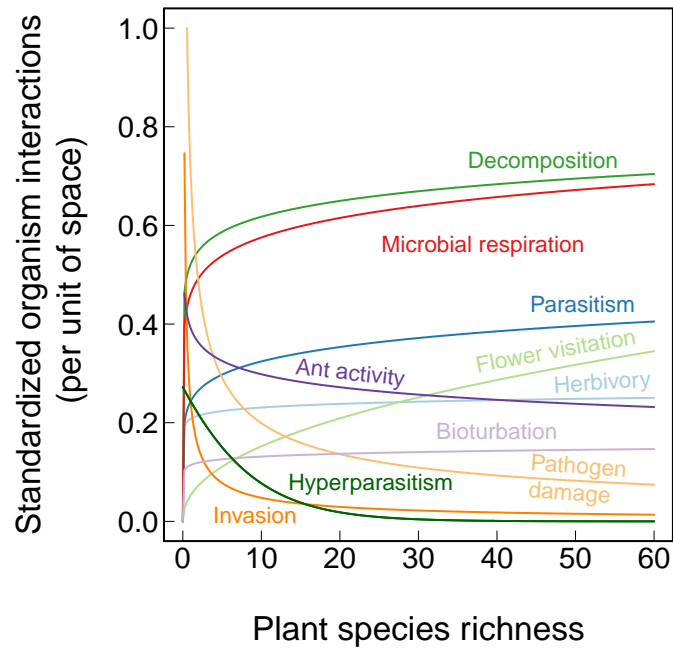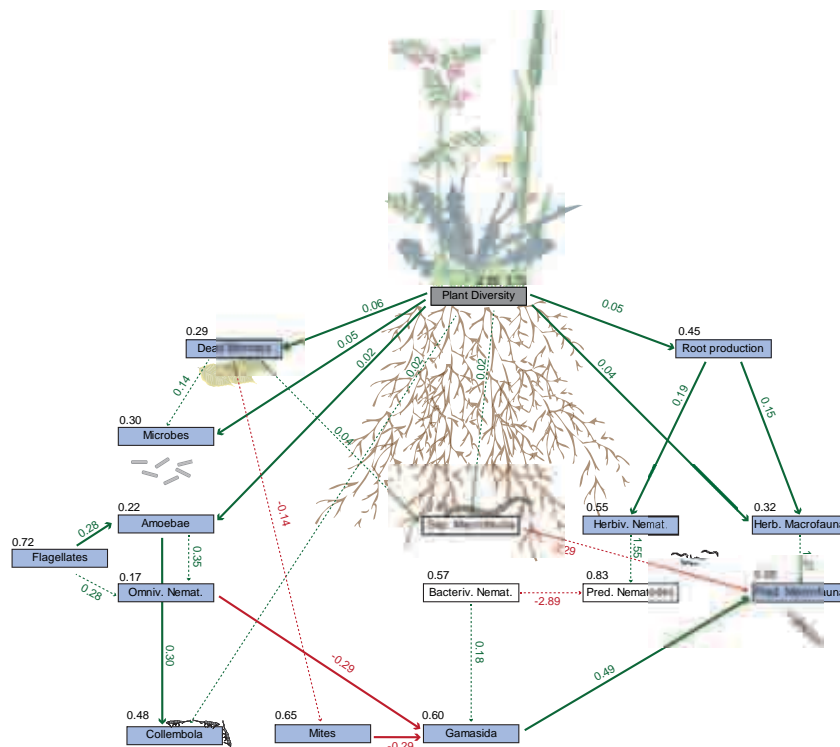## Supplementary Figures and Legends


Supplementary Figure 1 | Biodiversity effects on organism interactions. Sample size: N=82 except for hyperparasitism (extrapolated from smaller plots).

Supplementary Figure 2 | Effects of plant species richness on organism abundances in the belowground food web. Sample size: N=82 (missing values replaced by the mean), Chi²= 108.424, df=91 (61 estimated parameters), P=0.103; RMSEA= 0.049, 90%CI=[0;0.08]. The model is the result of a specification search over 50 models that started off with a maximal model (containing all hypothesized relationships), with subsequent deletions of arrows not supported by the data. The model shows unstandardized parameter estimates. The Supplementary Figure shows the minimal adequate model (defined by lowest AIC, BIC and lowest difference between observed and implied covariance matrices). Arrows connecting boxes show structural relationships; parameters next to solid arrows are significant at P≤0.05. Parameter estimates next to dashed arrows are not significant but were retained in the minimal adequate model. Green arrows show significantly positive relationships, red arrows significantly negative ones. Grey arrows and text show error terms. Plant species richness (grey box) was experimentally manipulated. Light blue boxes indicate variables that are linked by at least one solid arrow.

