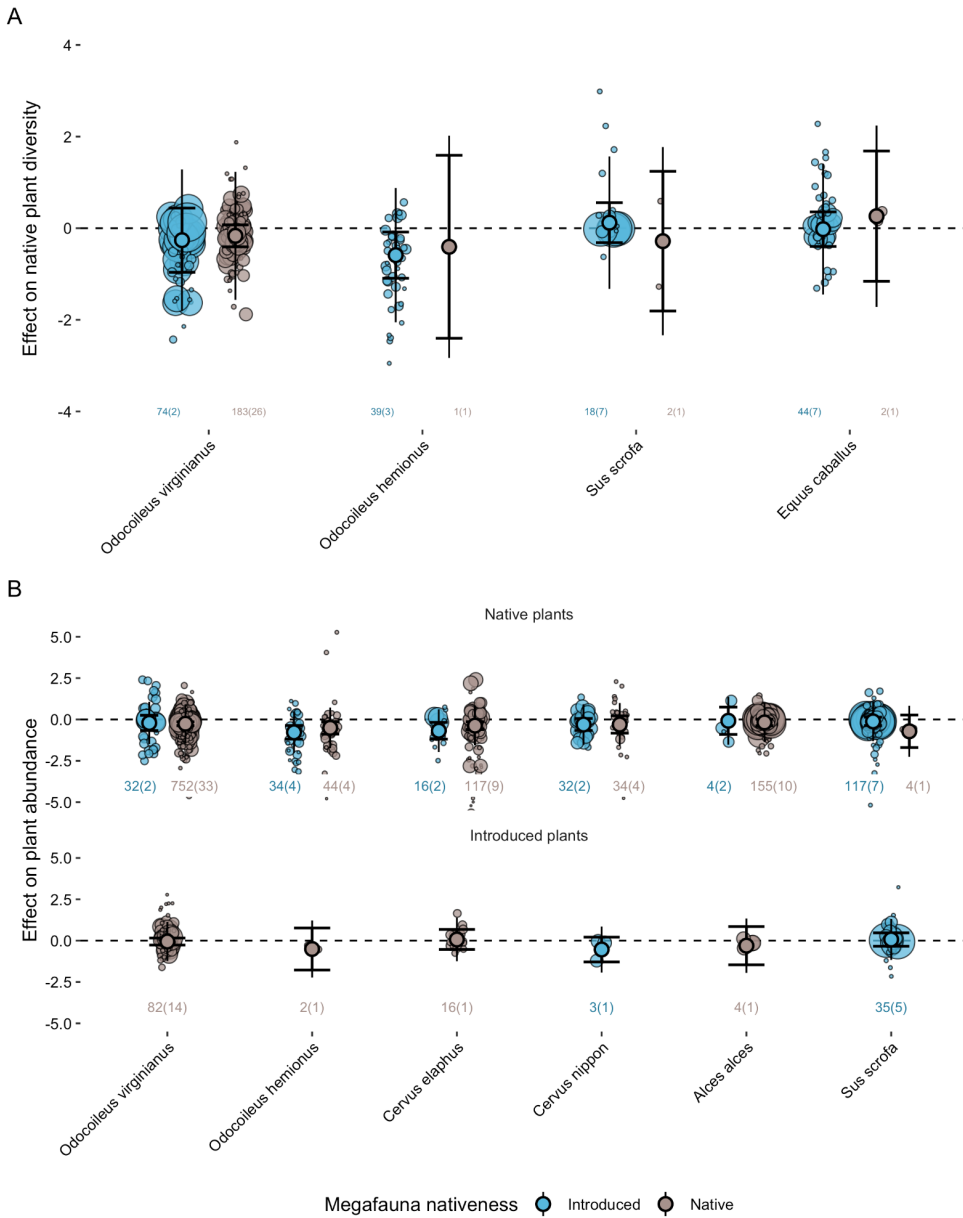
2 **Fig. S1.**

3 Map of study locations showing bias towards North America, Europe, and Australia. The meta-
4 analysis data consisted of 170 distinct study locations (considered distinct if >100 km apart).

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3 **Fig. S2.**

4 Nativeness does not shape the effects of megafauna on plant diversity (A) or abundance (B) when
5 controlling for species identity, for those species with studies in their native and introduced ranges.
6 Nativeness did not improve model quality (LR=[0.5, 3.49], p-values=0.75–0.97) and there was no
7 significant difference between native and introduced megafauna (contrast: $z=[-1.89, 0.62]$, p-
8 values=0.30–0.94, Table S2).

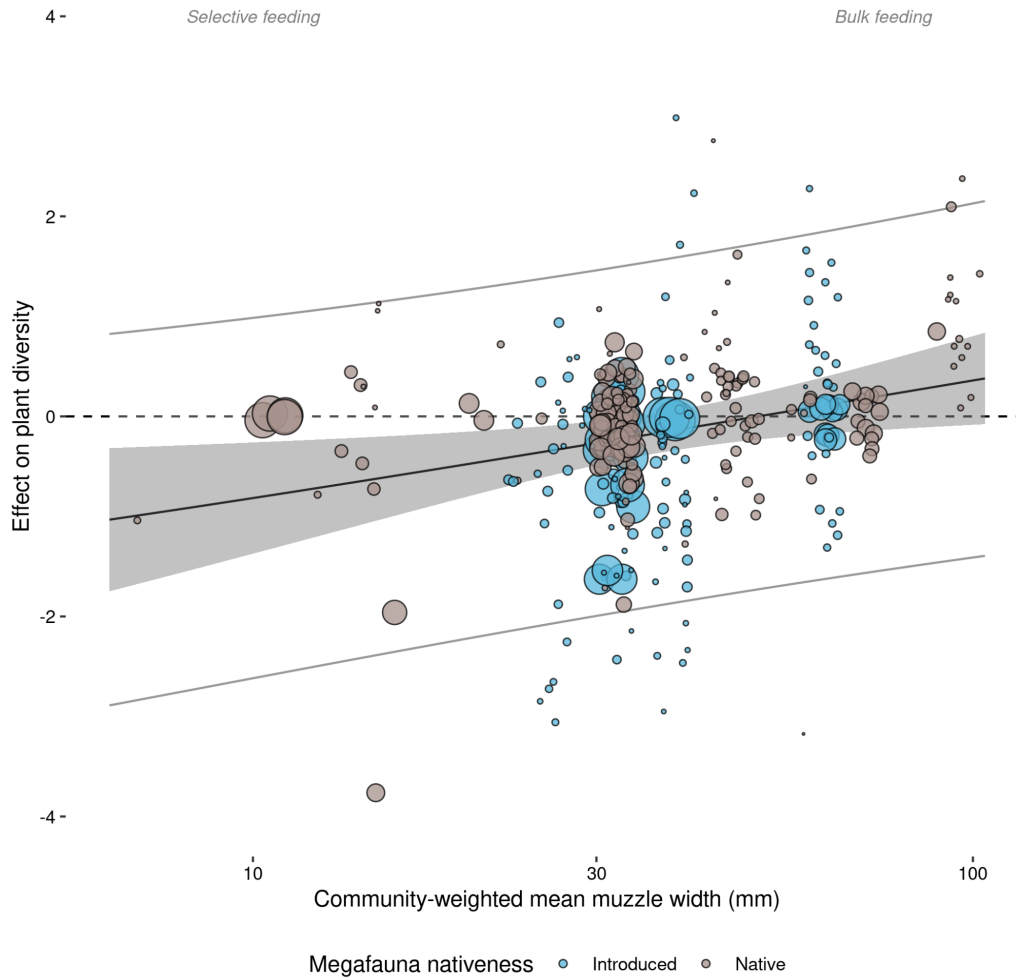
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5 **Fig. S3.**

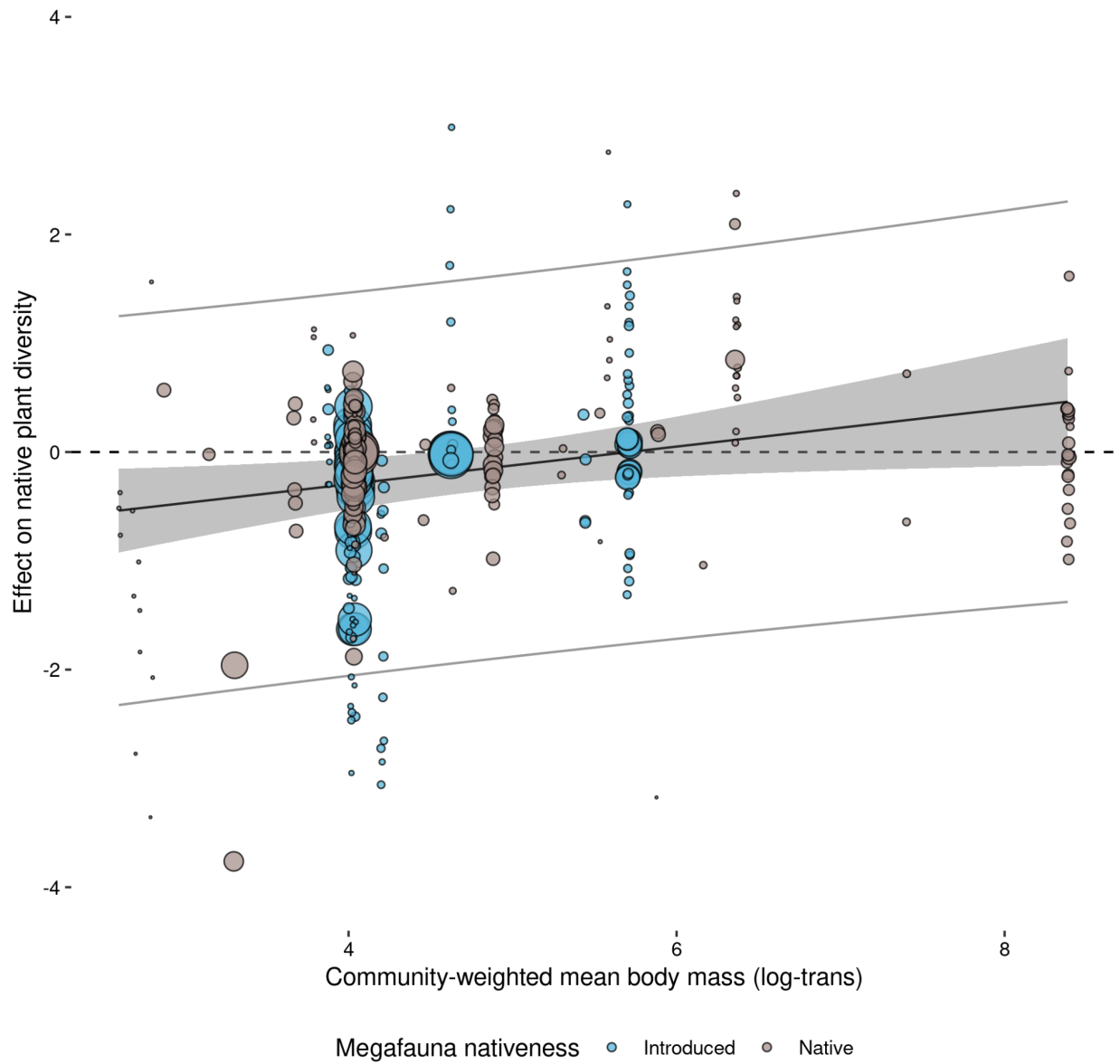
6 Community-weighted mean muzzle width shaped megafauna effects on plant diversity ($g=0.20$,
7 $CI_s=[0.05, 0.36]$, $p\text{-value}=0.01$, Table S1) and improved model quality relative to an intercept-
8 only null model ($LR=5.8$, $p\text{-value}=0.02$, Table S2).

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3 **Fig. S4.**

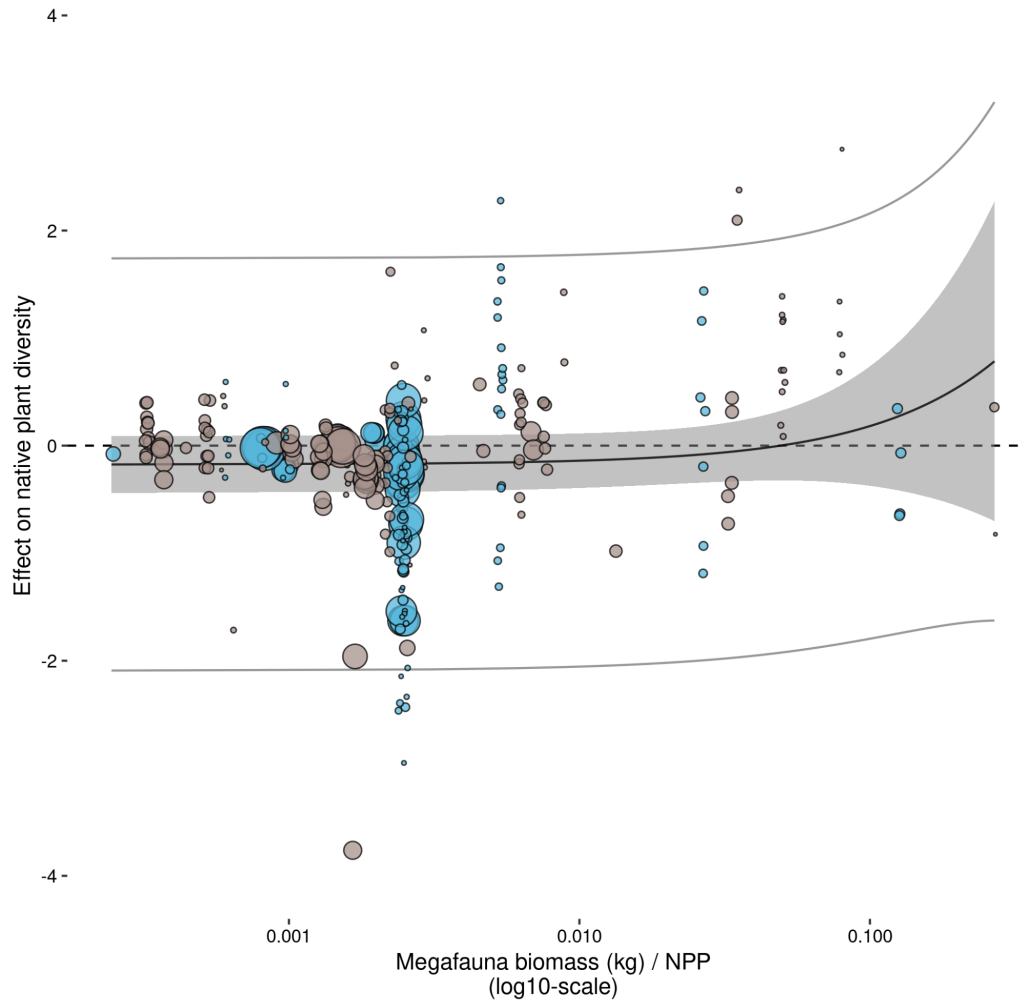
4 Community-weighted mean megafauna body mass also had a positive relationship with impacts
5 on plant diversity (slope=0.20, CIs=[0.03, 0.38], p-value=0.02, Table S1) and improved model
6 quality relative to an intercept-only null model (LR=4.6, p-value=0.03, Table S2).

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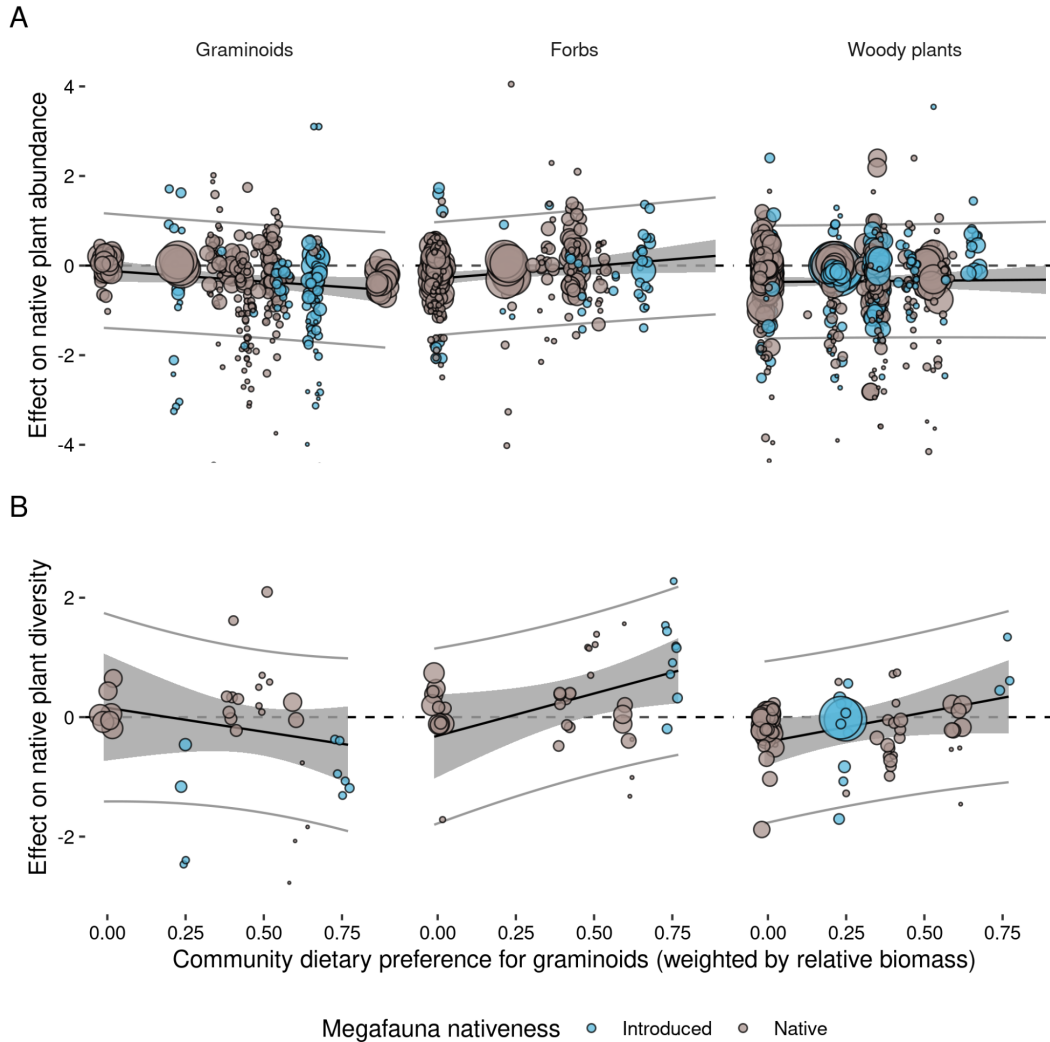
3 **Fig. S5.**

4 Megafauna biomass (kg), relativized by net primary productivity, did not influence megafauna
5 effects on native plant diversity (slope=0.10, CIs=[-0.06, 0.26], p-value=0.21, Table S1) and did
6 not improve model quality relative to an intercept-only null model (LR=1.3, p-value=0.26, Table
7 S2).

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4 **Fig. S6.**

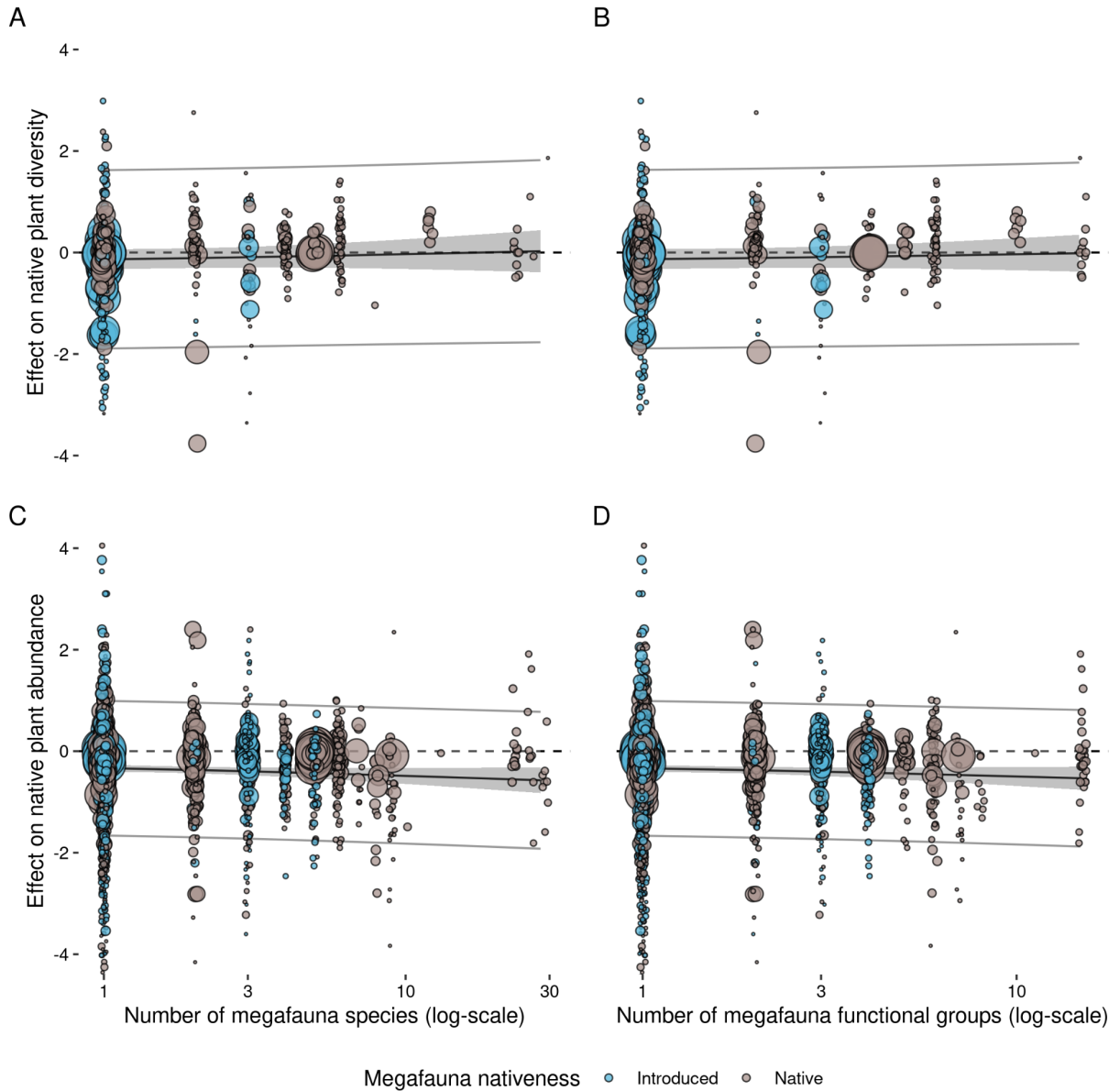
5 Megafauna dietary preference for graminoids interacts with plant growth forms to shape
6 megafauna impacts on (A) plant diversity (interaction p-values=0.02–0.03) and (B) abundance (p-
7 values=0.02–0.001). See Table S1 for all coefficient estimates. Dietary preference was weighted
8 by relative biomass of each species (see Eq. 2). This model significantly improved model quality
9 relative to intercept-only model (diversity: LR=15.1, p-value=0.01, abundance: LR=16.3, p-
10 value=0.006, Table S2).