Supplementary Figure 3 | Effects of plant species richness on all response variables on the original scale. Variables are sorted in alphabetic order. Fitted green and blue lines show 1st and 2nd order local polynomial regressions fit by weighted least squares; black lines show linear regression fits. Note that local polynomial regressions are for illustrative purposes only.
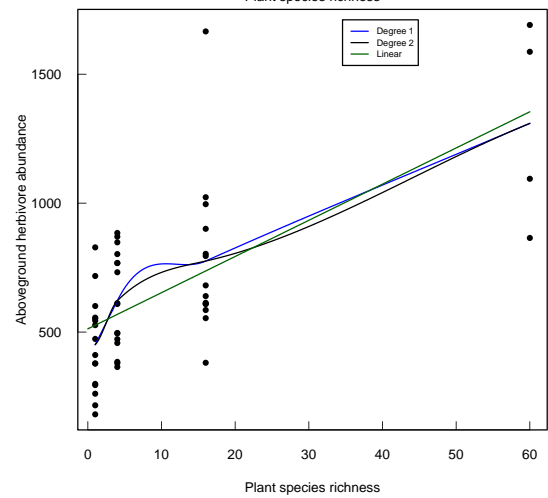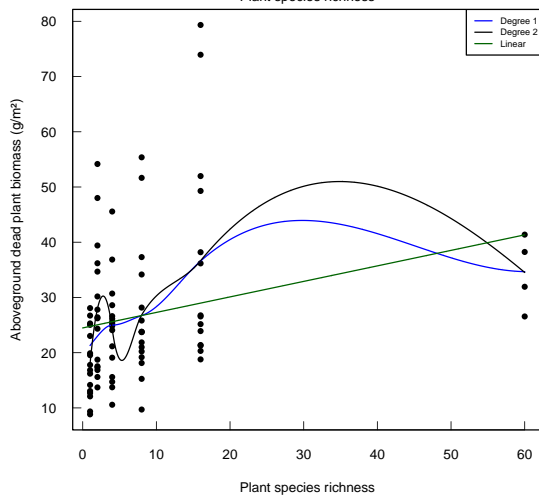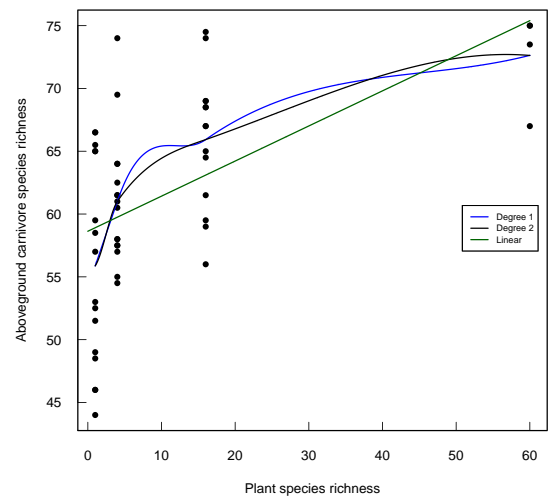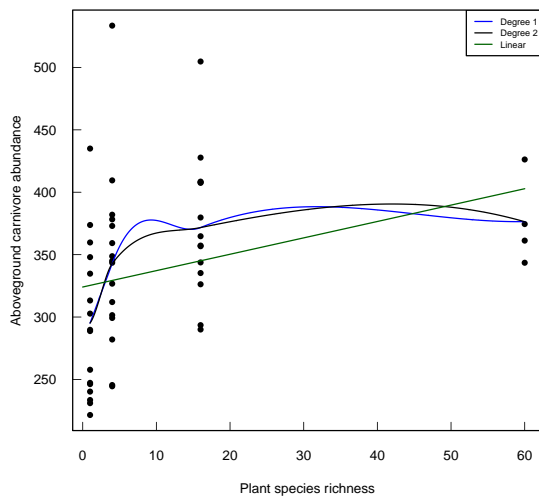
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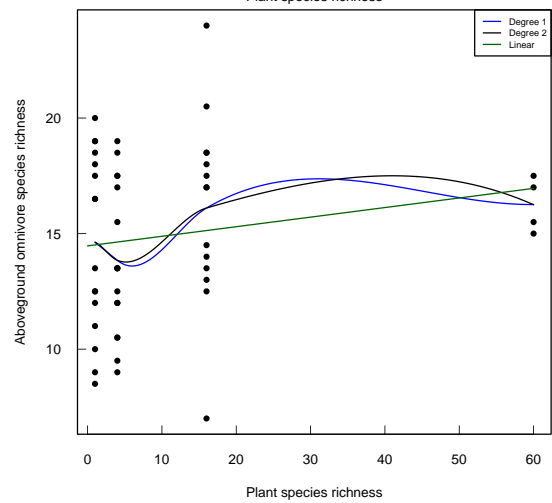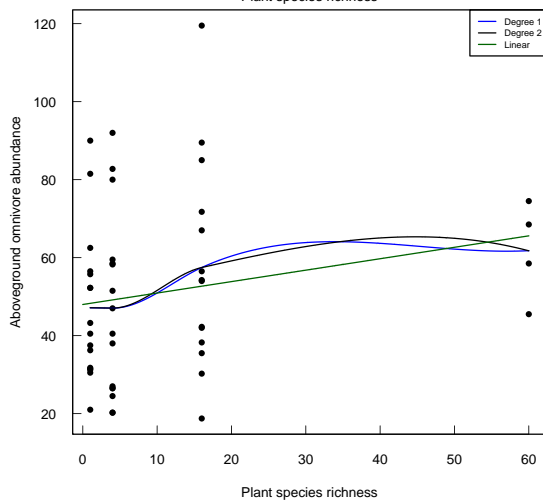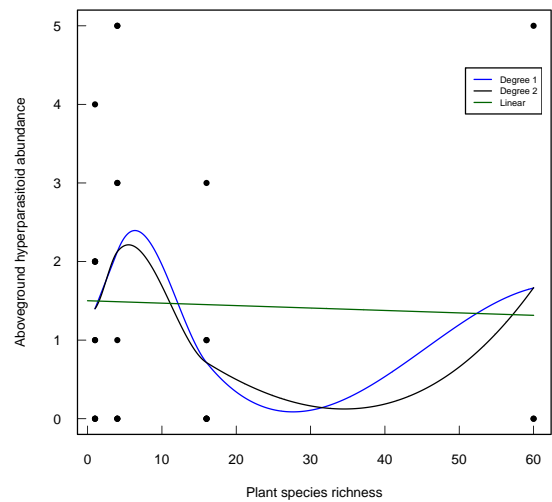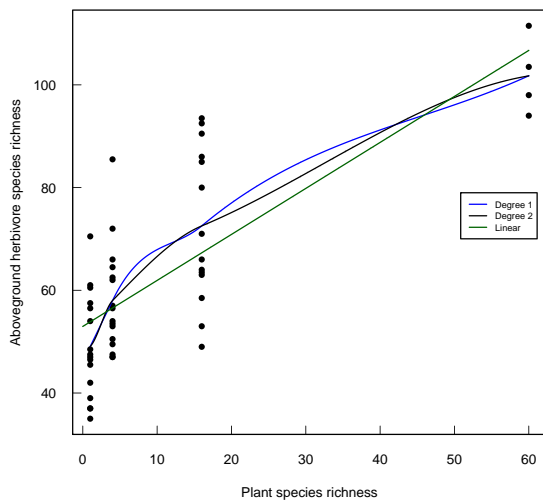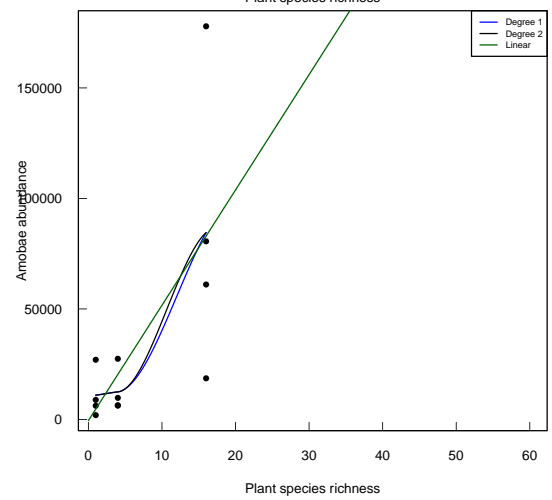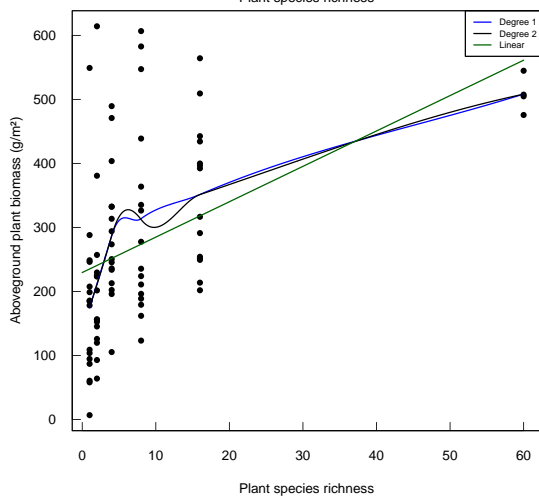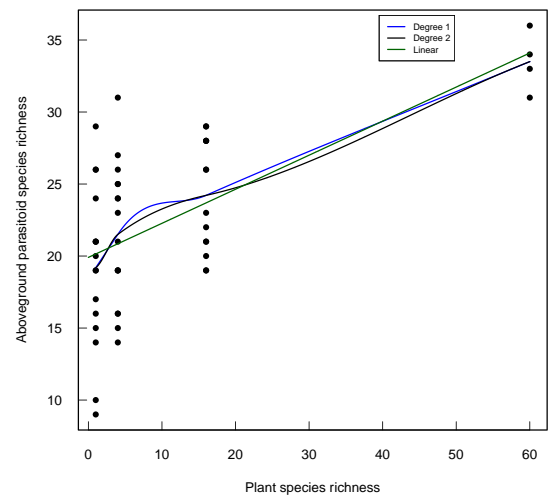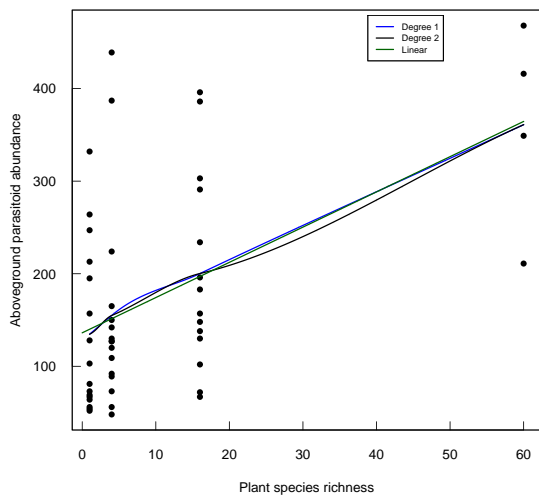
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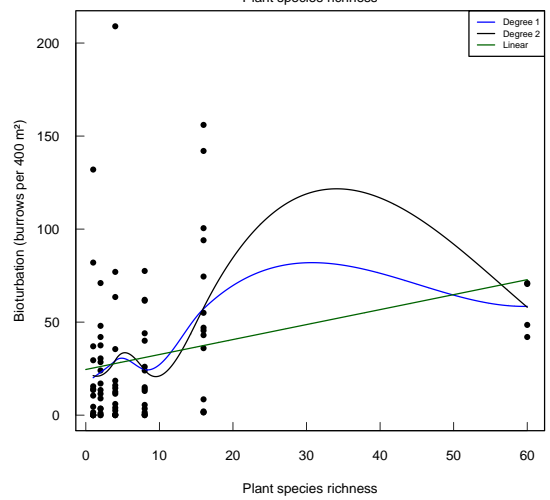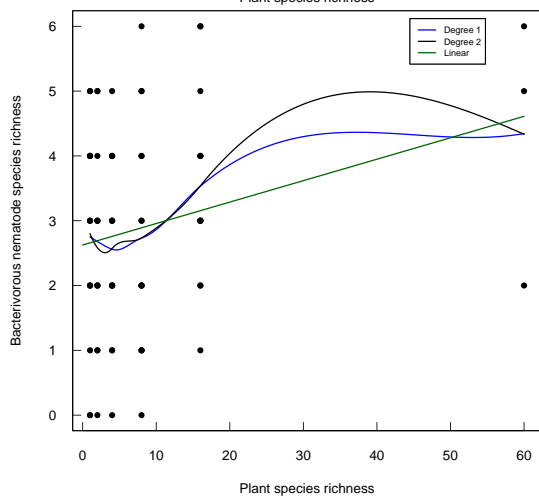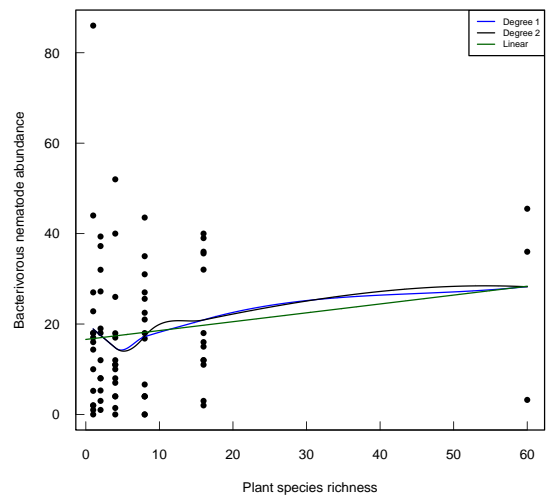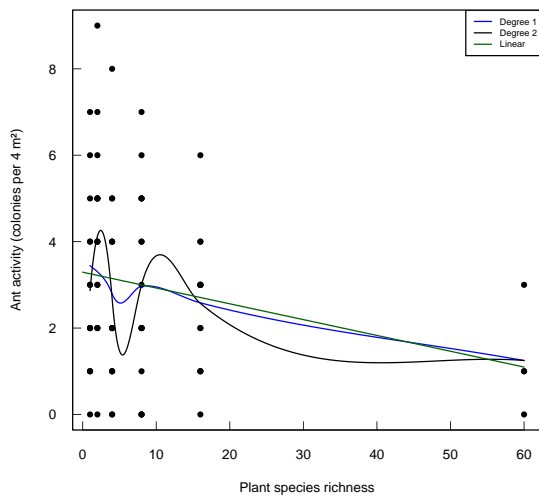
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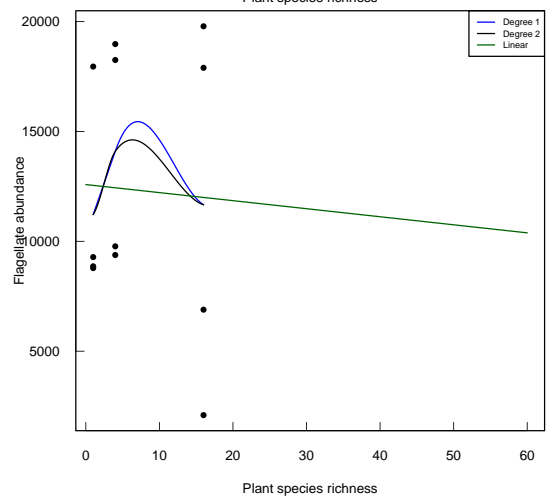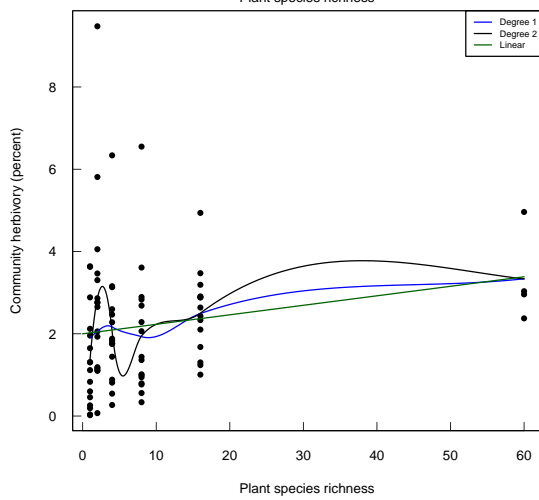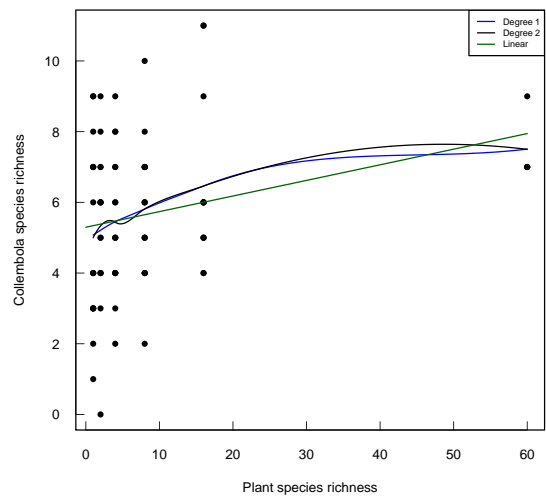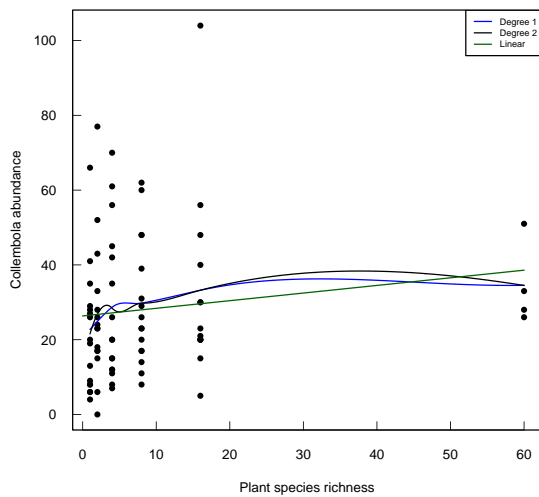
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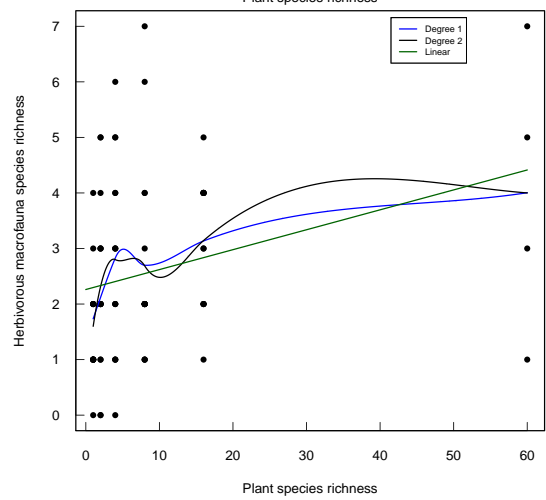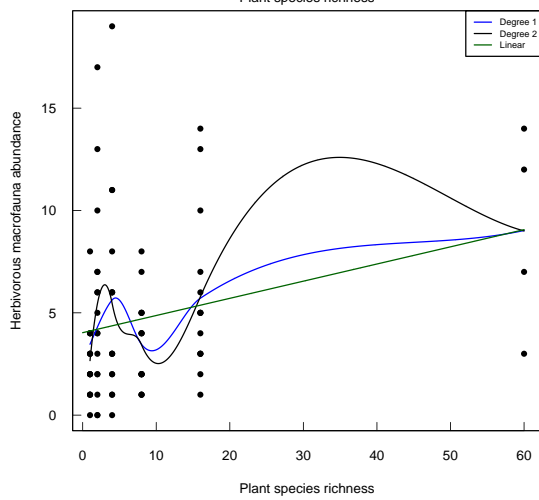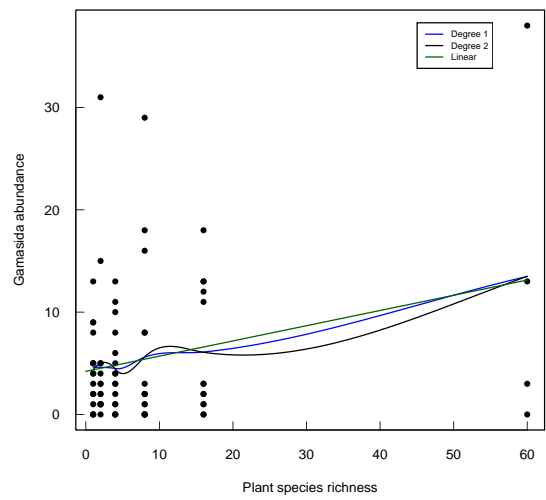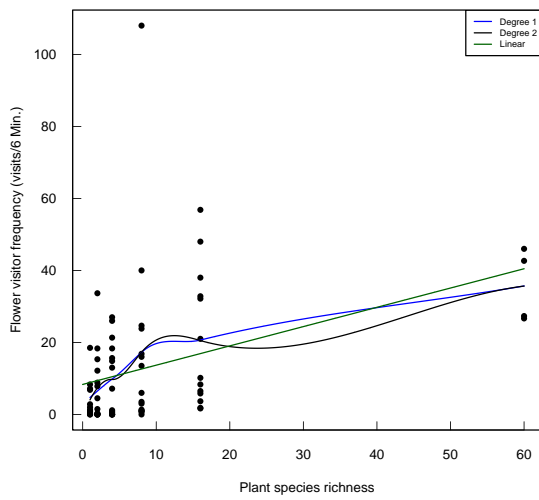
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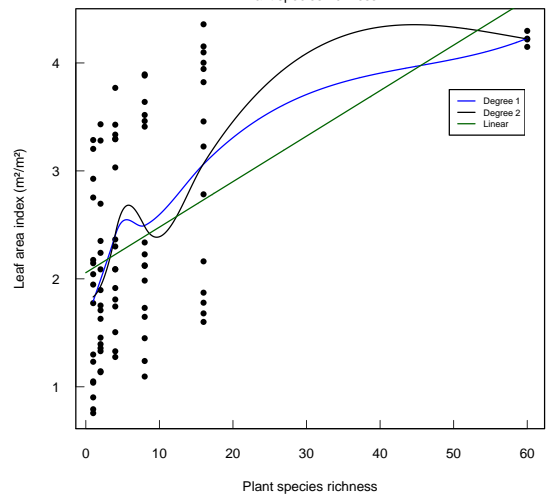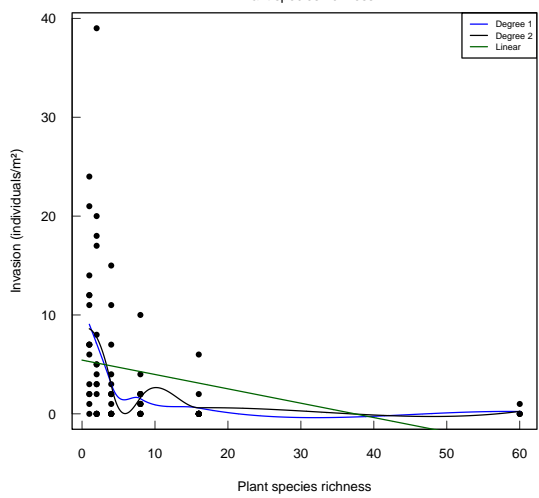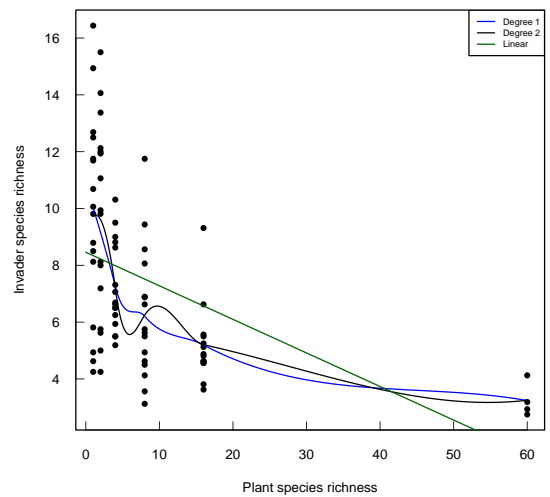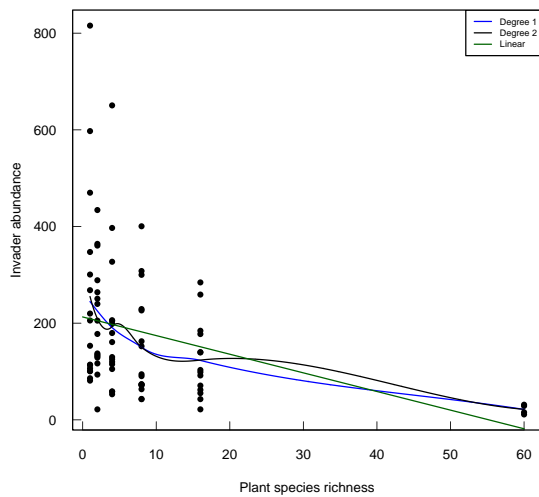
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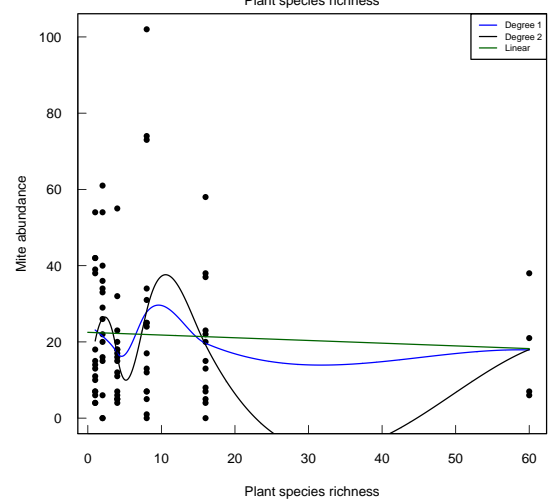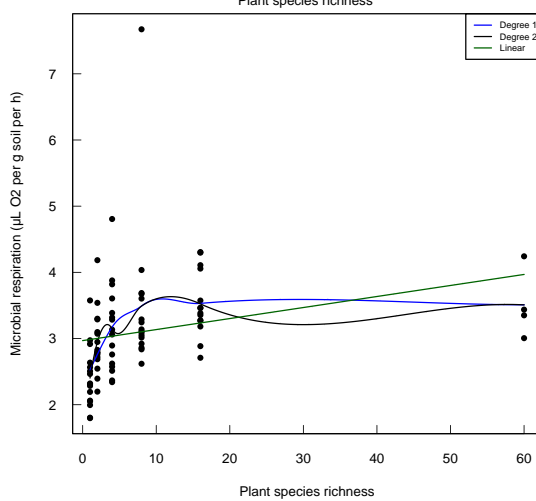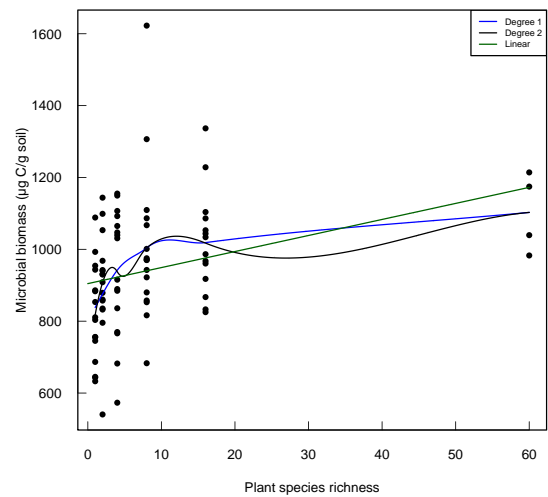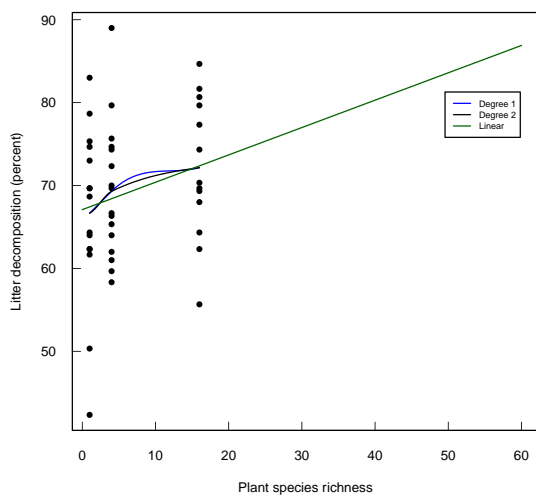
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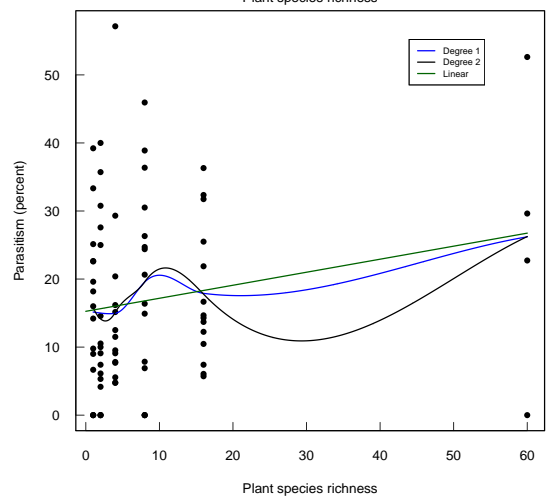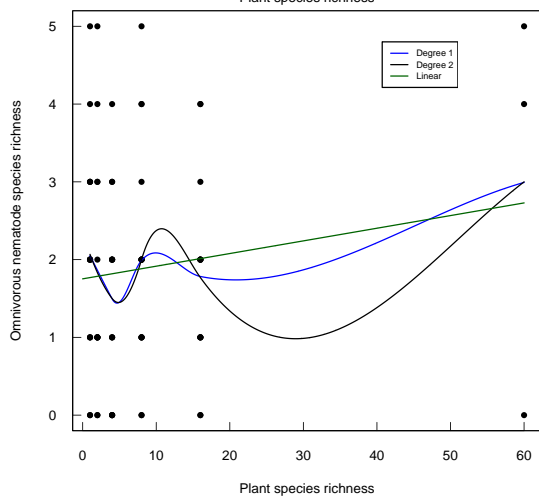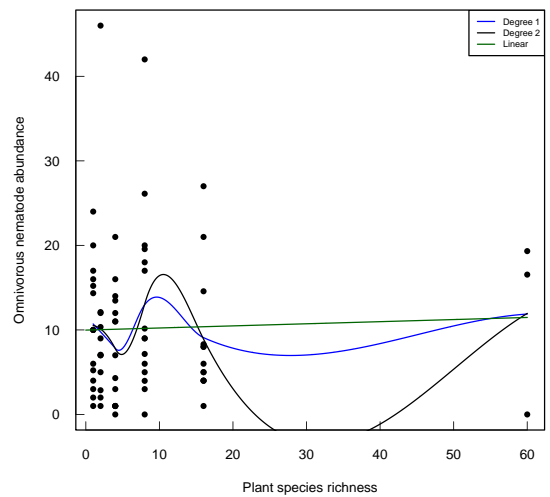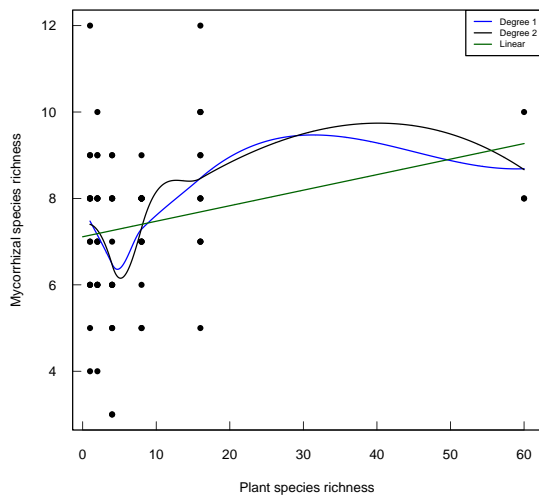
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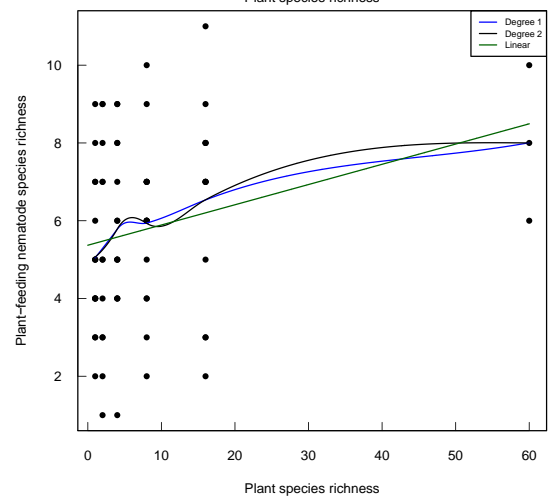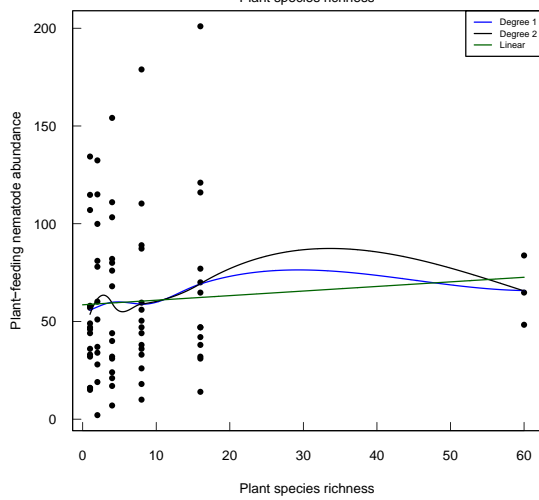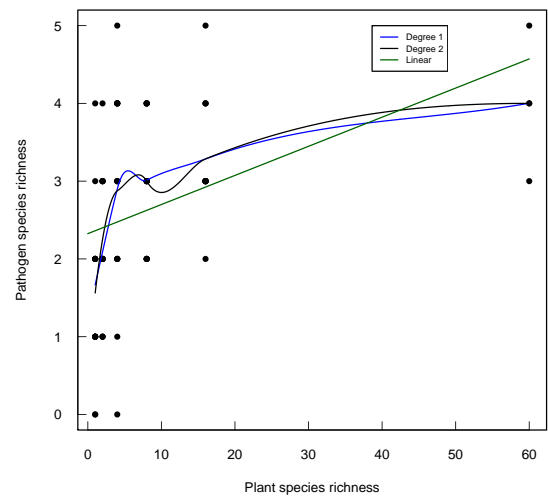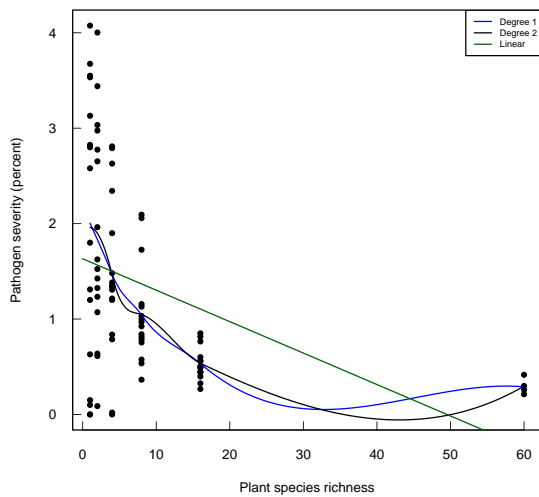
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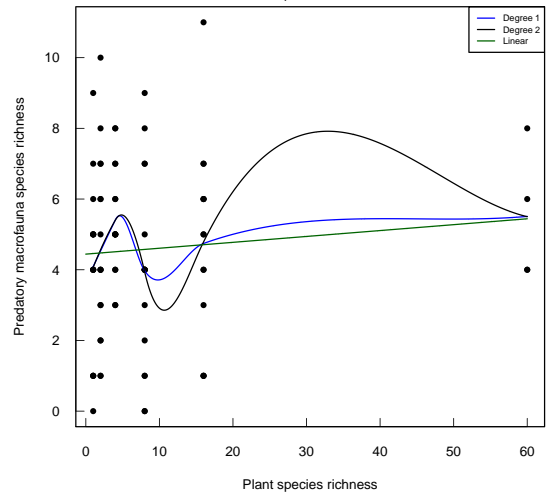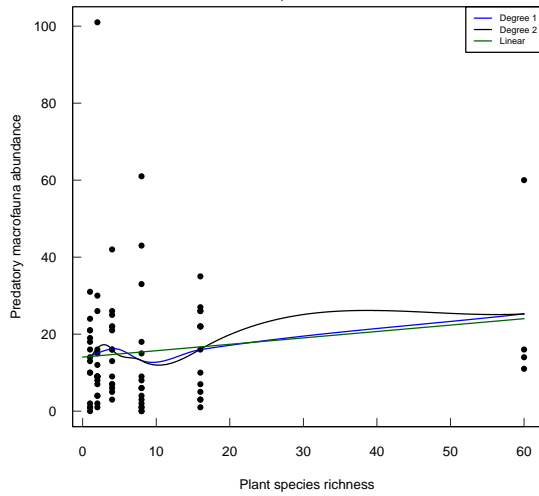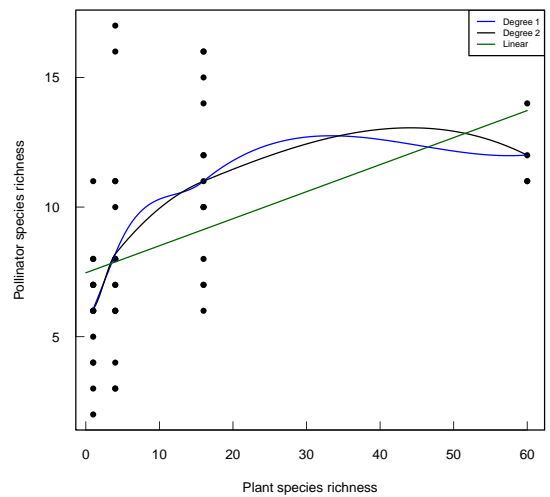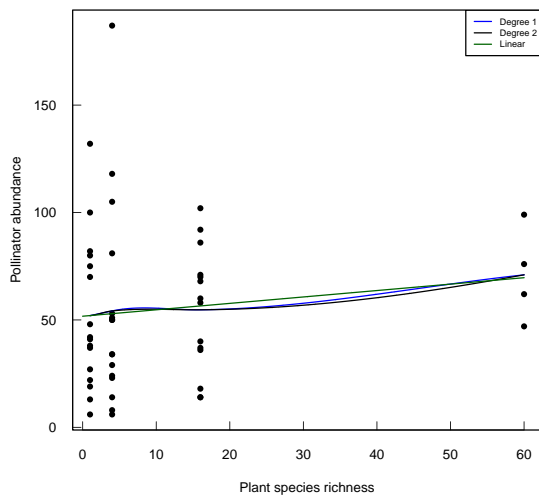
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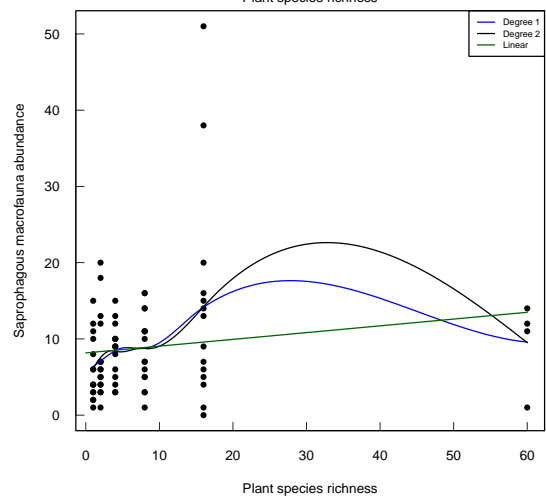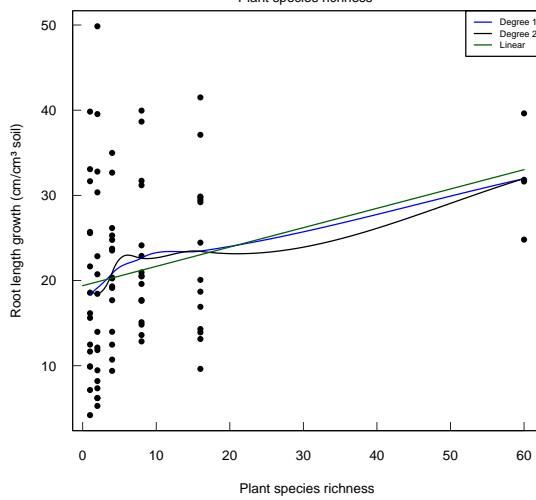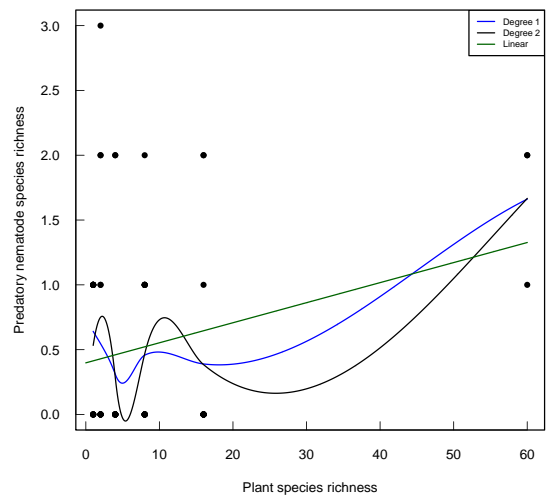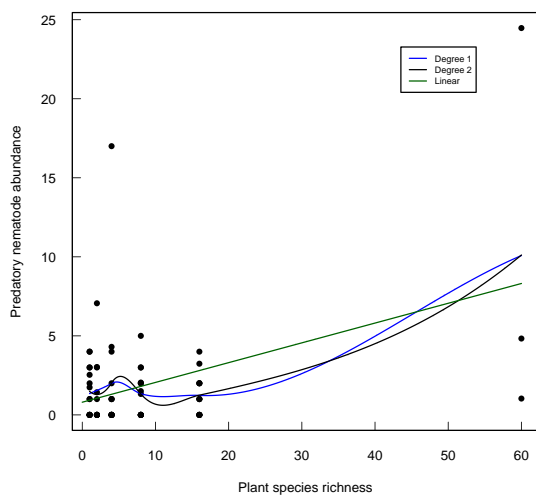
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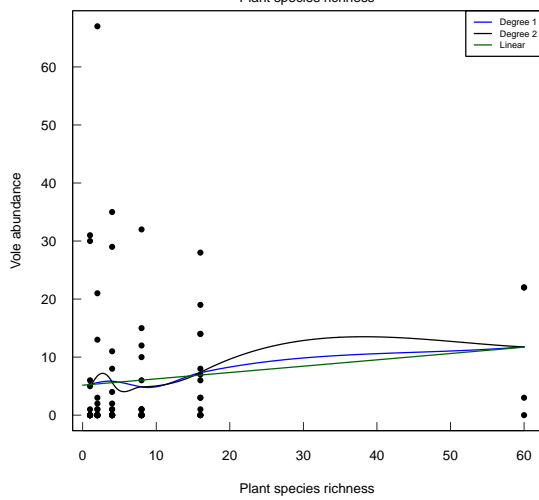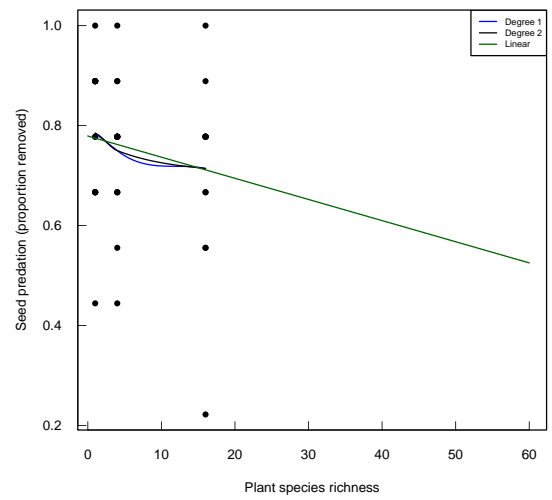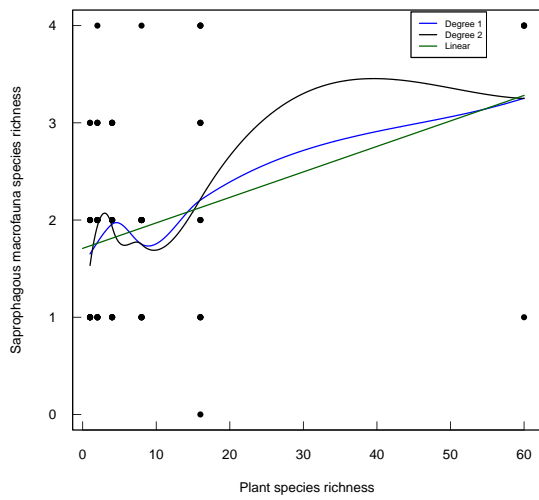
Supplementary Methods

Sampling of aboveground organisms

The population density of **small rodents** was estimated by placing two Ugglan multiple capture live-traps in each plot, with trapping between June and October 2005 (11 trapping sessions). Each trapping session lasted for two trap nights with traps activated in the morning of day 1, and three trap checks in the morning and evening of day 2 and the morning of day 3. Traps were baited with standard rodent feeding pellets and weather-protected by a metal cover. Every individual captured for the first time in a trapping session was etherized and marked individually using transponders (Trovan®). Individuals weighing less than 20 g did not receive a transponder, but were marked using fur-clipping. For every individual capture, we recorded species, body weight, sex, and breeding condition.

The population density and species richness of **aboveground invertebrates** (including herbivores, carnivores, parasitoids, omnivores and pollinators) were measured in N=50 plots (1, 4, 16, 60 plant species) using an electric suction sampler combined with a biocenometer that covered a base area of 0.75 x 0.75 m. In contrast to other approaches (e.g. sweepnetting), the biocenometer method allows **volume-specific sampling** (i.e. exactly the same biovolume is sampled on every plot, similar to taking a soil core). Thus, our data on aboveground and belowground organism abundances/species richness are highly comparable. Every plot received six suction samplings that were randomly placed without replacement. Samples were taken five times per year from May to October (2003 and 2005).

**Pollination** was estimated as the number of flower visits in subplots per main plot. Flower visits were quantified by counting flower-visiting insects in randomly placed quadrats of 80 x 80 cm per 20x20 m plot. Only N=73 plots containing forbs were observed (i.e. excluding plots containing only wind-pollinated grasses). Flower visitors were counted during six observation periods: 24-25 May 2005, 15-16 June 2005, 18-19 August 2005, 6-9 June 2006, 17-18 June 2006 and 1-5 August 2006. Observations were restricted to sunny days characterized by at least 18°C air temperature, with no or little wind (<2 m s-1), between 09:00 and 17:00 h. Observations within a block were carried out within two days, assuring constant weather conductions within blocks. The sequence of plot observations was independent of plant richness. We observed pollinating insects for 6 minutes per quadrat, plot and observation period, resulting in a total of 36 minutes per plot. Pollinators were identified directly in the field to genus or morphospecies and species level in the field. After each observation period we collected all unknown species for further identification in the laboratory.

In addition, we exposed N=164 standardized trap nests made from reed internodes in the exact centre of every plot (N=82). This allowed us to calculate **parasitism rate** of trap-nesting bees and wasps.

To measure the activity density and species richness of **epigeic invertebrates** (mainly Carabids, Staphylinids and spiders), two **pitfall traps** were placed near the centre of each plot (N=50) and replaced six times per year from May to October (2003 and 2005). All species were identified and their relative population densities (per unit of space) estimated.

Sampling of belowground organisms

Belowground meso- and macrofauna were sampled twice a year in 2004, 2006 and 2008 from N=82 plots. The subplot positions (2 x 4 m) for sampling were drawn at random. Samples were taken using soil cores of a diameter of 5 and 21 cm for extraction of meso- and macrofauna, respectively. Because most soil animals populate the upper soil layers, the upper 10 cm of the soil cores were used for extraction. Soil animals were extracted over a period of 10 days by heat[30].

Earthworm sampling was performed each year in April and October between 2003-2006 on N=46 plots (1, 4 and 16 plant species mixtures) using an electroshocking method[31], employing a combination of four octet devices (DEKA 4000, Deka Gerätebau, Marsberg, Germany). Positions for earthworm sampling were randomized once at the beginning of the experiment (2003). Earthworms were extracted from an area of 1 x 1 m.