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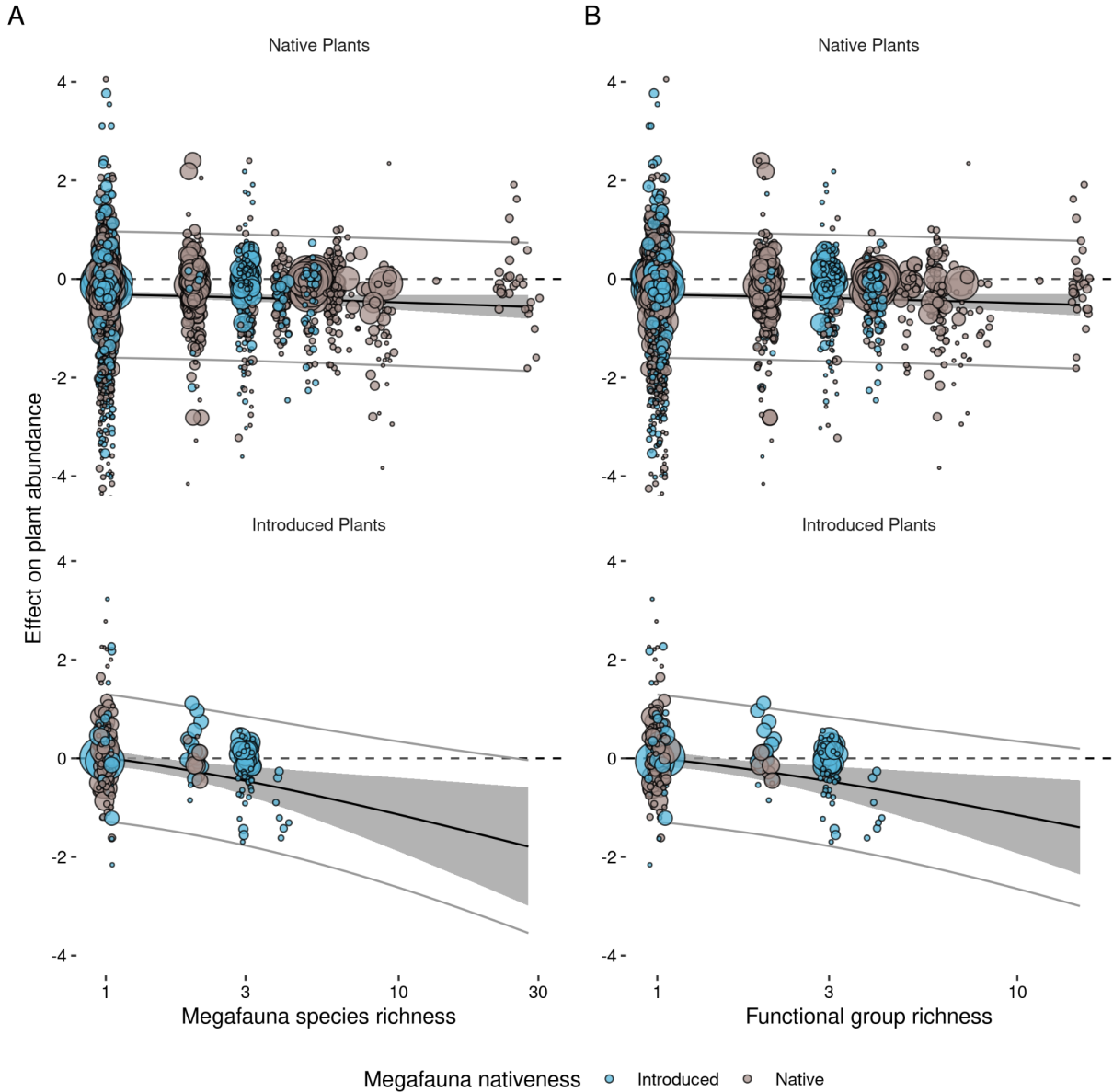
3

4 **Fig. S7**

5 There was no evidence that megafauna community species (A, C) and functional group (B, D)
6 richness shaped impacts on native plant diversity (A, B) or plant abundance (C, D) (p -values=0.08–
7 0.50, Table S1). Likewise, these measures of megafauna diversity did not improve model quality
8 relative to an intercept-only null model (LR=[0.46, 3.0], p -values=0.08–0.50, Table S2)

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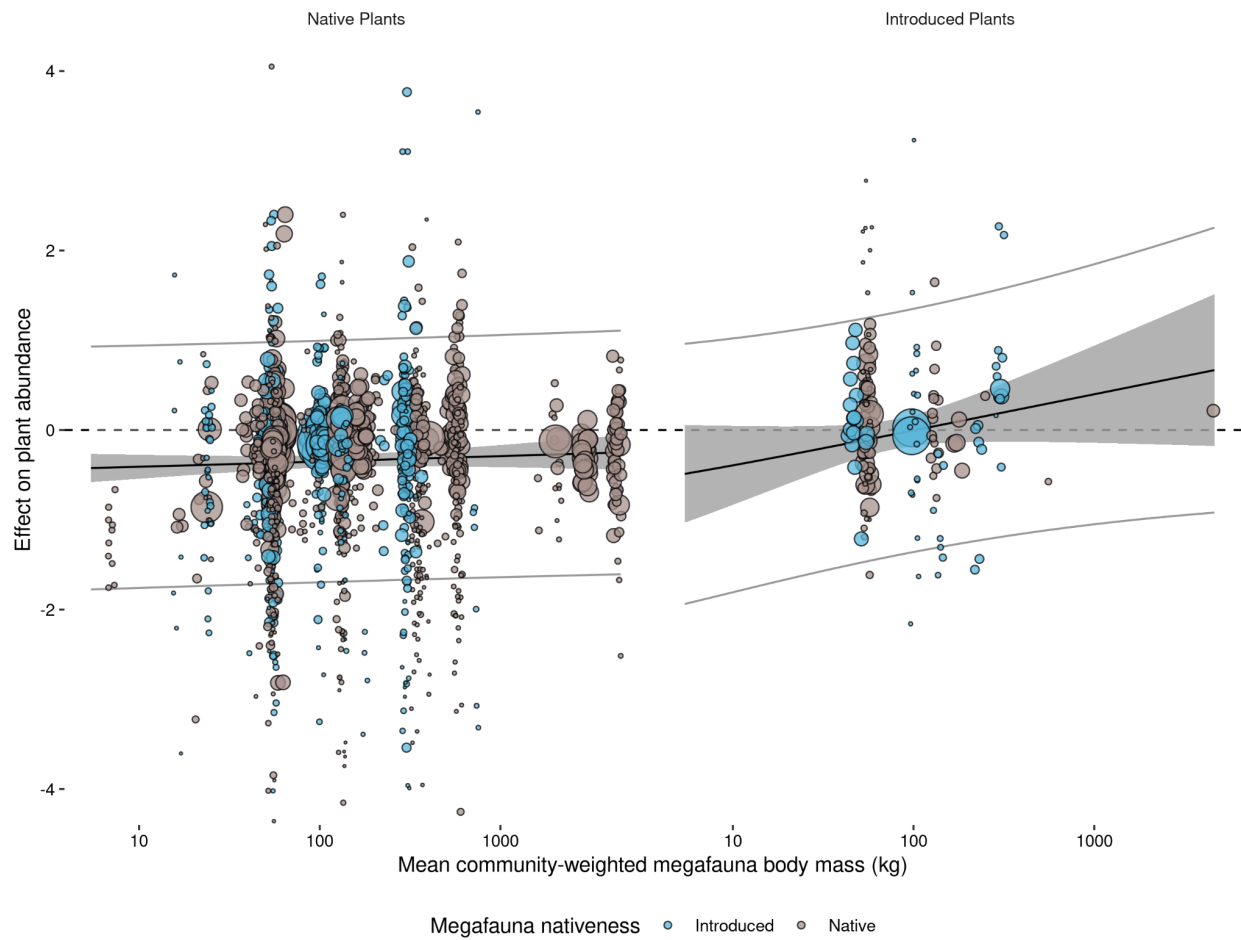
2 **Fig. S8**

3 Megafauna species richness (A) and functional group richness (B) had a significant but weak
4 negative relationship with introduced plant abundance (bottom row, p-values=0.005–0.007, Table
5 S1). These factors improved model quality relative to an intercept-only null model (LR=[14.9,
6 15.3], p-values=0.0005, Table S2)

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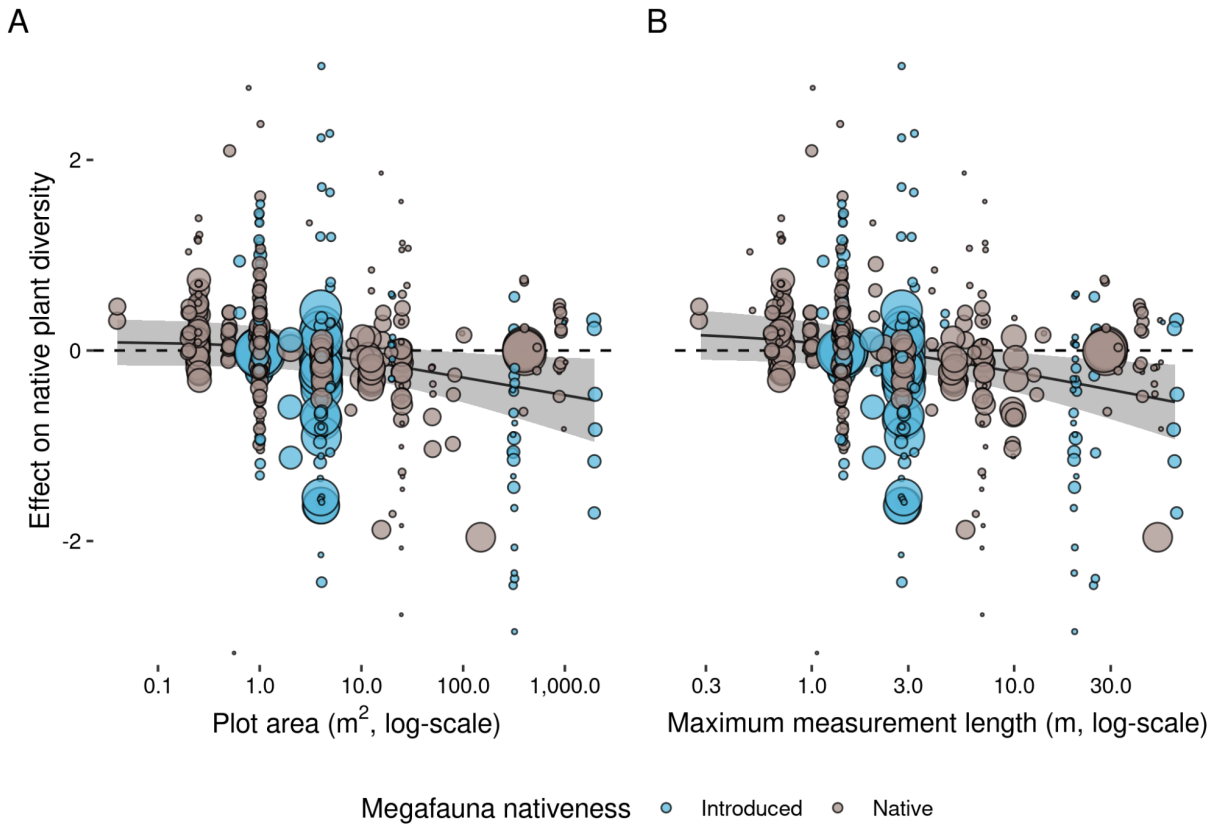
5 **Fig. S9**

6 The interaction between megafauna body mass and plant nativeness improved model quality in
7 explaining impacts on plant abundance (LR=15.4, p-value=0.0005, Table S2) with a non-
8 significant positive interaction with introduced plants (p-value=0.09, Table S1).

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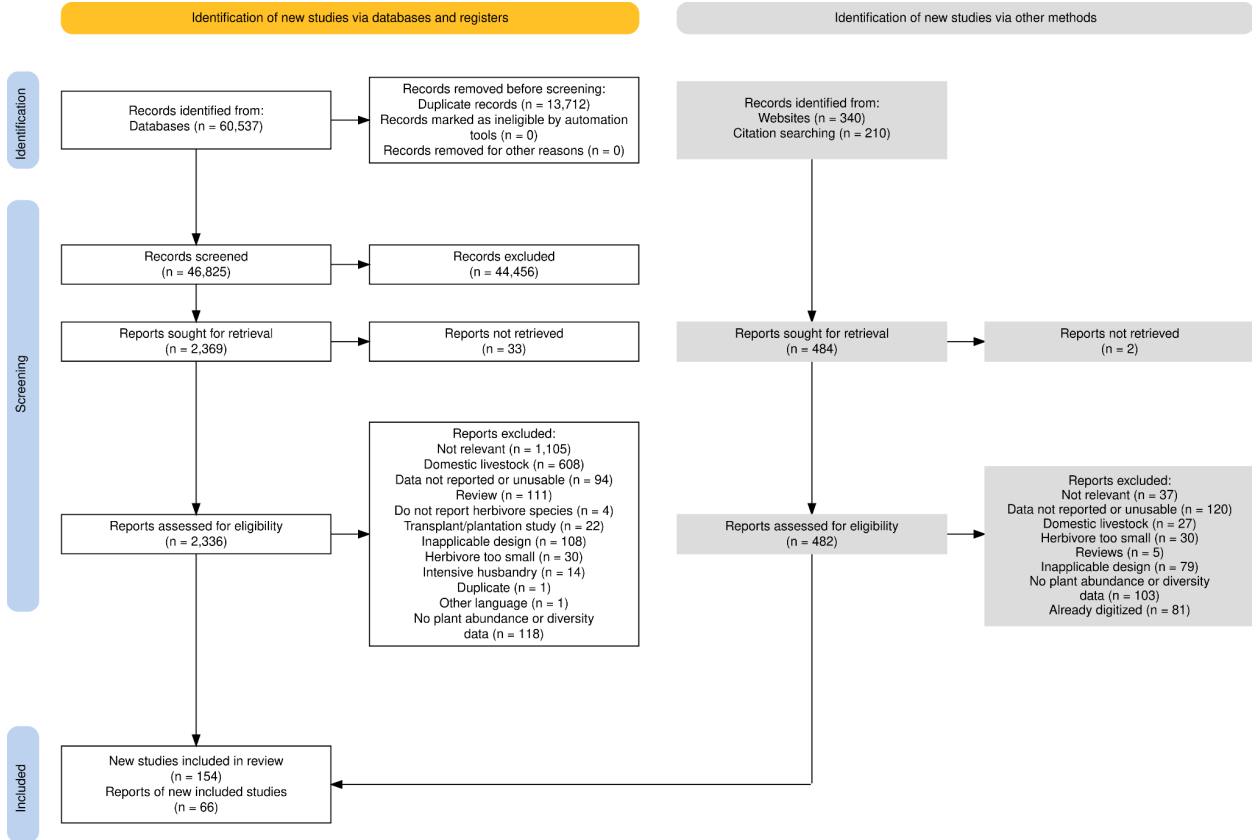


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3 **Fig. S10**

4 Measurement scale significantly improved model quality (LR=[4.5, 5.9], p-values=0.01–0.03,
5 Table S2) relative to intercept-only models. Measurement scale was estimated both as plot area
6 (A), which excluded transect-based measurements and as maximum measurement length (B),
7 which included transect length, the hypotenuse of rectangular and square plots and the diameter of
8 circular plots. Both had a negative relationship with plant diversity impacts (p-values=0.01–0.03,
9 Table S1).

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4 **Fig. S11**

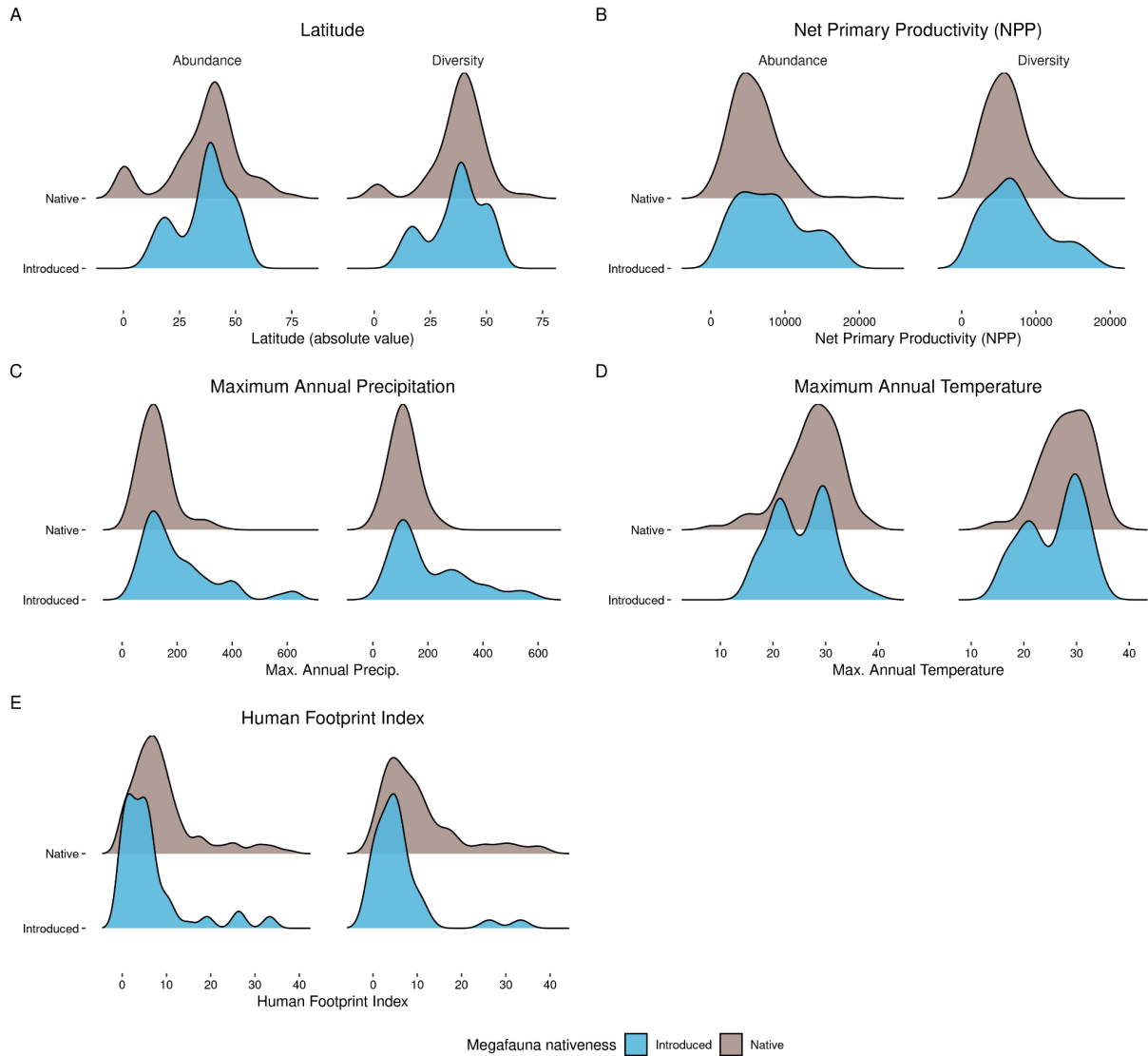
5 PRISMA diagram (58) indicating systematic literature review process. The left pathway indicates
 6 the total number of studies identified from Web of Science, the number removed through title
 7 screening, the number unavailable, and the number excluded due to ineligibility. On the right, the
 8 diagram indicates the number of additional studies identified from Google Scholar, bibliographies,
 9 and other meta-analyses, with the number excluded due to ineligibility.