Nematodes were sampled in autumn 2005 from 5 soil cores (2 cm in diameter, 5 cm deep) taken at a randomized subplot position (2 x 4 m) per plot (N=82). Samples were homogenized, nematodes extracted by a modified wet extraction technique[32], counted and determined to species level.

For the quantification of **Protozoa (Amoebae and Flagellates)**, five soil samples were taken on a randomized position on N=12 plots using a metal corer (diameter 5 cm, soil depth ~10 cm) in October 2009. The soil was homogenized and stored at 5 °C until usage. Amoebae and Flagellates were counted using a modified most probable number method[33]. Briefly, 5 g fresh weight of soil was suspended in 20 mL sterile Neff's modified amoebae saline (NMAS; see ref.[34]) and gently shaken for 20 min on a vertical shaker. Threefold dilution series with nutrient broth (Merck, Darmstadt, Germany) and NMAS at 1:9 v/v were prepared in 96-well microtiter plates (VWR, Darmstadt, Germany) with four replicates, each. The microtiter plates were incubated at 15 °C in darkness and the wells were inspected for presence of protozoa using an inverted microscope at x 100 and x 200 magnification (Nikon, Eclipse TE 2000-E, Tokyo, Japan) after 3, 6 ,11, 19 and 26 days. Densities of protozoa were calculated according to ref.[35].

Microbial biomass and respiration were measured from five cores (diameter 5 cm, depth 5 cm) taken on randomized subplot positions (2 x 4 m) per plot in May 2002, 2003, 2004, 2006, 2007 and 2008. Soil samples were homogenized from each plot and microbial respiration and microbial biomass were measured using an O_2 microcompensation apparatus[36]. Microbial biomass was determined by the substrate-induced respiration method (SIR; see Ref.[37]).

Diversity of **arbuscular mycorrhizal fungi** was determined by amplification of DNA derived directly from soil on a subset of 23 plots. Plots were selected at random, constrained of equal representation of levels of plant species richness. DNA was extracted under utilization of FastDNA Spin Kit for Soil (MP Biomedicals, Illkirch, France) according to manufacturers' protocol. The internal transcribed spacer (ITS) within the rDNA was amplified by nested PCR (see Ref.[38]) using the primer pair LSU-Glom1/ SSU-Glom1 for the first PCR reaction and ITS4/ ITS5 for the second PCR step, Between the PCR steps, an intermediate AluI digestion was performed to exclude non-mycorrhizal DNA after the first PCR. Cloning, clone fingerprinting by RFLP and sequencing were performed as in Ref.[39]. Sequences were pre-sorted into syngeneic clusters using the contig-tool as implemented in

Sequencher 4.8 (Gene Codes Corp., Ann Arbor, USA).Closest matches to each sequence cluster were determined using the BLASTN sequence similarity search tool in GenBank[40] and used as references. Sequences were pre-aligned in MultAlin[41], alignments were corrected by hand. The phylogenetic relations were inferred based on the Kimura 2-parameter method[42] with the neighbour-joining analysis[43] as implemented in PAUP 4.0b8 (see Ref. [44]). The confidence of branching was assessed using 1000 bootstrap resamplings. Sequences falling into one clade, and showing sequence identities of at least 92% were regarded as distinct taxa. The cutoff value of 92% was chosen according to Ref. [45] in order to reflect the natural sequence diversity found within and between the spores of the same AMF species[46].

Spatial **soil exploitation by roots** was assessed with the ingrowth-core technique[47]. In June 2003, five soil cores (4.8 cm diameter, 30 cm deep) were removed per plot and replaced by root-free soil from the field site. In September 2003, the initially root-free in-growth cores were removed and the holes were re-filled with root-free soil until the following withdrawal in July 2004. To extract the newly formed roots, each in-growth core was first weighed and carefully homogenized. A subsample of 50 g of soil was suspended in water and rinsed over a 0.5-mm screen. Roots collected in the screen were transferred into a water-filled clear acrylic tray and scanned. Total root length was determined from images using WinRhizo (Regent Instruments, Quebec, Canada). Afterwards, root length density (cm root length per cm^3 soil volume) was calculated.

Classification of organisms into groups

All organisms collected were classified into functional groups (guilds) based on extensive literature and database searches. Functional groups were defined based on trophic position (feeding guild) and interaction type (consumers, mutualists, pathogens, decomposers).

Aboveground herbivores: Phytophagous beetles (mainly Chrysomelidae and Curculionidae), Leafhoppers (Cicadina), gall-forming and other phytophagous Hymenoptera, phytophagous Heteroptera, Grasshoppers (Saltatoria: Acrididae), phytophagous Diptera.

Aboveground carnivores: Zoophagous Hymenoptera (excl. Parasitica), zoophagous beetles (mainly Carabidae and Staphylinidae), Zoophagous Heteroptera, Zoophagous Diptera, Spiders (Arachnidae).

Aboveground omnivores: Omnivorous beetles (mainly Staphylinid beetles) and Diptera

Parasitoids: Parasitoid Hymenoptera and Diptera. No parasitoid Coleoptera were found.

Hyperparasitoids: Hyperparasitoid Hymenoptera (mainly *Alloxysta* sp., Hymenoptera: Cynipidae) and mummy parasitoids (*Dendrocerus* sp., Hymenoptera: Megaspilidae)

Pollinators: Hymenoptera (mainly Apidae), Diptera (mainly Syrphidae).

Pathogens: Plant-pathogenic fungi of the groups Peronosporaceae (Downy Mildews), Erysiphales (Powdery Mildews), Ustilaginales (Smut diseases) and Uredinales (Rust fungi). Further, we included Bacteria and Fungi causing Leafspot diseases.

Invaders: Abundance (dry weight/m²) and species richness of (weedy) plant species not

present in the pool of 60 plant species present in the Jena Experiment (so-called external invaders).

Belowground microfauna: Amoebae and Flagellates.

Belowground mesofauna: Collembola, Herbivorous Nematodes, Bacterivorous Nema-todes, Fungivorous Nematodes, Omnivorous Nematodes, Oribatid mites, pro- meso- and astigmatic mites.

Saprophagous Macrofauna: Earthworms (Lumbricidae), Isopoda, Diplopoda, Enchytraei-dae

Predatory Macrofauna: Araneida, Geophilidae, Lithobiidae, Carabidae, Staphylinidae, Elateridae, zoophagous insect larvae, Hymenoptera

Herbivorous Macrofauna: Gastropoda, Curculionidae, herbivorous larvae iof Diptera, Symphyla, herbivorous Hemiptera groups.

Definition and quantification of organism interactions

We included only those interactions between organisms that were directly and quantitatively observed in the field (as opposed to correlative approaches where interaction partners are generally unknown). Hence, every interaction considered here contains information about the exact process rates. For example, "decomposition" is the amount of material of known quantity decomposed over a given period of time per unit area.

The specific definitions for each interaction are:

Herbivory: The percentage of intact leaf area of an average sample of each plant community consumed by invertebrate herbivores over a given period of time on subplots of 2 x 4 m, averaged across time. Plant community herbivory was visually estimated in May and August 2003, 2004 and 2005 by sampling a given number of plant individuals along transects through each of the 82 experimental plots and noting the percentage of leaf area eaten by invertebrate herbivores (insects and molluscs).

Parasitism: The percentage of wildbee (Hymenoptera: Apidae) cells parasitized in artificially exposed trap nests (measured in 2005 and 2006). Trap nests consisted of reed internodes cut to a standardized length and enclosed in plastic tubes of c. 14 cm diameter. There were 4 trap nests installed on a wooden post in the middle of each plot; trap nests were installed in early spring each year and removed in autumn, and all reed internodes were checked for colonization by trap-nesting bees, wasps and their natural enemies. We used parasitized wildbee cells because these measurements were performed in all N=82 large plots. Qualitatively similar results were obtained using parasitism rates estimated from aphid mummies.

Hyperparasitism: The percentage of aphid mummies that were parasitized by Hymenopteran hyperparasitoids. All stationary aphids (including alates within colonies) were counted 4 times (twice before the first mowing, twice after) in c. 3 m x 20 cm transects in 47 small extra plots on all sown plant species (plant species richness here ranged from 1 to 9 plant species). All mummies (parasitized aphids) were collected in the same transect at the same 4 dates and checked for parasitoids and hyperparasitoids. Analyses were performed separately from all other data, and lines in Fig. 1 show predicted values extrapolated to more species-rich mixtures. Hyperparasitism was additionally measured in 23 large plots (20 x 20 m) and a binary regression analysis showed qualitatively the same result.

Pollination: The number of flower visits by Dipteran and Hymenopteran pollinators per time interval (6 minutes) visually counted on 0.64 m² subplots in each plot (excluding those plots containing only grasses) in May, June and August 2005 and 2006, averaged over time.

Pathogen severity: The mean percentage of leaf area damaged by plant pathogenic fungi across the whole plant community of every plot. Pathogen infection was visually assessed in 2006 for all species in all 82 large plots. Screening focussed on the pathogen groups downy mildew, powdery mildew, rusts and smuts. In addition, infection of fungal-caused leaf spots was assessed. Fungal pathogen infection was registered for each species per plot as the mean percentage infected individuals per species.

Bioturbation: The number of burrowing holes of the Common Vole (*Microtus arvalis*)

found in June and September 2005 in an area of 20 x 20 m on every plot, averaged across time. Activity of other bioturbators (e.g. earthworms) was not assessed, but data on earthworm densities are available upon request.

Decomposition: The percentage of litter remaining in standardized exposed litter bags per plot after four months of time. Litter of three plant functional groups (grasses, herbs and legumes) was used to establish four litter treatments [grasses (G), herbs (H), legumes (L) and mixed (M)]. Each litterbag contained 3 g dry weight of plant material. Litter of each functional group was obtained by mixing 1 g of senesced litter of three plant species: grasses (*Festuca rubra*, *Lolium perenne*, *Poa pratensis*) (N 2.0%, C:N 22.6), herbs (*Cirsium oleraceum*, *Daucus carota*, *Plantago lanceolata*) (N 2.3%, C:N 19.6), legumes (*Lathyrus pratensis*, *Lotus corniculatus*, *Trifolium repens*) (3.0%, C:N 15.5). For the mixed litter treatment we used 3 g dry weight litter (N 2.4%, C:N 19.3) from a homogenous mixture created by mixing all 9 plant species. The litter material was collected from the Jena Experiment field site in the previous season (2003), sorted, dried for 3 days at 60 °C and cut into pieces ~ 3 cm in length. Litterbags were built using 4 mm mesh to allow access of soil animals including large earthworms such as *Lumbricus terrestris*. Litterbags of each of the four litter treatments were placed on the soil surface of four decomposer treatments (reduced and increased earthworm density, ambient and reduced springtail density) of the 1, 4, 16 plant species diversity plots in February 2004. The litterbags were collected in June 2004, after 4 months of exposure, dried three days at 60 °C and weighed. The percentage of litter remaining in the mixed litter treatment after these four months was used as a measure of decomposition rate. Measurements were performed on plots containing 1, 4 and 16 plant species.

Biological invasion: The population density (individuals per 4 m²) of an invading weedy plant species (*Cirsium arvense*), measured in 2004 on randomly placed positions in the core area of every plot.

Microbial respiration: Microbial respiration was measured from five cores (diameter 5 cm, depth 5 cm) taken on randomized subplot positions (2 x 4 m) per plot in May 2002, 2003, 2004, 2006, 2007 and 2008. Soil samples were homogenized from each plot and microbial respiration was measured using an O_2 microcompensation apparatus[36].

Ant activity: Between 4th July 2006 and 16th August 2006, ant colonies were counted in each plot in an area of 4m². The surface of the plots was searched visually. Every entrance was counted as a measure of colony number. An entrance was defined by the observation of ants passing in and out and by recruiting behaviour occurring when the entrance was disturbed using tweezers.

Statistical Methods

We used R 2.11.0 (see Ref. [48]) for data analyses. In addition, we calculated structural equation models using AMOS 16.0 (SPSS, Inc.). Code printed below refers to R 2.11.0.

General approach

For most of our analyses, we present results on a unified scale [0;1]. This allows direct comparisons of slopes, intercepts and other model parameters across all taxonomic groups.

A small example dataset shall serve to introduce the methodology used; let y_1 and y_2 be carnivore and herbivore abundance, respectively; let x_1 be the explanatory variable (plant

x_1	y_1	y_2	$y_1´$	$y_2´$
1	10	100	0	0
2	22	220	0.4	0.4
3	34	340	0.8	0.8
4	40	400	1	1

species richness). $y_1´$ and $y_2´$ are the transformed versions of the response variables y_1 and y_2. A possible dataset may then look like this:

The slopes of corresponding regression lines are then 10.2 for carnivores or 102 for herbivores. On the transformed scale, however, both slopes are exactly 0.34. Thus, standardizing the response variables to [0;1] reveals that both groups actually respond in exactly the same way to plant species richness. Such a conclusion would, however, not have been possible on the original scale.

Our approach to data analysis consists of four steps:

(1) Standardization of response variables to a unified scale [0...1]
(2) Separate analysis of every response variable using a common set of 572 linear and nonlinear models per response variable
(3) Combined analysis of all response variables using a common power law function
(4) Combined multivariate analyses of groups of response variables using (i) multivariate linear models and (ii) structural equation models.

We chose a transformation to range [0,1] rather than a z transformation because (i) the resulting values are easier to compare and to interpret, (ii) because this transformation is more robust than the z transformation [49], and (iii) because information about the variation of variables is lost with the z transformation (all variables having a standard deviation of 1 after transformation).

Note that scaling variables to [0;1] may introduce a bias when dividing by the maximum observed value for each variable, especially if the underlying distributions are skewed. In particular, a large maximum:median ratio could lead to lower values of the exponent z reported in power functions. However, the z values calculated by us were based on highly aggregated data, for which the arithmetic mean is likely to be an unbiased estimater of the

true population mean.

We additionally ran our analyses using a z transformation and found no principal differences.

Univariate linear and nonlinear models

The set of linear and nonlinear models was carefully chosen from biologically meaningful models:

(1) **Linear models** containing block, plant species richness, number of plant functional groups, grass and legume presence
(2) **Saturating** non-linear models (Michaelis-Menten, asymptotic regression models, logistic regression models)
(3) **Exponential** non-linear models (including biexponential models)
(4) **Power law models** covering a wide range of possible shapes of responses

To make linear and non-linear models comparable, legume presence, grass presence and number of functional groups were included as covariates into the nonlinear models.

If model diagnostic plots showed variance heterogeneity or non-normality of variance, we updated our models using variance functions. In two cases (vertebrate herbivore abundance and hyperparasitism rates) we additionally used generalized linear models for analysis[50].

Blocks were treated as fixed rather than random effects because there were only four levels of blocks, and because treatments were unequally represented within blocks (see Ref. [51] for a similar approach).

We used AICc (Akaike´s Information Criterion, corrected for small sample sizes; see Ref. [52]) for model simplification and model selection. Manual deletions of terms from models (comparing models using conditional F-tests) lead to qualitatively very similar results.

Abundances and numbers of distinct species per sample were summed during data aggregation. For non-count data (organism interactions), we calculated mean values for every plot. The total sample size was at least 50 for abundance and species richness data, and 82 for organism interactions. For practical reasons, hyperparasitism and belowground protozoa had a smaller sample size. These variables were therefore not included into the multivariate linear models. Every response variable was transformed using a transformation to [0;1] prior to analyses to allow comparisons of model parameters. Vertebrate herbivore abundance was log-transformed before transformation to [o;1] to reduce non-constancy of variance. For every response variable, we set up a set of linear and nonlinear candidate models. In generalized non-linear least squares models, we used variance functions to account for heteroscedasticity. For every response variable, the set of candidate models considered was created using linear and nonlinear models.

To give every model the same chance of being selected, the same principal set of initial models was considered for every response variable in turn.

This makes the overall model selection process entirely reproducible.

The R code for the general model selection function was:

```
evaluate.all=function(response=quote(response),DF=quote(DF),i){
require(MASS)
require(pgirmess)
require(nlme)
options(width=500,show.error.messages=T)

DF <- cbind(response = DF[[response]], DF)
options(show.error.messages=F)
L=list(
        modelname1=try(model.formula1,DF)),
        modelname2=try(model.formula2,DF)),
        modelname3=try(model.formula3,DF))
        #the full list of model formulae is available upon request
        #[...]
        )

L2=Filter(function(x) !inherits(x, "try-error"), L) #to select only those models that converged
without error
nn=names(L2)

# actual model selection based on AICc:
        df=data.frame(selMod(L2))
        nn=nn[as.numeric(row.names(df))]
        df=cbind(nn,df)

# return the i´th selected model
selected=which(seq(1:length(nn))==as.numeric(rownames(selMod(L2)))[i])

# return the model formula (this has the structure response~...,data=DF)
called=lapply(L2[selected],function(x)x$call)

# Some text replacement to have the correct response variables and dataframes in there:

called=sub("response",response,called)
replacevec<-c("newsynthesis.ranged")

called=sub("DF",replacevec,called)

# Finally, return the selected models

returnlist=list(response=response,models=df,selected.model=called,all.models=L2)

return(returnlist)
}
```

The full list of model formulae used inside the function is available on request.

The `gnls()` function from the `MASS` library in R[53] was used to fit generalized nonlinear least-squares models that allow for covariates in nonlinear models, and variance heteroscedasticity can be modelled using variance functions.

The `try()` command prevents the function to exit with an error if initial parameter values do not lead to model convergence. Initial parameter values for nonlinear models were based on previous manual model fitting approaches.
The index `i` allows the i´th model to be extracted from the resulting list of models (ordered by AICc) for manual inspection and modification.

For all models we calculated the number of parameters, log-Likelihood, Akaike´s An Information Criterion, corrected for small sample size (AICc), delta-AICc values and Akaike weights. The five models with lowest AICc values were inspected in detail by plotting model predictions and model diagnostic plots to inspect the variance structure. The model with lowest AICc and highest Akaike weight was taken to be the best model of the subset, with some exceptions where biological knowledge made competing models more likely (for example if theory predicted saturating rather than exponential kinetics).

To allow the reader a full assessment of all competing models, we supply two Excel tables containing all models considered. Model convergence was different for every response variable, and we provide these outputs to allow a precise judgement of which patterns are strongly supported by the data, and which not.

Fitting a more parsimonious unified power law model

Using the `evaluate.all()` function defined above revealed that 25 out of 54 response variables (i.e. 46%) showed clearly nonlinear relationships with plant species richness (8 exponential, 7 Michaelis-Menten, 10 power law relationships).

For parsimony, we decided to fit a **common power law function** to all response variables (Adler 1998), covering a broad range of possible non-linear and linear biodiversity effects.

The common power law function used was

$$y = a + b \times sowndiv^{c}$$

Where y is the response variable, sowdiv is sown plant species richness, and a, b and c are parameters to be estimated from the data.

Note that this model also allows linear models (for c=1) and null models (for c=0).

Because many response variables can be assumed to be zero for zero plant species richness, we excluded the intercept from the model in cases where the c parameter was compared across different response variables (model named `Pa4` below).

The power law models were fitted using the following R code:

```
evaluate.small=function(response=quote(response),DF=quote(DF)){
require(MASS)
require(pgirmess)
require(nlme)
options(width=500,show.error.messages=T)

DF <- cbind(response = DF[[response]], DF)

L=list(
     Pa1=try(nls(response~a+b*sowndiv^c,start=list(a=1,b=1,c=1),DF)),
     Pa2=try(nls(response~a+b*sowndiv,start=list(a=1,b=1),DF)),
     Pa3=try(nls(response~a+sowndiv^c,start=list(a=1,c=1),DF)),
     Pa4=try(nls(response~b*sowndiv^c,start=list(b=1,c=1),DF)),
     Pa5=try(nls(response~sowndiv^c,start=list(c=1),DF))
)

L2=Filter(function(x) !inherits(x, "try-error"), L) #to select only those models
that converged without error
nn=names(L2)

called=lapply(L2[1],function(x)x$call)

params=lapply(L2[1],function(x)summary(x)[10])

summary=lapply(L2[1],function(x)summary(x))

called=sub("response",response,called)
replacevec<-c("newsynthesis.ranged")

called=sub("DF",replacevec,called)

returnlist=list(response=response,selected.model=called,all.models=L2,params=par
ams,summary=summary)
return(returnlist)
}
```

Multivariate linear models

Measurements collected on the same 82 plots cannot be considered statistically independent; for example, herbivory and decomposition can be indirectly correlated via faeces of herbivorous insects or induced leaf abscission. Hence, we used multivariate linear models[54] to compare the responses of different variables to biodiversity. For parsimony, multivariate linear models consisted of a matrix of response variables, and log (plant species richness) as the only explanatory variable.

We used the log of plant species richness to linearize individual relationships between each response and explanatory variable, and to reduce leverage. The model was fitted like this:

```
model1<-lm(cbind(response.variable1,response.variable2...)~logdiv)
```

We constructed three multivariate models, one for organism abundances, one for organism species richness, and one for biotic interactions. The overall output from these models yielded Pillai´s trace and approximate F values cited in the manuscript text.

For every model, we further constructed a matrix of contrast coefficients for the response variables that was used to compare the slopes of the response variables with one another. In all cases, we used so-called successive difference contrasts[53].

For example, the successive difference contrasts for a set of 8 response variables was specified using

```
require(MASS)
contr.sdif(8)
```

In this case, the first comparison is between herbivores and carnivores, the second comparison is between parasitoids and carnivores, and so on.

F- and P-values for each comparison were calculated from the diagonal elements of the resulting hypothesis and error sum of squares-and products matrices (here termed `SSPH` and `SSPE`; see also Ref. [54]) using the following formulae:

```
f.value=diag(linhyp$SSPH)/(diag(linhyp1$SSPE)/res.df)
p.value=1-pf(f.value,1,res.df)
```

where `linhyp` is the linear hypothesis constructed using the matrix of contrast coefficients, and `res.df` are the residual degrees of freedom of the multivariate linear model under consideration.

Structural equation models

As effects of plant species richness on organism abundances or diversity may also be mediated indirectly, we decided to employ structural equation models (SEMs; see Refs. [55,56]) to allow multiple pathways for the effects of plant species richness.

SEMs are particularly well suited also in an experimental context, i.e. where some variables are deliberately manipulated experimentally (Grace 2006, pp. 233 ff). Further, SEMs "can be used to develop accurate and meaningful final multiple regression models when collinearities among explanatory variables are thought to be present" (see Ref. [57]).

We use the following terminology for graphical representations of structural equation models:
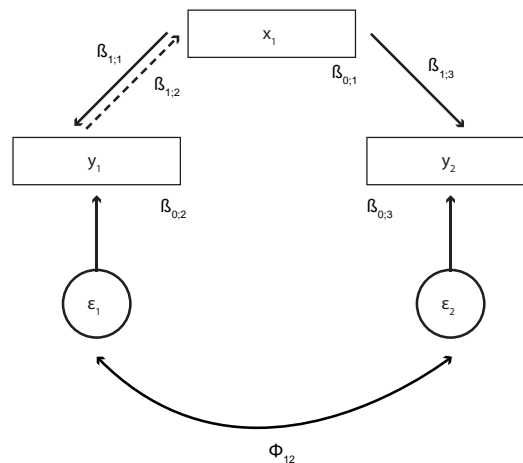
x_1, y_1 and y_2 are observed variables; $\beta_{0;1}$, $\beta_{0;2}$ and $\beta_{0;3}$ are intercepts, $\beta_{1;1}$, $\beta_{1;2}$ and $\beta_{1;3}$ are path coefficients representing directed effects of x_1 on y_1, y_1 on x_1, and x_1 on y_2. ε_1 and ε_2 are residual errors, and ϕ_{12} represents the residual co-variance between ε_1 and ε_2. The corresponding structural equations are:

$$\varepsilon_1 \sim N(0, \sigma_1)$$
$$\varepsilon_2 \sim N(0, \sigma_2)$$

$$y_1 = \beta_{0;1} + \beta_{1;1} x_1 + \varepsilon_1$$
$$x_1 = \beta_{0;2} + \beta_{1;2} y_1$$
$$y_2 = \beta_{0;1} + \beta_{1;3} x_1 + \varepsilon_2,$$

where x_1 is treated as an "explanatory" variable measured without error, and ε_1 and ε_2 follow standard normal distributions N with mean 0 and standard deviations $\sigma_{1\ldots2}$.

Because plant species richness was our main experimentally manipulated variable, all SEMs started off with plant species richness and further trophic groups were added both above- and below ground. All "response" variables were log-transformed and scaled to [0;1] before analysis to avoid non-positive definite residual covariance matrices. Plant species richness was log-transformed before analysis to reduce leverage. In essence, we therefore fitted log-log models that were essentially linearized versions of the individual non-linear regression models. Missing values were replaced by the mean. The total sample size was N=50 data points.

This allowed us to use up k<49 degrees of freedom for all SEMs. Hence, with a total of about 50 variables for all above- and belowground organism groups, it was not possible to fit a "complete" above-/belowground food web model.

We therefore present two types of SEMs:

(1) An above-/belowground SEM incorporating only organism groups with a size of >2mm (macrofauna).

(2) A belowground SEM incorporating only belowground organism groups.

For both types of SEMs, we decided on the initial model by considering published food webs (e.g. Coleman et al. 2003) and collecting expert opinions before the actual model-fitting process. The resulting initial models were then simplified using the "Specification search" command in AMOS 16.0 for Windows XP (SPSS, Inc). The minimal adequate model was considered to be the one that minimized Akaike´s An Information Criterion [58]. For the minimal adequate model, the 95% confidence interval of the root mean square error of approximation (RMSEA) was further required to include 0 (see Ref. [59]).

Supplementary Tables

Supplementary Table 1 | Summaries of response variables on original scale.

Statistical summaries and units of measurement for the response variables used in this study on their original scale. The values of each observation y_i on the transformed scale can easily be computed using this table and the formula: $y' = (y_i - y_{min})/(y_{max} - y_{min})$. For example, a herbivory value of 3% corresponds to $(3-0.02)/(9.48-0.02) = 2.98/9.46 = 0.32$ on the transformed scale. N is the number of plots with non-missing values (sample size).

	Minimum	Median	Mean	Maximum	N
Design variables					
Grass presence (1=absent, 2=present)	1	1	1.46	2	82
Legume presence (1=absent, 2=present)	1	1	1.48	2	82
Small herb presence (1=absent, 2=present)	1	2	1.52	2	82
Tall herb presence (1=absent, 2=present)	1	2	1.54	2	82
Plant functional group richness (1-4)	1	2	2.12	4	82
Sown plant species richness (1-60)	1	4	8.59	60	82
Organism abundances					
Microbial biomass (µg C/g soil)	5.40×10^2	9.41×10^2	9.43×102	1.62×10^3	82
Amobae abundance	1.95×10^3	1.42×10^4	3.60×10^4	1.78×10^5	12
Flagellate abundance	2.09×10^3	9.58×10^3	1.23×10^4	1.98×10^4	12
Saprophagous macrofauna abundance	0	7	8.94	51	80
Saprophagous mesofauna abundance	0	4	7.51	64	80
Herbivorous macrofauna abundance	0	4	4.76	19	80
Predatory macrofauna abundance	0	11.5	15.49	101	80
Bacterivorous nematode abundance	0	16	18.22	86	73
Fungivorous nematode abundance	0	13	17.17	78	73
Plant-feeding nematode abundance	2.07	47	60.47	201	73
Predatory nematode abundance	0	1	1.84	24.47	73
Omnivorous nematode abundance	0	8	10.19	46	73
Collembola abundance	0	23	28.1	104	80
Mite abundance	0	16.5	21.9	102	80
Gamasida abundance	0	3	5.49	38	80
Aboveground herbivore abundance	181	609	665.16	1691	50
Aboveground carnivore abundance	221.5	343.62	338.33	533.5	50
Aboveground omnivore abundance	18.75	49.25	51.17	119.5	50
Aboveground parasitoid abundance	48	140	177.6	468	50
Aboveground hyperparasitoid abundance	0	1	1.46	5	28
Pollinator abundance	6	49	54.98	187	50
Invader abundance	11.14	133.14	179.78	815.67	82
Vole abundance	0	0.5	6.1	67	82

Supplementary Table 1 (continued)

	Minimum	Median	Mean	Maximum	N
Organism species richness					
Mycorrhizal species richness	3	8	7.4	12	77
Saprophagous macrofauna species richness	0	2	1.94	4	80
Saprophagous mesofauna species richness	0	1	1.39	3	80
Herbivorous macrofauna species richness	0	2	2.58	7	80
Predatory macrofauna species richness	0	4.5	4.59	11	80
Bacterivorous nematode species richness	0	3	2.9	6	72
Fungivorous nematode species richness	0	3	2.42	4	72
Plant-feeding nematode species richness	1	6	5.81	11	72
Predatory nematode species richness	0	0	0.53	3	72
Omnivorous nematode species richness	0	2	1.89	5	72
Collembola species richness	0	6	5.67	11	80
Aboveground herbivore species richness	35	58	62.71	111.5	50
Aboveground carnivore species richness	44	61.5	61.67	75	50
Aboveground omnivore species richness	7	15.25	14.92	24	50
Aboveground parasitoid species richness	9	21.5	22.48	36	50
Pollinator species richness	2	8	8.6	17	50
Invader species richness	2.75	6.62	7.45	16.44	82
Pathogen species richness	0	3	2.65	5	82
Organism interactions					
Community herbivory (percent)	0.02	2.01	2.2	9.48	82
Parasitism (percent)	0	14.43	16.95	57.14	78
Flower visitor frequency (visits/6 Min.)	0	6.83	13.24	108	73
Litter decomposition (percent)	42.33	69.67	69.24	89	44
Seed predation (proportion removed)	0.22	0.78	0.75	1	46
Pathogen severity (percent)	0	1.05	1.35	4.08	82
Invasion (individuals/m²)	0	1.5	4.19	39	80
Bioturbation (burrows per 400 m²)	0	14.75	31.45	209	82
Ant activity (colonies per 4 m²)	0	3	2.98	9	81
Microbial respiration ($\mu L\ O_2$ g soil^{-1} x h^{-1})	1.8	3.05	3.11	7.67	82
Other covariates					
Aboveground plant biomass (g/m²)	6.71	240.68	277	614.21	82
Aboveground dead plant biomass (g/m²)	8.84	24.59	26.89	79.34	82
Leaf area index (m²/m²)	0.76	2.13	2.42	4.36	82
Root length growth (cm/cm³ soil)	4.2	20.26	21.37	49.85	81

Supplementary Table 2 | Model selection tables for all response variables and all models considered (see following pages) Column names: **model name**, an internal name used to uniquely label all models fitted per response variable; **model formula**, the model formula used (in R notation); variance functions and covariate formulae for gnls models not shown here (see **Supplementary Table 3** for the full specification of all models); **LL** maximized log-likelihood of the model, given the data; **K**, number of estimated parameters in the model; **N2K**, the number of observations, divided by K; **AICc**, Akaike´s An Information Criterion, corrected for small sample sizes; **deltAICc**, the difference between AICc and the lowest AICc value in the set of models considered for a given response variable; **w_ic**, the AICc weights.

Supplementary Table 2 (continued)

Long variable name	model name	model formula	LL	K	N2K	AICc	deltAICc	w_ic
Microbial biomass	L02	block + (sowndiv + funcgr + grass + leg)^2	61.935	16	5.125	-83.500	0.000	0.52
Microbial biomass	L01	block + (sowndiv + funcgr + grass + leg)^2	61.260	16	5.125	-82.152	1.348	0.26
Microbial biomass	L0	block + (sowndiv + funcgr + grass + leg)^2	57.717	15	5.467	-78.161	5.339	0.04
Microbial biomass	M1	a * sowndiv/(b + sowndiv)	41.150	3	27.333	-75.993	7.507	0.01
Microbial biomass	M1a	SSmicmen(sowndiv, Vm, k)	41.150	3	27.333	-75.993	7.507	0.01
Microbial biomass	Pa3	a + sowndiv^c	41.021	3	27.333	-75.734	7.766	0.01
Microbial biomass	Pb31	a + sowndiv^c	41.021	3	27.333	-75.734	7.766	0.01
Microbial biomass	L011	block + (sowndiv + funcgr + grass + leg)^2	57.847	16	5.125	-75.324	8.176	0.01
Microbial biomass	L021	block + (sowndiv + funcgr + grass + leg)^2	57.769	16	5.125	-75.169	8.331	0.01
Microbial biomass	Pa4	b * sowndiv^c	40.738	3	27.333	-75.168	8.332	0.01
Microbial biomass	Pb41	b * sowndiv^c	40.738	3	27.333	-75.168	8.332	0.01
Microbial biomass	M3	a * sowndiv/(b + sowndiv)	42.879	5	16.400	-74.969	8.531	0.01
Microbial biomass	Pc331	a + sowndiv^c	41.405	4	20.500	-74.290	9.210	0.01
Microbial biomass	M2	d + a * sowndiv/(b + sowndiv)	41.252	4	20.500	-73.984	9.515	0.00
Microbial biomass	Pc321	a + sowndiv^c	41.210	4	20.500	-73.901	9.599	0.00
Microbial biomass	Pc431	b * sowndiv^c	41.111	4	20.500	-73.703	9.797	0.00
Microbial biomass	M321	a * sowndiv/(b + sowndiv)	43.375	6	13.667	-73.630	9.870	0.00
Microbial biomass	AS3	SSasympOrig(sowndiv, Asym, lrc)	39.966	3	27.333	-73.624	9.876	0.00
Microbial biomass	Pg181	a + sowndiv^c	42.122	5	16.400	-73.455	10.045	0.00
Microbial biomass	AS1	SSasymp(sowndiv, Asym, R0, lrc)	40.914	4	20.500	-73.309	10.191	0.00
Microbial biomass	AS2	SSasympOff(sowndiv, Asym, lrc, c0)	40.914	4	20.500	-73.309	10.191	0.00
Microbial biomass	Pc421	b * sowndiv^c	40.914	4	20.500	-73.308	10.192	0.00
Microbial biomass	LG2	SSlogis(sowndiv, Asym, xmid, scal)	40.793	4	20.500	-73.067	10.433	0.00
Microbial biomass	M141	d + a * sowndiv/(b + sowndiv)	48.042	10	8.200	-72.985	10.515	0.00
Microbial biomass	Pg191	b * sowndiv^c	41.860	5	16.400	-72.930	10.570	0.00
Microbial biomass	M311	a * sowndiv/(b + sowndiv)	42.938	6	13.667	-72.756	10.744	0.00
Microbial biomass	Pf131	a + sowndiv^c	41.721	5	16.400	-72.653	10.846	0.00
Microbial biomass	M222	d + a * sowndiv/(b + sowndiv)	41.564	5	16.400	-72.338	11.162	0.00
Microbial biomass	M5	a * sowndiv/(b + sowndiv)	41.513	5	16.400	-72.237	11.263	0.00
Microbial biomass	M211	d + a * sowndiv/(b + sowndiv)	41.488	5	16.400	-72.188	11.312	0.00
Microbial biomass	Pf141	b * sowndiv^c	41.487	5	16.400	-72.185	11.315	0.00
Microbial biomass	M4	a * sowndiv/(b + sowndiv)	41.483	5	16.400	-72.176	11.324	0.00
Microbial biomass	Pn1831	a + sowndiv^c	42.529	6	13.667	-71.939	11.561	0.00

Supplementary Table 2 (continued)

Long variable name	model name	model formula	LL	K	N2K	AICc	deltAICc	w_ic
Microbial biomass	Pd81	a + sowndiv^c	41.282	5	16.400	-71.775	11.725	0.00
Microbial biomass	Pd91	b * sowndiv^c	41.275	5	16.400	-71.761	11.739	0.00
Microbial biomass	Pn1931	b * sowndiv^c	42.277	6	13.667	-71.434	12.066	0.00
Microbial biomass	Pn1821	a + sowndiv^c	42.208	6	13.667	-71.296	12.204	0.00
Microbial biomass	Pm1331	a + sowndiv^c	42.069	6	13.667	-71.017	12.483	0.00
Microbial biomass	M81	a * sowndiv/(b + sowndiv)	43.195	7	11.714	-70.877	12.623	0.00
Microbial biomass	M6	a * sowndiv/(b + sowndiv)	43.172	7	11.714	-70.831	12.669	0.00
Microbial biomass	Pn1921	b * sowndiv^c	41.937	6	13.667	-70.755	12.745	0.00
Microbial biomass	M522	a * sowndiv/(b + sowndiv)	41.927	6	13.667	-70.734	12.766	0.00
Microbial biomass	Ph241	b * sowndiv^c	43.117	7	11.714	-70.720	12.780	0.00
Microbial biomass	Pm1321	a + sowndiv^c	41.916	6	13.667	-70.713	12.787	0.00
Microbial biomass	Pd61	a + b * sowndiv^c	43.040	7	11.714	-70.567	12.933	0.00
Microbial biomass	Pm1431	b * sowndiv^c	41.836	6	13.667	-70.553	12.947	0.00
Microbial biomass	Ph231	a + sowndiv^c	43.004	7	11.714	-70.494	13.006	0.00
Microbial biomass	M411	a * sowndiv/(b + sowndiv)	41.768	6	13.667	-70.417	13.083	0.00
Microbial biomass	Pj331	a + sowndiv^c	42.934	7	11.714	-70.354	13.146	0.00
Microbial biomass	Pe831	a + sowndiv^c	41.699	6	13.667	-70.278	13.222	0.00
Microbial biomass	Pe931	b * sowndiv^c	41.695	6	13.667	-70.269	13.231	0.00
Microbial biomass	M511	a * sowndiv/(b + sowndiv)	41.694	6	13.667	-70.268	13.232	0.00
Microbial biomass	Pm1421	b * sowndiv^c	41.678	6	13.667	-70.236	13.264	0.00
Microbial biomass	M422	a * sowndiv/(b + sowndiv)	41.613	6	13.667	-70.107	13.393	0.00
Microbial biomass	Pj341	b * sowndiv^c	42.749	7	11.714	-69.984	13.516	0.00
Microbial biomass	Pe821	a + sowndiv^c	41.476	6	13.667	-69.833	13.667	0.00
Microbial biomass	Pe921	b * sowndiv^c	41.466	6	13.667	-69.812	13.688	0.00
Microbial biomass	M7	a * sowndiv/(b + sowndiv)	42.497	7	11.714	-69.481	14.019	0.00
Microbial biomass	M622	a * sowndiv/(b + sowndiv)	43.634	8	10.250	-69.296	14.204	0.00
Microbial biomass	Pd71	a + b * sowndiv	40.033	5	16.400	-69.276	14.224	0.00
Microbial biomass	M832	a * sowndiv/(b + sowndiv)	43.624	8	10.250	-69.275	14.225	0.00
Microbial biomass	Pi291	b * sowndiv^c	42.357	7	11.714	-69.201	14.299	0.00
Microbial biomass	Pi281	a + sowndiv^c	42.355	7	11.714	-69.197	14.303	0.00
Microbial biomass	Pp2431	b * sowndiv^c	43.584	8	10.250	-69.195	14.305	0.00
Microbial biomass	Pp2331	a + sowndiv^c	43.487	8	10.250	-69.002	14.498	0.00
Microbial biomass	Pr3331	a + sowndiv^c	43.340	8	10.250	-68.707	14.792	0.00

Supplementary Table 2 (continued)

Long variable name	model name	model formula	LL	K	N2K	AICc	deltAICc	w_ic
Microbial biomass	M111	d + a * sowndiv/(b + sowndiv)	42.028	7	11.714	-68.542	14.958	0.00
Microbial biomass	M821	a * sowndiv/(b + sowndiv)	43.254	8	10.250	-68.535	14.965	0.00
Microbial biomass	M611	a * sowndiv/(b + sowndiv)	43.222	8	10.250	-68.470	15.029	0.00
Microbial biomass	Pp2421	b * sowndiv^c	43.181	8	10.250	-68.389	15.111	0.00
Microbial biomass	Pr3431	b * sowndiv^c	43.154	8	10.250	-68.336	15.164	0.00
Microbial biomass	Pp2321	a + sowndiv^c	43.063	8	10.250	-68.154	15.346	0.00
Microbial biomass	Pr3321	a + sowndiv^c	43.019	8	10.250	-68.066	15.434	0.00
Microbial biomass	Ph221	a + b * sowndiv	41.695	7	11.714	-67.877	15.623	0.00
Microbial biomass	Pe731	a + b * sowndiv	40.482	6	13.667	-67.843	15.657	0.00
Microbial biomass	M722	a * sowndiv/(b + sowndiv)	42.872	8	10.250	-67.771	15.729	0.00
Microbial biomass	Pr3421	b * sowndiv^c	42.839	8	10.250	-67.705	15.795	0.00
Microbial biomass	Ec2121	a + exp(c * sowndiv)	40.373	6	13.667	-67.627	15.873	0.00
Microbial biomass	Pb21	a + b * sowndiv	36.961	3	27.333	-67.614	15.886	0.00
Microbial biomass	Pa2	a + b * sowndiv	36.961	3	27.333	-67.614	15.886	0.00
Microbial biomass	Pq2831	a + sowndiv^c	42.717	8	10.250	-67.461	16.039	0.00
Microbial biomass	Pq2931	b * sowndiv^c	42.712	8	10.250	-67.451	16.049	0.00
Microbial biomass	L2	sowndiv + funcgr + leg	39.107	5	16.400	-67.424	16.076	0.00
Microbial biomass	Pe721	a + b * sowndiv	40.207	6	13.667	-67.295	16.205	0.00
Microbial biomass	Pg171	a + b * sowndiv	39.038	5	16.400	-67.287	16.213	0.00
Microbial biomass	M711	a * sowndiv/(b + sowndiv)	42.621	8	10.250	-67.268	16.232	0.00
Microbial biomass	Pq2921	b * sowndiv^c	42.514	8	10.250	-67.056	16.444	0.00
Microbial biomass	Pq2821	a + sowndiv^c	42.505	8	10.250	-67.038	16.462	0.00
Microbial biomass	Pf121	a + b * sowndiv	38.854	5	16.400	-66.919	16.581	0.00
Microbial biomass	M1132	d + a * sowndiv/(b + sowndiv)	42.436	8	10.250	-66.899	16.601	0.00
Microbial biomass	Pp2231	a + b * sowndiv	42.176	8	10.250	-66.380	17.120	0.00
Microbial biomass	Pc231	a + b * sowndiv	37.344	4	20.500	-66.168	17.332	0.00
Microbial biomass	Pn1731	a + b * sowndiv	39.613	6	13.667	-66.107	17.393	0.00
Microbial biomass	Pi271	a + b * sowndiv	40.783	7	11.714	-66.052	17.448	0.00
Microbial biomass	L222	sowndiv + funcgr + leg	39.577	6	13.667	-66.034	17.465	0.00
Microbial biomass	M91	a * sowndiv/(b + sowndiv)	43.240	9	9.111	-65.980	17.520	0.00
Microbial biomass	Ea921	a + exp(c * sowndiv)	39.536	6	13.667	-65.952	17.548	0.00
Microbial biomass	Pk391	b * sowndiv^c	43.163	9	9.111	-65.825	17.675	0.00
Microbial biomass	E32	a + exp(c * sowndiv)	37.167	4	20.500	-65.814	17.686	0.00

Supplementary Table 2 (continued)

Long variable name	model name	model formula	LL	K	N2K	AICc	deltAICc	w_ic
Microbial biomass	Pk381	a + sowndiv^c	43.083	9	9.111	-65.666	17.834	0.00
Microbial biomass	Pj321	a + b * sowndiv	40.566	7	11.714	-65.618	17.882	0.00
Microbial biomass	Pp2221	a + b * sowndiv	41.779	8	10.250	-65.585	17.915	0.00
Microbial biomass	M131	d + a * sowndiv/(b + sowndiv)	44.339	10	8.200	-65.579	17.921	0.00
Microbial biomass	Pc221	a + b * sowndiv	37.024	4	20.500	-65.529	17.971	0.00
Microbial biomass	L21	sowndiv + funcgr + leg	39.316	6	13.667	-65.511	17.989	0.00
Microbial biomass	L22	sowndiv + funcgr + leg	39.212	6	13.667	-65.305	18.195	0.00
Microbial biomass	Pm1231	a + b * sowndiv	39.193	6	13.667	-65.266	18.234	0.00
Microbial biomass	L211	sowndiv + funcgr + leg	39.163	6	13.667	-65.206	18.294	0.00
Microbial biomass	E31	a + exp(c * sowndiv)	36.782	4	20.500	-65.044	18.456	0.00
Microbial biomass	Pq2631	a + b * sowndiv^c	45.387	11	7.455	-65.002	18.498	0.00
Microbial biomass	Pn1721	a + b * sowndiv	39.049	6	13.667	-64.978	18.522	0.00
Microbial biomass	Pm1221	a + b * sowndiv	39.013	6	13.667	-64.906	18.594	0.00
Microbial biomass	Eb1521	a + exp(c * sowndiv)	38.963	6	13.667	-64.806	18.694	0.00
Microbial biomass	Ea911	a + exp(c * sowndiv)	38.943	6	13.667	-64.767	18.733	0.00
Microbial biomass	Pq2731	a + b * sowndiv	41.190	8	10.250	-64.407	19.093	0.00
Microbial biomass	Eb1511	a + exp(c * sowndiv)	38.741	6	13.667	-64.362	19.138	0.00
Microbial biomass	M932	a * sowndiv/(b + sowndiv)	43.680	10	8.200	-64.262	19.238	0.00
Microbial biomass	Ps3931	b * sowndiv^c	43.610	10	8.200	-64.121	19.379	0.00
Microbial biomass	Pr3231	a + b * sowndiv	41.003	8	10.250	-64.033	19.466	0.00
Microbial biomass	Ps3831	a + sowndiv^c	43.533	10	8.200	-63.967	19.533	0.00
Microbial biomass	Pq2721	a + b * sowndiv	40.935	8	10.250	-63.897	19.603	0.00
Microbial biomass	Ef3921	a + exp(c * sowndiv)	40.852	8	10.250	-63.731	19.769	0.00
Microbial biomass	M921	a * sowndiv/(b + sowndiv)	43.294	10	8.200	-63.490	20.010	0.00
Microbial biomass	Ps3921	b * sowndiv^c	43.234	10	8.200	-63.370	20.130	0.00
Microbial biomass	Pr3221	a + b * sowndiv	40.651	8	10.250	-63.330	20.170	0.00
Microbial biomass	Ps3821	a + sowndiv^c	43.155	10	8.200	-63.212	20.288	0.00
Microbial biomass	Pk371	a + b * sowndiv	41.722	9	9.111	-62.945	20.555	0.00
Microbial biomass	E2	a + b * exp(sowndiv)	34.222	3	27.333	-62.137	21.363	0.00
Microbial biomass	Ps3731	a + b * sowndiv	42.217	10	8.200	-61.336	22.164	0.00
Microbial biomass	E22	a + b * exp(sowndiv)	34.840	4	20.500	-61.161	22.339	0.00
Microbial biomass	M1332	d + a * sowndiv/(b + sowndiv)	43.226	11	7.455	-60.680	22.820	0.00
Microbial biomass	Ps3721	a + b * sowndiv	41.798	10	8.200	-60.497	23.003	0.00

Supplementary Table 2 (continued)

Long variable name	model name	model formula	LL	K	N2K	AICc	deltAICc	w_ic
Microbial biomass	E21	a + b * exp(sowndiv)	34.224	4	20.500	-59.929	23.571	0.00
Microbial biomass	M1621	d + a * sowndiv/(b + sowndiv)	43.829	14	5.857	-53.389	30.111	0.00
Microbial biomass	Ec2411	exp(c * sowndiv)	-16.779	4	20.500	42.077	125.577	0.00
Microbial biomass	Ef4211	exp(c * sowndiv)	-18.452	5	16.400	47.693	131.193	0.00
Microbial biomass	Ec2421	exp(c * sowndiv)	-22.010	4	20.500	52.539	136.039	0.00
Microbial biomass	Pe1021	sowndiv^c	-23.004	4	20.500	54.528	138.028	0.00
Microbial biomass	Ed3021	exp(c * sowndiv)	-21.873	5	16.400	54.535	138.035	0.00
Microbial biomass	Ef4221	exp(c * sowndiv)	-22.298	5	16.400	55.385	138.885	0.00
Microbial biomass	Pp2521	sowndiv^c	-22.318	5	16.400	55.426	138.926	0.00
Microbial biomass	Pq3021	sowndiv^c	-22.751	5	16.400	56.291	139.791	0.00
Microbial biomass	Pr3521	sowndiv^c	-23.330	5	16.400	57.449	140.949	0.00
Microbial biomass	Ps4021	sowndiv^c	-22.318	6	13.667	57.757	141.257	0.00
Microbial biomass	Ec24	exp(c * sowndiv)	-25.822	3	27.333	57.952	141.452	0.00
Microbial biomass	E61	exp(c * sowndiv)	-25.837	3	27.333	57.982	141.482	0.00
Microbial biomass	Ea121	exp(c * sowndiv)	-24.809	4	20.500	58.138	141.638	0.00
Microbial biomass	Eb1811	exp(c * sowndiv)	-24.874	4	20.500	58.268	141.768	0.00
Microbial biomass	Pn2021	sowndiv^c	-25.447	4	20.500	59.414	142.914	0.00
Microbial biomass	Ea1221	exp(c * sowndiv)	-27.410	4	20.500	63.338	146.838	0.00
Microbial biomass	Eb1821	exp(c * sowndiv)	-28.062	4	20.500	64.644	148.144	0.00
Microbial biomass	Ea12	exp(c * sowndiv)	-29.323	3	27.333	64.953	148.453	0.00
Microbial biomass	Pm1521	sowndiv^c	-29.450	4	20.500	67.419	150.919	0.00
Microbial biomass	Eb18	exp(c * sowndiv)	-30.733	3	27.333	67.775	151.275	0.00
Microbial biomass	E62	exp(c * sowndiv)	-31.043	3	27.333	68.394	151.894	0.00
Microbial biomass	Pc521	sowndiv^c	-31.052	3	27.333	68.411	151.911	0.00
Microbial biomass	Pe1031	sowndiv^c	-33.608	4	20.500	75.736	159.236	0.00
Microbial biomass	Pp2531	sowndiv^c	-33.351	5	16.400	77.491	160.991	0.00
Microbial biomass	Pq3031	sowndiv^c	-33.507	5	16.400	77.803	161.303	0.00
Microbial biomass	Ps4031	sowndiv^c	-33.349	6	13.667	79.818	163.318	0.00
Microbial biomass	Pr3531	sowndiv^c	-34.584	5	16.400	79.957	163.456	0.00
Microbial biomass	E5	b * exp(sowndiv)	-39.024	2	41.000	82.200	165.700	0.00
Microbial biomass	E52	b * exp(sowndiv)	-38.413	3	27.333	83.133	166.633	0.00
Microbial biomass	Pn2031	sowndiv^c	-37.755	4	20.500	84.029	167.529	0.00
Microbial biomass	Pm1531	sowndiv^c	-40.766	4	20.500	90.051	173.551	0.00

Supplementary Table 2 (continued)