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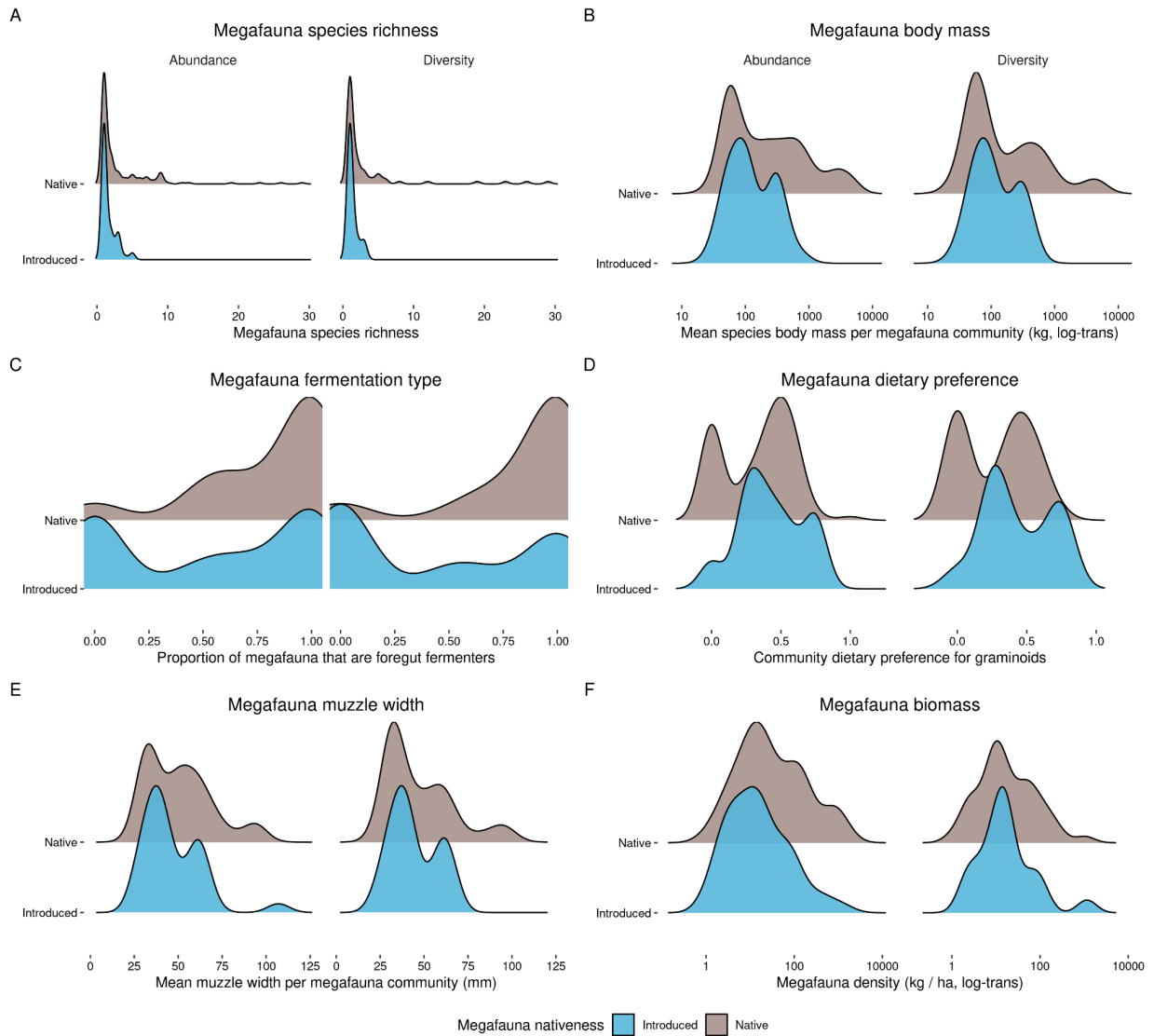
2

3 **Fig. S12.**

4 Distributions of environmental variables were similar between native and introduced megafauna
5 communities. Each plot shows environmental distributions for studies reporting on plant
6 abundance responses (left) and diversity responses (right), with native distributions in brown and
7 introduced in blue.

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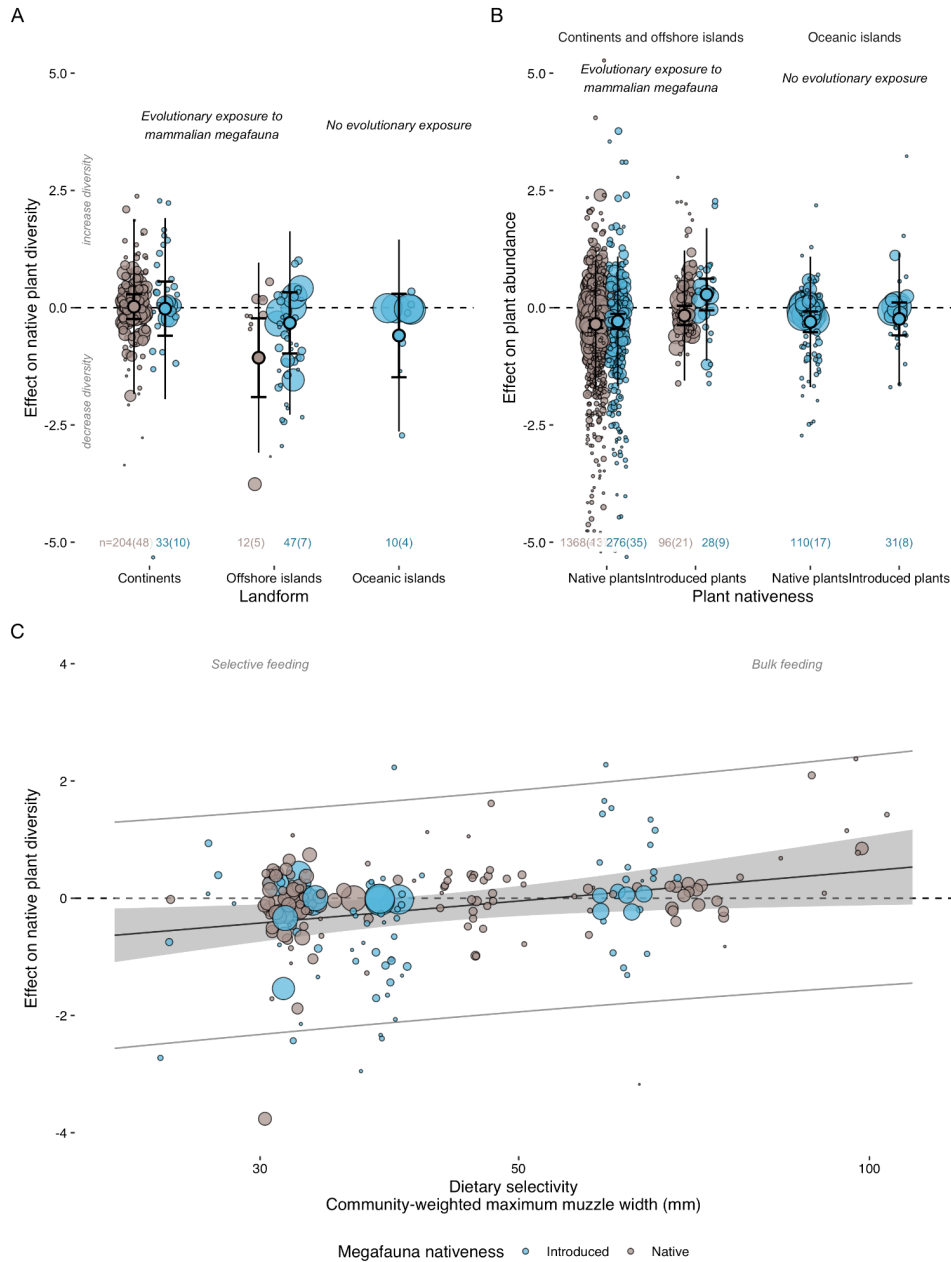


2

3 **Fig. S13.**

4 Distributions of megafauna species richness and trait distributions were roughly similar between
5 native and introduced megafauna communities. Each plot shows trait distributions for studies
6 reporting on plant abundance responses (left) and diversity responses (right), with native
7 distributions in brown and introduced in blue.

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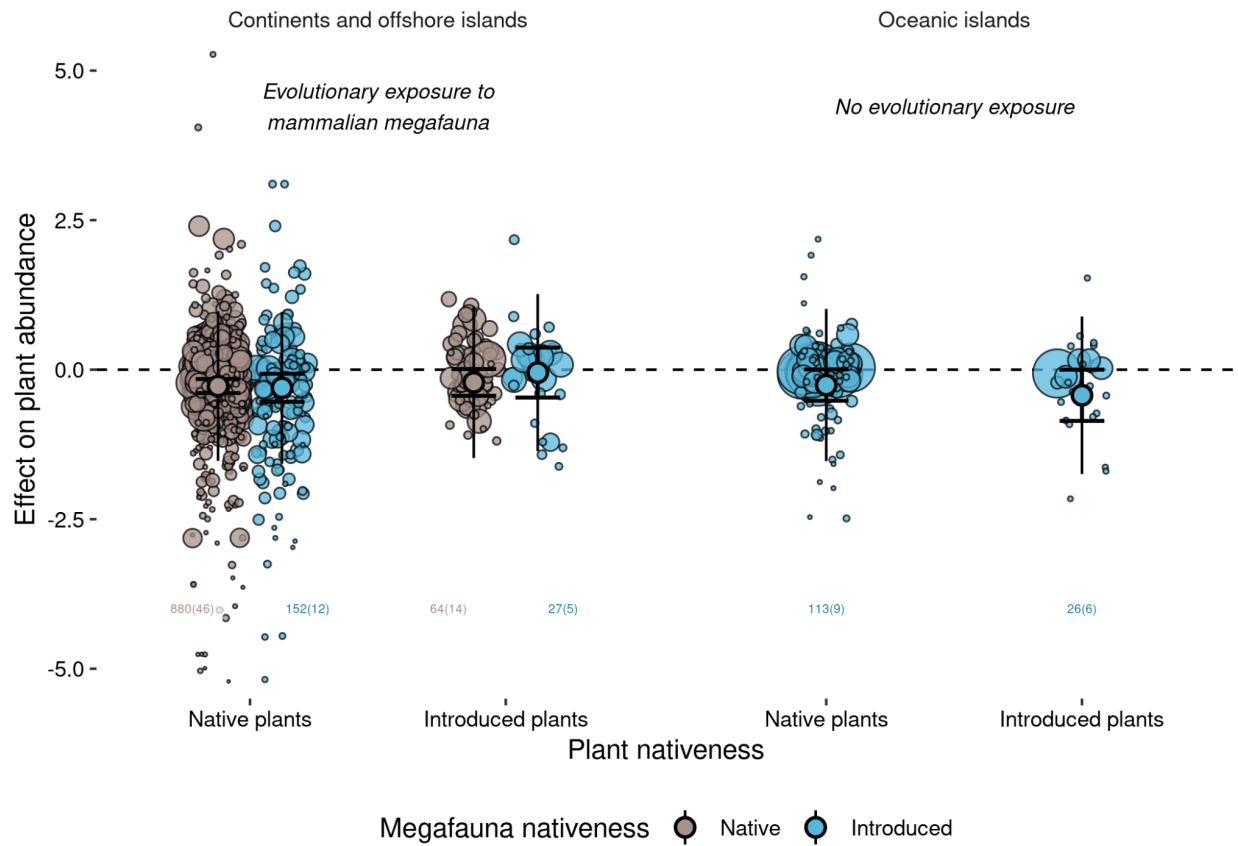


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2 **Fig. S14**

3 Main results selecting only the final time point in time series, or the largest measurement scale in
 4 experiments that reported time series or multiple scales from the same site / species led to the same
 5 results as controlling for non-independence with random effects. Nativeness did not improve
 6 model quality (p-values=0.06-0.38, Table S2) and there was no difference between native and
 7 introduced megafauna (p-values=0.07-0.65, Table S1). Muzzle width still significantly affected
 8 impacts on plant diversity (slope=0.24, 95% CIs=[0.04, 0.44], p=0.02, Table S1) and improved
 9 model quality (LR=5.4, p=0.02, Table S2). See Table S1 and Table S2 for additional models that
 10 also evaluated only the final time point / measurement scale.
 11

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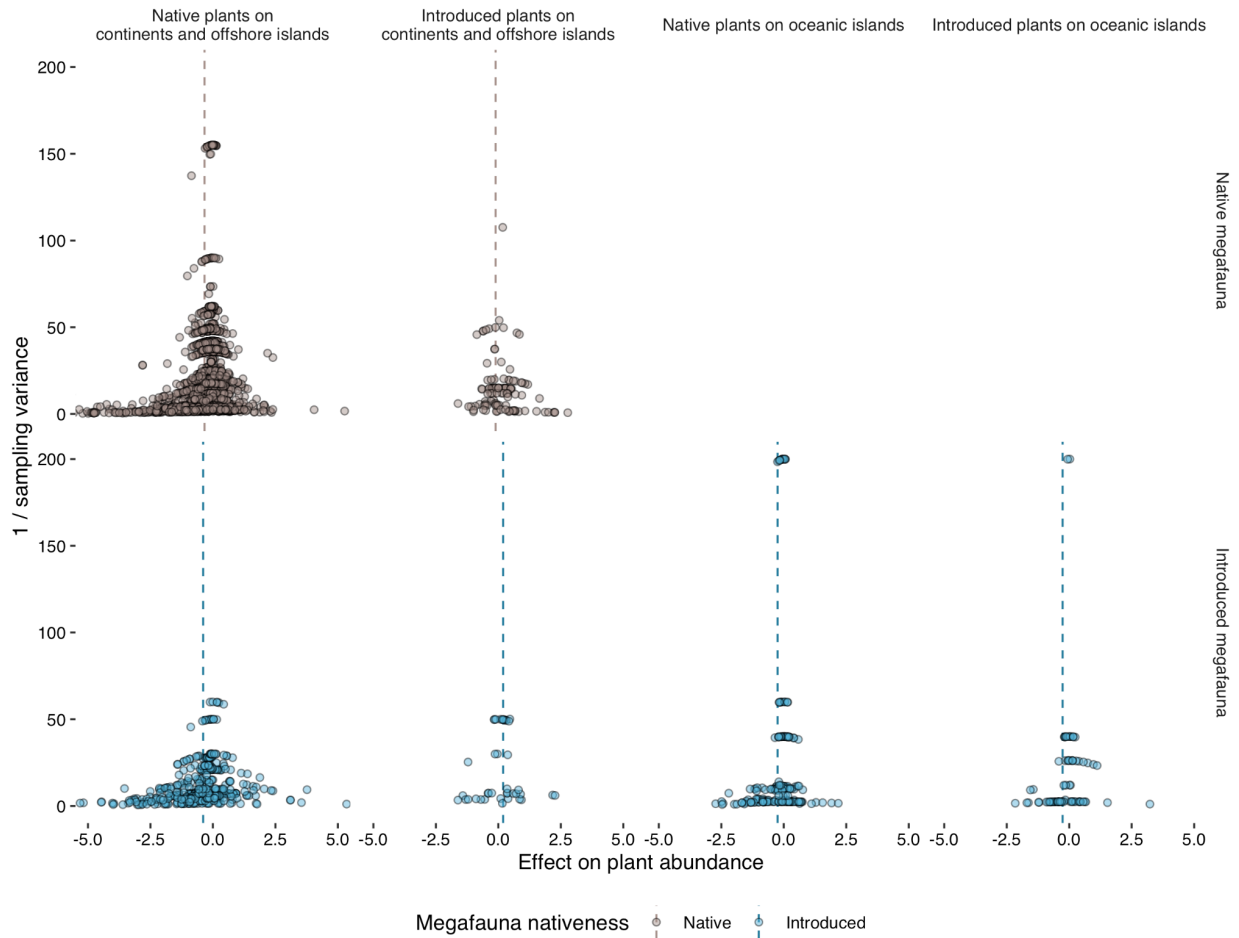
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3 **Fig. S15**

4 There was no difference between the impacts of native and introduced megafauna on plant
5 abundance across landforms when only considering species-level responses (for which plant
6 nativeness was more certain, $z=[-0.9, 0.68]$, p -values=0.84–0.99, Table S1). Nor did megafauna
7 nativeness improve model quality (LR=0.7, p -value=0.7, Table S2).

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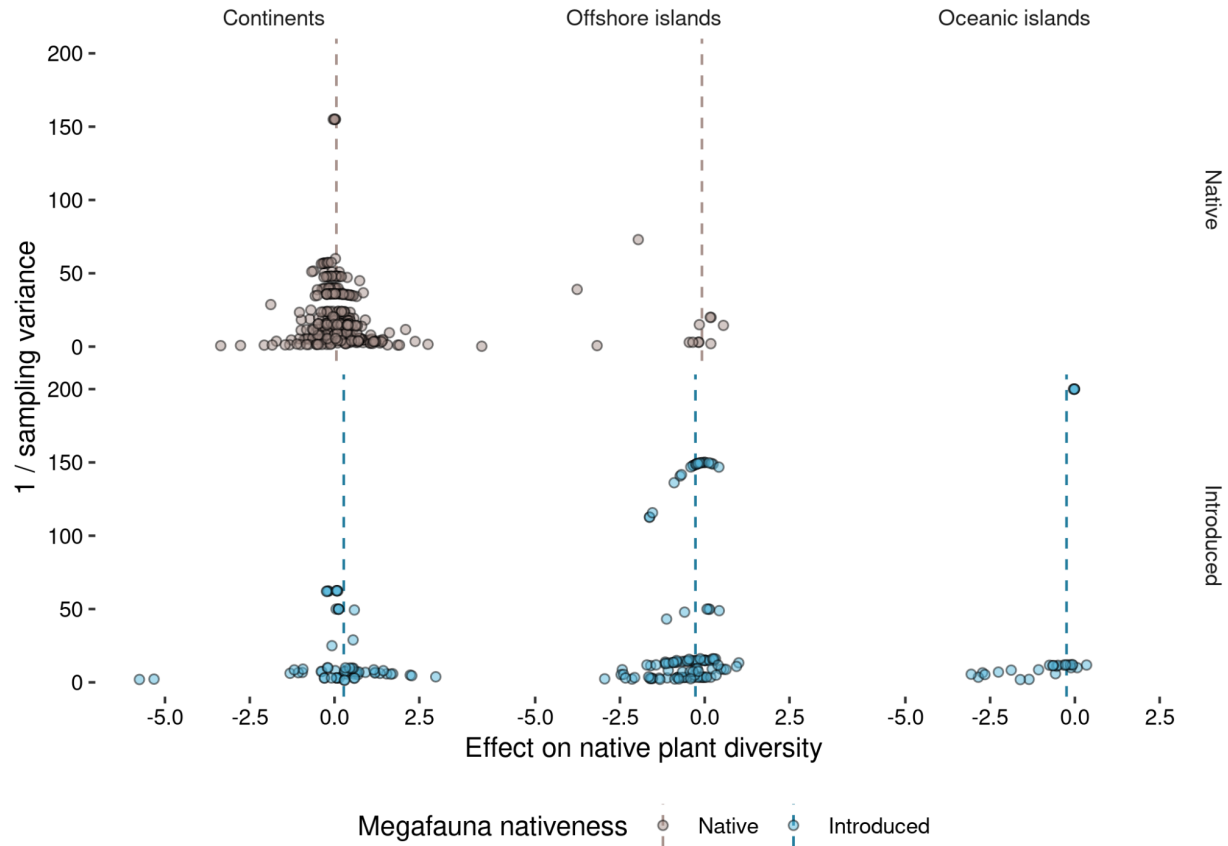
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3 **Fig. S16**

4 Funnel plot of megafauna impacts on native and introduced plant abundance. Model estimate (e.g.,
5 pooled effect size) for each group is shown with a vertical dashed line. Larger values on y axis
6 (e.g., lower sampling variance) have higher weight in model and should be closer to model
7 estimate. Low-sample size publication bias should result in asymmetrical funnel plots due the non-
8 publication of non-significant results (high sampling variance, low position on y axis). While the
9 funnel plot suggests some evidence of low small size publication bias, these make our conclusions
10 more conservative to prevailing views.

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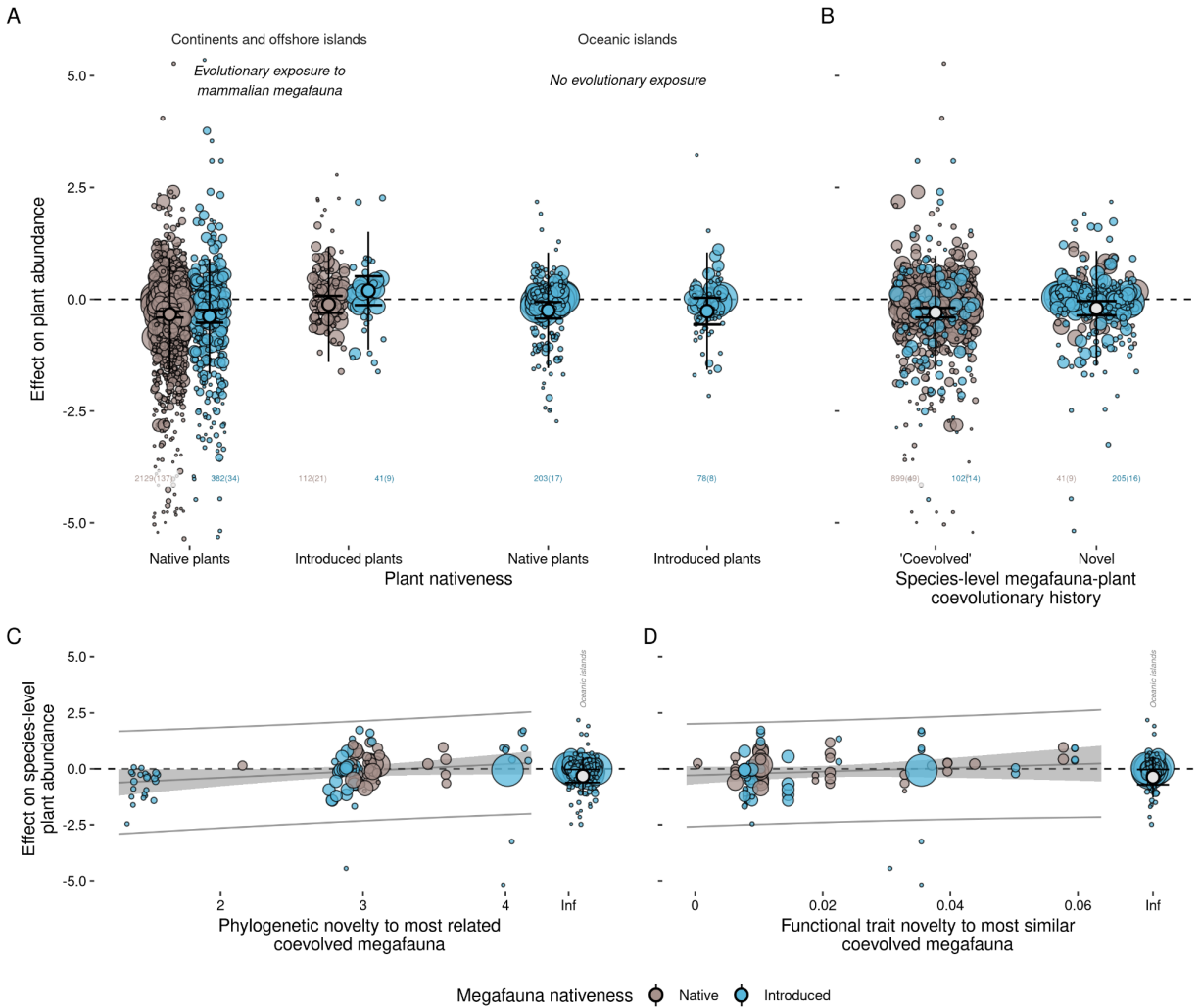
3 **Fig. S17**

4 Funnel plot of megafauna impacts on native plant diversity. Model estimate (e.g., pooled effect
5 size) for each group is shown with a vertical dashed line. Larger values on y axis (e.g., lower
6 sampling variance) have higher weight in model and should be closer to model estimate. Low-
7 sample size publication bias should result in asymmetrical funnel plots due the non-publication of
8 non-significant results (high sampling variance, low position on y axis). While the funnel plot
9 suggests some evidence of small sample size publication bias (introduced megafauna on offshore
10 islands and oceanic islands), these make our conclusions more conservative.

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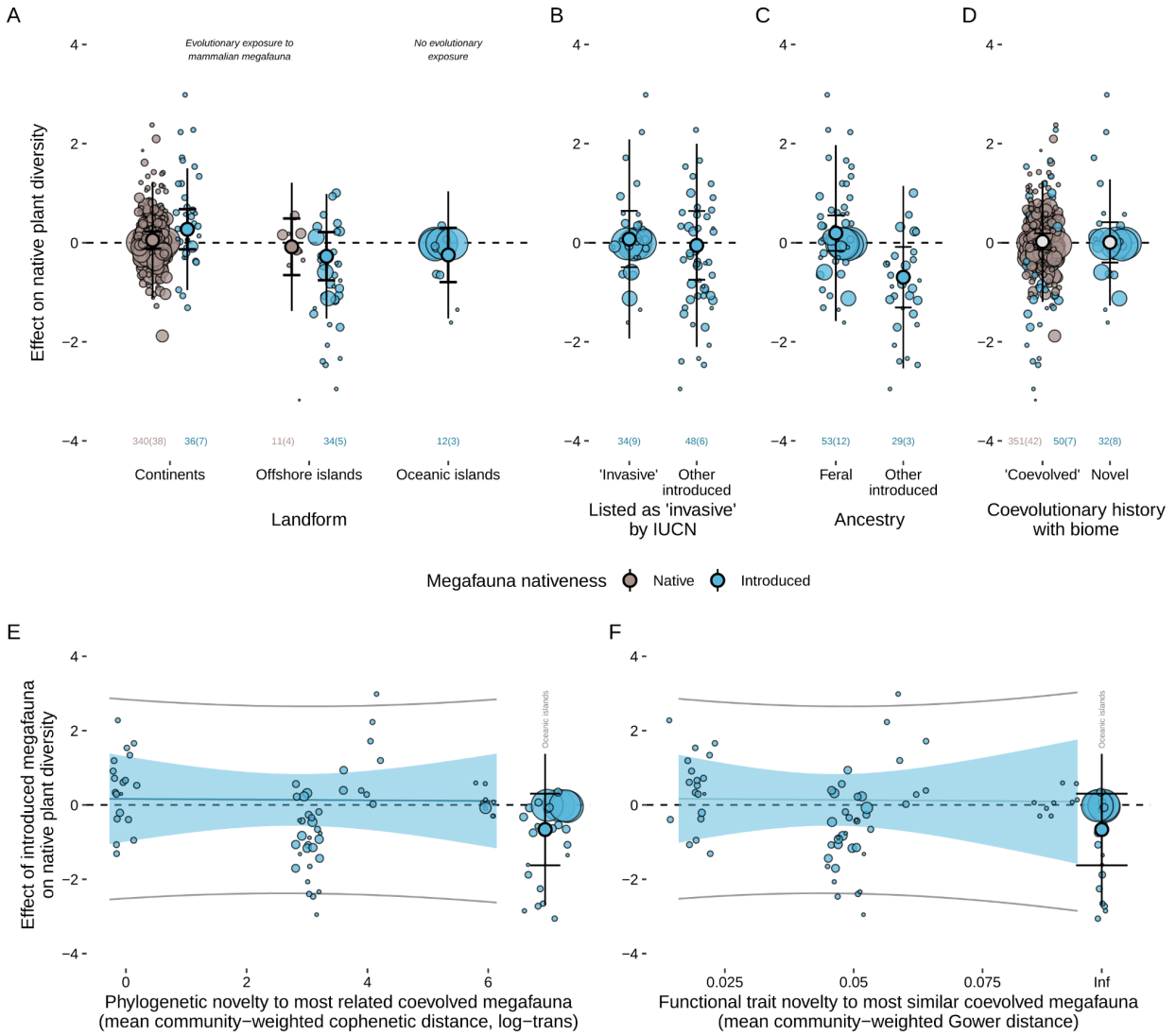


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4 **Fig. S18**

5 Effects of megafauna on plant abundance when only considered pure-nativeness megafauna
 6 communities, which involved excluding one study. As with main text results, there was no
 7 significant difference between native and introduced megafauna ($z=[-0.84, 1.65]$, $p=[0.25, 0.98]$,
 8 Table S1).
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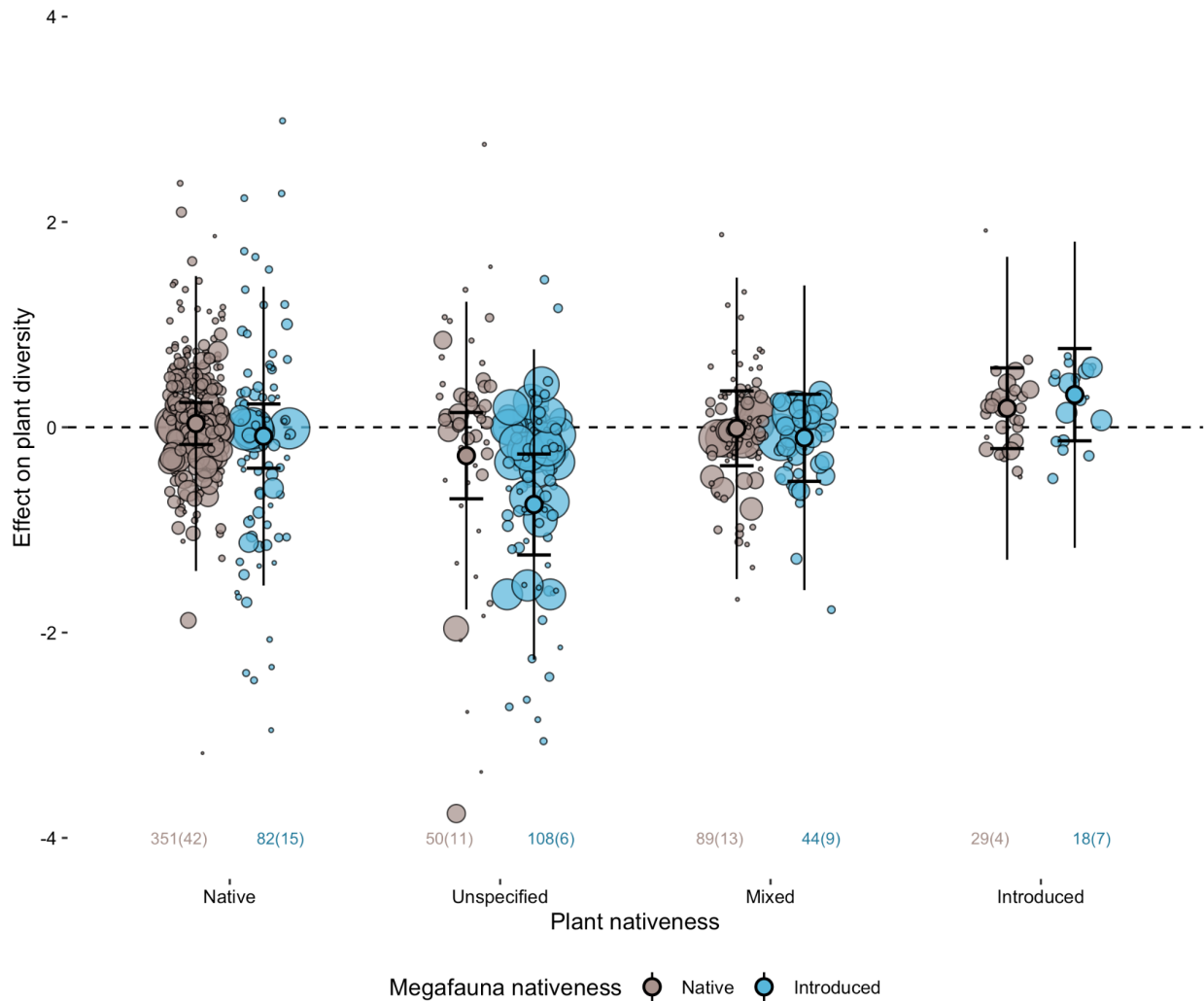
2

3 Fig. S19

4 Effects of megafauna on plant diversity with plants of unspecified nativeness excluded. As with
5 main text results (Figs. 1, 3), there was no significant difference between native and introduced
6 megafauna ($z=[-1.05, 1.01]$, $p=[0.69, 0.98]$, Table S1)

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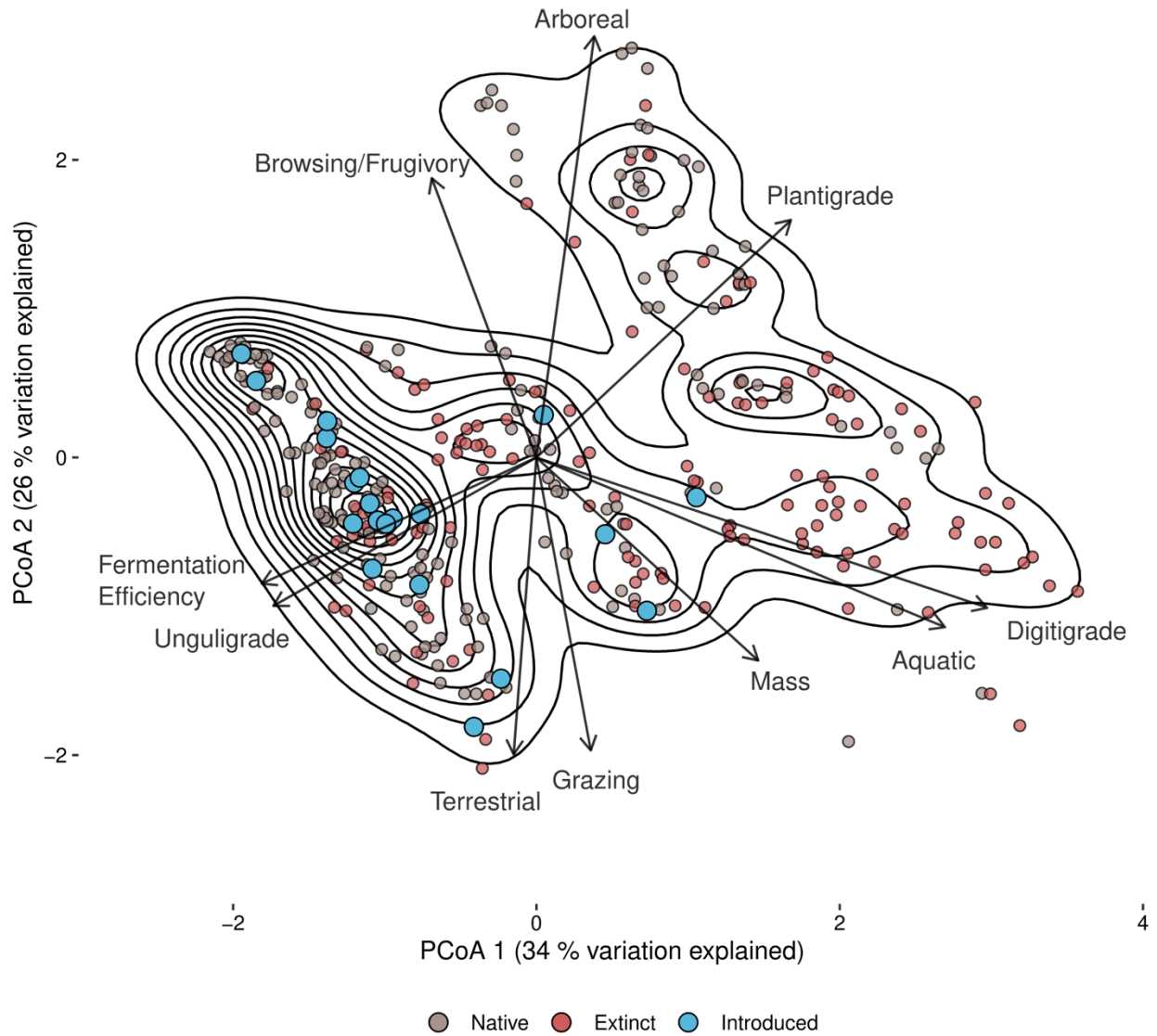
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3 **Fig. S20**

4 Effects of megafauna on plant diversity, showing responses reported as native, unspecified plant
5 diversity responses (treated as 'native' in main text), mixed plant responses (excluded from main
6 text), and introduced plant responses (Fig 3B). As in main text analysis, there was no difference
7 between the impacts of native and introduced megafauna ($z=[-1.4, 0.7]$, $p=[0.51, 0.93]$) and
8 nativeness did not improve model quality ($LR=4.30$, $p=0.37$, Table S2). See Fig. S19 for analyses
9 with unspecified nativeness plants excluded.

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3 **Fig. S21.**

4 Megafauna functional space derived from key traits that control the effects of megafauna on the
5 environment. Functional traits are derived from (54). Points indicate species, colored by their
6 status (indicating introduced species in the meta-analytic dataset). Overlaid arrows and text
7 indicate relationship between traits and principal coordinate analysis axes.

8

Table S1

Main effects of all models for main text results ('Primary Analyses') as well as sensitivity analyses. Model formulas and sample sizes are given per model as are the model estimates, standard error of the estimates ('SE'), lower and upper 95% confidence intervals ('Lower CI', 'Upper CI'), t-statistic, and p-value. Sample sizes are given following each formula, with number of individual responses followed by number of studies in parentheses. Note that the t-statistics and p-values are testing if the coefficient is significantly different from zero. See Table S2 for planned contrast test results comparing native and introduced megafauna impacts. Note that interactions between categorical variables were formulated as single concatenated variables, leading to identical but more interpretable results. Finally, we removed intercepts from models containing categorical variables. Sensitivity analyses include: 'Simple Random'=models do not include a temporal autocorrelation term; 'Final in Time Series / Largest Scale Measure Only'=the last time point and the largest scale measurement from each experiment were selected, instead of being controlled for with random effects; 'Species-level Responses Only'=collective plant abundance responses omitted, only species-level abundances included; 'Pure Megafauna Nativeness'=data from studies with more than one nativeness of manipulated megafauna were excluded (1 study); and 'Unspecified Nativeness Plants Excluded'=plants of unspecified nativeness were excluded from diversity analyses.

Primary Analyses**Responses to Native and Introduced Megafauna**

*Abundance ~ Megafauna Nativeness * Plant Nativeness * Landform Evo. History, N=2974(196)*

Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
Introduced-Introduced-absent	-0.2636	0.1521	-0.562	0.0348	-1.7335	0.0833
Introduced-Introduced-present	0.1905	0.1646	-0.1323	0.5134	1.1574	0.2472
Introduced-Native-absent	-0.246	0.0936	-0.4297	-0.0622	-2.6271	0.0087
Introduced-Native-present	-0.3903	0.0702	-0.528	-0.2526	-5.5581	<0.0001
Native-Introduced-present	-0.1114	0.0961	-0.3	0.0771	-1.1591	0.2465
Native-Native-present	-0.338	0.0359	-0.4084	-0.2676	-9.4125	<0.0001

*Abundance ~ Megafauna Nativeness * Landform Evo. History, N=2974(196)*

Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
Introduced-absent	-0.2536	0.0914	-0.4342	-0.0729	-2.7742	0.0062
Introduced-present	-0.3328	0.0698	-0.4707	-0.1948	-4.7662	<0.0001
Native-present	-0.3306	0.0364	-0.4025	-0.2586	-9.0806	<0.0001

*Diversity ~ Megafauna Nativeness * Landform Evo. History * Island, N=591(73)*

Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
Introduced-absent-yes	-0.6869	0.3815	-1.4488	0.075	-1.8006	0.0764
Introduced-present-no	-0.1659	0.2326	-0.6304	0.2986	-0.7133	0.4782
Introduced-present-yes	-0.2651	0.2864	-0.837	0.3068	-0.9257	0.358
Native-present-no	0.0401	0.1147	-0.1891	0.2692	0.3491	0.7281
Native-present-yes	-0.8339	0.3767	-1.5862	-0.0816	-2.2137	0.0304

Diversity ~ Invasive, N=591(73)

Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
100 Worst	0.0602	0.2813	-0.5011	0.6215	0.2139	0.8312
Other	-0.1437	0.1037	-0.3506	0.0633	-1.3855	0.1704

Abundance ~ Invasive, N=2743(188)

Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
100 Worst	-0.2429	0.0869	-0.4148	-0.0711	-2.7944	0.0059
Other	-0.3797	0.0354	-0.4498	-0.3097	-10.7147	<0.0001

Diversity ~ Feral, N=591(73)

Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
Feral	-0.2136	0.2041	-0.6208	0.1937	-1.0464	0.2991
Non Feral	-0.0976	0.1076	-0.3123	0.1172	-0.9065	0.3679

Abundance ~ Feral, N=2743(188)

Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
Feral	-0.3089	0.072	-0.4512	-0.1666	-4.2907	<0.0001
Non Feral	-0.3751	0.037	-0.4482	-0.3019	-10.1402	<0.0001

*Diversity ~ Megafauna Nativeness * Plant Nativeness, N=638(74)*

Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
Introduced-Introduced	0.2578	0.254	-0.2417	0.7574	1.0151	0.3108
Introduced-Native	-0.3145	0.1633	-0.6357	0.0066	-1.9262	0.0549
Native-Introduced	0.1329	0.2158	-0.2915	0.5572	0.6158	0.5384
Native-Native	-0.0366	0.11	-0.2529	0.1798	-0.3323	0.7398

*Abundance ~ Megafauna Nativeness * Plant Nativeness, N=2974(196)*

Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
Introduced-Introduced	-0.0747	0.1115	-0.2934	0.144	-0.6699	0.503
Introduced-Native	-0.3358	0.0564	-0.4465	-0.2251	-5.9492	<0.0001
Native-Introduced	-0.121	0.0964	-0.31	0.0681	-1.2547	0.2098
Native-Native	-0.339	0.0361	-0.4098	-0.2683	-9.3942	<0.0001

Primary Analyses

Coevolutionary History and Novelty

Abundance ~ Plant-Megafauna Coev., N=1247(76)

Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
No	-0.1983	0.0781	-0.3517	-0.045	-2.5397	0.0113
Yes	-0.2964	0.0536	-0.4017	-0.1912	-5.5336	<0.0001

Abundance ~ Plant-Megafauna Phylogenetic Novelty (CWM), N=115(17)

Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
intercept	-0.1573	0.1086	-0.3889	0.0743	-1.4479	0.1682
Plant-Megafauna Phylogenetic Novelty (CWM)	0.1403	0.1171	-0.092	0.3727	1.1985	0.2336

Abundance ~ Plant-Megafauna Functional Novelty (CWM), N=115(17)

Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
intercept	-0.1469	0.1091	-0.3794	0.0856	-1.3465	0.1981
Plant-Megafauna Functional Novelty (CWM)	0.1009	0.1087	-0.1147	0.3166	0.9288	0.3553

Diversity ~ Coevolved Biome, N=591(73)

Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
No	-0.0092	0.2978	-0.6034	0.5849	-0.031	0.9754
Yes	-0.1326	0.1032	-0.3386	0.0733	-1.2853	0.2031

Diversity ~ Megafauna Phylogenetic Novelty (CWM), N=162(15)

Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
intercept	-0.1459	0.3418	-0.8981	0.6063	-0.4268	0.6777
Megafauna Phylogenetic Novelty (CWM)	0.1913	0.2859	-0.438	0.8206	0.6691	0.5172

Diversity ~ Megafauna Functional Novelty (CWM), N=162(15)

Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
intercept	-0.2343	0.3942	-1.1019	0.6333	-0.5945	0.5642
Megafauna Functional Novelty (CWM)	-0.0033	0.3456	-0.7641	0.7575	-0.0095	0.9926

Primary Analyses

Functional Traits

Abundance ~ Max. Muzzle Width (CWM), N=2103(152)

Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
intercept	-0.3716	0.0379	-0.4467	-0.2966	-9.8081	<0.0001
Max. Muzzle Width (CWM)	0.0185	0.0348	-0.0499	0.0868	0.5301	0.5961

Diversity ~ Max. Muzzle Width (CWM), N=407(60)

Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
Term						

intercept	-0.1896	0.0838	-0.3576	-0.0216	-2.2633	0.0277
Max. Muzzle Width (CWM)	0.2597	0.069	0.1237	0.3956	3.7625	2.00E-04
<i>Abundance ~ Mean Muzzle Width (CWM), N=2103(152)</i>						
Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
intercept	-0.3712	0.0377	-0.4459	-0.2964	-9.8335	<0.0001
Mean Muzzle Width (CWM)	0.0515	0.0319	-0.011	0.114	1.6157	0.1064
<i>Diversity ~ Mean Muzzle Width (CWM), N=407(60)</i>						
Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
intercept	-0.1577	0.1001	-0.3583	0.043	-1.5757	0.121
Mean Muzzle Width (CWM)	0.2018	0.0782	0.0477	0.3558	2.5802	0.0105
<i>Abundance ~ Mean Body Mass (CWM), N=2135(154)</i>						
Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
intercept	-0.3736	0.0373	-0.4475	-0.2997	-10.0157	<0.0001
Mean Body Mass (CWM)	0.0349	0.03	-0.024	0.0938	1.1633	0.2449
<i>Diversity ~ Mean Body Mass (CWM), N=420(62)</i>						
Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
intercept	-0.1915	0.102	-0.3957	0.0126	-1.878	0.0654
Mean Body Mass (CWM)	0.2031	0.0885	0.0288	0.3774	2.295	0.0225
<i>Abundance ~ Max. Body Mass (CWM), N=2135(154)</i>						
Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
intercept	-0.3716	0.0375	-0.4458	-0.2975	-9.9226	<0.0001
Max. Body Mass (CWM)	0.0127	0.0309	-0.0478	0.0732	0.4119	0.6804
<i>Diversity ~ Max. Body Mass (CWM), N=420(62)</i>						
Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
intercept	-0.196	0.1046	-0.4053	0.0133	-1.8745	0.0659
Max. Body Mass (CWM)	0.1756	0.087	0.0043	0.3469	2.0181	0.0446
<i>Abundance ~ Megafauna Biomass / NPP, N=1638(112)</i>						
Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
intercept	-0.3276	0.0403	-0.4078	-0.2475	-8.1255	<0.0001
Megafauna Biomass / NPP	-0.04	0.0259	-0.0908	0.0107	-1.5467	0.1221
<i>Diversity ~ Megafauna Biomass / NPP, N=317(44)</i>						
Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
intercept	-0.141	0.1256	-0.3949	0.1128	-1.1228	0.2682
Megafauna Biomass / NPP	0.101	0.0804	-0.0573	0.2593	1.2553	0.2103
<i>Abundance ~ Plant Growth Form * Graminoid Preference (CWM), N=1730(120)</i>						
Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
intercept	-0.1579	0.0583	-0.2736	-0.0422	-2.7109	0.008
Plant Growth FormGraminoid	-0.0701	0.0889	-0.2447	0.1045	-0.7878	0.4311
Plant Growth FormWoody	-0.1951	0.0664	-0.3254	-0.0648	-2.9389	0.0034
Graminoid Preference (CWM)	0.1385	0.0593	0.0222	0.2549	2.3352	0.0197
Plant Growth FormGraminoid:Graminoid Preference (CWM)	-0.2553	0.0787	-0.4096	-0.1009	-3.2437	0.0012
Plant Growth FormWoody:Graminoid Preference (CWM)	-0.1247	0.0704	-0.2628	0.0133	-1.7727	0.0765
<i>Diversity ~ Plant Growth Form * Graminoid Preference (CWM), N=167(27)</i>						
Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
intercept	0.1185	0.1971	-0.2914	0.5285	0.6012	0.5541
Plant Growth FormGraminoid	-0.2066	0.2769	-0.7634	0.3502	-0.7459	0.4594
Plant Growth FormWoody	-0.2325	0.2197	-0.6743	0.2093	-1.058	0.2954
Graminoid Preference (CWM)	0.3874	0.1705	0.0338	0.7411	2.2724	0.0332
Plant Growth FormGraminoid:Graminoid Preference (CWM)	-0.6075	0.2462	-1.0952	-0.1198	-2.4674	0.0151

Plant Growth FormWoody:Graminoid Preference (CWM)	-0.1186	0.1948	-0.5045	0.2673	-0.6087	0.5439
<i>Abundance ~ Max. Body Mass (CWM) * Plant Nativeness, N=2306(161)</i>						
Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
Max. Body Mass (CWM)	0.1098	0.1138	-0.1134	0.3331	0.9651	0.3346
Plant NativenessIntroduced	-0.0102	0.0908	-0.1884	0.168	-0.1124	0.9106
Plant NativenessNative	-0.3479	0.0349	-0.4165	-0.2793	-9.9553	<0.0001
Max. Body Mass (CWM):Plant NativenessNative	-0.1023	0.1136	-0.325	0.1205	-0.9004	0.368
<i>Diversity ~ Max. Body Mass (CWM) * Plant Nativeness, N=460(63)</i>						
Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
Max. Body Mass (CWM)	-0.0279	0.3077	-0.6336	0.5778	-0.0907	0.9278
Plant NativenessIntroduced	0.1805	0.2106	-0.2364	0.5973	0.857	0.3931
Plant NativenessNative	-0.1861	0.1059	-0.3958	0.0235	-1.7574	0.0814
Max. Body Mass (CWM):Plant NativenessNative	0.2005	0.3046	-0.399	0.8	0.6582	0.5109
<i>Abundance ~ Mean Body Mass (CWM) * Plant Nativeness, N=2306(161)</i>						
Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
Mean Body Mass (CWM)	0.1992	0.1183	-0.0327	0.4312	1.6847	0.0922
Plant NativenessIntroduced	-9.00E-04	0.0885	-0.1747	0.1729	-0.0099	0.9921
Plant NativenessNative	-0.3502	0.0348	-0.4185	-0.282	-10.0728	<0.0001
Mean Body Mass (CWM):Plant NativenessNative	-0.1694	0.1179	-0.4007	0.0619	-1.4367	0.151
<i>Diversity ~ Mean Body Mass (CWM) * Plant Nativeness, N=460(63)</i>						
Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
Mean Body Mass (CWM)	-0.1267	0.4044	-0.9228	0.6693	-0.3134	0.7542
Plant NativenessIntroduced	0.2172	0.2208	-0.2198	0.6543	0.9841	0.327
Plant NativenessNative	-0.1815	0.1044	-0.3882	0.0252	-1.7383	0.0847
Mean Body Mass (CWM):Plant NativenessNative	0.321	0.4015	-0.4692	1.1112	0.7995	0.4247
<i>Abundance ~ Proportion Hindgut (CWM), N=2135(154)</i>						
Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
intercept	-0.3726	0.0375	-0.4469	-0.2983	-9.9306	<0.0001
Proportion Hindgut (CWM)	0.0179	0.0329	-0.0466	0.0823	0.5433	0.587
<i>Diversity ~ Proportion Hindgut (CWM), N=420(62)</i>						
Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
intercept	-0.1784	0.1105	-0.3997	0.0428	-1.6141	0.1119
Proportion Hindgut (CWM)	0.0454	0.0904	-0.1327	0.2236	0.5025	0.6157
Primary Analyses						
Environmental Factors						
<i>Abundance ~ Max. Annual Precip., N=2743(188)</i>						
Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
intercept	-0.3647	0.033	-0.4299	-0.2994	-11.0465	<0.0001
Max. Annual Precip.	-0.0445	0.0365	-0.116	0.0271	-1.219	0.223
<i>Diversity ~ Max. Annual Precip., N=591(73)</i>						
Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
intercept	-0.0963	0.0927	-0.2812	0.0886	-1.0393	0.3024
Max. Annual Precip.	-0.1586	0.0849	-0.3256	0.0083	-1.8693	0.0625
<i>Abundance ~ Max. Annual Temp., N=2743(188)</i>						
Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
intercept	-0.3553	0.0333	-0.4213	-0.2894	-10.6564	<0.0001
Max. Annual Temp.	0.0213	0.0331	-0.0436	0.0863	0.6447	0.5192
<i>Diversity ~ Max. Annual Temp., N=591(73)</i>						
Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value

intercept	-0.1055	0.0972	-0.2994	0.0884	-1.0857	0.2814
Max. Annual Temp.	0.0912	0.0984	-0.1024	0.2849	0.927	0.3546
<i>Abundance ~ Net Primary Productivity, N=2743(188)</i>						
Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
intercept	-0.3618	0.0328	-0.4266	-0.2969	-11.0273	<0.0001
Net Primary Productivity	-0.0427	0.0318	-0.105	0.0196	-1.3435	0.1793
<i>Diversity ~ Net Primary Productivity, N=591(73)</i>						
Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
intercept	-0.1092	0.0989	-0.3066	0.0883	-1.1035	0.2737
Net Primary Productivity	-0.0398	0.0735	-0.1844	0.1048	-0.5421	0.5881
<i>Abundance ~ Human Footprint Index, N=2743(188)</i>						
Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
intercept	-0.3599	0.033	-0.4251	-0.2948	-10.9228	<0.0001
Human Footprint Index	0.005	0.0344	-0.0624	0.0724	0.1463	0.8837
<i>Diversity ~ Human Footprint Index, N=591(73)</i>						
Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
intercept	-0.1406	0.1029	-0.3459	0.0647	-1.3663	0.1763
Human Footprint Index	0.0425	0.0647	-0.0849	0.1698	0.6563	0.5121
<i>Abundance ~ Island, N=2743(188)</i>						
Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
no	-0.3604	0.0377	-0.435	-0.2859	-9.5595	<0.0001
yes	-0.3604	0.0672	-0.4932	-0.2276	-5.3644	<0.0001
<i>Diversity ~ Island, N=591(73)</i>						
Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
no	0.0076	0.1048	-0.2015	0.2168	0.0729	0.9421
yes	-0.5213	0.19	-0.9003	-0.1422	-2.7441	0.0078

Primary Analyses

Megafauna Diversity

<i>Abundance ~ Number of Megafauna Species, N=2743(188)</i>						
Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
intercept	-0.3606	0.0327	-0.4252	-0.2959	-11.0302	<0.0001
Number of Megafauna Species	-0.0433	0.0249	-0.0921	0.0056	-1.7382	0.0823
<i>Diversity ~ Number of Megafauna Species, N=591(73)</i>						
Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
intercept	-0.1144	0.0976	-0.3091	0.0804	-1.1717	0.2454
Number of Megafauna Species	0.0329	0.0414	-0.0485	0.1144	0.7958	0.4267
<i>Abundance ~ Number of Megafauna Functional Groups, N=2743(188)</i>						
Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
intercept	-0.3624	0.0329	-0.4274	-0.2975	-11.0315	<0.0001
Number of Megafauna Functional Groups	-0.0405	0.026	-0.0914	0.0104	-1.5619	0.1185
<i>Diversity ~ Number of Megafauna Functional Groups, N=591(73)</i>						
Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
intercept	-0.1137	0.0979	-0.3091	0.0817	-1.1611	0.2496
Number of Megafauna Functional Groups	0.0286	0.0419	-0.0539	0.111	0.682	0.4958
<i>Abundance ~ Number of Megafauna Species * Plant Nativeness, N=2974(196)</i>						
Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
Number of Megafauna Species	-0.322	0.1156	-0.5488	-0.0952	-2.7841	0.0054
Plant NativenessIntroduced	-0.182	0.08	-0.339	-0.025	-2.2752	0.0231
Plant NativenessNative	-0.3411	0.0307	-0.4013	-0.2809	-11.1212	<0.0001

Number of Megafauna Species:Plant NativenessNative	0.277	0.1159	0.0498	0.5043	2.3914	0.0169
<i>Diversity ~ Number of Megafauna Species * Plant Nativeness, N=638(74)</i>						
Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
Number of Megafauna Species	-0.2172	0.2718	-0.7517	0.3172	-0.7994	0.4246
Plant NativenessIntroduced	0.1045	0.2112	-0.3132	0.5222	0.4948	0.6216
Plant NativenessNative	-0.1072	0.0954	-0.2959	0.0815	-1.1237	0.2632
Number of Megafauna Species:Plant NativenessNative	0.2495	0.272	-0.2855	0.7845	0.9173	0.3596
<i>Abundance ~ Number of Megafauna Functional Groups * Plant Nativeness, N=2974(196)</i>						
Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
Number of Megafauna Functional Groups	-0.2866	0.1061	-0.4946	-0.0786	-2.7018	0.007
Plant NativenessIntroduced	-0.1719	0.0787	-0.3264	-0.0175	-2.184	0.0292
Plant NativenessNative	-0.3434	0.0309	-0.404	-0.2828	-11.1211	<0.0001
Number of Megafauna Functional Groups:Plant NativenessNative	0.2445	0.1062	0.0362	0.4527	2.3025	0.0214
<i>Diversity ~ Number of Megafauna Functional Groups * Plant Nativeness, N=638(74)</i>						
Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
Number of Megafauna Functional Groups	-0.2606	0.2952	-0.8412	0.3201	-0.8826	0.3781
Plant NativenessIntroduced	0.0845	0.2192	-0.3491	0.5181	0.3853	0.7006
Plant NativenessNative	-0.1061	0.0954	-0.2948	0.0827	-1.1112	0.2685
Number of Megafauna Functional Groups:Plant NativenessNative	0.2881	0.2952	-0.2924	0.8687	0.9762	0.3296
Primary Analyses						
Methodological Factors						
<i>Diversity ~ Measurement Area (m2), N=567(66)</i>						
Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
intercept	-0.0508	0.0954	-0.2415	0.1399	-0.5322	0.5965
Measurement Area (m2)	-0.1402	0.0632	-0.2644	-0.0159	-2.2193	0.0272
<i>Diversity ~ Max. Measurement Length (m), N=573(69)</i>						
Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
intercept	-0.046	0.0898	-0.2253	0.1334	-0.512	0.6104
Max. Measurement Length (m)	-0.1582	0.0611	-0.2785	-0.0379	-2.5874	0.0101
<i>Abundance ~ Treatment Duration / NPP, N=2535(173)</i>						
Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
intercept	-0.3705	0.0355	-0.4408	-0.3001	-10.4261	<0.0001
Treatment Duration / NPP	0.0071	0.0269	-0.0457	0.0599	0.2634	0.7923
<i>Diversity ~ Treatment Duration / NPP, N=576(68)</i>						
Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
intercept	-0.1035	0.1026	-0.3086	0.1017	-1.0084	0.3172
Treatment Duration / NPP	-0.0355	0.0501	-0.1338	0.0629	-0.7079	0.4793
<i>Abundance ~ Treatment Duration, N=2535(173)</i>						
Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
intercept	-0.371	0.0359	-0.442	-0.3	-10.34	<0.0001
Treatment Duration	-0.0201	0.0172	-0.0538	0.0137	-1.1651	0.2441
<i>Diversity ~ Treatment Duration, N=576(68)</i>						
Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
intercept	-0.1055	0.1025	-0.3103	0.0994	-1.0293	0.3073
Treatment Duration	-0.0208	0.0345	-0.0886	0.047	-0.6019	0.5475
<i>Abundance ~ Treatment Duration * Net Primary Productivity, N=2535(173)</i>						
Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
intercept	-0.3732	0.0355	-0.4436	-0.3029	-10.5006	<0.0001
Treatment Duration	-0.0107	0.0177	-0.0453	0.024	-0.6048	0.5454

Net Primary Productivity	-0.0415	0.0341	-0.1084	0.0254	-1.2177	0.2235
Treatment Duration:Net Primary Productivity	-0.0313	0.0136	-0.0581	-0.0045	-2.294	0.0219

*Diversity ~ Treatment Duration * Net Primary Productivity, N=576(68)*

Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
intercept	-0.1171	0.106	-0.3291	0.0949	-1.1052	0.2735
Treatment Duration	-0.0306	0.0348	-0.0989	0.0377	-0.8798	0.3794
Net Primary Productivity	0.024	0.0817	-0.1367	0.1847	0.2938	0.7691
Treatment Duration:Net Primary Productivity	-0.1169	0.0582	-0.2312	-0.0026	-2.0089	0.0451

Simple Random

Responses to Native and Introduced Megafauna

*Abundance ~ Megafauna Nativeness * Plant Nativeness * Landform Evo. History, N=2974(196)*

Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
Introduced-Introduced-absent	-0.2691	0.1461	-0.5557	0.0175	-1.8422	0.0657
Introduced-Introduced-present	0.2545	0.1543	-0.048	0.557	1.6493	0.0992
Introduced-Native-absent	-0.2404	0.0907	-0.4184	-0.0624	-2.6497	0.0082
Introduced-Native-present	-0.3461	0.069	-0.4813	-0.2109	-5.0195	<0.0001
Native-Introduced-present	-0.1365	0.0923	-0.3175	0.0445	-1.4785	0.1394
Native-Native-present	-0.3355	0.0355	-0.4052	-0.2658	-9.4426	<0.0001

*Diversity ~ Megafauna Nativeness * Landform Evo. History * Island, N=591(73)*

Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
Introduced-absent-yes	-0.702	0.385	-1.4709	0.0669	-1.8234	0.0728
Introduced-present-no	-0.302	0.2212	-0.7438	0.1397	-1.3655	0.1768
Introduced-present-yes	-0.2222	0.2935	-0.8082	0.3639	-0.757	0.4518
Native-present-no	0.0545	0.1158	-0.1768	0.2858	0.4709	0.6393
Native-present-yes	-0.7778	0.3807	-1.5382	-0.0174	-2.0428	0.0451

Diversity ~ Invasive, N=591(73)

Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
100 Worst	0.0412	0.2816	-0.5207	0.603	0.1462	0.8842
Other	-0.1416	0.1044	-0.3498	0.0667	-1.3567	0.1794

Abundance ~ Invasive, N=2743(188)

Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
100 Worst	-0.2321	0.0838	-0.3978	-0.0663	-2.768	0.0064
Other	-0.3642	0.0347	-0.4328	-0.2956	-10.4999	<0.0001

Diversity ~ Feral, N=591(73)

Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
Feral	-0.3168	0.1962	-0.7084	0.0748	-1.6142	0.1111
Non Feral	-0.0743	0.1076	-0.2891	0.1404	-0.6907	0.4921

Abundance ~ Feral, N=2743(188)

Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
Feral	-0.284	0.0693	-0.421	-0.1469	-4.0964	1.00E-04
Non Feral	-0.363	0.0362	-0.4345	-0.2915	-10.0397	<0.0001

*Diversity ~ Megafauna Nativeness * Plant Nativeness, N=638(74)*

Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
Introduced-Introduced	0.2586	0.2414	-0.2154	0.7326	1.0713	0.2844
Introduced-Native	-0.3712	0.1564	-0.6784	-0.0641	-2.3732	0.0179
Native-Introduced	0.1305	0.2116	-0.285	0.546	0.6167	0.5376
Native-Native	-0.0153	0.1078	-0.2271	0.1964	-0.1423	0.8869

Simple Random

Coevolutionary History and Novelty

<i>Abundance ~ Plant-Megafauna Coev., N=1247(76)</i>						
Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
No	-0.1918	0.0751	-0.3394	-0.0443	-2.5531	0.0109
Yes	-0.2862	0.0527	-0.3897	-0.1827	-5.4296	<0.0001
<i>Abundance ~ Plant-Megafauna Phylogenetic Novelty (CWM), N=115(17)</i>						
Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
intercept	-0.1266	0.0864	-0.3107	0.0575	-1.4653	0.1635
Plant-Megafauna Phylogenetic Novelty (CWM)	0.1937	0.1092	-0.0226	0.41	1.7746	0.0787
<i>Abundance ~ Plant-Megafauna Functional Novelty (CWM), N=115(17)</i>						
Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
intercept	-0.1046	0.0857	-0.2873	0.0782	-1.2197	0.2414
Plant-Megafauna Functional Novelty (CWM)	0.134	0.087	-0.0383	0.3063	1.5411	0.1261
<i>Diversity ~ Coevolved Biome, N=591(73)</i>						
Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
No	-0.0295	0.2979	-0.6239	0.5649	-0.0991	0.9214
Yes	-0.1305	0.1038	-0.3377	0.0766	-1.2575	0.2129
<i>Diversity ~ Megafauna Phylogenetic Novelty (CWM), N=162(15)</i>						
Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
intercept	-0.1484	0.3377	-0.8917	0.595	-0.4393	0.669
Megafauna Phylogenetic Novelty (CWM)	0.188	0.2709	-0.4084	0.7843	0.6938	0.5022
<i>Diversity ~ Megafauna Functional Novelty (CWM), N=162(15)</i>						
Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
intercept	-0.212	0.3673	-1.0205	0.5965	-0.5772	0.5755
Megafauna Functional Novelty (CWM)	0.0256	0.2796	-0.5897	0.6409	0.0917	0.9286
Simple Random						
Functional Traits						
<i>Abundance ~ Max. Muzzle Width (CWM), N=2103(152)</i>						
Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
intercept	-0.3525	0.0365	-0.4247	-0.2802	-9.6659	<0.0001
Max. Muzzle Width (CWM)	0.0143	0.0284	-0.0414	0.0701	0.505	0.6136
<i>Diversity ~ Max. Muzzle Width (CWM), N=407(60)</i>						
Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
intercept	-0.1798	0.0838	-0.3479	-0.0117	-2.1456	0.0365
Max. Muzzle Width (CWM)	0.2596	0.0692	0.1237	0.3956	3.7542	2.00E-04
<i>Abundance ~ Mean Muzzle Width (CWM), N=2103(152)</i>						
Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
intercept	-0.3527	0.0363	-0.4246	-0.2807	-9.7035	<0.0001
Mean Muzzle Width (CWM)	0.0526	0.0253	0.003	0.1022	2.0783	0.0378
<i>Diversity ~ Mean Muzzle Width (CWM), N=407(60)</i>						
Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
intercept	-0.1529	0.0961	-0.3456	0.0399	-1.591	0.1176
Mean Muzzle Width (CWM)	0.1947	0.0734	0.0503	0.339	2.6516	0.0083
<i>Abundance ~ Mean Body Mass (CWM), N=2135(154)</i>						
Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
intercept	-0.3524	0.0359	-0.4236	-0.2813	-9.813	<0.0001
Mean Body Mass (CWM)	0.0131	0.0216	-0.0292	0.0554	0.6069	0.544
<i>Diversity ~ Mean Body Mass (CWM), N=420(62)</i>						
Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
intercept	-0.1864	0.1001	-0.3867	0.0138	-1.8635	0.0675