Long variable name	model name	model formula	LL	K	N2K	AICc	deltAICc	w_ic
Microbial biomass	Pd101	sowndiv^c	-42.131	3	27.333	90.570	174.070	0.00
Microbial biomass	Pg201	sowndiv^c	-43.048	3	27.333	92.403	175.903	0.00
Microbial biomass	Ph251	sowndiv^c	-41.970	4	20.500	92.459	175.958	0.00
Microbial biomass	Pi301	sowndiv^c	-42.003	4	20.500	92.526	176.026	0.00
Microbial biomass	Pc531	sowndiv^c	-43.207	3	27.333	92.721	176.221	0.00
Microbial biomass	Pb51	sowndiv^c	-44.520	2	41.000	93.193	176.693	0.00
Microbial biomass	Pa5	sowndiv^c	-44.520	2	41.000	93.193	176.693	0.00
Microbial biomass	Pj351	sowndiv^c	-42.416	4	20.500	93.351	176.851	0.00
Microbial biomass	Pf151	sowndiv^c	-44.034	3	27.333	94.377	177.877	0.00
Microbial biomass	Pk401	sowndiv^c	-41.948	5	16.400	94.686	178.186	0.00
Microbial biomass	Ec2221	a + exp(sowndiv)	-794.328	4	20.500	1597.176	1680.676	0.00
Microbial biomass	Ed2821	a + exp(sowndiv)	-794.328	5	16.400	1599.445	1682.945	0.00
Microbial biomass	Ee342	a + exp(sowndiv)	-794.328	5	16.400	1599.446	1682.946	0.00
Microbial biomass	Eg4621	a + exp(sowndiv)	-794.328	6	13.667	1601.775	1685.275	0.00
Microbial biomass	E42	a + exp(sowndiv)	-800.988	3	27.333	1608.285	1691.785	0.00
Microbial biomass	Eb1621	a + exp(sowndiv)	-800.869	4	20.500	1610.258	1693.758	0.00
Microbial biomass	Ea1021	a + exp(sowndiv)	-800.886	4	20.500	1610.291	1693.791	0.00
Microbial biomass	Ef4021	a + exp(sowndiv)	-800.642	5	16.400	1612.074	1695.574	0.00
Microbial biomass	E51	b * exp(sowndiv)	-1656.492	3	27.333	3319.291	3402.791	0.00
Microbial biomass	E41	a + exp(sowndiv)	-1729.079	3	27.333	3464.466	3547.966	0.00
Microbial biomass	Ea1011	a + exp(sowndiv)	-1728.390	4	20.500	3465.300	3548.800	0.00
Microbial biomass	Eb1611	a + exp(sowndiv)	-1729.038	4	20.500	3466.596	3550.096	0.00
Microbial biomass	Ec2211	a + exp(sowndiv)	-1729.079	4	20.500	3466.678	3550.178	0.00
Microbial biomass	Ef4011	a + exp(sowndiv)	-1728.384	5	16.400	3467.558	3551.058	0.00
Microbial biomass	Ed2811	a + exp(sowndiv)	-1728.390	5	16.400	3467.570	3551.070	0.00
Microbial biomass	Ee341	a + exp(sowndiv)	-1729.038	5	16.400	3468.866	3552.366	0.00
Microbial biomass	Eg4611	a + exp(sowndiv)	-1728.384	6	13.667	3469.888	3553.388	0.00
Microbial biomass	Ef3721	a + b * exp(c * sowndiv)	-2719.873	11	7.455	5465.518	5549.017	0.00
Microbial biomass	Ec1921	a + b * exp(c * sowndiv)	-2877.534	8	10.250	5773.040	5856.540	0.00
Microbial biomass	E4	a + exp(sowndiv)	-4912.516	2	41.000	9829.183	9912.683	0.00
Microbial biomass	Ea10	a + exp(sowndiv)	-4912.516	3	27.333	9831.339	9914.839	0.00
Microbial biomass	Eb16	a + exp(sowndiv)	-4912.516	3	27.333	9831.339	9914.839	0.00
Microbial biomass	Ec22	a + exp(sowndiv)	-4912.516	3	27.333	9831.339	9914.839	0.00

Supplementary Table 2 (continued)

Long variable name	model name	model formula	LL	K	N2K	AICc	deltAICc	w_ic
Microbial biomass	Ed28	a + exp(sowndiv)	-4912.516	4	20.500	9833.551	9917.051	0.00
Microbial biomass	Ee40	a + exp(sowndiv)	-4912.516	4	20.500	9833.551	9917.051	0.00
Microbial biomass	Ef40	a + exp(sowndiv)	-4912.516	4	20.500	9833.551	9917.051	0.00
Microbial biomass	Eg46	a + exp(sowndiv)	-4912.516	5	16.400	9835.821	9919.321	0.00
Microbial respiration	M211	d + a * sowndiv/(b + sowndiv)	62.409	5	16.400	-114.029	0.000	0.14
Microbial respiration	AS3	SSasympOrig(sowndiv, Asym, lrc)	60.009	3	27.333	-113.711	0.318	0.12
Microbial respiration	M1a	SSmicmen(sowndiv, Vm, k)	59.730	3	27.333	-113.152	0.878	0.09
Microbial respiration	M1	a * sowndiv/(b + sowndiv)	59.730	3	27.333	-113.152	0.878	0.09
Microbial respiration	M411	a * sowndiv/(b + sowndiv)	62.783	6	13.667	-112.446	1.583	0.06
Microbial respiration	Pc321	a + sowndiv^c	60.190	4	20.500	-111.861	2.168	0.05
Microbial respiration	M2	d + a * sowndiv/(b + sowndiv)	60.138	4	20.500	-111.756	2.273	0.05
Microbial respiration	AS2	SSasympOff(sowndiv, Asym, lrc, c0)	60.010	4	20.500	-111.501	2.528	0.04
Microbial respiration	AS1	SSasymp(sowndiv, Asym, R0, lrc)	60.010	4	20.500	-111.501	2.528	0.04
Microbial respiration	LG2	SSlogis(sowndiv, Asym, xmid, scal)	59.677	4	20.500	-110.835	3.194	0.03
Microbial respiration	M511	a * sowndiv/(b + sowndiv)	61.900	6	13.667	-110.680	3.349	0.03
Microbial respiration	M311	a * sowndiv/(b + sowndiv)	61.884	6	13.667	-110.647	3.382	0.03
Microbial respiration	Pm1321	a + sowndiv^c	61.709	6	13.667	-110.298	3.731	0.02
Microbial respiration	M4	a * sowndiv/(b + sowndiv)	60.326	5	16.400	-109.862	4.167	0.02
Microbial respiration	M222	d + a * sowndiv/(b + sowndiv)	60.224	5	16.400	-109.659	4.371	0.02
Microbial respiration	Pe821	a + sowndiv^c	61.067	6	13.667	-109.014	5.015	0.01
Microbial respiration	Pa3	a + sowndiv^c	57.578	3	27.333	-108.848	5.181	0.01
Microbial respiration	Pb31	a + sowndiv^c	57.578	3	27.333	-108.848	5.181	0.01
Microbial respiration	M5	a * sowndiv/(b + sowndiv)	59.764	5	16.400	-108.738	5.292	0.01
Microbial respiration	M3	a * sowndiv/(b + sowndiv)	59.731	5	16.400	-108.672	5.357	0.01
Microbial respiration	Pc421	b * sowndiv^c	58.486	4	20.500	-108.452	5.577	0.01
Microbial respiration	Pe921	b * sowndiv^c	60.555	6	13.667	-107.990	6.040	0.01
Microbial respiration	Pm1421	b * sowndiv^c	60.552	6	13.667	-107.983	6.046	0.01
Microbial respiration	M711	a * sowndiv/(b + sowndiv)	62.960	8	10.250	-107.947	6.082	0.01
Microbial respiration	M821	a * sowndiv/(b + sowndiv)	62.821	8	10.250	-107.670	6.359	0.01
Microbial respiration	M422	a * sowndiv/(b + sowndiv)	60.387	6	13.667	-107.654	6.376	0.01
Microbial respiration	Pn1821	a + sowndiv^c	60.321	6	13.667	-107.521	6.508	0.01
Microbial respiration	Pf131	a + sowndiv^c	58.961	5	16.400	-107.133	6.897	0.00
Microbial respiration	Pd81	a + sowndiv^c	58.841	5	16.400	-106.892	7.137	0.00

Supplementary Table 2 (continued)

Long variable name	model name	model formula	LL	K	N2K	AICc	deltAICc	w_ic
Microbial respiration	Pc331	a + sowndiv^c	57.625	4	20.500	-106.731	7.298	0.00
Microbial respiration	Pd91	b * sowndiv^c	58.712	5	16.400	-106.635	7.394	0.00
Microbial respiration	M522	a * sowndiv/(b + sowndiv)	59.846	6	13.667	-106.572	7.458	0.00
Microbial respiration	M321	a * sowndiv/(b + sowndiv)	59.800	6	13.667	-106.480	7.550	0.00
Microbial respiration	Pa4	b * sowndiv^c	56.348	3	27.333	-106.389	7.640	0.00
Microbial respiration	Pb41	b * sowndiv^c	56.348	3	27.333	-106.389	7.640	0.00
Microbial respiration	Pq2821	a + sowndiv^c	62.032	8	10.250	-106.092	7.937	0.00
Microbial respiration	Pr3321	a + sowndiv^c	61.957	8	10.250	-105.942	8.087	0.00
Microbial respiration	M611	a * sowndiv/(b + sowndiv)	61.940	8	10.250	-105.908	8.121	0.00
Microbial respiration	Pf141	b * sowndiv^c	58.114	5	16.400	-105.439	8.591	0.00
Microbial respiration	Pr3421	b * sowndiv^c	61.701	8	10.250	-105.429	8.600	0.00
Microbial respiration	M7	a * sowndiv/(b + sowndiv)	60.422	7	11.714	-105.331	8.698	0.00
Microbial respiration	Pq2921	b * sowndiv^c	61.647	8	10.250	-105.321	8.708	0.00
Microbial respiration	M1221	d + a * sowndiv/(b + sowndiv)	61.631	8	10.250	-105.289	8.740	0.00
Microbial respiration	Pg181	a + sowndiv^c	58.011	5	16.400	-105.233	8.796	0.00
Microbial respiration	M81	a * sowndiv/(b + sowndiv)	60.369	7	11.714	-105.224	8.805	0.00
Microbial respiration	Pn1921	b * sowndiv^c	58.998	6	13.667	-104.877	9.152	0.00
Microbial respiration	Pm1331	a + sowndiv^c	58.961	6	13.667	-104.802	9.227	0.00
Microbial respiration	Pe831	a + sowndiv^c	58.904	6	13.667	-104.688	9.342	0.00
Microbial respiration	Pe931	b * sowndiv^c	58.832	6	13.667	-104.544	9.486	0.00
Microbial respiration	Pp2321	a + sowndiv^c	61.104	8	10.250	-104.235	9.794	0.00
Microbial respiration	Pc431	b * sowndiv^c	56.374	4	20.500	-104.228	9.801	0.00
Microbial respiration	M6	a * sowndiv/(b + sowndiv)	59.767	7	11.714	-104.021	10.008	0.00
Microbial respiration	Pj341	b * sowndiv^c	59.744	7	11.714	-103.974	10.055	0.00
Microbial respiration	Pg191	b * sowndiv^c	57.215	5	16.400	-103.641	10.388	0.00
Microbial respiration	M921	a * sowndiv/(b + sowndiv)	63.323	10	8.200	-103.548	10.481	0.00
Microbial respiration	Pi291	b * sowndiv^c	59.440	7	11.714	-103.366	10.664	0.00
Microbial respiration	Pi281	a + sowndiv^c	59.425	7	11.714	-103.336	10.694	0.00
Microbial respiration	Pj331	a + sowndiv^c	59.394	7	11.714	-103.274	10.755	0.00
Microbial respiration	Pp2421	b * sowndiv^c	60.588	8	10.250	-103.203	10.826	0.00
Microbial respiration	Pm1431	b * sowndiv^c	58.119	6	13.667	-103.118	10.911	0.00
Microbial respiration	M722	a * sowndiv/(b + sowndiv)	60.475	8	10.250	-102.977	11.052	0.00
Microbial respiration	Pe721	a + b * sowndiv	58.032	6	13.667	-102.943	11.086	0.00

Supplementary Table 2 (continued)

Long variable name	model name	model formula	LL	K	N2K	AICc	deltAICc	w_ic
Microbial respiration	Pn1831	a + sowndiv^c	58.016	6	13.667	-102.913	11.116	0.00
Microbial respiration	M832	a * sowndiv/(b + sowndiv)	60.439	8	10.250	-102.906	11.123	0.00
Microbial respiration	Ph231	a + sowndiv^c	58.844	7	11.714	-102.175	11.855	0.00
Microbial respiration	Ph241	b * sowndiv^c	58.713	7	11.714	-101.912	12.118	0.00
Microbial respiration	Pd71	a + b * sowndiv	56.350	5	16.400	-101.910	12.119	0.00
Microbial respiration	M622	a * sowndiv/(b + sowndiv)	59.847	8	10.250	-101.721	12.308	0.00
Microbial respiration	Pr3431	b * sowndiv^c	59.846	8	10.250	-101.720	12.309	0.00
Microbial respiration	Ps3821	a + sowndiv^c	62.343	10	8.200	-101.587	12.442	0.00
Microbial respiration	Pn1931	b * sowndiv^c	57.254	6	13.667	-101.388	12.641	0.00
Microbial respiration	Pq2931	b * sowndiv^c	59.530	8	10.250	-101.086	12.943	0.00
Microbial respiration	Pq2831	a + sowndiv^c	59.468	8	10.250	-100.964	13.066	0.00
Microbial respiration	M91	a * sowndiv/(b + sowndiv)	60.720	9	9.111	-100.939	13.090	0.00
Microbial respiration	Ps3921	b * sowndiv^c	62.017	10	8.200	-100.936	13.094	0.00
Microbial respiration	Pr3331	a + sowndiv^c	59.423	8	10.250	-100.873	13.156	0.00
Microbial respiration	M1521	d + a * sowndiv/(b + sowndiv)	63.319	11	7.455	-100.867	13.162	0.00
Microbial respiration	M1421	d + a * sowndiv/(b + sowndiv)	63.110	11	7.455	-100.449	13.580	0.00
Microbial respiration	Pe731	a + b * sowndiv	56.506	6	13.667	-99.891	14.138	0.00
Microbial respiration	Pp2331	a + sowndiv^c	58.905	8	10.250	-99.837	14.192	0.00
Microbial respiration	Pm1221	a + b * sowndiv	56.415	6	13.667	-99.711	14.318	0.00
Microbial respiration	Pp2431	b * sowndiv^c	58.836	8	10.250	-99.699	14.330	0.00
Microbial respiration	Pq2721	a + b * sowndiv	58.828	8	10.250	-99.684	14.345	0.00
Microbial respiration	Ec2121	a + exp(c * sowndiv)	56.300	6	13.667	-99.480	14.549	0.00
Microbial respiration	Pk391	b * sowndiv^c	59.873	9	9.111	-99.245	14.784	0.00
Microbial respiration	Eb1511	a + exp(c * sowndiv)	56.116	6	13.667	-99.112	14.917	0.00
Microbial respiration	Pr3221	a + b * sowndiv	58.507	8	10.250	-99.041	14.988	0.00
Microbial respiration	Pk381	a + sowndiv^c	59.658	9	9.111	-98.816	15.213	0.00
Microbial respiration	Pf121	a + b * sowndiv	54.674	5	16.400	-98.558	15.471	0.00
Microbial respiration	M932	a * sowndiv/(b + sowndiv)	60.766	10	8.200	-98.433	15.597	0.00
Microbial respiration	Ef3911	a + exp(c * sowndiv)	58.200	8	10.250	-98.428	15.601	0.00
Microbial respiration	Pj321	a + b * sowndiv	56.839	7	11.714	-98.164	15.865	0.00
Microbial respiration	Pi271	a + b * sowndiv	56.834	7	11.714	-98.154	15.876	0.00
Microbial respiration	Pp2221	a + b * sowndiv	58.033	8	10.250	-98.093	15.936	0.00
Microbial respiration	Ph221	a + b * sowndiv	56.387	7	11.714	-97.260	16.769	0.00

Supplementary Table 2 (continued)

Long variable name	model name	model formula	LL	K	N2K	AICc	deltAICc	w_ic
Microbial respiration	Pg171	a + b * sowndiv	53.904	5	16.400	-97.019	17.010	0.00
Microbial respiration	Ps3931	b * sowndiv^c	59.968	10	8.200	-96.836	17.193	0.00
Microbial respiration	Pm1231	a + b * sowndiv	54.756	6	13.667	-96.392	17.637	0.00
Microbial respiration	Ps3831	a + sowndiv^c	59.692	10	8.200	-96.285	17.745	0.00
Microbial respiration	Pn1721	a + b * sowndiv	54.636	6	13.667	-96.153	17.876	0.00
Microbial respiration	Eb1521	a + exp(c * sowndiv)	54.591	6	13.667	-96.063	17.967	0.00
Microbial respiration	Pr3231	a + b * sowndiv	56.998	8	10.250	-96.023	18.007	0.00
Microbial respiration	Pq2731	a + b * sowndiv	56.970	8	10.250	-95.968	18.061	0.00
Microbial respiration	Ea911	a + exp(c * sowndiv)	54.458	6	13.667	-95.795	18.234	0.00
Microbial respiration	Ef3921	a + exp(c * sowndiv)	56.781	8	10.250	-95.589	18.440	0.00
Microbial respiration	Pn1731	a + b * sowndiv	54.192	6	13.667	-95.263	18.766	0.00
Microbial respiration	L211	sowndiv + funcgr + leg	54.155	6	13.667	-95.191	18.838	0.00
Microbial respiration	Pa2	a + b * sowndiv	50.749	3	27.333	-95.190	18.839	0.00
Microbial respiration	Pb21	a + b * sowndiv	50.749	3	27.333	-95.190	18.839	0.00
Microbial respiration	Pp2231	a + b * sowndiv	56.569	8	10.250	-95.164	18.865	0.00
Microbial respiration	Ps3721	a + b * sowndiv	59.097	10	8.200	-95.095	18.934	0.00
Microbial respiration	Ea921	a + exp(c * sowndiv)	54.095	6	13.667	-95.070	18.959	0.00
Microbial respiration	Pc221	a + b * sowndiv	51.769	4	20.500	-95.019	19.010	0.00
Microbial respiration	L2	sowndiv + funcgr + leg	52.741	5	16.400	-94.693	19.336	0.00
Microbial respiration	E31	a + exp(c * sowndiv)	51.405	4	20.500	-94.291	19.738	0.00
Microbial respiration	L02	block + (sowndiv + funcgr + grass + leg)^2	67.299	16	5.125	-94.229	19.801	0.00
Microbial respiration	Pk371	a + b * sowndiv	57.122	9	9.111	-93.744	20.285	0.00
Microbial respiration	Pc231	a + b * sowndiv	50.802	4	20.500	-93.084	20.945	0.00
Microbial respiration	E32	a + exp(c * sowndiv)	50.668	4	20.500	-92.816	21.213	0.00
Microbial respiration	L22	sowndiv + funcgr + leg	52.937	6	13.667	-92.753	21.276	0.00
Microbial respiration	L222	sowndiv + funcgr + leg	52.839	6	13.667	-92.558	21.471	0.00
Microbial respiration	L21	sowndiv + funcgr + leg	52.799	6	13.667	-92.477	21.552	0.00
Microbial respiration	M1432	d + a * sowndiv/(b + sowndiv)	59.112	11	7.455	-92.452	21.578	0.00
Microbial respiration	L01	block + (sowndiv + funcgr + grass + leg)^2	66.292	16	5.125	-92.215	21.815	0.00
Microbial respiration	Ps3731	a + b * sowndiv	57.261	10	8.200	-91.423	22.606	0.00
Microbial respiration	E2	a + b * exp(sowndiv)	48.244	3	27.333	-90.180	23.850	0.00
Microbial respiration	E22	a + b * exp(sowndiv)	48.708	4	20.500	-88.896	25.133	0.00
Microbial respiration	M161	d + a * sowndiv/(b + sowndiv)	59.883	13	6.308	-88.413	25.616	0.00

Supplementary Table 2 (continued)

Long variable name	model name	model formula	LL	K	N2K	AICc	deltAICc	w_ic
Microbial respiration	M1621	d + a * sowndiv/(b + sowndiv)	61.225	14	5.857	-88.182	25.847	0.00
Microbial respiration	LO	block + (sowndiv + funcgr + grass + leg)^2	61.919	15	5.467	-86.565	27.465	0.00
Microbial respiration	LO11	block + (sowndiv + funcgr + grass + leg)^2	63.317	16	5.125	-86.265	27.764	0.00
Microbial respiration	LO21	block + (sowndiv + funcgr + grass + leg)^2	62.589	16	5.125	-84.809	29.220	0.00
Microbial respiration	M1632	d + a * sowndiv/(b + sowndiv)	59.482	14	5.857	-84.695	29.334	0.00
Microbial respiration	Ec2411	exp(c * sowndiv)	10.156	4	20.500	-11.793	102.236	0.00
Microbial respiration	Ef4211	exp(c * sowndiv)	10.038	5	16.400	-9.286	104.743	0.00
Microbial respiration	E61	exp(c * sowndiv)	4.334	3	27.333	-2.360	111.670	0.00
Microbial respiration	Eb1811	exp(c * sowndiv)	4.924	4	20.500	-1.328	112.701	0.00
Microbial respiration	Ea121	exp(c * sowndiv)	4.341	4	20.500	-0.163	113.866	0.00
Microbial respiration	Ec2421	exp(c * sowndiv)	2.870	4	20.500	2.780	116.809	0.00
Microbial respiration	Ef4221	exp(c * sowndiv)	3.632	5	16.400	3.526	117.555	0.00
Microbial respiration	Ed3021	exp(c * sowndiv)	2.873	5	16.400	5.044	119.073	0.00
Microbial respiration	Ec24	exp(c * sowndiv)	0.615	3	27.333	5.078	119.107	0.00
Microbial respiration	E51	b * exp(sowndiv)	-0.183	3	27.333	6.673	120.702	0.00
Microbial respiration	E5	b * exp(sowndiv)	-3.785	2	41.000	11.721	125.751	0.00
Microbial respiration	E62	exp(c * sowndiv)	-2.729	3	27.333	11.765	125.794	0.00
Microbial respiration	Eb1821	exp(c * sowndiv)	-2.195	4	20.500	12.910	126.940	0.00
Microbial respiration	E52	b * exp(sowndiv)	-3.732	3	27.333	13.772	127.801	0.00
Microbial respiration	Ea1221	exp(c * sowndiv)	-2.700	4	20.500	13.919	127.948	0.00
Microbial respiration	Eb18	exp(c * sowndiv)	-3.830	3	27.333	13.968	127.998	0.00
Microbial respiration	Ea12	exp(c * sowndiv)	-4.269	3	27.333	14.845	128.874	0.00
Microbial respiration	Pe1021	sowndiv^c	-20.441	4	20.500	49.401	163.430	0.00
Microbial respiration	Pq3021	sowndiv^c	-20.252	5	16.400	51.294	165.324	0.00
Microbial respiration	Pp2521	sowndiv^c	-20.310	5	16.400	51.409	165.438	0.00
Microbial respiration	Ps4021	sowndiv^c	-20.224	6	13.667	53.569	167.598	0.00
Microbial respiration	Pr3521	sowndiv^c	-21.788	5	16.400	54.366	168.396	0.00
Microbial respiration	Pm1521	sowndiv^c	-24.079	4	20.500	56.678	170.708	0.00
Microbial respiration	Pn2021	sowndiv^c	-25.634	4	20.500	59.788	173.817	0.00
Microbial respiration	Pc521	sowndiv^c	-28.002	3	27.333	62.312	176.342	0.00
Microbial respiration	Pe1031	sowndiv^c	-37.730	4	20.500	83.979	198.008	0.00
Microbial respiration	Pq3031	sowndiv^c	-37.693	5	16.400	86.175	200.204	0.00
Microbial respiration	Pp2531	sowndiv^c	-37.717	5	16.400	86.223	200.252	0.00

Supplementary Table 2 (continued)

Long variable name	model name	model formula	LL	K	N2K	AICc	deltAICc	w_ic
Microbial respiration	Ps4031	sowndiv^c	-37.691	6	13.667	88.503	202.532	0.00
Microbial respiration	Pr3531	sowndiv^c	-38.999	5	16.400	88.788	202.817	0.00
Microbial respiration	Pm1531	sowndiv^c	-42.138	4	20.500	92.795	206.825	0.00
Microbial respiration	Pn2031	sowndiv^c	-43.376	4	20.500	95.271	209.301	0.00
Microbial respiration	Pc531	sowndiv^c	-47.571	3	27.333	101.449	215.478	0.00
Microbial respiration	Pd101	sowndiv^c	-49.733	3	27.333	105.774	219.803	0.00
Microbial respiration	Pb51	sowndiv^c	-51.460	2	41.000	107.072	221.101	0.00
Microbial respiration	Pa5	sowndiv^c	-51.460	2	41.000	107.072	221.101	0.00
Microbial respiration	Pf151	sowndiv^c	-50.453	3	27.333	107.213	221.243	0.00
Microbial respiration	Pi301	sowndiv^c	-49.710	4	20.500	107.940	221.969	0.00
Microbial respiration	Ph251	sowndiv^c	-49.733	4	20.500	107.985	222.014	0.00
Microbial respiration	Pj351	sowndiv^c	-49.758	4	20.500	108.035	222.064	0.00
Microbial respiration	Pg201	sowndiv^c	-50.899	3	27.333	108.106	222.135	0.00
Microbial respiration	Pk401	sowndiv^c	-49.680	5	16.400	110.149	224.178	0.00
Microbial respiration	Ec2221	a + exp(sowndiv)	-794.154	4	20.500	1596.827	1710.856	0.00
Microbial respiration	Ee342	a + exp(sowndiv)	-794.152	5	16.400	1599.094	1713.124	0.00
Microbial respiration	Ed2821	a + exp(sowndiv)	-794.154	5	16.400	1599.097	1713.126	0.00
Microbial respiration	Eg4621	a + exp(sowndiv)	-794.152	6	13.667	1601.425	1715.454	0.00
Microbial respiration	E42	a + exp(sowndiv)	-800.938	3	27.333	1608.183	1722.212	0.00
Microbial respiration	Ea1021	a + exp(sowndiv)	-800.816	4	20.500	1610.151	1724.181	0.00
Microbial respiration	Eb1621	a + exp(sowndiv)	-800.839	4	20.500	1610.198	1724.227	0.00
Microbial respiration	Ef4021	a + exp(sowndiv)	-800.595	5	16.400	1611.979	1726.008	0.00
Microbial respiration	Eb1611	a + exp(sowndiv)	-1703.664	4	20.500	3415.847	3529.876	0.00
Microbial respiration	E41	a + exp(sowndiv)	-1705.469	3	27.333	3417.246	3531.275	0.00
Microbial respiration	Ef4011	a + exp(sowndiv)	-1703.572	5	16.400	3417.933	3531.962	0.00
Microbial respiration	Ee341	a + exp(sowndiv)	-1703.664	5	16.400	3418.117	3532.146	0.00
Microbial respiration	Ea1011	a + exp(sowndiv)	-1705.442	4	20.500	3419.403	3533.433	0.00
Microbial respiration	Ec2211	a + exp(sowndiv)	-1705.469	4	20.500	3419.457	3533.487	0.00
Microbial respiration	Eg4611	a + exp(sowndiv)	-1703.572	6	13.667	3420.263	3534.293	0.00
Microbial respiration	Ed2811	a + exp(sowndiv)	-1705.442	5	16.400	3421.673	3535.703	0.00
Microbial respiration	Ef3721	a + b * exp(c * sowndiv)	-2708.060	11	7.455	5441.891	5555.921	0.00
Microbial respiration	Ec1921	a + b * exp(c * sowndiv)	-2845.250	8	10.250	5708.472	5822.502	0.00
Microbial respiration	E4	a + exp(sowndiv)	-4912.516	2	41.000	9829.183	9943.212	0.00

Supplementary Table 2 (continued)