Mean Body Mass (CWM)	0.1912	0.0855	0.0231	0.3593	2.2353	0.0259
<i>Abundance ~ Max. Body Mass (CWM), N=2135(154)</i>						
Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
intercept	-0.3515	0.0362	-0.4231	-0.2798	-9.7192	<0.0001
Max. Body Mass (CWM)	-0.0076	0.0232	-0.0531	0.0378	-0.33	0.7414
<i>Diversity ~ Max. Body Mass (CWM), N=420(62)</i>						
Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
intercept	-0.1907	0.1026	-0.3962	0.0147	-1.8581	0.0682
Max. Body Mass (CWM)	0.1632	0.084	-0.0019	0.3283	1.943	0.0527
<i>Abundance ~ Megafauna Biomass / NPP, N=1638(112)</i>						
Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
intercept	-0.3172	0.039	-0.3948	-0.2395	-8.1221	<0.0001
Megafauna Biomass / NPP	-0.0465	0.0174	-0.0806	-0.0124	-2.6747	0.0076
<i>Diversity ~ Megafauna Biomass / NPP, N=317(44)</i>						
Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
intercept	-0.1281	0.1225	-0.3756	0.1194	-1.0461	0.3018
Megafauna Biomass / NPP	0.0993	0.0783	-0.0548	0.2534	1.2677	0.2058
<i>Abundance ~ Plant Growth Form * Graminoid Preference (CWM), N=1730(120)</i>						
Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
intercept	-0.1675	0.0582	-0.283	-0.0519	-2.8776	0.005
Plant Growth FormGraminoid	-0.0547	0.0866	-0.2247	0.1153	-0.6317	0.5278
Plant Growth FormWoody	-0.1836	0.0655	-0.3121	-0.0551	-2.8047	0.0052
Graminoid Preference (CWM)	0.1468	0.0593	0.0306	0.2631	2.4772	0.0133
Plant Growth FormGraminoid:Graminoid Preference (CWM)	-0.2419	0.0768	-0.3925	-0.0913	-3.1508	0.0017
Plant Growth FormWoody:Graminoid Preference (CWM)	-0.1102	0.0694	-0.2463	0.0259	-1.588	0.1125
<i>Diversity ~ Plant Growth Form * Graminoid Preference (CWM), N=167(27)</i>						
Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
intercept	0.1137	0.2008	-0.3039	0.5312	0.5661	0.5773
Plant Growth FormGraminoid	-0.177	0.2796	-0.7392	0.3853	-0.6329	0.5298
Plant Growth FormWoody	-0.2225	0.2217	-0.6682	0.2232	-1.0037	0.3205
Graminoid Preference (CWM)	0.4029	0.1732	0.0436	0.7621	2.3255	0.0297
Plant Growth FormGraminoid:Graminoid Preference (CWM)	-0.6367	0.2463	-1.1232	-0.1503	-2.5848	0.0106
Plant Growth FormWoody:Graminoid Preference (CWM)	-0.1199	0.1948	-0.5045	0.2647	-0.6157	0.5389
<i>Abundance ~ Max. Body Mass (CWM) * Plant Nativeness, N=2306(161)</i>						
Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
Max. Body Mass (CWM)	0.102	0.1082	-0.1102	0.3142	0.9424	0.3461
Plant NativenessIntroduced	-0.0131	0.0879	-0.1857	0.1595	-0.1484	0.882
Plant NativenessNative	-0.3316	0.0341	-0.3985	-0.2648	-9.734	<0.0001
Max. Body Mass (CWM):Plant NativenessNative	-0.1116	0.108	-0.3234	0.1002	-1.033	0.3017
<i>Diversity ~ Max. Body Mass (CWM) * Plant Nativeness, N=460(63)</i>						
Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
Max. Body Mass (CWM)	-0.0148	0.3091	-0.6221	0.5925	-0.0479	0.9618
Plant NativenessIntroduced	0.1822	0.2121	-0.2377	0.602	0.8589	0.3921
Plant NativenessNative	-0.1829	0.1041	-0.3889	0.0232	-1.7568	0.0815
Max. Body Mass (CWM):Plant NativenessNative	0.1719	0.3068	-0.431	0.7748	0.5603	0.5756
<i>Abundance ~ Mean Body Mass (CWM) * Plant Nativeness, N=2306(161)</i>						
Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
Mean Body Mass (CWM)	0.1874	0.1115	-0.0312	0.406	1.6814	0.0928
Plant NativenessIntroduced	-0.0038	0.0854	-0.1715	0.1639	-0.0445	0.9645

Plant NativenessNative	-0.3329	0.0338	-0.3991	-0.2666	-9.8574	<0.0001
Mean Body Mass (CWM):Plant NativenessNative	-0.1759	0.1112	-0.394	0.0422	-1.5816	0.1139
<i>Diversity ~ Mean Body Mass (CWM) * Plant Nativeness, N=460(63)</i>						
Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
Mean Body Mass (CWM)	-0.1158	0.4035	-0.9087	0.6771	-0.287	0.7742
Plant NativenessIntroduced	0.2201	0.223	-0.2213	0.6615	0.9873	0.3255
Plant NativenessNative	-0.179	0.1026	-0.3822	0.0242	-1.7442	0.0837
Mean Body Mass (CWM):Plant NativenessNative	0.2962	0.4009	-0.4916	1.0841	0.739	0.4603
<i>Abundance ~ Proportion Hindgut (CWM), N=2135(154)</i>						
Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
intercept	-0.3526	0.0361	-0.424	-0.2812	-9.779	<0.0001
Proportion Hindgut (CWM)	0.0088	0.0275	-0.0452	0.0628	0.3186	0.7501
<i>Diversity ~ Proportion Hindgut (CWM), N=420(62)</i>						
Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
intercept	-0.1729	0.1091	-0.3913	0.0456	-1.5842	0.1186
Proportion Hindgut (CWM)	0.0176	0.0843	-0.1481	0.1834	0.209	0.8346
Simple Random						
Megafauna Diversity						
<i>Abundance ~ Number of Megafauna Species, N=2743(188)</i>						
Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
intercept	-0.3471	0.032	-0.4104	-0.2838	-10.8459	<0.0001
Number of Megafauna Species	-0.0555	0.019	-0.0928	-0.0182	-2.9167	0.0036
<i>Diversity ~ Number of Megafauna Species, N=591(73)</i>						
Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
intercept	-0.1127	0.0978	-0.308	0.0825	-1.152	0.2533
Number of Megafauna Species	0.0436	0.0315	-0.0184	0.1055	1.3806	0.1679
<i>Abundance ~ Number of Megafauna Functional Groups, N=2743(188)</i>						
Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
intercept	-0.3498	0.0322	-0.4135	-0.2861	-10.8555	<0.0001
Number of Megafauna Functional Groups	-0.0555	0.0195	-0.0937	-0.0172	-2.8424	0.0045
<i>Diversity ~ Number of Megafauna Functional Groups, N=591(73)</i>						
Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
intercept	-0.1115	0.0982	-0.3074	0.0845	-1.1349	0.2604
Number of Megafauna Functional Groups	0.0401	0.0319	-0.0225	0.1026	1.2582	0.2088
Final in Time Series / Largest Scale Measure Only						
Responses to Native and Introduced Megafauna						
<i>Abundance ~ Megafauna Nativeness * Plant Nativeness * Landform Evo. History, N=1909(196)</i>						
Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
Introduced-Introduced-absent	-0.24	0.1784	-0.5902	0.1101	-1.3451	0.1789
Introduced-Introduced-present	0.2813	0.1724	-0.0568	0.6194	1.6316	0.1029
Introduced-Native-absent	-0.3016	0.1119	-0.5212	-0.082	-2.6951	0.0072
Introduced-Native-present	-0.2915	0.0821	-0.4525	-0.1304	-3.5485	4.00E-04
Native-Introduced-present	-0.1674	0.1054	-0.374	0.0393	-1.5884	0.1124
Native-Native-present	-0.3505	0.0425	-0.4339	-0.267	-8.2373	<0.0001
<i>Diversity ~ Megafauna Nativeness * Landform Evo. History * Island, N=306(73)</i>						
Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
Introduced-absent-yes	-0.593	0.4456	-1.483	0.297	-1.3307	0.1879
Introduced-present-no	-0.0209	0.2887	-0.5975	0.5557	-0.0724	0.9425
Introduced-present-yes	-0.3248	0.3267	-0.9772	0.3276	-0.9941	0.3238

Native-present-no	0.0224	0.1313	-0.2398	0.2847	0.1707	0.865
Native-present-yes	-1.0669	0.4206	-1.9068	-0.227	-2.5368	0.0136
<i>Diversity ~ Invasive, N=306(73)</i>						
Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
100 Worst	0.1145	0.327	-0.5381	0.767	0.35	0.7274
Other	-0.1584	0.1179	-0.3937	0.0768	-1.3439	0.1834
<i>Abundance ~ Invasive, N=1754(188)</i>						
Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
100 Worst	-0.3068	0.1034	-0.5112	-0.1024	-2.9677	0.0035
Other	-0.3616	0.0417	-0.444	-0.2791	-8.6709	<0.0001
<i>Diversity ~ Feral, N=306(73)</i>						
Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
Feral	-0.1003	0.2455	-0.5902	0.3896	-0.4085	0.6842
Non Feral	-0.1334	0.1224	-0.3775	0.1108	-1.0901	0.2795
<i>Abundance ~ Feral, N=1754(188)</i>						
Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
Feral	-0.2476	0.0832	-0.4121	-0.0831	-2.9759	0.0034
Non Feral	-0.3823	0.0432	-0.4677	-0.2969	-8.851	<0.0001
<i>Diversity ~ Megafauna Nativeness * Plant Nativeness, N=344(74)</i>						
Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
Introduced-Introduced	0.2944	0.311	-0.3173	0.9061	0.9465	0.3445
Introduced-Native	-0.263	0.1936	-0.6439	0.1178	-1.3584	0.1752
Native-Introduced	0.1207	0.2445	-0.3603	0.6017	0.4935	0.622
Native-Native	-0.0737	0.1257	-0.3209	0.1735	-0.5863	0.5581
Final in Time Series / Largest Scale Measure Only						
Coevolutionary History and Novelty						
<i>Abundance ~ Plant-Megafauna Coev., N=959(76)</i>						
Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
No	-0.186	0.0728	-0.3288	-0.0431	-2.5562	0.0108
Yes	-0.249	0.0493	-0.3458	-0.1522	-5.0512	<0.0001
<i>Abundance ~ Plant-Megafauna Phylogenetic Novelty (CWM), N=93(17)</i>						
Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
intercept	-0.0912	0.091	-0.2853	0.1028	-1.002	0.3322
Plant-Megafauna Phylogenetic Novelty (CWM)	0.1817	0.1062	-0.0293	0.3927	1.7108	0.0905
<i>Abundance ~ Plant-Megafauna Functional Novelty (CWM), N=93(17)</i>						
Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
intercept	-0.0965	0.0913	-0.2912	0.0982	-1.0569	0.3073
Plant-Megafauna Functional Novelty (CWM)	0.1245	0.0944	-0.0631	0.3121	1.3186	0.1906
<i>Diversity ~ Coevolved Biome, N=306(73)</i>						
Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
No	0.0468	0.3477	-0.647	0.7406	0.1346	0.8933
Yes	-0.1469	0.1173	-0.3811	0.0872	-1.2525	0.2147
<i>Diversity ~ Megafauna Phylogenetic Novelty (CWM), N=78(15)</i>						
Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
intercept	-0.1457	0.3583	-0.9342	0.6428	-0.4067	0.692
Megafauna Phylogenetic Novelty (CWM)	0.1581	0.2947	-0.4904	0.8067	0.5367	0.6022
<i>Diversity ~ Megafauna Functional Novelty (CWM), N=78(15)</i>						
Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
intercept	-0.1482	0.3637	-0.9487	0.6523	-0.4074	0.6916

Megafauna Functional Novelty (CWM)	0.0245	0.2516	-0.5293	0.5783	0.0974	0.9241
Final in Time Series / Largest Scale Measure Only						
Functional Traits						
<i>Abundance ~ Max. Muzzle Width (CWM), N=1500(152)</i>						
Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
intercept	-0.3516	0.0431	-0.4369	-0.2663	-8.1604	<0.0001
Max. Muzzle Width (CWM)	0.0243	0.0317	-0.0378	0.0864	0.7675	0.4429
<i>Diversity ~ Max. Muzzle Width (CWM), N=238(60)</i>						
Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
intercept	-0.1787	0.1169	-0.4132	0.0557	-1.529	0.1322
Max. Muzzle Width (CWM)	0.2371	0.1002	0.0397	0.4345	2.3663	0.0188
<i>Abundance ~ Mean Muzzle Width (CWM), N=1500(152)</i>						
Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
intercept	-0.3487	0.0429	-0.4337	-0.2637	-8.128	<0.0001
Mean Muzzle Width (CWM)	0.0567	0.0261	0.0055	0.1079	2.174	0.0299
<i>Diversity ~ Mean Muzzle Width (CWM), N=238(60)</i>						
Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
intercept	-0.1453	0.1198	-0.3855	0.095	-1.2126	0.2307
Mean Muzzle Width (CWM)	0.2264	0.0928	0.0436	0.4092	2.4395	0.0154
<i>Abundance ~ Mean Body Mass (CWM), N=1532(154)</i>						
Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
intercept	-0.3518	0.0426	-0.4362	-0.2675	-8.2576	<0.0001
Mean Body Mass (CWM)	0.0166	0.0241	-0.0306	0.0638	0.6902	0.4902
<i>Diversity ~ Mean Body Mass (CWM), N=251(62)</i>						
Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
intercept	-0.1916	0.12	-0.4318	0.0486	-1.5968	0.1158
Mean Body Mass (CWM)	0.1814	0.1123	-0.0399	0.4027	1.6147	0.1077
<i>Abundance ~ Max. Body Mass (CWM), N=1532(154)</i>						
Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
intercept	-0.3519	0.043	-0.4369	-0.2668	-8.1928	<0.0001
Max. Body Mass (CWM)	-0.0048	0.0258	-0.0554	0.0457	-0.188	0.8509
<i>Diversity ~ Max. Body Mass (CWM), N=251(62)</i>						
Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
intercept	-0.1922	0.1222	-0.4369	0.0524	-1.5728	0.1212
Max. Body Mass (CWM)	0.1157	0.1074	-0.0957	0.3272	1.0778	0.2822
<i>Abundance ~ Megafauna Biomass / NPP, N=1142(112)</i>						
Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
intercept	-0.3177	0.0486	-0.4143	-0.2212	-6.5427	<0.0001
Megafauna Biomass / NPP	-0.0297	0.0174	-0.0639	0.0045	-1.7042	0.0886
<i>Diversity ~ Megafauna Biomass / NPP, N=165(44)</i>						
Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
intercept	-0.1626	0.1478	-0.4614	0.1362	-1.0996	0.2781
Megafauna Biomass / NPP	0.0898	0.1103	-0.128	0.3076	0.8142	0.4167
<i>Abundance ~ Plant Growth Form * Graminoid Preference (CWM), N=1301(120)</i>						
Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
intercept	-0.161	0.0602	-0.2807	-0.0414	-2.6729	0.0089
Plant Growth FormGraminoid	-0.0448	0.0897	-0.2208	0.1312	-0.5	0.6172
Plant Growth FormWoody	-0.1998	0.0687	-0.3347	-0.0648	-2.9069	0.0038
Graminoid Preference (CWM)	0.1519	0.0631	0.028	0.2758	2.4052	0.0163

Plant Growth FormGraminoid:Graminoid Preference (CWM)	-0.2502	0.0825	-0.4121	-0.0883	-3.031	0.0025
Plant Growth FormWoody:Graminoid Preference (CWM)	-0.1368	0.0748	-0.2837	0.01	-1.8283	0.0677
<i>Diversity ~ Plant Growth Form * Graminoid Preference (CWM), N=121(27)</i>						
Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
intercept	0.1449	0.2075	-0.2866	0.5763	0.6982	0.4927
Plant Growth FormGraminoid	-0.2656	0.2835	-0.8356	0.3044	-0.9369	0.3535
Plant Growth FormWoody	-0.2578	0.2275	-0.7152	0.1995	-1.1335	0.2626
Graminoid Preference (CWM)	0.4603	0.1882	0.07	0.8505	2.4457	0.0229
Plant Growth FormGraminoid:Graminoid Preference (CWM)	-0.6762	0.263	-1.1971	-0.1552	-2.5709	0.0114
Plant Growth FormWoody:Graminoid Preference (CWM)	-0.1547	0.2064	-0.5636	0.2542	-0.7494	0.4551
<i>Abundance ~ Max. Body Mass (CWM) * Plant Nativeness, N=1661(161)</i>						
Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
Max. Body Mass (CWM)	0.1049	0.1257	-0.1418	0.3515	0.834	0.4044
Plant NativenessIntroduced	-0.0018	0.1015	-0.2009	0.1974	-0.0175	0.986
Plant NativenessNative	-0.3273	0.0397	-0.4052	-0.2493	-8.2392	<0.0001
Max. Body Mass (CWM):Plant NativenessNative	-0.1109	0.1254	-0.3569	0.1351	-0.8842	0.3767
<i>Diversity ~ Max. Body Mass (CWM) * Plant Nativeness, N=284(63)</i>						
Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
Max. Body Mass (CWM)	-0.3121	0.3445	-0.9902	0.366	-0.9059	0.3658
Plant NativenessIntroduced	0.2054	0.2205	-0.2311	0.6418	0.9315	0.3535
Plant NativenessNative	-0.1824	0.122	-0.4238	0.0591	-1.4954	0.1374
Max. Body Mass (CWM):Plant NativenessNative	0.4252	0.3388	-0.2417	1.0921	1.2549	0.2105
<i>Abundance ~ Mean Body Mass (CWM) * Plant Nativeness, N=1661(161)</i>						
Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
Mean Body Mass (CWM)	0.1989	0.1301	-0.0563	0.4542	1.5285	0.1266
Plant NativenessIntroduced	0.0152	0.0994	-0.1799	0.2102	0.1525	0.8788
Plant NativenessNative	-0.3275	0.0393	-0.4046	-0.2503	-8.3295	<0.0001
Mean Body Mass (CWM):Plant NativenessNative	-0.1834	0.1298	-0.4379	0.0712	-1.413	0.1579
<i>Diversity ~ Mean Body Mass (CWM) * Plant Nativeness, N=284(63)</i>						
Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
Mean Body Mass (CWM)	-0.4118	0.4649	-1.3269	0.5033	-0.8858	0.3765
Plant NativenessIntroduced	0.2341	0.226	-0.2134	0.6816	1.0357	0.3024
Plant NativenessNative	-0.1815	0.1203	-0.4197	0.0566	-1.5089	0.1339
Mean Body Mass (CWM):Plant NativenessNative	0.5839	0.4597	-0.321	1.4887	1.2702	0.2051
<i>Abundance ~ Proportion Hindgut (CWM), N=1532(154)</i>						
Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
intercept	-0.3528	0.0427	-0.4374	-0.2683	-8.2663	<0.0001
Proportion Hindgut (CWM)	0.0244	0.0309	-0.0362	0.0849	0.7887	0.4304
<i>Diversity ~ Proportion Hindgut (CWM), N=251(62)</i>						
Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
intercept	-0.1859	0.1242	-0.4344	0.0627	-1.4967	0.1399
Proportion Hindgut (CWM)	0.073	0.1098	-0.1433	0.2894	0.665	0.5067
Final in Time Series / Largest Scale Measure Only						
Megafauna Diversity						
<i>Abundance ~ Number of Megafauna Species, N=1754(188)</i>						
Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
intercept	-0.3501	0.0384	-0.426	-0.2742	-9.1131	<0.0001
Number of Megafauna Species	-0.0358	0.0217	-0.0784	0.0067	-1.651	0.0989
<i>Diversity ~ Number of Megafauna Species, N=306(73)</i>						

Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
intercept	-0.1255	0.1109	-0.3468	0.0957	-1.1324	0.2615
Number of Megafauna Species	0.0588	0.0364	-0.0128	0.1305	1.616	0.1071

Abundance ~ Number of Megafauna Functional Groups, N=1754(188)

Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
intercept	-0.3512	0.0385	-0.4274	-0.275	-9.1113	<0.0001
Number of Megafauna Functional Groups	-0.0315	0.0224	-0.0753	0.0124	-1.4059	0.1599

Diversity ~ Number of Megafauna Functional Groups, N=306(73)

Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
intercept	-0.1243	0.1111	-0.346	0.0974	-1.1187	0.2672
Number of Megafauna Functional Groups	0.061	0.0361	-0.01	0.132	1.6906	0.0919

Species-level Responses Only

Responses to Native and Introduced Megafauna

*Abundance ~ Megafauna Nativeness * Plant Nativeness * Landform Evo. History, N=1262(76)*

Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
Introduced-Introduced-absent	-0.428	0.2182	-0.8566	5.00E-04	-1.9615	0.0503
Introduced-Introduced-present	-0.0485	0.2126	-0.466	0.3691	-0.2279	0.8198
Introduced-Native-absent	-0.2571	0.1335	-0.5192	0.0051	-1.9258	0.0546
Introduced-Native-present	-0.3029	0.1198	-0.5382	-0.0676	-2.5283	0.0117
Native-Introduced-present	-0.2127	0.1138	-0.4361	0.0108	-1.8694	0.0621
Native-Native-present	-0.2735	0.0598	-0.3908	-0.1561	-4.5755	<0.0001

Abundance ~ Invasive, N=1145(67)

Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
100 Worst	-0.1679	0.1265	-0.4211	0.0852	-1.3274	0.1895
Other	-0.2999	0.054	-0.4079	-0.1919	-5.5569	<0.0001

Abundance ~ Feral, N=1145(67)

Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
Feral	-0.2505	0.106	-0.4626	-0.0385	-2.3639	0.0214
Non Feral	-0.2906	0.0571	-0.4049	-0.1764	-5.0891	<0.0001

Pure Megafauna Nativeness

Responses to Native and Introduced Megafauna

*Abundance ~ Megafauna Nativeness * Plant Nativeness * Landform Evo. History, N=2945(195)*

Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
Introduced-Introduced-absent	-0.2649	0.1523	-0.5638	0.0341	-1.7386	0.0824
Introduced-Introduced-present	0.1932	0.1648	-0.13	0.5164	1.1723	0.2412
Introduced-Native-absent	-0.2467	0.0941	-0.4314	-0.0621	-2.6224	0.0089
Introduced-Native-present	-0.3797	0.0728	-0.5224	-0.2369	-5.217	<0.0001
Native-Introduced-present	-0.1128	0.0962	-0.3014	0.0758	-1.1725	0.2411
Native-Native-present	-0.3392	0.0361	-0.41	-0.2685	-9.4047	<0.0001

Abundance ~ Invasive, N=2714(187)

Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
100 Worst	-0.2436	0.0873	-0.4162	-0.071	-2.7901	0.006
Other	-0.3786	0.0358	-0.4494	-0.3078	-10.5712	<0.0001

Abundance ~ Feral, N=2714(187)

Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
Feral	-0.2949	0.0741	-0.4414	-0.1485	-3.9813	1.00E-04
Non Feral	-0.3757	0.037	-0.4489	-0.3024	-10.143	<0.0001

Pure Megafauna Nativeness

Coevolutionary History and Novelty

Abundance ~ Plant-Megafauna Coev., N=1247(76)

Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
No	-0.2009	0.0816	-0.361	-0.0407	-2.4629	0.0141
Yes	-0.2988	0.0552	-0.4072	-0.1905	-5.4174	<0.0001

Abundance ~ Plant-Megafauna Phylogenetic Novelty (CWM), N=105(16)

Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
intercept	-0.1612	0.1154	-0.4087	0.0863	-1.3972	0.1841
Plant-Megafauna Phylogenetic Novelty (CWM)	0.2384	0.1241	-0.0081	0.485	1.9219	0.0578

Abundance ~ Plant-Megafauna Functional Novelty (CWM), N=105(16)

Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
intercept	-0.1369	0.1183	-0.3907	0.1168	-1.1573	0.2665
Plant-Megafauna Functional Novelty (CWM)	0.124	0.1174	-0.1094	0.3573	1.0559	0.2939

Unspecified Nativeness Plants Excluded**Responses to Native and Introduced Megafauna**

*Diversity ~ Megafauna Nativeness * Reported Plant Nativeness, N=771(92)*

Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
Introduced-Introduced	0.3174	0.2287	-0.1321	0.7669	1.388	0.1659
Introduced-Mixed	-0.1021	0.2158	-0.5263	0.322	-0.4733	0.6363
Introduced-Native	-0.0862	0.159	-0.3987	0.2262	-0.5425	0.5877
Introduced-Unspecified	-0.752	0.2491	-1.244	-0.26	-3.019	0.003
Native-Introduced	0.1853	0.2	-0.2077	0.5784	0.9268	0.3546
Native-Mixed	-0.0105	0.1855	-0.3751	0.3542	-0.0563	0.9551
Native-Native	0.0367	0.1039	-0.1676	0.241	0.3526	0.7245
Native-Unspecified	-0.2763	0.2113	-0.6966	0.144	-1.3075	0.1946

*Diversity ~ Megafauna Nativeness * Landform Evo. History * Island, N=433(56)*

Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
Introduced-absent-yes	-0.2494	0.2744	-0.801	0.3023	-0.9088	0.368
Introduced-present-no	0.2602	0.2013	-0.1445	0.6649	1.2929	0.2022
Introduced-present-yes	-0.2677	0.2432	-0.7567	0.2212	-1.1009	0.2764
Native-present-no	0.0556	0.0863	-0.118	0.2292	0.6439	0.5227
Native-present-yes	-0.0819	0.2857	-0.6563	0.4924	-0.2869	0.7754

Diversity ~ Invasive, N=433(56)

Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
100 Worst	0.0703	0.1923	-0.3157	0.4564	0.3658	0.7161
Other	0.0129	0.083	-0.1537	0.1794	0.1549	0.8775

Diversity ~ Feral, N=433(56)

Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
Feral	0.0759	0.161	-0.2473	0.399	0.4712	0.6395
Non Feral	0.0079	0.0843	-0.1613	0.1772	0.0941	0.9254

Unspecified Nativeness Plants Excluded**Coevolutionary History and Novelty**

Diversity ~ Coevolved Biome, N=433(56)

Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
No	0.0071	0.2026	-0.3996	0.4139	0.0352	0.9721
Yes	0.0243	0.0823	-0.141	0.1896	0.2952	0.769

Diversity ~ Megafauna Phylogenetic Novelty (CWM), N=66(10)

Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
intercept	0.1391	0.284	-0.5559	0.8342	0.4899	0.6416
Megafauna Phylogenetic Novelty (CWM)	-0.0193	0.2635	-0.664	0.6255	-0.0731	0.9441

Diversity ~ Megafauna Functional Novelty (CWM), N=66(10)

Term	Estimate	SE	Lower CI	Upper CI	t-statistic	p-value
intercept	0.1366	0.284	-0.5584	0.8316	0.4809	0.6476
Megafauna Functional Novelty (CWM)	-0.0238	0.2922	-0.7389	0.6912	-0.0816	0.9376

Table S2.

Model comparison table indicating model formulas per each comparison, sample size, likelihood ratio test results, and nativeness planned contrast test results. Each row is a model comparison series consisting of a null model, a base model, and a nativeness model, each with increasing level of complexity and all trained on the same data. Note that some analyses (e.g., 'Invasive' and Feral) lack a null model. Sample sizes for each analysis are indicated with number of responses and number of studies in parentheses for native megafauna and introduced megafauna respectively. Likelihood ratio test results for the base model compared to the null model ("Base LRT") and the nativeness model compared to the base model ("Nativeness LRT") are indicated with likelihood ratios (LR) and p-values. Planned contrast tests compare native and introduced megafauna impacts. In models with more than one contrast between native and introduced megafauna impacts (e.g., per plant nativeness level or landform type), the minimum and maximum of test statistics and p values are given within square brackets. Main text analyses ('Primary Analyses') are followed by sensitivity analyses, which include: 'Simple Random'=models do not include a temporal autocorrelation term; 'Final in Time Series / Largest Scale Measure Only'=the last time point and the largest scale measurement from each experiment were selected, instead of being controlled for with random effects; 'Species-level Responses Only'=collective plant abundance responses omitted, only species-level abundances included; 'Pure Megafauna Nativeness'=data from studies with more than one nativeness of manipulated megafauna were excluded (1 study); and 'Unspecified Nativeness Plants Excluded'=plants of unspecified nativeness were excluded from diversity analysis.

Models	Sample Size	Base LRT (LR, p-value)	Nativeness LRT (LR, p-value)	Planned contrast (z, p-value ranges)
Primary Analyses				
Responses to Native and Introduced Megafauna				
Null: Abundance ~ Landform Evo. History				
Base: Abundance ~ Plant Nativeness * Landform Evo. History	2,241(141)			
Nativeness: Abundance ~ Megafauna Nativeness * Plant Nativeness * Landform Evo. History	733(56)	13.01, 0.001***	3.52, 0.172	[-0.85, 1.63], [0.347, 0.936]
Null: Abundance ~ 1				
Base: Abundance ~ Landform Evo. History	2,241(141)			
Nativeness: Abundance ~ Megafauna Nativeness * Landform Evo. History	733(56)	0.64, 0.425	0, 0.978	[-0.03, 0.78], [0.676, 0.999]
Null: Diversity ~ Island				
Base: Diversity ~ Landform Evo. History * Island	401(53)			
Nativeness: Diversity ~ Megafauna Nativeness * Landform Evo. History * Island	190(21)	0.23, 0.63	2, 0.368	[-1.82, 1.2], [0.218, 0.996]
Null:				
Base: Diversity ~ 1	401(53)			
Nativeness: Diversity ~ Invasive	190(21)		0.46, 0.497	0.68, 0.497
Null:				
Base: Abundance ~ 1	2,129(137)			
Nativeness: Abundance ~ Invasive	614(52)		2.12, 0.145	1.46, 0.145
Null:				
Base: Diversity ~ 1	401(53)			
Nativeness: Diversity ~ Feral	190(21)		0.25, 0.617	-0.52, 0.601
Null:				
Base: Abundance ~ 1	2,129(137)			
Nativeness: Abundance ~ Feral	614(52)		0.67, 0.413	0.82, 0.412
Null: Diversity ~ 1				
Base: Diversity ~ Plant Nativeness	430(53)			
Nativeness: Diversity ~ Megafauna Nativeness * Plant Nativeness	208(22)	3.15, 0.076	3.04, 0.219	[-1.49, 0.43], [0.249, 0.884]
Null: Abundance ~ 1				
Base: Abundance ~ Plant Nativeness	2,241(141)			
Nativeness: Abundance ~ Megafauna Nativeness * Plant Nativeness	733(56)	9.98, 0.002***	0.1, 0.95	[0.05, 0.32], [0.936, 0.998]
Coevolutionary History and Novelty				
Null:				
Base: Abundance ~ 1	932(52)			
Nativeness: Abundance ~ Plant-Megafauna Coev.	315(24)		1.37, 0.241	1.17, 0.24
Null:				
Base: Abundance ~ 1	41(9)			
Nativeness: Abundance ~ Plant-Megafauna Phylogenetic Novelty (CWM)	74(8)		1.38, 0.24	
Null:				
Base: Abundance ~ 1	41(9)			
Nativeness: Abundance ~ Plant-Megafauna Functional Novelty (CWM)	74(8)		0.85, 0.358	
Null:				
Base: Diversity ~ 1	401(53)			
Nativeness: Diversity ~ Coevolved Biome	190(21)		0.15, 0.696	0.39, 0.695
Null:				
Base: Diversity ~ 1	162(15)			
Nativeness: Diversity ~ Megafauna Phylogenetic Novelty (CWM)	162(15)		0.44, 0.508	
Null:				
Base: Diversity ~ 1	162(15)			
Nativeness: Diversity ~ Megafauna Functional Novelty (CWM)	162(15)		0, 0.992	
Functional Traits				
Null: Abundance ~ 1				
Base: Abundance ~ Max. Muzzle Width (CWM)	1,650(112)			
Nativeness: Abundance ~ Megafauna Nativeness + Max. Muzzle Width (CWM)	453(41)	0.28, 0.597	0.72, 0.396	-0.86, 0.389
Null: Diversity ~ 1				
Base: Diversity ~ Max. Muzzle Width (CWM)	223(43)			
Nativeness: Diversity ~ Megafauna Nativeness + Max. Muzzle Width (CWM)	184(18)	9.3, 0.002***	0.83, 0.362	-0.92, 0.359
Null: Abundance ~ 1				
Base: Abundance ~ Mean Muzzle Width (CWM)	1,650(112)			
Nativeness: Abundance ~ Megafauna Nativeness + Mean Muzzle Width (CWM)	453(41)	2.6, 0.107	0.86, 0.353	-0.94, 0.347
Null: Diversity ~ 1				
Base: Diversity ~ Mean Muzzle Width (CWM)	223(43)			
Nativeness: Diversity ~ Megafauna Nativeness + Mean Muzzle Width (CWM)	184(18)	5.77, 0.016*	1.26, 0.261	-1.17, 0.242
Null: Abundance ~ 1				
Base: Abundance ~ Mean Body Mass (CWM)	1,682(114)			
Nativeness: Abundance ~ Megafauna Nativeness + Mean Body Mass (CWM)	453(41)	1.35, 0.245	0.62, 0.432	-0.8, 0.424
Null: Diversity ~ 1				
Base: Diversity ~ Mean Body Mass (CWM)	236(45)			
Nativeness: Diversity ~ Megafauna Nativeness + Mean Body Mass (CWM)	184(18)	4.59, 0.032*	0.47, 0.491	-0.7, 0.483

Null: Abundance ~ 1					
Base: Abundance ~ Max. Body Mass (CWM)	1,682(114)				
Nativeness: Abundance ~ Megafauna Nativeness + Max. Body Mass (CWM)	453(41)	0.17, 0.681	0.69, 0.406	-0.84, 0.398	
Null: Diversity ~ 1					
Base: Diversity ~ Max. Body Mass (CWM)	236(45)				
Nativeness: Diversity ~ Megafauna Nativeness + Max. Body Mass (CWM)	184(18)	3.52, 0.061	0.32, 0.573	-0.57, 0.569	
Null: Abundance ~ 1					
Base: Abundance ~ Megafauna Biomass / NPP	1,268(82)				
Nativeness: Abundance ~ Megafauna Nativeness + Megafauna Biomass / NPP	370(30)	2.37, 0.123	2.27, 0.132	-1.53, 0.126	
Null: Diversity ~ 1					
Base: Diversity ~ Megafauna Biomass / NPP	156(31)				
Nativeness: Diversity ~ Megafauna Nativeness + Megafauna Biomass / NPP	161(13)	1.25, 0.263	1.46, 0.228	-1.23, 0.218	
Null: Abundance ~ 1					
Base: Abundance ~ Plant Growth Form * Graminoid Preference (CWM)	1,407(92)				
Nativeness: Abundance ~ Megafauna Nativeness + Plant Growth Form * Graminoid Preference (CWM)	323(28)	16.29, 0.006***	0.01, 0.939	0.08, 0.937	
Null: Diversity ~ 1					
Base: Diversity ~ Plant Growth Form * Graminoid Preference (CWM)	133(22)				
Nativeness: Diversity ~ Megafauna Nativeness + Plant Growth Form * Graminoid Preference (CWM)	34(5)	15.09, 0.01***	0.15, 0.701	-0.39, 0.7	
Null: Abundance ~ Max. Body Mass (CWM)					
Base: Abundance ~ Max. Body Mass (CWM) * Plant Nativeness	1,789(118)				
Nativeness: Abundance ~ Max. Body Mass (CWM) * Megafauna Nativeness * Plant Nativeness	517(44)	13.81, 0.001***	2.43, 0.658	[-1.01, 0.54], [0.521, 0.827]	
Null: Diversity ~ Max. Body Mass (CWM)					
Base: Diversity ~ Max. Body Mass (CWM) * Plant Nativeness	261(45)				
Nativeness: Diversity ~ Max. Body Mass (CWM) * Megafauna Nativeness * Plant Nativeness	199(19)	3.47, 0.177	2.23, 0.694	[-0.46, 0.74], [0.696, 0.866]	
Null: Abundance ~ Mean Body Mass (CWM)					
Base: Abundance ~ Mean Body Mass (CWM) * Plant Nativeness	1,789(118)				
Nativeness: Abundance ~ Mean Body Mass (CWM) * Megafauna Nativeness * Plant Nativeness	517(44)	15.4, 0**	5.36, 0.252	[-1, 0.17], [0.533, 0.882]	
Null: Diversity ~ Mean Body Mass (CWM)					
Base: Diversity ~ Mean Body Mass (CWM) * Plant Nativeness	261(45)				
Nativeness: Diversity ~ Mean Body Mass (CWM) * Megafauna Nativeness * Plant Nativeness	199(19)	3.67, 0.16	1.95, 0.745	[-0.55, 0.47], [0.817, 0.864]	
Null: Abundance ~ 1					
Base: Abundance ~ Proportion Hindgut (CWM)	1,682(114)				
Nativeness: Abundance ~ Megafauna Nativeness + Proportion Hindgut (CWM)	453(41)	0.29, 0.587	1.28, 0.257	-1.16, 0.248	
Null: Diversity ~ 1					
Base: Diversity ~ Proportion Hindgut (CWM)	236(45)				
Nativeness: Diversity ~ Megafauna Nativeness + Proportion Hindgut (CWM)	184(18)	0.24, 0.626	0.9, 0.343	-0.96, 0.335	

Environmental Factors

Null: Abundance ~ 1					
Base: Abundance ~ Max. Annual Precip.	2,129(137)				
Nativeness: Abundance ~ Megafauna Nativeness + Max. Annual Precip.	614(52)	1.48, 0.224	0.34, 0.562	0.58, 0.561	
Null: Diversity ~ 1					
Base: Diversity ~ Max. Annual Precip.	401(53)				
Nativeness: Diversity ~ Megafauna Nativeness + Max. Annual Precip.	190(21)	3.2, 0.074	0.27, 0.604	-0.54, 0.586	
Null: Abundance ~ 1					
Base: Abundance ~ Max. Annual Temp.	2,129(137)				
Nativeness: Abundance ~ Megafauna Nativeness + Max. Annual Temp.	614(52)	0.41, 0.521	0.02, 0.876	0.16, 0.876	
Null: Diversity ~ 1					
Base: Diversity ~ Max. Annual Temp.	401(53)				
Nativeness: Diversity ~ Megafauna Nativeness + Max. Annual Temp.	190(21)	0.82, 0.365	1.45, 0.229	-1.23, 0.219	
Null: Abundance ~ 1					
Base: Abundance ~ Net Primary Productivity	2,129(137)				
Nativeness: Abundance ~ Megafauna Nativeness + Net Primary Productivity	614(52)	1.8, 0.179	0.25, 0.619	0.5, 0.618	
Null: Diversity ~ 1					
Base: Diversity ~ Net Primary Productivity	401(53)				
Nativeness: Diversity ~ Megafauna Nativeness + Net Primary Productivity	190(21)	0.29, 0.591	1.59, 0.207	-1.29, 0.197	
Null: Abundance ~ 1					
Base: Abundance ~ Human Footprint Index	2,129(137)				
Nativeness: Abundance ~ Megafauna Nativeness + Human Footprint Index	614(52)	0.02, 0.884	0, 0.968	0.04, 0.968	
Null: Diversity ~ 1					
Base: Diversity ~ Human Footprint Index	401(53)				
Nativeness: Diversity ~ Megafauna Nativeness + Human Footprint Index	190(21)	0.42, 0.518	1.42, 0.234	-1.23, 0.217	
Null: Abundance ~ 1					
Base: Abundance ~ Island	2,129(137)				
Nativeness: Abundance ~ Megafauna Nativeness * Island	614(52)	0, 1	0.42, 0.81	[-0.52, 0.39], [0.841, 0.91]	
Null: Diversity ~ 1					
Base: Diversity ~ Island	401(53)				
Nativeness: Diversity ~ Megafauna Nativeness * Island	190(21)	5.59, 0.018*	1.46, 0.483	[-0.83, 0.94], [0.575, 0.645]	

Megafauna Diversity

Null: Abundance ~ 1					
Base: Abundance ~ Number of Megafauna Species	2,129(137)				
Nativeness: Abundance ~ Megafauna Nativeness + Number of Megafauna Species	614(52)	3.01, 0.083	0, 0.965	-0.04, 0.965	
Null: Diversity ~ 1					
Base: Diversity ~ Number of Megafauna Species	401(53)				
Nativeness: Diversity ~ Megafauna Nativeness + Number of Megafauna Species	190(21)	0.63, 0.427	1.57, 0.211	-1.28, 0.201	
Null: Abundance ~ 1					
Base: Abundance ~ Number of Megafauna Functional Groups	2,129(137)				
Nativeness: Abundance ~ Megafauna Nativeness + Number of Megafauna Species	614(52)	2.43, 0.119	0.58, 0.448	-0.04, 0.965	
Null: Diversity ~ 1					
Base: Diversity ~ Number of Megafauna Functional Groups	401(53)				
Nativeness: Diversity ~ Megafauna Nativeness + Number of Megafauna Species	190(21)	0.46, 0.496	1.73, 0.188	-1.28, 0.201	
Null: Abundance ~ Number of Megafauna Species					
Base: Abundance ~ Number of Megafauna Species * Plant Nativeness	2,241(141)				
Nativeness: Abundance ~ Number of Megafauna Species * Megafauna Nativeness * Plant Nativeness	733(56)	15.28, 0**	3.13, 0.536	[0.01, 1.11], [0.462, 1]	
Null: Diversity ~ Number of Megafauna Species					
Base: Diversity ~ Number of Megafauna Species * Plant Nativeness	430(53)				
Nativeness: Diversity ~ Number of Megafauna Species * Megafauna Nativeness * Plant Nativeness	208(22)	4, 0.135	3.09, 0.543	[-0.88, 0.46], [0.593, 0.865]	
Null: Abundance ~ Number of Megafauna Functional Groups					
Base: Abundance ~ Number of Megafauna Functional Groups * Plant Nativeness	2,241(141)				
Nativeness: Abundance ~ Number of Megafauna Functional Groups * Megafauna Nativeness * Plant Nativeness	733(56)	14.92, 0.001**	4.19, 0.381	[0.08, 1.47], [0.264, 0.996]	

Null: Diversity ~ Number of Megafauna Functional Groups				
Base: Diversity ~ Number of Megafauna Functional Groups * Plant Nativeness	430(53)			[-1.09, 0.89]
Nativeness: Diversity ~ Number of Megafauna Functional Groups * Megafauna Nativeness * Plant Nativeness	208(22)	4.11, 0.128	3.98, 0.408	[0.461, 0.592]
Methodological Factors				
Null: Diversity ~ 1				
Base: Diversity ~ Measurement Area (m2)	396(50)			
Nativeness: Diversity ~ Megafauna Nativeness + Measurement Area (m2)	171(17)	4.44, 0.035*	1.16, 0.282	-1.11, 0.269
Null: Diversity ~ 1				
Base: Diversity ~ Max. Measurement Length (m)	400(52)			
Nativeness: Diversity ~ Megafauna Nativeness + Max. Measurement Length (m)	173(18)	5.86, 0.015*	0.85, 0.356	-0.95, 0.343
Null: Abundance ~ 1				
Base: Abundance ~ Treatment Duration / NPP	1,934(125)			
Nativeness: Abundance ~ Megafauna Nativeness + Treatment Duration / NPP	601(49)	0.07, 0.796	0, 0.959	-0.05, 0.959
Null: Diversity ~ 1				
Base: Diversity ~ Treatment Duration / NPP	393(49)			
Nativeness: Diversity ~ Megafauna Nativeness + Treatment Duration / NPP	183(20)	0.5, 0.481	2.61, 0.106	-1.66, 0.097
Null: Abundance ~ 1				
Base: Abundance ~ Treatment Duration	1,934(125)			
Nativeness: Abundance ~ Megafauna Nativeness + Treatment Duration	601(49)	1.18, 0.278	0.01, 0.916	-0.11, 0.916
Null: Diversity ~ 1				
Base: Diversity ~ Treatment Duration	393(49)			
Nativeness: Diversity ~ Megafauna Nativeness + Treatment Duration	183(20)	0.36, 0.549	2.72, 0.099	-1.7, 0.089
Null: Abundance ~ 1				
Base: Abundance ~ Treatment Duration * Net Primary Productivity	1,934(125)			
Nativeness: Abundance ~ Megafauna Nativeness + Treatment Duration * Net Primary Productivity	601(49)	7.8, 0.05	0.18, 0.669	0.43, 0.669
Null: Diversity ~ 1				
Base: Diversity ~ Treatment Duration * Net Primary Productivity	393(49)			
Nativeness: Diversity ~ Megafauna Nativeness + Treatment Duration * Net Primary Productivity	183(20)	4.47, 0.215	2.24, 0.135	-1.53, 0.125
Simple Random Responses to Native and Introduced Megafauna				
Null: Abundance ~ Landform Evo. History				
Base: Abundance ~ Plant Nativeness * Landform Evo. History	2,241(141)			[-0.77, 2.3]
Nativeness: Abundance ~ Megafauna Nativeness * Plant Nativeness * Landform Evo. History	733(56)	12.34, 0.002***	5.51, 0.064	[0.082, 1]
Null: Diversity ~ Island				
Base: Diversity ~ Landform Evo. History * Island	401(53)			[-1.88, 1.16]
Nativeness: Diversity ~ Megafauna Nativeness * Landform Evo. History * Island	190(21)	0.4, 0.528	3.28, 0.194	[0.195, 1]
Null:				
Base: Diversity ~ 1	401(53)			
Nativeness: Diversity ~ Invasive	190(21)		0.37, 0.543	0.61, 0.543
Null:				
Base: Abundance ~ 1	2,129(137)			
Nativeness: Abundance ~ Invasive	614(52)		2.12, 0.146	1.46, 0.145
Null:				
Base: Diversity ~ 1	401(53)			
Nativeness: Diversity ~ Feral	190(21)		1.14, 0.286	-1.16, 0.248
Null:				
Base: Abundance ~ 1	2,129(137)			
Nativeness: Abundance ~ Feral	614(52)		1.03, 0.31	1.02, 0.309
Null: Diversity ~ 1				
Base: Diversity ~ Plant Nativeness	430(53)			[-2.03, 0.51]
Nativeness: Diversity ~ Megafauna Nativeness * Plant Nativeness	208(22)	3.05, 0.081	5.42, 0.067	[0.082, 0.843]
Coevolutionary History and Novelty				
Null:				
Base: Abundance ~ 1	932(52)			
Nativeness: Abundance ~ Plant-Megafauna Coev.	315(24)		1.41, 0.236	1.19, 0.235
Null:				
Base: Abundance ~ 1	41(9)			
Nativeness: Abundance ~ Plant-Megafauna Phylogenetic Novelty (CWM)	74(8)		2.86, 0.091	
Null:				
Base: Abundance ~ 1	41(9)			
Nativeness: Abundance ~ Plant-Megafauna Functional Novelty (CWM)	74(8)		2.09, 0.148	
Null:				
Base: Diversity ~ 1	401(53)			
Nativeness: Diversity ~ Coevolved Biome	190(21)		0.1, 0.749	0.32, 0.749
Null:				
Base: Diversity ~ 1	401(53)			
Nativeness: Diversity ~ Megafauna Phylogenetic Novelty (CWM)	162(15)		0.47, 0.491	
Null:				
Base: Diversity ~ 1	162(15)			
Nativeness: Diversity ~ Megafauna Functional Novelty (CWM)	162(15)		0.01, 0.927	
Functional Traits				
Null: Abundance ~ 1				
Base: Abundance ~ Max. Muzzle Width (CWM)	1,650(112)			
Nativeness: Abundance ~ Megafauna Nativeness + Max. Muzzle Width (CWM)	453(41)	0.25, 0.615	0.26, 0.609	-0.52, 0.604
Null: Diversity ~ 1				
Base: Diversity ~ Max. Muzzle Width (CWM)	223(43)			
Nativeness: Diversity ~ Megafauna Nativeness + Max. Muzzle Width (CWM)	184(18)	10.21, 0.001***	0.74, 0.389	-0.87, 0.386
Null: Abundance ~ 1				
Base: Abundance ~ Mean Muzzle Width (CWM)	1,650(112)			
Nativeness: Abundance ~ Megafauna Nativeness + Mean Muzzle Width (CWM)	453(41)	4.32, 0.038*	0.35, 0.557	-0.59, 0.552
Null: Diversity ~ 1				
Base: Diversity ~ Mean Muzzle Width (CWM)	223(43)			
Nativeness: Diversity ~ Megafauna Nativeness + Mean Muzzle Width (CWM)	184(18)	5.88, 0.015*	1.77, 0.183	-1.38, 0.169
Null: Abundance ~ 1				
Base: Abundance ~ Mean Body Mass (CWM)	1,682(114)			
Nativeness: Abundance ~ Megafauna Nativeness + Mean Body Mass (CWM)	453(41)	0.37, 0.545	0.26, 0.611	-0.52, 0.606
Null: Diversity ~ 1				
Base: Diversity ~ Mean Body Mass (CWM)	236(45)			
Nativeness: Diversity ~ Megafauna Nativeness + Mean Body Mass (CWM)	184(18)	4.37, 0.037*	0.82, 0.366	-0.92, 0.357

Null: Abundance ~ 1				
Base: Abundance ~ Max. Body Mass (CWM)	1,682(114)			
Nativeness: Abundance ~ Megafauna Nativeness + Max. Body Mass (CWM)	453(41)	0.11, 0.742	0.31, 0.577	-0.57, 0.571
Null: Diversity ~ 1				
Base: Diversity ~ Max. Body Mass (CWM)	236(45)			
Nativeness: Diversity ~ Megafauna Nativeness + Max. Body Mass (CWM)	184(18)	3.31, 0.069	0.59, 0.444	-0.78, 0.438
Null: Abundance ~ 1				
Base: Abundance ~ Megafauna Biomass / NPP	1,268(82)			
Nativeness: Abundance ~ Megafauna Nativeness + Megafauna Biomass / NPP	370(30)	7.14, 0.008***	1.82, 0.177	-1.37, 0.17
Null: Diversity ~ 1				
Base: Diversity ~ Megafauna Biomass / NPP	156(31)			
Nativeness: Diversity ~ Megafauna Nativeness + Megafauna Biomass / NPP	161(13)	1.37, 0.241	1.14, 0.285	-1.09, 0.277
Null: Abundance ~ 1				
Base: Abundance ~ Plant Growth Form * Graminoid Preference (CWM)	1,407(92)			
Nativeness: Abundance ~ Megafauna Nativeness + Plant Growth Form * Graminoid Preference (CWM)	323(28)	15.81, 0.007***	0.05, 0.815	0.24, 0.811
Null: Diversity ~ 1				
Base: Diversity ~ Plant Growth Form * Graminoid Preference (CWM)	133(22)			
Nativeness: Diversity ~ Megafauna Nativeness + Plant Growth Form * Graminoid Preference (CWM)	34(5)	15.51, 0.008***	0.15, 0.697	-0.39, 0.696
Null: Abundance ~ Max. Body Mass (CWM)				
Base: Abundance ~ Max. Body Mass (CWM) * Plant Nativeness	1,789(118)			[-0.7, 0.65],
Nativeness: Abundance ~ Max. Body Mass (CWM) * Megafauna Nativeness * Plant Nativeness	517(44)	13.06, 0.001***	3.03, 0.553	[0.729, 0.76]
Null: Diversity ~ Max. Body Mass (CWM)				
Base: Diversity ~ Max. Body Mass (CWM) * Plant Nativeness	261(45)			[-0.58, 0.54],
Nativeness: Diversity ~ Max. Body Mass (CWM) * Megafauna Nativeness * Plant Nativeness	199(19)	3.33, 0.189	2.35, 0.672	[0.798, 0.821]
Null: Abundance ~ Mean Body Mass (CWM)				
Base: Abundance ~ Mean Body Mass (CWM) * Plant Nativeness	1,789(118)			[-0.73, 0.16],
Nativeness: Abundance ~ Mean Body Mass (CWM) * Megafauna Nativeness * Plant Nativeness	517(44)	14.84, 0.001**	6.58, 0.16	[0.71, 0.984]
Null: Diversity ~ Mean Body Mass (CWM)				
Base: Diversity ~ Mean Body Mass (CWM) * Plant Nativeness	261(45)			[-0.64, 0.29],
Nativeness: Diversity ~ Mean Body Mass (CWM) * Megafauna Nativeness * Plant Nativeness	199(19)	3.55, 0.169	2.32, 0.676	[0.761, 0.946]
Null: Abundance ~ 1				
Base: Abundance ~ Proportion Hindgut (CWM)	1,682(114)			
Nativeness: Abundance ~ Megafauna Nativeness + Proportion Hindgut (CWM)	453(41)	0.1, 0.75	0.46, 0.496	-0.69, 0.488
Null: Diversity ~ 1				
Base: Diversity ~ Proportion Hindgut (CWM)	236(45)			
Nativeness: Diversity ~ Megafauna Nativeness + Proportion Hindgut (CWM)	184(18)	0.04, 0.841	1.17, 0.278	-1.1, 0.27

Megafauna Diversity

Null: Abundance ~ 1				
Base: Abundance ~ Number of Megafauna Species	2,129(137)			
Nativeness: Abundance ~ Megafauna Nativeness + Number of Megafauna Species	614(52)	8.5, 0.004***	0.11, 0.743	0.33, 0.743
Null: Diversity ~ 1				
Base: Diversity ~ Number of Megafauna Species	401(53)			
Nativeness: Diversity ~ Megafauna Nativeness + Number of Megafauna Species	190(21)	1.9, 0.168	2.67, 0.102	-1.72, 0.085
Null: Abundance ~ 1				
Base: Abundance ~ Number of Megafauna Functional Groups	2,129(137)			
Nativeness: Abundance ~ Megafauna Nativeness + Number of Megafauna Species	614(52)	8.08, 0.004***	0.53, 0.467	0.33, 0.743
Null: Diversity ~ 1				
Base: Diversity ~ Number of Megafauna Functional Groups	401(53)			
Nativeness: Diversity ~ Megafauna Nativeness + Number of Megafauna Species	190(21)	1.58, 0.209	2.99, 0.084	-1.72, 0.085

Final in Time Series / Largest Scale Measure Only Responses to Native and Introduced Megafauna

Null: Abundance ~ Landform Evo. History				
Base: Abundance ~ Plant Nativeness * Landform Evo. History	1,464(141)			[-0.35, 2.39],
Nativeness: Abundance ~ Megafauna Nativeness * Plant Nativeness * Landform Evo. History	445(56)	8.58, 0.014*	5.71, 0.058	[0.065, 0.994]
Null: Diversity ~ Island				
Base: Diversity ~ Landform Evo. History * Island	216(53)			[-1.32, 1.39],
Nativeness: Diversity ~ Megafauna Nativeness * Landform Evo. History * Island	90(21)	0, 0.985	1.93, 0.38	[0.456, 1]
Null:				
Base: Diversity ~ 1	216(53)			
Nativeness: Diversity ~ Invasive	90(21)		0.61, 0.433	0.79, 0.432
Null:				
Base: Abundance ~ 1	1,368(137)			
Nativeness: Abundance ~ Invasive	386(52)		0.24, 0.623	0.49, 0.623
Null:				
Base: Diversity ~ 1	216(53)			
Nativeness: Diversity ~ Feral	90(21)		0.01, 0.904	0.12, 0.902
Null:				
Base: Abundance ~ 1	1,368(137)			
Nativeness: Abundance ~ Feral	386(52)		2.11, 0.147	1.45, 0.146
Null: Diversity ~ 1				
Base: Diversity ~ Plant Nativeness	245(53)			[-0.84, 0.46],
Nativeness: Diversity ~ Megafauna Nativeness * Plant Nativeness	99(22)	2.72, 0.099	1.35, 0.508	[0.627, 0.865]

Coevolutionary History and Novelty

Null:				
Base: Abundance ~ 1	740(52)			
Nativeness: Abundance ~ Plant-Megafauna Coev.	219(24)		0.64, 0.425	0.8, 0.423
Null:				
Base: Abundance ~ 1	36(9)			
Nativeness: Abundance ~ Plant-Megafauna Phylogenetic Novelty (CWM)	57(8)		2.79, 0.095	
Null:				
Base: Abundance ~ 1	36(9)			
Nativeness: Abundance ~ Plant-Megafauna Functional Novelty (CWM)	57(8)		1.62, 0.203	
Null:				
Base: Diversity ~ 1	216(53)			
Nativeness: Diversity ~ Coevolved Biome	90(21)		0.28, 0.598	0.53, 0.597
Null:				
Base: Diversity ~ 1	216(53)			
Nativeness: Diversity ~ Megafauna Phylogenetic Novelty (CWM)	78(15)		0.29, 0.593	

Null:				
Base: Diversity ~ 1				
Nativeness: Diversity ~ Megafauna Functional Novelty (CWM)	78(15)		0.01, 0.922	
Functional Traits				
Null: Abundance ~ 1				
Base: Abundance ~ Max. Muzzle Width (CWM)	1,183(112)			
Nativeness: Abundance ~ Megafauna Nativeness + Max. Muzzle Width (CWM)	317(41)	0.58, 0.447	0.01, 0.922	-0.1, 0.921
Null: Diversity ~ 1				
Base: Diversity ~ Max. Muzzle Width (CWM)	151(43)			
Nativeness: Diversity ~ Megafauna Nativeness + Max. Muzzle Width (CWM)	87(18)	4.92, 0.027*	0.04, 0.847	-0.19, 0.847
Null: Abundance ~ 1				
Base: Abundance ~ Mean Muzzle Width (CWM)	1,183(112)			
Nativeness: Abundance ~ Megafauna Nativeness + Mean Muzzle Width (CWM)	317(41)	4.71, 0.03*	0.04, 0.847	-0.19, 0.846
Null: Diversity ~ 1				
Base: Diversity ~ Mean Muzzle Width (CWM)	151(43)			
Nativeness: Diversity ~ Megafauna Nativeness + Mean Muzzle Width (CWM)	87(18)	5.54, 0.019*	0.26, 0.611	-0.51, 0.608
Null: Abundance ~ 1				
Base: Abundance ~ Mean Body Mass (CWM)	1,215(114)			
Nativeness: Abundance ~ Megafauna Nativeness + Mean Body Mass (CWM)	317(41)	0.47, 0.492	0.01, 0.928	-0.09, 0.927
Null: Diversity ~ 1				
Base: Diversity ~ Mean Body Mass (CWM)	164(45)			
Nativeness: Diversity ~ Megafauna Nativeness + Mean Body Mass (CWM)	87(18)	2.43, 0.119	0.02, 0.881	-0.15, 0.88
Null: Abundance ~ 1				
Base: Abundance ~ Max. Body Mass (CWM)	1,215(114)			
Nativeness: Abundance ~ Megafauna Nativeness + Max. Body Mass (CWM)	317(41)	0.04, 0.851	0.02, 0.896	-0.13, 0.896
Null: Diversity ~ 1				
Base: Diversity ~ Max. Body Mass (CWM)	164(45)			
Nativeness: Diversity ~ Megafauna Nativeness + Max. Body Mass (CWM)	87(18)	1.09, 0.296	0.01, 0.929	-0.09, 0.929
Null: Abundance ~ 1				
Base: Abundance ~ Megafauna Biomass / NPP	900(82)			
Nativeness: Abundance ~ Megafauna Nativeness + Megafauna Biomass / NPP	242(30)	2.9, 0.088	0.49, 0.482	-0.71, 0.479
Null: Diversity ~ 1				
Base: Diversity ~ Megafauna Biomass / NPP	86(31)			
Nativeness: Diversity ~ Megafauna Nativeness + Megafauna Biomass / NPP	79(13)	0.65, 0.419	0.54, 0.464	-0.74, 0.462
Null: Abundance ~ 1				
Base: Abundance ~ Plant Growth Form * Graminoid Preference (CWM)	1,053(92)			
Nativeness: Abundance ~ Megafauna Nativeness + Plant Growth Form * Graminoid Preference (CWM)	248(28)	14.88, 0.011*	0.27, 0.607	-0.52, 0.601
Null: Diversity ~ 1				
Base: Diversity ~ Plant Growth Form * Graminoid Preference (CWM)	97(22)			
Nativeness: Diversity ~ Megafauna Nativeness + Plant Growth Form * Graminoid Preference (CWM)	24(5)	15.82, 0.007***	0.12, 0.726	-0.35, 0.726
Null: Abundance ~ Max. Body Mass (CWM)				
Base: Abundance ~ Max. Body Mass (CWM) * Plant Nativeness	1,306(118)			[-0.2, 1.03],
Nativeness: Abundance ~ Max. Body Mass (CWM) * Megafauna Nativeness * Plant Nativeness	355(44)	10.4, 0.006***	3.43, 0.488	[0.513, 0.976]
Null: Diversity ~ Max. Body Mass (CWM)				
Base: Diversity ~ Max. Body Mass (CWM) * Plant Nativeness	189(45)			[-0.15, 0.85],
Nativeness: Diversity ~ Max. Body Mass (CWM) * Megafauna Nativeness * Plant Nativeness	95(19)	4.26, 0.119	1.76, 0.78	[0.611, 0.985]
Null: Abundance ~ Mean Body Mass (CWM)				
Base: Abundance ~ Mean Body Mass (CWM) * Plant Nativeness	1,306(118)			[-0.22, 0.63],
Nativeness: Abundance ~ Mean Body Mass (CWM) * Megafauna Nativeness * Plant Nativeness	355(44)	11.87, 0.003***	5.59, 0.232	[0.773, 0.969]
Null: Diversity ~ Mean Body Mass (CWM)				
Base: Diversity ~ Mean Body Mass (CWM) * Plant Nativeness	189(45)			[-0.2, 0.61],
Nativeness: Diversity ~ Mean Body Mass (CWM) * Megafauna Nativeness * Plant Nativeness	95(19)	4.26, 0.119	0.78, 0.941	[0.776, 0.974]
Null: Abundance ~ 1				
Base: Abundance ~ Proportion Hindgut (CWM)	1,215(114)			
Nativeness: Abundance ~ Megafauna Nativeness + Proportion Hindgut (CWM)	317(41)	0.62, 0.431	0.16, 0.693	-0.4, 0.688
Null: Diversity ~ 1				
Base: Diversity ~ Proportion Hindgut (CWM)	164(45)			
Nativeness: Diversity ~ Megafauna Nativeness + Proportion Hindgut (CWM)	87(18)	0.43, 0.512	0.24, 0.622	-0.5, 0.62
Megafauna Diversity				
Null: Abundance ~ 1				
Base: Abundance ~ Number of Megafauna Species	1,368(137)			
Nativeness: Abundance ~ Megafauna Nativeness + Number of Megafauna Species	386(52)	2.72, 0.099	0.3, 0.586	0.55, 0.585
Null: Diversity ~ 1				
Base: Diversity ~ Number of Megafauna Species	216(53)			
Nativeness: Diversity ~ Megafauna Nativeness + Number of Megafauna Species	90(21)	2.6, 0.107	0.34, 0.559	-0.59, 0.557
Null: Abundance ~ 1				
Base: Abundance ~ Number of Megafauna Functional Groups	1,368(137)			
Nativeness: Abundance ~ Megafauna Nativeness + Number of Megafauna Species	386(52)	1.97, 0.16	1.04, 0.308	0.55, 0.585
Null: Diversity ~ 1				
Base: Diversity ~ Number of Megafauna Functional Groups	216(53)			
Nativeness: Diversity ~ Megafauna Nativeness + Number of Megafauna Species	90(21)	2.85, 0.091	0.09, 0.765	-0.59, 0.557
Species-level Responses Only				
Responses to Native and Introduced Megafauna				
Null: Abundance ~ Landform Evo. History				
Base: Abundance ~ Plant Nativeness * Landform Evo. History	944(52)			[-0.88, 0.68],
Nativeness: Abundance ~ Megafauna Nativeness * Plant Nativeness * Landform Evo. History	318(24)	1.78, 0.41	0.7, 0.703	[0.839, 1]
Null:				
Base: Abundance ~ 1	880(46)			
Nativeness: Abundance ~ Invasive	265(21)		0.91, 0.339	0.96, 0.337
Null:				
Base: Abundance ~ 1	880(46)			
Nativeness: Abundance ~ Feral	265(21)		0.11, 0.739	0.33, 0.739
Pure Megafauna Nativeness				
Null: Abundance ~ Landform Evo. History				
Base: Abundance ~ Plant Nativeness * Landform Evo. History	2,241(141)			[-0.84, 1.65],
Nativeness: Abundance ~ Megafauna Nativeness * Plant Nativeness * Landform Evo. History	704(55)	12.9, 0.002***	3.33, 0.19	[0.335, 0.977]
Null:				
Base: Abundance ~ 1	2,129(137)			
Nativeness: Abundance ~ Invasive	585(51)		2.05, 0.153	1.43, 0.152

Null:				
Base: Abundance ~ 1	2,129(137)			
Nativeness: Abundance ~ Feral	585(51)		0.96, 0.328	0.98, 0.328
Coevolutionary History and Novelty				
Null:				
Base: Abundance ~ 1	940(52)			
Nativeness: Abundance ~ Plant-Megafauna Coev.	307(24)		1.31, 0.252	1.15, 0.251
Null:				
Base: Abundance ~ 1	41(9)			
Nativeness: Abundance ~ Plant-Megafauna Phylogenetic Novelty (CWM)	64(7)		3.4, 0.065	
Null:				
Base: Abundance ~ 1	41(9)			
Nativeness: Abundance ~ Plant-Megafauna Functional Novelty (CWM)	64(7)		1.09, 0.297	
Unspecified Nativeness Plants Excluded				
Responses to Native and Introduced Megafauna				
Null: Diversity ~ 1				
Base: Diversity ~ Reported Plant Nativeness	519(65)			[-0.68, 0.49]
Nativeness: Diversity ~ Megafauna Nativeness * Reported Plant Nativeness	252(28)	10.67, 0.014*	2.74, 0.602	[0.743, 0.853]
Null: Diversity ~ Island				
Base: Diversity ~ Landform Evo. History * Island	351(42)			[-1.06, 0.96]
Nativeness: Diversity ~ Megafauna Nativeness * Landform Evo. History * Island	82(15)	0.04, 0.833	1.11, 0.574	[0.688, 0.98]
Null:				
Base: Diversity ~ 1	351(42)			
Nativeness: Diversity ~ Invasive	82(15)		0.08, 0.784	0.27, 0.784
Null:				
Base: Diversity ~ 1	351(42)			
Nativeness: Diversity ~ Feral	82(15)		0.14, 0.705	0.38, 0.703
Coevolutionary History and Novelty				
Null:				
Base: Diversity ~ 1	351(42)			
Nativeness: Diversity ~ Coevolved Biome	82(15)		0.01, 0.937	-0.08, 0.937
Null:				
Base: Diversity ~ 1				
Nativeness: Diversity ~ Megafauna Phylogenetic Novelty (CWM)	66(10)		0.01, 0.943	
Null:				
Base: Diversity ~ 1				
Nativeness: Diversity ~ Megafauna Functional Novelty (CWM)	66(10)		0.01, 0.937	

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