Long variable name	model name	model formula	LL	K	N2K	AICc	deltAICc	w_ic
Microbial respiration	Ea10	a + exp(sowndiv)	-4912.516	3	27.333	9831.339	9945.368	0.00
Microbial respiration	Eb16	a + exp(sowndiv)	-4912.516	3	27.333	9831.339	9945.368	0.00
Microbial respiration	Ec22	a + exp(sowndiv)	-4912.516	3	27.333	9831.339	9945.368	0.00
Microbial respiration	Ed28	a + exp(sowndiv)	-4912.516	4	20.500	9833.551	9947.580	0.00
Microbial respiration	Ee40	a + exp(sowndiv)	-4912.516	4	20.500	9833.551	9947.580	0.00
Microbial respiration	Ef40	a + exp(sowndiv)	-4912.516	4	20.500	9833.551	9947.580	0.00
Microbial respiration	Eg46	a + exp(sowndiv)	-4912.516	5	16.400	9835.821	9949.850	0.00
Saprophagous macrofauna abundance	M1	a * sowndiv/(b + sowndiv)	42.594	3	26.667	-78.872	0.000	0.20
Saprophagous macrofauna abundance	M1a	SSmicmen(sowndiv, Vm, k)	42.594	3	26.667	-78.872	0.000	0.20
Saprophagous macrofauna abundance	Pa3	a + sowndiv^c	42.493	3	26.667	-78.670	0.202	0.18
Saprophagous macrofauna abundance	Pa4	b * sowndiv^c	42.280	3	26.667	-78.244	0.628	0.15
Saprophagous macrofauna abundance	LG2	SSlogis(sowndiv, Asym, xmid, scal)	43.253	4	20.000	-77.972	0.899	0.13
Saprophagous macrofauna abundance	M2	d + a * sowndiv/(b + sowndiv)	42.838	4	20.000	-77.142	1.730	0.09
Saprophagous macrofauna abundance	Pa2	a + b * sowndiv	40.425	3	26.667	-74.535	4.337	0.02
Saprophagous macrofauna abundance	L2	sowndiv + funcgr + leg	42.370	5	16.000	-73.929	4.943	0.02
Saprophagous macrofauna abundance	E2	a + b * exp(sowndiv)	39.508	3	26.667	-72.700	6.171	0.01
Saprophagous macrofauna abundance	L0	block + (sowndiv + funcgr + grass + leg)^2	52.730	15	5.333	-67.960	10.911	0.00
Saprophagous macrofauna abundance	E5	b * exp(sowndiv)	5.689	2	40.000	-7.221	71.650	0.00
Saprophagous macrofauna abundance	Pa5	sowndiv^c	-46.774	2	40.000	97.704	176.576	0.00
Saprophagous macrofauna abundance	E4	a + exp(sowndiv)	-4793.686	2	40.000	9591.527	9670.399	0.00
Saprophagous macrofauna diversity	Pa2	a + b * sowndiv	2.962	3	26.667	0.393	0.000	0.23
Saprophagous macrofauna diversity	L2	sowndiv + funcgr + leg	4.621	5	16.000	1.569	1.176	0.13
Saprophagous macrofauna diversity	Pa4	b * sowndiv^c	1.968	3	26.667	2.380	1.988	0.08
Saprophagous macrofauna diversity	E2	a + b * exp(sowndiv)	1.918	3	26.667	2.479	2.086	0.08
Saprophagous macrofauna diversity	LG2	SSlogis(sowndiv, Asym, xmid, scal)	2.976	4	20.000	2.581	2.188	0.08
Saprophagous macrofauna diversity	Pa1	a + b * sowndiv^c	2.975	4	20.000	2.583	2.190	0.08
Saprophagous macrofauna diversity	AS2	SSasympOff(sowndiv, Asym, lrc, c0)	2.972	4	20.000	2.589	2.196	0.08
Saprophagous macrofauna diversity	AS1	SSasymp(sowndiv, Asym, R0, lrc)	2.972	4	20.000	2.589	2.196	0.08
Saprophagous macrofauna diversity	M2	d + a * sowndiv/(b + sowndiv)	2.972	4	20.000	2.589	2.196	0.08
Saprophagous macrofauna diversity	Pa3	a + sowndiv^c	1.784	3	26.667	2.748	2.355	0.07
Saprophagous macrofauna diversity	M1a	SSmicmen(sowndiv, Vm, k)	0.283	3	26.667	5.750	5.357	0.02
Saprophagous macrofauna diversity	M1	a * sowndiv/(b + sowndiv)	0.283	3	26.667	5.750	5.357	0.02
Saprophagous macrofauna diversity	AS3	SSasympOrig(sowndiv, Asym, lrc)	-0.271	3	26.667	6.858	6.466	0.01

Supplementary Table 2 (continued)

Long variable name	model name	model formula	LL	K	N2K	AICc	deltAICc	w_ic
Saprophagous macrofauna diversity	L0	block + (sowndiv + funcgr + grass + leg)^2	11.769	15	5.333	13.963	13.570	0.00
Saprophagous macrofauna diversity	Pa5	sowndiv^c	-42.094	2	40.000	88.344	87.952	0.00
Saprophagous macrofauna diversity	E5	b * exp(sowndiv)	-60.104	2	40.000	124.364	123.971	0.00
Saprophagous macrofauna diversity	E4	a + exp(sowndiv)	-4793.686	2	40.000	9591.527	9591.135	0.00
Herbivorous macrofauna abundance	Pa2	a + b * sowndiv	13.870	3	26.667	-21.424	0.000	0.18
Herbivorous macrofauna abundance	Pa4	b * sowndiv^c	13.487	3	26.667	-20.659	0.766	0.12
Herbivorous macrofauna abundance	Pa3	a + sowndiv^c	13.358	3	26.667	-20.399	1.025	0.10
Herbivorous macrofauna abundance	E2	a + b * exp(sowndiv)	13.291	3	26.667	-20.266	1.158	0.10
Herbivorous macrofauna abundance	AS3	SSasympOrig(sowndiv, Asym, lrc)	12.845	3	26.667	-19.374	2.050	0.06
Herbivorous macrofauna abundance	M1	a * sowndiv/(b + sowndiv)	12.817	3	26.667	-19.318	2.106	0.06
Herbivorous macrofauna abundance	M1a	SSmicmen(sowndiv, Vm, k)	12.817	3	26.667	-19.318	2.106	0.06
Herbivorous macrofauna abundance	Pa1	a + b * sowndiv^c	13.876	4	20.000	-19.219	2.205	0.06
Herbivorous macrofauna abundance	LG2	SSlogis(sowndiv, Asym, xmid, scal)	13.876	4	20.000	-19.218	2.206	0.06
Herbivorous macrofauna abundance	AS2	SSasympOff(sowndiv, Asym, lrc, c0)	13.871	4	20.000	-19.209	2.215	0.06
Herbivorous macrofauna abundance	AS1	SSasymp(sowndiv, Asym, R0, lrc)	13.871	4	20.000	-19.209	2.215	0.06
Herbivorous macrofauna abundance	M2	d + a * sowndiv/(b + sowndiv)	13.871	4	20.000	-19.209	2.215	0.06
Herbivorous macrofauna abundance	L2	sowndiv + funcgr + leg	14.184	5	16.000	-17.557	3.867	0.03
Herbivorous macrofauna abundance	L0	block + (sowndiv + funcgr + grass + leg)^2	24.697	15	5.333	-11.894	9.530	0.00
Herbivorous macrofauna abundance	E5	b * exp(sowndiv)	-19.873	2	40.000	43.901	65.326	0.00
Herbivorous macrofauna abundance	Pa5	sowndiv^c	-50.540	2	40.000	105.237	126.661	0.00
Herbivorous macrofauna abundance	E4	a + exp(sowndiv)	-4793.686	2	40.000	9591.527	9612.952	0.00
Herbivorous macrofauna diversity	Pa3	a + sowndiv^c	10.690	3	26.667	-15.064	0.000	0.19
Herbivorous macrofauna diversity	Pa4	b * sowndiv^c	10.557	3	26.667	-14.798	0.266	0.17
Herbivorous macrofauna diversity	M1a	SSmicmen(sowndiv, Vm, k)	10.553	3	26.667	-14.790	0.274	0.17
Herbivorous macrofauna diversity	M1	a * sowndiv/(b + sowndiv)	10.553	3	26.667	-14.790	0.274	0.17
Herbivorous macrofauna diversity	AS3	SSasympOrig(sowndiv, Asym, lrc)	10.081	3	26.667	-13.846	1.218	0.11
Herbivorous macrofauna diversity	M2	d + a * sowndiv/(b + sowndiv)	10.554	4	20.000	-12.575	2.489	0.06
Herbivorous macrofauna diversity	AS1	SSasymp(sowndiv, Asym, R0, lrc)	10.059	4	20.000	-11.584	3.480	0.03
Herbivorous macrofauna diversity	AS2	SSasympOff(sowndiv, Asym, lrc, c0)	10.059	4	20.000	-11.584	3.480	0.03
Herbivorous macrofauna diversity	LG2	SSlogis(sowndiv, Asym, xmid, scal)	9.860	4	20.000	-11.187	3.877	0.03
Herbivorous macrofauna diversity	Pa2	a + b * sowndiv	8.722	3	26.667	-11.129	3.935	0.03
Herbivorous macrofauna diversity	L2	sowndiv + funcgr + leg	9.906	5	16.000	-9.002	6.062	0.01
Herbivorous macrofauna diversity	E2	a + b * exp(sowndiv)	6.931	3	26.667	-7.547	7.518	0.00

Supplementary Table 2 (continued)

Long variable name	model name	model formula	LL	K	N2K	AICc	deltAICc	w_ic
Herbivorous macrofauna diversity	L0	block + (sowndiv + funcgr + grass + leg)^2	21.929	15	5.333	-6.359	8.705	0.00
Herbivorous macrofauna diversity	E5	b * exp(sowndiv)	-42.733	2	40.000	89.621	104.685	0.00
Herbivorous macrofauna diversity	Pa5	sowndiv^c	-49.612	2	40.000	103.380	118.444	0.00
Herbivorous macrofauna diversity	E4	a + exp(sowndiv)	-4793.686	2	40.000	9591.527	9606.592	0.00
Predatory macrofauna abundance	E2	a + b * exp(sowndiv)	35.938	3	26.667	-65.560	0.000	0.20
Predatory macrofauna abundance	Pa2	a + b * sowndiv	35.865	3	26.667	-65.414	0.145	0.18
Predatory macrofauna abundance	Pa4	b * sowndiv^c	35.471	3	26.667	-64.626	0.934	0.12
Predatory macrofauna abundance	Pa3	a + sowndiv^c	35.441	3	26.667	-64.567	0.993	0.12
Predatory macrofauna abundance	AS3	SSasympOrig(sowndiv, Asym, lrc)	35.269	3	26.667	-64.223	1.337	0.10
Predatory macrofauna abundance	M1a	SSmicmen(sowndiv, Vm, k)	35.267	3	26.667	-64.218	1.342	0.10
Predatory macrofauna abundance	M1	a * sowndiv/(b + sowndiv)	35.267	3	26.667	-64.218	1.342	0.10
Predatory macrofauna abundance	L2	sowndiv + funcgr + leg	36.535	5	16.000	-62.260	3.300	0.04
Predatory macrofauna abundance	L0	block + (sowndiv + funcgr + grass + leg)^2	49.549	15	5.333	-61.599	3.961	0.03
Predatory macrofauna abundance	E5	b * exp(sowndiv)	10.776	2	40.000	-17.397	48.163	0.00
Predatory macrofauna abundance	Pa5	sowndiv^c	-44.448	2	40.000	93.053	158.612	0.00
Predatory macrofauna abundance	E4	a + exp(sowndiv)	-4793.686	2	40.000	9591.527	9657.087	0.00
Predatory macrofauna diversity	L0	block + (sowndiv + funcgr + grass + leg)^2	23.649	15	5.333	-9.798	0.000	0.18
Predatory macrofauna diversity	AS3	SSasympOrig(sowndiv, Asym, lrc)	7.652	3	26.667	-8.988	0.811	0.12
Predatory macrofauna diversity	M1	a * sowndiv/(b + sowndiv)	7.521	3	26.667	-8.726	1.073	0.11
Predatory macrofauna diversity	M1a	SSmicmen(sowndiv, Vm, k)	7.521	3	26.667	-8.726	1.073	0.11
Predatory macrofauna diversity	Pa2	a + b * sowndiv	7.513	3	26.667	-8.709	1.089	0.11
Predatory macrofauna diversity	E2	a + b * exp(sowndiv)	7.498	3	26.667	-8.681	1.118	0.11
Predatory macrofauna diversity	Pa4	b * sowndiv^c	7.467	3	26.667	-8.618	1.181	0.10
Predatory macrofauna diversity	Pa3	a + sowndiv^c	7.466	3	26.667	-8.617	1.181	0.10
Predatory macrofauna diversity	Pa1	a + b * sowndiv^c	7.519	4	20.000	-6.506	3.293	0.04
Predatory macrofauna diversity	L2	sowndiv + funcgr + leg	8.364	5	16.000	-5.918	3.881	0.03
Predatory macrofauna diversity	Pa5	sowndiv^c	-37.843	2	40.000	79.841	89.640	0.00
Predatory macrofauna diversity	E5	b * exp(sowndiv)	-51.152	2	40.000	106.460	116.259	0.00
Predatory macrofauna diversity	E4	a + exp(sowndiv)	-4793.686	2	40.000	9591.527	9601.326	0.00
Amoebae abundance	L2	sowndiv + funcgr + leg	4.083	5	2.400	11.834	Inf	NA
Amoebae abundance	E1	a + b * exp(c * sowndiv)	2.516	4	3.000	8.682	Inf	NA
Amoebae abundance	E2	a + b * exp(sowndiv)	2.514	3	4.000	3.971	Inf	NA
Amoebae abundance	E3	a + exp(c * sowndiv)	2.395	3	4.000	4.211	Inf	NA

Supplementary Table 2 (continued)

Long variable name	model name	model formula	LL	K	N2K	AICc	deltAICc	w_ic
Amoebae abundance	E4	a + exp(sowndiv)	-200.003	2	6.000	405.339	Inf	NA
Amoebae abundance	E5	b * exp(sowndiv)	2.201	2	6.000	0.931	Inf	NA
Amoebae abundance	E6	exp(c * sowndiv)	-3.953	2	6.000	13.239	Inf	NA
Amoebae abundance	Pa2	a + b * sowndiv	2.344	3	4.000	4.313	Inf	NA
Amoebae abundance	Pa3	a + sowndiv^c	1.470	3	4.000	6.059	Inf	NA
Amoebae abundance	Pa4	b * sowndiv^c	2.424	3	4.000	4.151	Inf	NA
Amoebae abundance	Pa5	sowndiv^c	-11.612	2	6.000	28.557	Inf	NA
Amoebae abundance	L0	block + (sowndiv + funcgr + grass + leg)^2	Inf	13	0.923	#NAME?	NA	NA
Flagellate abundance	L2	sowndiv + funcgr + leg	-2.336	5	2.400	24.672	Inf	NA
Flagellate abundance	M1	a * sowndiv/(b + sowndiv)	-3.237	3	4.000	15.473	Inf	NA
Flagellate abundance	M1a	SSmicmen(sowndiv, Vm, k)	-3.237	3	4.000	15.473	Inf	NA
Flagellate abundance	E2	a + b * exp(sowndiv)	-3.254	3	4.000	15.508	Inf	NA
Flagellate abundance	E3	a + exp(c * sowndiv)	-3.285	3	4.000	15.570	Inf	NA
Flagellate abundance	E4	a + exp(sowndiv)	-200.003	2	6.000	405.339	Inf	NA
Flagellate abundance	E5	b * exp(sowndiv)	-10.527	2	6.000	26.387	Inf	NA
Flagellate abundance	E6	exp(c * sowndiv)	-6.344	2	6.000	18.021	Inf	NA
Flagellate abundance	Pa2	a + b * sowndiv	-3.285	3	4.000	15.570	Inf	NA
Flagellate abundance	Pa3	a + sowndiv^c	-3.290	3	4.000	15.579	Inf	NA
Flagellate abundance	Pa4	b * sowndiv^c	-3.290	3	4.000	15.580	Inf	NA
Flagellate abundance	Pa5	sowndiv^c	-6.575	2	6.000	18.483	Inf	NA
Flagellate abundance	L0	block + (sowndiv + funcgr + grass + leg)^2	Inf	13	0.923	#NAME?	NA	NA
Bacteria-feeding nematode diversity	L2	sowndiv + funcgr + leg	-0.372	5	14.400	11.653	0.000	0.52
Bacteria-feeding nematode diversity	Pa2	a + b * sowndiv	-4.300	3	24.000	14.953	3.301	0.10
Bacteria-feeding nematode diversity	Pa4	b * sowndiv^c	-4.858	3	24.000	16.068	4.416	0.06
Bacteria-feeding nematode diversity	Pa3	a + sowndiv^c	-4.961	3	24.000	16.275	4.623	0.05
Bacteria-feeding nematode diversity	LG2	SSlogis(sowndiv, Asym, xmid, scal)	-4.085	4	18.000	16.767	5.114	0.04
Bacteria-feeding nematode diversity	AS2	SSasympOff(sowndiv, Asym, lrc, c0)	-4.125	4	18.000	16.848	5.195	0.04
Bacteria-feeding nematode diversity	AS1	SSasymp(sowndiv, Asym, R0, lrc)	-4.125	4	18.000	16.848	5.195	0.04
Bacteria-feeding nematode diversity	M2	d + a * sowndiv/(b + sowndiv)	-4.140	4	18.000	16.877	5.225	0.04
Bacteria-feeding nematode diversity	E2	a + b * exp(sowndiv)	-5.317	3	24.000	16.986	5.333	0.04
Bacteria-feeding nematode diversity	Pa1	a + b * sowndiv^c	-4.227	4	18.000	17.050	5.397	0.04
Bacteria-feeding nematode diversity	M1a	SSmicmen(sowndiv, Vm, k)	-6.102	3	24.000	18.557	6.904	0.02
Bacteria-feeding nematode diversity	M1	a * sowndiv/(b + sowndiv)	-6.102	3	24.000	18.557	6.904	0.02

Supplementary Table 2 (continued)

Long variable name	model name	model formula	LL	K	N2K	AICc	deltAICc	w_ic
Bacteria-feeding nematode diversity	AS3	SSasympOrig(sowndiv, Asym, Irc)	-6.552	3	24.000	19.457	7.804	0.01
Bacteria-feeding nematode diversity	L0	block + (sowndiv + funcgr + grass + leg)^2	5.619	15	4.800	27.333	15.680	0.00
Bacteria-feeding nematode diversity	Pa5	sowndiv^c	-38.237	2	36.000	80.648	68.996	0.00
Bacteria-feeding nematode diversity	E5	b * exp(sowndiv)	-56.678	2	36.000	117.529	105.877	0.00
Bacteria-feeding nematode diversity	E4	a + exp(sowndiv)	-4307.754	2	36.000	8619.681	8608.029	0.00
Hyphenophagous nematode diversity	E2	a + b * exp(sowndiv)	-6.338	3	24.000	19.030	0.000	0.18
Hyphenophagous nematode diversity	Pa2	a + b * sowndiv	-6.442	3	24.000	19.237	0.207	0.16
Hyphenophagous nematode diversity	AS3	SSasympOrig(sowndiv, Asym, Irc)	-6.631	3	24.000	19.615	0.585	0.13
Hyphenophagous nematode diversity	Pa4	b * sowndiv^c	-6.682	3	24.000	19.716	0.686	0.13
Hyphenophagous nematode diversity	Pa3	a + sowndiv^c	-6.683	3	24.000	19.719	0.689	0.12
Hyphenophagous nematode diversity	M1a	SSmicmen(sowndiv, Vm, k)	-6.714	3	24.000	19.781	0.751	0.12
Hyphenophagous nematode diversity	M1	a * sowndiv/(b + sowndiv)	-6.714	3	24.000	19.781	0.751	0.12
Hyphenophagous nematode diversity	L2	sowndiv + funcgr + leg	-5.536	5	14.400	21.982	2.952	0.04
Hyphenophagous nematode diversity	L0	block + (sowndiv + funcgr + grass + leg)^2	-2.443	15	4.800	43.457	24.427	0.00
Hyphenophagous nematode diversity	Pa5	sowndiv^c	-27.188	2	36.000	58.551	39.521	0.00
Hyphenophagous nematode diversity	E5	b * exp(sowndiv)	-70.270	2	36.000	144.713	125.683	0.00
Hyphenophagous nematode diversity	E4	a + exp(sowndiv)	-4307.754	2	36.000	8619.681	8600.651	0.00
Omnivorous nematode diversity	L0	block + (sowndiv + funcgr + grass + leg)^2	9.273	15	4.800	20.025	0.000	0.95
Omnivorous nematode diversity	E2	a + b * exp(sowndiv)	-11.048	3	24.000	28.450	8.425	0.01
Omnivorous nematode diversity	Pa2	a + b * sowndiv	-11.332	3	24.000	29.016	8.992	0.01
Omnivorous nematode diversity	Pa4	b * sowndiv^c	-11.932	3	24.000	30.217	10.192	0.01
Omnivorous nematode diversity	Pa3	a + sowndiv^c	-11.939	3	24.000	30.231	10.207	0.01
Omnivorous nematode diversity	M1	a * sowndiv/(b + sowndiv)	-11.967	3	24.000	30.286	10.261	0.01
Omnivorous nematode diversity	M1a	SSmicmen(sowndiv, Vm, k)	-11.967	3	24.000	30.286	10.261	0.01
Omnivorous nematode diversity	L2	sowndiv + funcgr + leg	-10.388	5	14.400	31.685	11.661	0.00
Omnivorous nematode diversity	Pa5	sowndiv^c	-41.636	2	36.000	87.446	67.421	0.00
Omnivorous nematode diversity	E5	b * exp(sowndiv)	-45.885	2	36.000	95.944	75.919	0.00
Omnivorous nematode diversity	E4	a + exp(sowndiv)	-4307.754	2	36.000	8619.681	8599.657	0.00
Plant-feeding nematode diversity	Pa4	b * sowndiv^c	5.971	3	24.000	-5.589	0.000	0.17
Plant-feeding nematode diversity	Pa3	a + sowndiv^c	5.918	3	24.000	-5.483	0.106	0.16
Plant-feeding nematode diversity	Pa2	a + b * sowndiv	5.551	3	24.000	-4.749	0.840	0.11
Plant-feeding nematode diversity	L2	sowndiv + funcgr + leg	7.367	5	14.400	-3.826	1.763	0.07
Plant-feeding nematode diversity	M1	a * sowndiv/(b + sowndiv)	5.036	3	24.000	-3.718	1.871	0.07

Supplementary Table 2 (continued)

Long variable name	model name	model formula	LL	K	N2K	AICc	deltAICc	w_ic
Plant-feeding nematode diversity	M1a	SSmicmen(sowndiv, Vm, k)	5.036	3	24.000	-3.718	1.871	0.07
Plant-feeding nematode diversity	Pa1	a + b * sowndiv^c	6.060	4	18.000	-3.523	2.066	0.06
Plant-feeding nematode diversity	M2	d + a * sowndiv/(b + sowndiv)	6.017	4	18.000	-3.437	2.152	0.06
Plant-feeding nematode diversity	AS1	SSasymp(sowndiv, Asym, R0, lrc)	6.000	4	18.000	-3.404	2.185	0.06
Plant-feeding nematode diversity	AS2	SSasympOff(sowndiv, Asym, lrc, c0)	6.000	4	18.000	-3.404	2.185	0.06
Plant-feeding nematode diversity	LG2	SSlogis(sowndiv, Asym, xmid, scal)	5.979	4	18.000	-3.360	2.229	0.06
Plant-feeding nematode diversity	E2	a + b * exp(sowndiv)	4.290	3	24.000	-2.227	3.362	0.03
Plant-feeding nematode diversity	AS3	SSasympOrig(sowndiv, Asym, lrc)	4.224	3	24.000	-2.096	3.493	0.03
Plant-feeding nematode diversity	L0	block + (sowndiv + funcgr + grass + leg)^2	18.509	15	4.800	1.554	7.143	0.00
Plant-feeding nematode diversity	Pa5	sowndiv^c	-36.718	2	36.000	77.610	83.199	0.00
Plant-feeding nematode diversity	E5	b * exp(sowndiv)	-54.298	2	36.000	112.770	118.359	0.00
Plant-feeding nematode diversity	E4	a + exp(sowndiv)	-4307.754	2	36.000	8619.681	8625.270	0.00
Predatory nematode diversity	E2	a + b * exp(sowndiv)	0.053	3	24.000	6.246	0.000	0.70
Predatory nematode diversity	Pa2	a + b * sowndiv	-1.425	3	24.000	9.204	2.958	0.16
Predatory nematode diversity	L2	sowndiv + funcgr + leg	-0.250	5	14.400	11.409	5.163	0.05
Predatory nematode diversity	Pa4	b * sowndiv^c	-3.313	3	24.000	12.979	6.733	0.02
Predatory nematode diversity	Pa3	a + sowndiv^c	-3.437	3	24.000	13.226	6.980	0.02
Predatory nematode diversity	M1a	SSmicmen(sowndiv, Vm, k)	-3.596	3	24.000	13.546	7.299	0.02
Predatory nematode diversity	M1	a * sowndiv/(b + sowndiv)	-3.596	3	24.000	13.546	7.299	0.02
Predatory nematode diversity	AS3	SSasympOrig(sowndiv, Asym, lrc)	-7.114	3	24.000	20.582	14.336	0.00
Predatory nematode diversity	L0	block + (sowndiv + funcgr + grass + leg)^2	5.297	15	4.800	27.977	21.731	0.00
Predatory nematode diversity	E5	b * exp(sowndiv)	-12.484	2	36.000	29.142	22.896	0.00
Predatory nematode diversity	Pa5	sowndiv^c	-47.020	2	36.000	98.214	91.968	0.00
Predatory nematode diversity	E4	a + exp(sowndiv)	-4307.754	2	36.000	8619.681	8613.435	0.00
Plant-feeding nematode abundance	Pa3	a + sowndiv^c	12.727	3	24.333	-19.105	0.000	0.13
Plant-feeding nematode abundance	Pa4	b * sowndiv^c	12.724	3	24.333	-19.101	0.004	0.13
Plant-feeding nematode abundance	M1a	SSmicmen(sowndiv, Vm, k)	12.696	3	24.333	-19.044	0.062	0.12
Plant-feeding nematode abundance	M1	a * sowndiv/(b + sowndiv)	12.696	3	24.333	-19.044	0.062	0.12
Plant-feeding nematode abundance	AS3	SSasympOrig(sowndiv, Asym, lrc)	12.647	3	24.333	-18.946	0.160	0.12
Plant-feeding nematode abundance	Pa2	a + b * sowndiv	12.552	3	24.333	-18.756	0.349	0.11
Plant-feeding nematode abundance	E2	a + b * exp(sowndiv)	12.404	3	24.333	-18.460	0.645	0.09
Plant-feeding nematode abundance	LG2	SSlogis(sowndiv, Asym, xmid, scal)	12.744	4	18.250	-16.900	2.205	0.04
Plant-feeding nematode abundance	AS2	SSasympOff(sowndiv, Asym, lrc, c0)	12.742	4	18.250	-16.895	2.211	0.04

Supplementary Table 2 (continued)

Long variable name	model name	model formula	LL	K	N2K	AICc	deltAICc	w_ic
Plant-feeding nematode abundance	AS1	SSasymp(sowndiv, Asym, R0, lrc)	12.742	4	18.250	-16.895	2.211	0.04
Plant-feeding nematode abundance	M2	d + a * sowndiv/(b + sowndiv)	12.729	4	18.250	-16.869	2.236	0.04
Plant-feeding nematode abundance	L2	sowndiv + funcgr + leg	12.645	5	14.600	-14.394	4.712	0.01
Plant-feeding nematode abundance	L0	block + (sowndiv + funcgr + grass + leg)^2	19.461	15	4.867	-0.501	18.604	0.00
Plant-feeding nematode abundance	E5	b * exp(sowndiv)	-27.302	2	36.500	58.774	77.880	0.00
Plant-feeding nematode abundance	Pa5	sowndiv^c	-41.221	2	36.500	86.613	105.719	0.00
Plant-feeding nematode abundance	E4	a + exp(sowndiv)	-4367.080	2	36.500	8738.332	8757.437	0.00
Omnivorous nematode abundance	E2	a + b * exp(sowndiv)	16.894	3	24.333	-27.440	0.000	0.20
Omnivorous nematode abundance	Pa2	a + b * sowndiv	16.873	3	24.333	-27.397	0.043	0.20
Omnivorous nematode abundance	Pa4	b * sowndiv^c	16.848	3	24.333	-27.349	0.091	0.19
Omnivorous nematode abundance	Pa3	a + sowndiv^c	16.848	3	24.333	-27.348	0.092	0.19
Omnivorous nematode abundance	M1a	SSmicmen(sowndiv, Vm, k)	16.831	3	24.333	-27.315	0.125	0.19
Omnivorous nematode abundance	L2	sowndiv + funcgr + leg	17.079	5	14.600	-23.263	4.178	0.02
Omnivorous nematode abundance	L0	block + (sowndiv + funcgr + grass + leg)^2	29.080	15	4.867	-19.739	7.701	0.00
Omnivorous nematode abundance	E5	b * exp(sowndiv)	-12.819	2	36.500	29.809	57.249	0.00
Omnivorous nematode abundance	Pa5	sowndiv^c	-41.112	2	36.500	86.396	113.836	0.00
Omnivorous nematode abundance	E4	a + exp(sowndiv)	-4367.080	2	36.500	8738.332	8765.772	0.00
Predatory nematode abundance	E2	a + b * exp(sowndiv)	45.837	3	24.333	-85.326	0.000	0.90
Predatory nematode abundance	Pa2	a + b * sowndiv	43.329	3	24.333	-80.310	5.016	0.07
Predatory nematode abundance	Pa4	b * sowndiv^c	41.916	3	24.333	-77.484	7.842	0.02
Predatory nematode abundance	L2	sowndiv + funcgr + leg	43.603	5	14.600	-76.311	9.015	0.01
Predatory nematode abundance	E5	b * exp(sowndiv)	38.795	2	36.500	-73.419	11.907	0.00
Predatory nematode abundance	Pa3	a + sowndiv^c	38.342	3	24.333	-70.336	14.990	0.00
Predatory nematode abundance	L0	block + (sowndiv + funcgr + grass + leg)^2	51.168	15	4.867	-63.914	21.412	0.00
Predatory nematode abundance	Pa5	sowndiv^c	-46.129	2	36.500	96.430	181.756	0.00
Predatory nematode abundance	E4	a + exp(sowndiv)	-4367.080	2	36.500	8738.332	8823.658	0.00
Bacteria-feeding nematode abundance	L2	sowndiv + funcgr + leg	23.367	5	14.600	-35.838	0.000	0.22
Bacteria-feeding nematode abundance	Pa2	a + b * sowndiv	20.918	3	24.333	-35.489	0.349	0.18
Bacteria-feeding nematode abundance	E2	a + b * exp(sowndiv)	20.746	3	24.333	-35.144	0.694	0.15
Bacteria-feeding nematode abundance	Pa4	b * sowndiv^c	20.445	3	24.333	-34.543	1.295	0.11
Bacteria-feeding nematode abundance	Pa3	a + sowndiv^c	20.406	3	24.333	-34.464	1.374	0.11
Bacteria-feeding nematode abundance	M1	a * sowndiv/(b + sowndiv)	20.123	3	24.333	-33.898	1.940	0.08
Bacteria-feeding nematode abundance	M1a	SSmicmen(sowndiv, Vm, k)	20.123	3	24.333	-33.898	1.940	0.08

Supplementary Table 2 (continued)

Long variable name	model name	model formula	LL	K	N2K	AICc	deltaAICc	w_ic
Bacteria-feeding nematode abundance	LG2	SSlogis(sowndiv, Asym, xmid, scal)	20.921	4	18.250	-33.253	2.585	0.06
Bacteria-feeding nematode abundance	L0	block + (sowndiv + funcgr + grass + leg)^2	33.511	15	4.867	-28.601	7.237	0.01
Bacteria-feeding nematode abundance	E5	b * exp(sowndiv)	-8.654	2	36.500	21.479	57.317	0.00
Bacteria-feeding nematode abundance	Pa5	sowndiv^c	-41.091	2	36.500	86.354	122.192	0.00
Bacteria-feeding nematode abundance	E4	a + exp(sowndiv)	-4367.080	2	36.500	8738.332	8774.169	0.00
Hyphenophagous nematode abundance	Pa2	a + b * sowndiv	16.299	3	24.333	-26.251	0.000	0.17
Hyphenophagous nematode abundance	E2	a + b * exp(sowndiv)	16.271	3	24.333	-26.193	0.058	0.17
Hyphenophagous nematode abundance	Pa3	a + sowndiv^c	16.075	3	24.333	-25.803	0.448	0.14
Hyphenophagous nematode abundance	Pa4	b * sowndiv^c	16.067	3	24.333	-25.785	0.466	0.14
Hyphenophagous nematode abundance	M1a	SSmicmen(sowndiv, Vm, k)	15.952	3	24.333	-25.556	0.695	0.12
Hyphenophagous nematode abundance	M1	a * sowndiv/(b + sowndiv)	15.952	3	24.333	-25.556	0.695	0.12
Hyphenophagous nematode abundance	LG2	SSlogis(sowndiv, Asym, xmid, scal)	16.308	4	18.250	-24.029	2.222	0.06
Hyphenophagous nematode abundance	M2	d + a * sowndiv/(b + sowndiv)	16.197	4	18.250	-23.807	2.444	0.05
Hyphenophagous nematode abundance	L2	sowndiv + funcgr + leg	16.657	5	14.600	-22.418	3.833	0.03
Hyphenophagous nematode abundance	BIEXP	SSbiexp(sowndiv, A1, lrc1, A2, lrc2)	16.345	5	14.600	-21.795	4.456	0.02
Hyphenophagous nematode abundance	L0	block + (sowndiv + funcgr + grass + leg)^2	18.821	15	4.867	0.779	27.030	0.00
Hyphenophagous nematode abundance	E5	b * exp(sowndiv)	-13.864	2	36.500	31.900	58.151	0.00
Hyphenophagous nematode abundance	Pa5	sowndiv^c	-40.837	2	36.500	85.845	112.096	0.00
Hyphenophagous nematode abundance	E4	a + exp(sowndiv)	-4367.080	2	36.500	8738.332	8764.583	0.00
Collembola abundance	M1	a * sowndiv/(b + sowndiv)	23.858	3	26.667	-41.400	0.000	0.15
Collembola abundance	M1a	SSmicmen(sowndiv, Vm, k)	23.858	3	26.667	-41.400	0.000	0.15
Collembola abundance	Pa3	a + sowndiv^c	23.795	3	26.667	-41.274	0.126	0.14
Collembola abundance	Pa4	b * sowndiv^c	23.747	3	26.667	-41.179	0.221	0.13
Collembola abundance	AS3	SSasympOrig(sowndiv, Asym, lrc)	23.630	3	26.667	-40.944	0.455	0.12
Collembola abundance	Pa2	a + b * sowndiv	22.952	3	26.667	-39.588	1.812	0.06
Collembola abundance	M2	d + a * sowndiv/(b + sowndiv)	23.870	4	20.000	-39.206	2.194	0.05
Collembola abundance	AS1	SSasymp(sowndiv, Asym, R0, lrc)	23.793	4	20.000	-39.052	2.348	0.05
Collembola abundance	AS2	SSasympOff(sowndiv, Asym, lrc, c0)	23.793	4	20.000	-39.052	2.348	0.05
Collembola abundance	LG2	SSlogis(sowndiv, Asym, xmid, scal)	23.765	4	20.000	-38.997	2.403	0.04
Collembola abundance	E2	a + b * exp(sowndiv)	22.427	3	26.667	-38.539	2.860	0.04
Collembola abundance	L0	block + (sowndiv + funcgr + grass + leg)^2	37.655	15	5.333	-37.810	3.590	0.02
Collembola abundance	L2	sowndiv + funcgr + leg	23.595	5	16.000	-36.379	5.021	0.01
Collembola abundance	E5	b * exp(sowndiv)	-21.858	2	40.000	47.872	89.272	0.00

Supplementary Table 2 (continued)

Long variable name	model name	model formula	LL	K	N2K	AICc	deltaAICc	w_ic
Collembola abundance	Pa5	sowndiv^c	-47.012	2	40.000	98.181	139.580	0.00
Collembola abundance	E4	a + exp(sowndiv)	-4793.686	2	40.000	9591.527	9632.927	0.00
Mite abundance	Pa2	a + b * sowndiv	19.716	3	26.667	-33.116	0.000	0.16
Mite abundance	E2	a + b * exp(sowndiv)	19.712	3	26.667	-33.108	0.008	0.16
Mite abundance	Pa3	a + sowndiv^c	19.637	3	26.667	-32.958	0.157	0.15
Mite abundance	Pa4	b * sowndiv^c	19.637	3	26.667	-32.957	0.158	0.15
Mite abundance	M1	a * sowndiv/(b + sowndiv)	19.631	3	26.667	-32.946	0.169	0.15
Mite abundance	M1a	SSmicmen(sowndiv, Vm, k)	19.631	3	26.667	-32.946	0.169	0.15
Mite abundance	LG2	SSlogis(sowndiv, Asym, xmid, scal)	19.722	4	20.000	-30.911	2.205	0.05
Mite abundance	L2	sowndiv + funcgr + leg	20.009	5	16.000	-29.207	3.908	0.02
Mite abundance	BIEXP	SSbiexp(sowndiv, A1, lrc1, A2, lrc2)	19.786	5	16.000	-28.761	4.355	0.02
Mite abundance	L0	block + (sowndiv + funcgr + grass + leg)^2	28.917	15	5.333	-20.333	12.783	0.00
Mite abundance	E5	b * exp(sowndiv)	-12.679	2	40.000	29.514	62.630	0.00
Mite abundance	Pa5	sowndiv^c	-45.163	2	40.000	94.483	127.598	0.00
Mite abundance	E4	a + exp(sowndiv)	-4793.686	2	40.000	9591.527	9624.643	0.00
Gamasida abundance	Pa2	a + b * sowndiv	22.832	3	26.667	-39.349	0.000	0.26
Gamasida abundance	E2	a + b * exp(sowndiv)	22.606	3	26.667	-38.895	0.454	0.21
Gamasida abundance	Pa4	b * sowndiv^c	22.019	3	26.667	-37.723	1.626	0.12
Gamasida abundance	LG2	SSlogis(sowndiv, Asym, xmid, scal)	22.867	4	20.000	-37.201	2.149	0.09
Gamasida abundance	Pa1	a + b * sowndiv^c	22.864	4	20.000	-37.195	2.154	0.09
Gamasida abundance	Pa3	a + sowndiv^c	21.600	3	26.667	-36.885	2.464	0.08
Gamasida abundance	L2	sowndiv + funcgr + leg	23.844	5	16.000	-36.877	2.472	0.08
Gamasida abundance	M1	a * sowndiv/(b + sowndiv)	20.714	3	26.667	-35.112	4.237	0.03
Gamasida abundance	M1a	SSmicmen(sowndiv, Vm, k)	20.714	3	26.667	-35.112	4.237	0.03
Gamasida abundance	AS3	SSasympOrig(sowndiv, Asym, lrc)	20.240	3	26.667	-34.164	5.185	0.02
Gamasida abundance	L0	block + (sowndiv + funcgr + grass + leg)^2	33.400	15	5.333	-29.301	10.049	0.00
Gamasida abundance	E5	b * exp(sowndiv)	6.190	2	40.000	-8.224	31.125	0.00
Gamasida abundance	Pa5	sowndiv^c	-50.302	2	40.000	104.760	144.109	0.00
Gamasida abundance	E4	a + exp(sowndiv)	-4793.686	2	40.000	9591.527	9630.877	0.00
Collembola diversity	L0	block + (sowndiv + funcgr + grass + leg)^2	36.161	15	5.333	-34.822	0.000	0.38
Collembola diversity	Pa4	b * sowndiv^c	19.349	3	26.667	-32.382	2.440	0.11
Collembola diversity	Pa3	a + sowndiv^c	19.305	3	26.667	-32.295	2.527	0.11
Collembola diversity	Pa2	a + b * sowndiv	18.847	3	26.667	-31.379	3.443	0.07

Supplementary Table 2 (continued)

Long variable name	model name	model formula	LL	K	N2K	AICc	deltAICc	w_ic
Collembola diversity	AS1	SSasymp(sowndiv, Asym, R0, lrc)	19.475	4	20.000	-30.416	4.406	0.04
Collembola diversity	AS2	SSasympOff(sowndiv, Asym, lrc, c0)	19.475	4	20.000	-30.416	4.406	0.04
Collembola diversity	LG2	SSlogis(sowndiv, Asym, xmid, scal)	19.473	4	20.000	-30.412	4.410	0.04
Collembola diversity	M2	d + a * sowndiv/(b + sowndiv)	19.472	4	20.000	-30.411	4.411	0.04
Collembola diversity	Pa1	a + b * sowndiv^c	19.453	4	20.000	-30.373	4.449	0.04
Collembola diversity	M1	a * sowndiv/(b + sowndiv)	18.207	3	26.667	-30.099	4.723	0.04
Collembola diversity	M1a	SSmicmen(sowndiv, Vm, k)	18.207	3	26.667	-30.099	4.723	0.04
Collembola diversity	E2	a + b * exp(sowndiv)	17.544	3	26.667	-28.772	6.050	0.02
Collembola diversity	AS3	SSasympOrig(sowndiv, Asym, lrc)	17.249	3	26.667	-28.183	6.639	0.01
Collembola diversity	L2	sowndiv + funcgr + leg	18.994	5	16.000	-27.178	7.644	0.01
Collembola diversity	Pa5	sowndiv^c	-32.542	2	40.000	69.240	104.063	0.00
Collembola diversity	E5	b * exp(sowndiv)	-62.899	2	40.000	129.954	164.777	0.00
Collembola diversity	E4	a + exp(sowndiv)	-4793.686	2	40.000	9591.527	9626.350	0.00
Aboveground herbivore abundance	Pa4	b * sowndiv^c	21.063	3	16.667	-35.603	0.000	0.25
Aboveground herbivore abundance	Pa2	a + b * sowndiv	20.600	3	16.667	-34.678	0.926	0.16
Aboveground herbivore abundance	Pa1	a + b * sowndiv^c	21.542	4	12.500	-34.196	1.408	0.13
Aboveground herbivore abundance	M2	d + a * sowndiv/(b + sowndiv)	21.247	4	12.500	-33.605	1.999	0.09
Aboveground herbivore abundance	AS1	SSasymp(sowndiv, Asym, R0, lrc)	21.222	4	12.500	-33.555	2.049	0.09
Aboveground herbivore abundance	AS2	SSasympOff(sowndiv, Asym, lrc, c0)	21.222	4	12.500	-33.555	2.049	0.09
Aboveground herbivore abundance	LG2	SSlogis(sowndiv, Asym, xmid, scal)	20.999	4	12.500	-33.109	2.494	0.07
Aboveground herbivore abundance	Pa3	a + sowndiv^c	19.713	3	16.667	-32.904	2.699	0.07
Aboveground herbivore abundance	L2	sowndiv + funcgr + leg	21.687	5	10.000	-32.011	3.593	0.04
Aboveground herbivore abundance	M1	a * sowndiv/(b + sowndiv)	16.580	3	16.667	-26.638	8.965	0.00
Aboveground herbivore abundance	M1a	SSmicmen(sowndiv, Vm, k)	16.580	3	16.667	-26.638	8.965	0.00
Aboveground herbivore abundance	E2	a + b * exp(sowndiv)	15.766	3	16.667	-25.011	10.593	0.00
Aboveground herbivore abundance	L0	block + (sowndiv + funcgr + grass + leg)^2	34.420	15	3.333	-24.722	10.881	0.00
Aboveground herbivore abundance	AS3	SSasympOrig(sowndiv, Asym, lrc)	14.098	3	16.667	-21.675	13.929	0.00
Aboveground herbivore abundance	E5	b * exp(sowndiv)	-14.632	2	25.000	33.519	69.122	0.00
Aboveground herbivore abundance	Pa5	sowndiv^c	-39.991	2	25.000	84.238	119.841	0.00
Aboveground herbivore abundance	E4	a + exp(sowndiv)	-3007.804	2	25.000	6019.863	6055.466	0.00
Aboveground carnivore abundance	M1	a * sowndiv/(b + sowndiv)	12.069	3	16.667	-17.617	0.000	0.20
Aboveground carnivore abundance	M1a	SSmicmen(sowndiv, Vm, k)	12.069	3	16.667	-17.617	0.000	0.20
Aboveground carnivore abundance	AS3	SSasympOrig(sowndiv, Asym, lrc)	11.573	3	16.667	-16.624	0.993	0.12

Supplementary Table 2 (continued)

Long variable name	model name	model formula	LL	K	N2K	AICc	deltAICc	w_ic
Aboveground carnivore abundance	Pa3	a + sowndiv^c	11.353	3	16.667	-16.183	1.434	0.10
Aboveground carnivore abundance	Pa4	b * sowndiv^c	10.999	3	16.667	-15.477	2.140	0.07
Aboveground carnivore abundance	AS1	SSasymp(sowndiv, Asym, R0, lrc)	12.078	4	12.500	-15.267	2.350	0.06
Aboveground carnivore abundance	AS2	SSasympOff(sowndiv, Asym, lrc, c0)	12.078	4	12.500	-15.267	2.350	0.06
Aboveground carnivore abundance	M2	d + a * sowndiv/(b + sowndiv)	12.076	4	12.500	-15.263	2.354	0.06
Aboveground carnivore abundance	LG2	SSlogis(sowndiv, Asym, xmid, scal)	12.075	4	12.500	-15.262	2.355	0.06
Aboveground carnivore abundance	L2	sowndiv + funcgr + leg	12.984	5	10.000	-14.605	3.012	0.05
Aboveground carnivore abundance	Pa2	a + b * sowndiv	8.122	3	16.667	-9.721	7.895	0.00
Aboveground carnivore abundance	E2	a + b * exp(sowndiv)	6.367	3	16.667	-6.213	11.404	0.00
Aboveground carnivore abundance	L0	block + (sowndiv + funcgr + grass + leg)^2	25.106	15	3.333	-6.094	11.522	0.00
Aboveground carnivore abundance	E5	b * exp(sowndiv)	-26.232	2	25.000	56.719	74.336	0.00
Aboveground carnivore abundance	Pa5	sowndiv^c	-36.012	2	25.000	76.280	93.897	0.00
Aboveground carnivore abundance	E4	a + exp(sowndiv)	-3007.804	2	25.000	6019.863	6037.480	0.00
Aboveground omnivore abundance	L2	sowndiv + funcgr + leg	17.487	5	10.000	-23.611	0.000	1.00
Aboveground omnivore abundance	L0	block + (sowndiv + funcgr + grass + leg)^2	26.922	15	3.333	-9.726	13.885	0.00
Aboveground omnivore abundance	Pa4	b * sowndiv^c	5.551	3	16.667	-4.580	19.031	0.00
Aboveground omnivore abundance	Pa3	a + sowndiv^c	5.517	3	16.667	-4.513	19.098	0.00
Aboveground omnivore abundance	Pa2	a + b * sowndiv	5.313	3	16.667	-4.103	19.507	0.00
Aboveground omnivore abundance	M1a	SSmicmen(sowndiv, Vm, k)	5.007	3	16.667	-3.492	20.119	0.00
Aboveground omnivore abundance	M1	a * sowndiv/(b + sowndiv)	5.007	3	16.667	-3.492	20.119	0.00
Aboveground omnivore abundance	E2	a + b * exp(sowndiv)	4.721	3	16.667	-2.920	20.691	0.00
Aboveground omnivore abundance	AS3	SSasympOrig(sowndiv, Asym, lrc)	4.623	3	16.667	-2.723	20.887	0.00
Aboveground omnivore abundance	LG2	SSlogis(sowndiv, Asym, xmid, scal)	5.728	4	12.500	-2.567	21.043	0.00
Aboveground omnivore abundance	AS2	SSasympOff(sowndiv, Asym, lrc, c0)	5.706	4	12.500	-2.523	21.087	0.00
Aboveground omnivore abundance	AS1	SSasymp(sowndiv, Asym, R0, lrc)	5.706	4	12.500	-2.523	21.087	0.00
Aboveground omnivore abundance	M2	d + a * sowndiv/(b + sowndiv)	5.675	4	12.500	-2.462	21.149	0.00
Aboveground omnivore abundance	Pa1	a + b * sowndiv^c	5.589	4	12.500	-2.289	21.321	0.00
Aboveground omnivore abundance	E5	b * exp(sowndiv)	-21.514	2	25.000	47.283	70.893	0.00
Aboveground omnivore abundance	Pa5	sowndiv^c	-35.116	2	25.000	74.487	98.097	0.00
Aboveground omnivore abundance	E4	a + exp(sowndiv)	-3007.804	2	25.000	6019.863	6043.473	0.00
Aboveground parasitoid abundance	L2	sowndiv + funcgr + leg	9.945	5	10.000	-8.527	0.000	0.77
Aboveground parasitoid abundance	L0	block + (sowndiv + funcgr + grass + leg)^2	25.076	15	3.333	-6.035	2.492	0.22
Aboveground parasitoid abundance	Pa2	a + b * sowndiv	1.345	3	16.667	3.831	12.358	0.00

Supplementary Table 2 (continued)

Long variable name	model name	model formula	LL	K	N2K	AICc	deltAICc	w_ic
Aboveground parasitoid abundance	Pa4	b * sowndiv^c	0.444	3	16.667	5.634	14.161	0.00
Aboveground parasitoid abundance	Pa1	a + b * sowndiv^c	1.373	4	12.500	6.143	14.670	0.00
Aboveground parasitoid abundance	M2	d + a * sowndiv/(b + sowndiv)	1.366	4	12.500	6.157	14.683	0.00
Aboveground parasitoid abundance	AS1	SSasymp(sowndiv, Asym, R0, lrc)	1.366	4	12.500	6.157	14.684	0.00
Aboveground parasitoid abundance	AS2	SSasympOff(sowndiv, Asym, lrc, c0)	1.366	4	12.500	6.157	14.684	0.00
Aboveground parasitoid abundance	LG2	SSlogis(sowndiv, Asym, xmid, scal)	1.353	4	12.500	6.183	14.709	0.00
Aboveground parasitoid abundance	E2	a + b * exp(sowndiv)	-0.256	3	16.667	7.033	15.559	0.00
Aboveground parasitoid abundance	Pa3	a + sowndiv^c	-0.521	3	16.667	7.565	16.091	0.00
Aboveground parasitoid abundance	M1a	SSmicmen(sowndiv, Vm, k)	-2.370	3	16.667	11.262	19.788	0.00
Aboveground parasitoid abundance	M1	a * sowndiv/(b + sowndiv)	-2.370	3	16.667	11.262	19.788	0.00
Aboveground parasitoid abundance	E5	b * exp(sowndiv)	-19.263	2	25.000	42.781	51.307	0.00
Aboveground parasitoid abundance	Pa5	sowndiv^c	-41.660	2	25.000	87.576	96.102	0.00
Aboveground parasitoid abundance	E4	a + exp(sowndiv)	-3007.804	2	25.000	6019.863	6028.389	0.00
Aboveground hyperparasitoid abundance	Pa3	a + sowndiv^c	-9.108	3	9.333	25.216	0.000	0.13
Aboveground hyperparasitoid abundance	Pa4	b * sowndiv^c	-9.110	3	9.333	25.221	0.005	0.13
Aboveground hyperparasitoid abundance	E2	a + b * exp(sowndiv)	-9.157	3	9.333	25.313	0.097	0.12
Aboveground hyperparasitoid abundance	Pa2	a + b * sowndiv	-9.166	3	9.333	25.332	0.116	0.12
Aboveground hyperparasitoid abundance	AS3	SSasympOrig(sowndiv, Asym, lrc)	-9.170	3	9.333	25.339	0.123	0.12
Aboveground hyperparasitoid abundance	M1a	SSmicmen(sowndiv, Vm, k)	-9.177	3	9.333	25.354	0.138	0.12
Aboveground hyperparasitoid abundance	M1	a * sowndiv/(b + sowndiv)	-9.177	3	9.333	25.354	0.138	0.12
Aboveground hyperparasitoid abundance	M2	d + a * sowndiv/(b + sowndiv)	-8.044	4	7.000	25.827	0.611	0.09
Aboveground hyperparasitoid abundance	Pa1	a + b * sowndiv^c	-9.103	4	7.000	27.946	2.730	0.03
Aboveground hyperparasitoid abundance	L2	sowndiv + funcgr + leg	-8.811	5	5.600	30.349	5.132	0.01
Aboveground hyperparasitoid abundance	E5	b * exp(sowndiv)	-16.232	2	14.000	36.944	11.728	0.00
Aboveground hyperparasitoid abundance	Pa5	sowndiv^c	-22.603	2	14.000	49.686	24.469	0.00
Aboveground hyperparasitoid abundance	L0	block + (sowndiv + funcgr + grass + leg)^2	-2.232	14	2.000	64.772	39.556	0.00
Aboveground hyperparasitoid abundance	E4	a + exp(sowndiv)	-1688.460	2	14.000	3381.400	3356.184	0.00
Pollinator abundance	L2	sowndiv + funcgr + leg	14.800	5	10.000	-18.236	0.000	0.71
Pollinator abundance	E2	a + b * exp(sowndiv)	9.723	3	16.667	-12.924	5.311	0.05
Pollinator abundance	Pa2	a + b * sowndiv	9.718	3	16.667	-12.913	5.322	0.05
Pollinator abundance	Pa4	b * sowndiv^c	9.554	3	16.667	-12.586	5.650	0.04
Pollinator abundance	Pa3	a + sowndiv^c	9.544	3	16.667	-12.567	5.668	0.04
Pollinator abundance	M1	a * sowndiv/(b + sowndiv)	9.416	3	16.667	-12.310	5.925	0.04

Supplementary Table 2 (continued)

Long variable name	model name	model formula	LL	K	N2K	AICc	deltAICc	w_ic
Pollinator abundance	M1a	SSmicmen(sowndiv, Vm, k)	9.416	3	16.667	-12.310	5.925	0.04
Pollinator abundance	AS3	SSasympOrig(sowndiv, Asym, lrc)	9.377	3	16.667	-12.232	6.004	0.04
Pollinator abundance	L0	block + (sowndiv + funcgr + grass + leg)^2	21.013	15	3.333	2.092	20.327	0.00
Pollinator abundance	E5	b * exp(sowndiv)	-14.188	2	25.000	32.632	50.868	0.00
Pollinator abundance	Pa5	sowndiv^c	-34.576	2	25.000	73.408	91.644	0.00
Pollinator abundance	E4	a + exp(sowndiv)	-3007.804	2	25.000	6019.863	6038.098	0.00
Plant invader abundance	Pn1831	a + sowndiv^c	48.697	6	13.667	-84.274	0.000	0.28
Plant invader abundance	Pp2231	a + b * sowndiv	50.809	8	10.250	-83.645	0.629	0.21
Plant invader abundance	Ef3921	a + exp(c * sowndiv)	49.460	8	10.250	-80.947	3.327	0.05
Plant invader abundance	Eb1521	a + exp(c * sowndiv)	47.019	6	13.667	-80.918	3.357	0.05
Plant invader abundance	Pm1231	a + b * sowndiv	46.962	6	13.667	-80.803	3.471	0.05
Plant invader abundance	Pr3231	a + b * sowndiv	49.301	8	10.250	-80.629	3.645	0.05
Plant invader abundance	Pp2331	a + sowndiv^c	48.984	8	10.250	-79.996	4.278	0.03
Plant invader abundance	Pr3331	a + sowndiv^c	48.974	8	10.250	-79.976	4.298	0.03
Plant invader abundance	Pc131	a + b * sowndiv^c	45.114	5	16.400	-79.439	4.836	0.03
Plant invader abundance	L222	sowndiv + funcgr + leg	46.251	6	13.667	-79.381	4.893	0.02
Plant invader abundance	Pc331	a + sowndiv^c	43.827	4	20.500	-79.135	5.139	0.02
Plant invader abundance	M222	d + a * sowndiv/(b + sowndiv)	44.888	5	16.400	-78.987	5.288	0.02
Plant invader abundance	Ps3731	a + b * sowndiv	50.947	10	8.200	-78.795	5.480	0.02
Plant invader abundance	Pe731	a + b * sowndiv	45.857	6	13.667	-78.595	5.679	0.02
Plant invader abundance	Ec2121	a + exp(c * sowndiv)	45.817	6	13.667	-78.513	5.761	0.02
Plant invader abundance	Ea921	a + exp(c * sowndiv)	45.525	6	13.667	-77.931	6.344	0.01
Plant invader abundance	E32	a + exp(c * sowndiv)	43.208	4	20.500	-77.897	6.377	0.01
Plant invader abundance	M1332	d + a * sowndiv/(b + sowndiv)	51.803	11	7.455	-77.835	6.439	0.01
Plant invader abundance	Pc231	a + b * sowndiv	42.975	4	20.500	-77.430	6.845	0.01
Plant invader abundance	Pn1731	a + b * sowndiv	45.232	6	13.667	-77.344	6.931	0.01
Plant invader abundance	Pq2731	a + b * sowndiv	47.461	8	10.250	-76.949	7.326	0.01
Plant invader abundance	L21	sowndiv + funcgr + leg	44.789	6	13.667	-76.459	7.816	0.01
Plant invader abundance	Pe831	a + sowndiv^c	44.568	6	13.667	-76.016	8.258	0.00
Plant invader abundance	Ps3831	a + sowndiv^c	49.274	10	8.200	-75.449	8.826	0.00
Plant invader abundance	Pm1331	a + sowndiv^c	44.253	6	13.667	-75.386	8.889	0.00
Plant invader abundance	Pp2221	a + b * sowndiv	46.641	8	10.250	-75.310	8.964	0.00
Plant invader abundance	Pn1821	a + sowndiv^c	44.155	6	13.667	-75.191	9.084	0.00

Supplementary Table 2 (continued)

Long variable name	model name	model formula	LL	K	N2K	AICc	deltAICc	w_ic
Plant invader abundance	Pq2831	a + sowndiv^c	45.974	8	10.250	-73.975	10.300	0.00
Plant invader abundance	Pe631	a + b * sowndiv^c	45.966	8	10.250	-73.959	10.316	0.00
Plant invader abundance	Pp2431	b * sowndiv^c	45.810	8	10.250	-73.647	10.627	0.00
Plant invader abundance	L021	block + (sowndiv + funcgr + grass + leg)^2	56.949	16	5.125	-73.529	10.745	0.00
Plant invader abundance	Pp2321	a + sowndiv^c	44.915	8	10.250	-71.858	12.416	0.00
Plant invader abundance	E22	a + b * exp(sowndiv)	40.118	4	20.500	-71.716	12.559	0.00
Plant invader abundance	Pr3221	a + b * sowndiv	44.782	8	10.250	-71.591	12.683	0.00
Plant invader abundance	Ps3931	b * sowndiv^c	47.285	10	8.200	-71.472	12.802	0.00
Plant invader abundance	Pn1921	b * sowndiv^c	42.293	6	13.667	-71.465	12.809	0.00
Plant invader abundance	Pr3321	a + sowndiv^c	44.683	8	10.250	-71.394	12.880	0.00
Plant invader abundance	Eb1511	a + exp(c * sowndiv)	42.254	6	13.667	-71.388	12.886	0.00
Plant invader abundance	Pm1221	a + b * sowndiv	42.183	6	13.667	-71.245	13.029	0.00
Plant invader abundance	L211	sowndiv + funcgr + leg	42.132	6	13.667	-71.144	13.131	0.00
Plant invader abundance	Pc321	a + sowndiv^c	39.601	4	20.500	-70.683	13.592	0.00
Plant invader abundance	Ps3721	a + b * sowndiv	46.849	10	8.200	-70.599	13.676	0.00
Plant invader abundance	Pc121	a + b * sowndiv^c	40.352	5	16.400	-69.915	14.360	0.00
Plant invader abundance	Pp2421	b * sowndiv^c	43.816	8	10.250	-69.658	14.616	0.00
Plant invader abundance	M211	d + a * sowndiv/(b + sowndiv)	40.146	5	16.400	-69.502	14.772	0.00
Plant invader abundance	Ea911	a + exp(c * sowndiv)	41.265	6	13.667	-69.410	14.865	0.00
Plant invader abundance	Pe721	a + b * sowndiv	41.204	6	13.667	-69.289	14.986	0.00
Plant invader abundance	Pn1931	b * sowndiv^c	41.149	6	13.667	-69.178	15.096	0.00
Plant invader abundance	E31	a + exp(c * sowndiv)	38.800	4	20.500	-69.080	15.194	0.00
Plant invader abundance	Pn1721	a + b * sowndiv	40.995	6	13.667	-68.870	15.405	0.00
Plant invader abundance	Pc221	a + b * sowndiv	38.588	4	20.500	-68.656	15.618	0.00
Plant invader abundance	Pe931	b * sowndiv^c	40.776	6	13.667	-68.432	15.843	0.00
Plant invader abundance	Pp2121	a + b * sowndiv^c	47.064	11	7.455	-68.357	15.917	0.00
Plant invader abundance	Pq2931	b * sowndiv^c	43.015	8	10.250	-68.058	16.216	0.00
Plant invader abundance	Ps3921	b * sowndiv^c	45.546	10	8.200	-67.994	16.281	0.00
Plant invader abundance	Ps3821	a + sowndiv^c	45.287	10	8.200	-67.475	16.799	0.00
Plant invader abundance	Pq2721	a + b * sowndiv	42.661	8	10.250	-67.349	16.925	0.00
Plant invader abundance	Pm1321	a + sowndiv^c	40.157	6	13.667	-67.194	17.080	0.00
Plant invader abundance	Pc421	b * sowndiv^c	37.776	4	20.500	-67.033	17.242	0.00
Plant invader abundance	Pr3431	b * sowndiv^c	42.487	8	10.250	-67.001	17.273	0.00

Supplementary Table 2 (continued)

Long variable name	model name	model formula	LL	K	N2K	AICc	deltAICc	w_ic
Plant invader abundance	Pr3421	b * sowndiv^c	42.481	8	10.250	-66.990	17.285	0.00
Plant invader abundance	Pm1121	a + b * sowndiv^c	42.423	8	10.250	-66.874	17.400	0.00
Plant invader abundance	Pe821	a + sowndiv^c	39.853	6	13.667	-66.586	17.688	0.00
Plant invader abundance	L011	block + (sowndiv + funcgr + grass + leg)^2	53.396	16	5.125	-66.423	17.852	0.00
Plant invader abundance	L22	sowndiv + funcgr + leg	39.721	6	13.667	-66.321	17.953	0.00
Plant invader abundance	L02	block + (sowndiv + funcgr + grass + leg)^2	53.251	16	5.125	-66.132	18.142	0.00
Plant invader abundance	M1521	d + a * sowndiv/(b + sowndiv)	45.930	11	7.455	-66.089	18.185	0.00
Plant invader abundance	Pe621	a + b * sowndiv^c	41.381	8	10.250	-64.790	19.485	0.00
Plant invader abundance	Pq2821	a + sowndiv^c	41.280	8	10.250	-64.587	19.687	0.00
Plant invader abundance	Pq2921	b * sowndiv^c	41.113	8	10.250	-64.254	20.021	0.00
Plant invader abundance	Pm1421	b * sowndiv^c	38.553	6	13.667	-63.987	20.288	0.00
Plant invader abundance	Pe921	b * sowndiv^c	38.531	6	13.667	-63.941	20.333	0.00
Plant invader abundance	Pc431	b * sowndiv^c	36.144	4	20.500	-63.768	20.507	0.00
Plant invader abundance	Pm1431	b * sowndiv^c	38.291	6	13.667	-63.462	20.812	0.00
Plant invader abundance	M1421	d + a * sowndiv/(b + sowndiv)	43.545	11	7.455	-61.319	22.955	0.00
Plant invader abundance	M611	a * sowndiv/(b + sowndiv)	39.484	8	10.250	-60.995	23.279	0.00
Plant invader abundance	Pg181	a + sowndiv^c	34.980	5	16.400	-59.171	25.103	0.00
Plant invader abundance	Pg191	b * sowndiv^c	34.617	5	16.400	-58.445	25.830	0.00
Plant invader abundance	M511	a * sowndiv/(b + sowndiv)	35.620	6	13.667	-58.121	26.154	0.00
Plant invader abundance	Ph221	a + b * sowndiv	36.486	7	11.714	-57.458	26.816	0.00
Plant invader abundance	L2	sowndiv + funcgr + leg	33.960	5	16.400	-57.130	27.144	0.00
Plant invader abundance	M522	a * sowndiv/(b + sowndiv)	34.949	6	13.667	-56.778	27.497	0.00
Plant invader abundance	Ph241	b * sowndiv^c	36.033	7	11.714	-56.553	27.722	0.00
Plant invader abundance	Ph231	a + sowndiv^c	35.822	7	11.714	-56.130	28.145	0.00
Plant invader abundance	M711	a * sowndiv/(b + sowndiv)	36.902	8	10.250	-55.832	28.443	0.00
Plant invader abundance	Pj331	a + sowndiv^c	35.634	7	11.714	-55.754	28.521	0.00
Plant invader abundance	M311	a * sowndiv/(b + sowndiv)	34.412	6	13.667	-55.703	28.571	0.00
Plant invader abundance	M411	a * sowndiv/(b + sowndiv)	34.382	6	13.667	-55.644	28.630	0.00
Plant invader abundance	Pj321	a + b * sowndiv	35.068	7	11.714	-54.623	29.652	0.00
Plant invader abundance	Pj341	b * sowndiv^c	35.063	7	11.714	-54.612	29.663	0.00
Plant invader abundance	Pf121	a + b * sowndiv	32.563	5	16.400	-54.337	29.938	0.00
Plant invader abundance	M722	a * sowndiv/(b + sowndiv)	36.121	8	10.250	-54.270	30.004	0.00
Plant invader abundance	M821	a * sowndiv/(b + sowndiv)	36.094	8	10.250	-54.216	30.059	0.00

Supplementary Table 2 (continued)

Long variable name	model name	model formula	LL	K	N2K	AICc	deltAICc	w_ic
Plant invader abundance	Pa3	a + sowndiv^c	30.134	3	27.333	-53.960	30.315	0.00
Plant invader abundance	Pb31	a + sowndiv^c	30.134	3	27.333	-53.960	30.315	0.00
Plant invader abundance	Pk391	b * sowndiv^c	37.000	9	9.111	-53.499	30.775	0.00
Plant invader abundance	M932	a * sowndiv/(b + sowndiv)	38.207	10	8.200	-53.315	30.959	0.00
Plant invader abundance	Pa4	b * sowndiv^c	29.788	3	27.333	-53.269	31.006	0.00
Plant invader abundance	Pb41	b * sowndiv^c	29.788	3	27.333	-53.269	31.006	0.00
Plant invader abundance	Pk371	a + b * sowndiv	36.720	9	9.111	-52.940	31.334	0.00
Plant invader abundance	Pf131	a + sowndiv^c	31.751	5	16.400	-52.712	31.563	0.00
Plant invader abundance	Pa1	a + b * sowndiv^c	30.270	4	20.500	-52.021	32.254	0.00
Plant invader abundance	Pb11	a + b * sowndiv^c	30.270	4	20.500	-52.021	32.254	0.00
Plant invader abundance	Pf141	b * sowndiv^c	31.388	5	16.400	-51.986	32.288	0.00
Plant invader abundance	Pk381	a + sowndiv^c	36.239	9	9.111	-51.977	32.297	0.00
Plant invader abundance	Pg171	a + b * sowndiv	31.246	5	16.400	-51.702	32.572	0.00
Plant invader abundance	M2	d + a * sowndiv/(b + sowndiv)	30.089	4	20.500	-51.658	32.616	0.00
Plant invader abundance	AS1	SSasymp(sowndiv, Asym, R0, lrc)	29.965	4	20.500	-51.410	32.864	0.00
Plant invader abundance	M3	a * sowndiv/(b + sowndiv)	30.972	5	16.400	-51.155	33.119	0.00
Plant invader abundance	Pa2	a + b * sowndiv	28.556	3	27.333	-50.805	33.470	0.00
Plant invader abundance	Pb21	a + b * sowndiv	28.556	3	27.333	-50.805	33.470	0.00
Plant invader abundance	M422	a * sowndiv/(b + sowndiv)	31.717	6	13.667	-50.315	33.960	0.00
Plant invader abundance	Pd71	a + b * sowndiv	30.410	5	16.400	-50.030	34.245	0.00
Plant invader abundance	Pi271	a + b * sowndiv	32.726	7	11.714	-49.939	34.335	0.00
Plant invader abundance	BIEXP	SSbiexp(sowndiv, A1, lrc1, A2, lrc2)	30.313	5	16.400	-49.837	34.437	0.00
Plant invader abundance	Pf111	a + b * sowndiv^c	32.652	7	11.714	-49.791	34.483	0.00
Plant invader abundance	M321	a * sowndiv/(b + sowndiv)	31.415	6	13.667	-49.710	34.565	0.00
Plant invader abundance	Pd81	a + sowndiv^c	30.161	5	16.400	-49.532	34.743	0.00
Plant invader abundance	M1	a * sowndiv/(b + sowndiv)	27.831	3	27.333	-49.354	34.920	0.00
Plant invader abundance	M1a	SSmicmen(sowndiv, Vm, k)	27.831	3	27.333	-49.354	34.920	0.00
Plant invader abundance	Pi291	b * sowndiv^c	32.283	7	11.714	-49.052	35.222	0.00
Plant invader abundance	Pi281	a + sowndiv^c	32.281	7	11.714	-49.048	35.226	0.00
Plant invader abundance	Pd91	b * sowndiv^c	29.914	5	16.400	-49.038	35.237	0.00
Plant invader abundance	M151	d + a * sowndiv/(b + sowndiv)	36.039	10	8.200	-48.980	35.295	0.00
Plant invader abundance	M81	a * sowndiv/(b + sowndiv)	32.234	7	11.714	-48.954	35.320	0.00
Plant invader abundance	M832	a * sowndiv/(b + sowndiv)	33.419	8	10.250	-48.866	35.409	0.00

Supplementary Table 2 (continued)

Long variable name	model name	model formula	LL	K	N2K	AICc	deltAICc	w_ic
Plant invader abundance	Pj311	a + b * sowndiv^c	35.961	10	8.200	-48.824	35.451	0.00
Plant invader abundance	M4	a * sowndiv/(b + sowndiv)	29.731	5	16.400	-48.672	35.602	0.00
Plant invader abundance	M91	a * sowndiv/(b + sowndiv)	34.291	9	9.111	-48.082	36.192	0.00
Plant invader abundance	M7	a * sowndiv/(b + sowndiv)	30.885	7	11.714	-46.256	38.019	0.00
Plant invader abundance	E2	a + b * exp(sowndiv)	26.173	3	27.333	-46.038	38.236	0.00
Plant invader abundance	Pd61	a + b * sowndiv^c	30.472	7	11.714	-45.431	38.844	0.00
Plant invader abundance	L0	block + (sowndiv + funcgr + grass + leg)^2	40.782	15	5.467	-44.291	39.983	0.00
Plant invader abundance	Pi261	a + b * sowndiv^c	32.917	10	8.200	-42.736	41.539	0.00
Plant invader abundance	Ea1221	exp(c * sowndiv)	24.206	4	20.500	-39.892	44.382	0.00
Plant invader abundance	Ef4221	exp(c * sowndiv)	25.198	5	16.400	-39.607	44.667	0.00
Plant invader abundance	Ed3021	exp(c * sowndiv)	25.091	5	16.400	-39.392	44.882	0.00
Plant invader abundance	Ec2421	exp(c * sowndiv)	21.536	4	20.500	-34.553	49.722	0.00
Plant invader abundance	Ea121	exp(c * sowndiv)	20.206	4	20.500	-31.893	52.382	0.00
Plant invader abundance	M921	a * sowndiv/(b + sowndiv)	27.032	10	8.200	-30.966	53.309	0.00
Plant invader abundance	Ef4211	exp(c * sowndiv)	20.862	5	16.400	-30.934	53.340	0.00
Plant invader abundance	M622	a * sowndiv/(b + sowndiv)	24.105	8	10.250	-30.237	54.037	0.00
Plant invader abundance	Ea12	exp(c * sowndiv)	16.695	3	27.333	-27.082	57.192	0.00
Plant invader abundance	E62	exp(c * sowndiv)	16.512	3	27.333	-26.716	57.558	0.00
Plant invader abundance	Eb1821	exp(c * sowndiv)	16.715	4	20.500	-24.910	59.364	0.00
Plant invader abundance	Ec2411	exp(c * sowndiv)	16.339	4	20.500	-24.158	60.116	0.00
Plant invader abundance	Ec24	exp(c * sowndiv)	13.667	3	27.333	-21.026	63.248	0.00
Plant invader abundance	E61	exp(c * sowndiv)	11.004	3	27.333	-15.700	68.574	0.00
Plant invader abundance	Eb1811	exp(c * sowndiv)	11.140	4	20.500	-13.760	70.515	0.00
Plant invader abundance	Pn2021	sowndiv^c	10.348	4	20.500	-12.176	72.099	0.00
Plant invader abundance	Pc521	sowndiv^c	8.497	3	27.333	-10.685	73.589	0.00
Plant invader abundance	Eb18	exp(c * sowndiv)	8.492	3	27.333	-10.676	73.599	0.00
Plant invader abundance	M6	a * sowndiv/(b + sowndiv)	13.077	7	11.714	-10.640	73.634	0.00
Plant invader abundance	Pp2521	sowndiv^c	10.517	5	16.400	-10.244	74.030	0.00
Plant invader abundance	Pr3521	sowndiv^c	10.352	5	16.400	-9.914	74.360	0.00
Plant invader abundance	Pe1021	sowndiv^c	8.958	4	20.500	-9.397	74.877	0.00
Plant invader abundance	Ps4021	sowndiv^c	10.956	6	13.667	-8.792	75.483	0.00
Plant invader abundance	Pm1521	sowndiv^c	8.558	4	20.500	-8.596	75.678	0.00
Plant invader abundance	Pq3021	sowndiv^c	8.990	5	16.400	-7.191	77.084	0.00

Supplementary Table 2 (continued)

Long variable name	model name	model formula	LL	K	N2K	AICc	deltAICc	w_ic
Plant invader abundance	E52	b * exp(sowndiv)	4.866	3	27.333	-3.424	80.850	0.00
Plant invader abundance	E51	b * exp(sowndiv)	-1.920	3	27.333	10.148	94.422	0.00
Plant invader abundance	Pn2031	sowndiv^c	-2.959	4	20.500	14.438	98.712	0.00
Plant invader abundance	Pc531	sowndiv^c	-4.439	3	27.333	15.186	99.460	0.00
Plant invader abundance	Pp2531	sowndiv^c	-2.463	5	16.400	15.715	99.990	0.00
Plant invader abundance	Pr3531	sowndiv^c	-2.779	5	16.400	16.347	100.621	0.00
Plant invader abundance	Pe1031	sowndiv^c	-4.182	4	20.500	16.884	101.158	0.00
Plant invader abundance	Pm1531	sowndiv^c	-4.434	4	20.500	17.387	101.661	0.00
Plant invader abundance	Ps4031	sowndiv^c	-2.209	6	13.667	17.539	101.813	0.00
Plant invader abundance	Pq3031	sowndiv^c	-3.964	5	16.400	18.718	102.992	0.00
Plant invader abundance	E5	b * exp(sowndiv)	-11.141	2	41.000	26.434	110.708	0.00
Plant invader abundance	Pg201	sowndiv^c	-31.336	3	27.333	68.980	153.255	0.00
Plant invader abundance	Pj351	sowndiv^c	-31.296	4	20.500	71.111	155.385	0.00
Plant invader abundance	Pb51	sowndiv^c	-33.511	2	41.000	71.173	155.448	0.00
Plant invader abundance	Pa5	sowndiv^c	-33.511	2	41.000	71.173	155.448	0.00
Plant invader abundance	Ph251	sowndiv^c	-31.336	4	20.500	71.192	155.466	0.00
Plant invader abundance	Pd101	sowndiv^c	-32.674	3	27.333	71.656	155.930	0.00
Plant invader abundance	Pk401	sowndiv^c	-31.175	5	16.400	73.140	157.414	0.00
Plant invader abundance	Pf151	sowndiv^c	-33.456	3	27.333	73.220	157.494	0.00
Plant invader abundance	Pi301	sowndiv^c	-32.365	4	20.500	73.249	157.523	0.00
Plant invader abundance	Ec2221	a + exp(sowndiv)	-794.702	4	20.500	1597.924	1682.199	0.00
Plant invader abundance	Ed2821	a + exp(sowndiv)	-794.689	5	16.400	1600.168	1684.442	0.00
Plant invader abundance	Ee342	a + exp(sowndiv)	-794.697	5	16.400	1600.183	1684.458	0.00
Plant invader abundance	Eg4621	a + exp(sowndiv)	-794.688	6	13.667	1602.496	1686.771	0.00
Plant invader abundance	E42	a + exp(sowndiv)	-801.511	3	27.333	1609.329	1693.603	0.00
Plant invader abundance	Eb1621	a + exp(sowndiv)	-801.342	4	20.500	1611.204	1695.479	0.00
Plant invader abundance	Ea1021	a + exp(sowndiv)	-801.450	4	20.500	1611.420	1695.694	0.00
Plant invader abundance	Ef4021	a + exp(sowndiv)	-801.165	5	16.400	1613.120	1697.394	0.00
Plant invader abundance	Ea1011	a + exp(sowndiv)	-1766.566	4	20.500	3541.651	3625.925	0.00
Plant invader abundance	E41	a + exp(sowndiv)	-1768.036	3	27.333	3542.379	3626.654	0.00
Plant invader abundance	Eb1611	a + exp(sowndiv)	-1767.522	4	20.500	3543.564	3627.838	0.00
Plant invader abundance	Ef4011	a + exp(sowndiv)	-1766.448	5	16.400	3543.685	3627.959	0.00
Plant invader abundance	Ed2811	a + exp(sowndiv)	-1766.566	5	16.400	3543.921	3628.195	0.00

Supplementary Table 2 (continued)

Long variable name	model name	model formula	LL	K	N2K	AICc	deltAICc	w_ic
Plant invader abundance	Ec2211	a + exp(sowndiv)	-1768.036	4	20.500	3544.591	3628.865	0.00
Plant invader abundance	Ee341	a + exp(sowndiv)	-1767.522	5	16.400	3545.834	3630.108	0.00
Plant invader abundance	Eg4611	a + exp(sowndiv)	-1766.448	6	13.667	3546.015	3630.290	0.00
Plant invader abundance	Ef3721	a + b * exp(c * sowndiv)	-2739.352	11	7.455	5504.476	5588.751	0.00
Plant invader abundance	E4	a + exp(sowndiv)	-4912.516	2	41.000	9829.183	9913.457	0.00
Plant invader abundance	Ea10	a + exp(sowndiv)	-4912.516	3	27.333	9831.339	9915.613	0.00
Plant invader abundance	Eb16	a + exp(sowndiv)	-4912.516	3	27.333	9831.339	9915.613	0.00
Plant invader abundance	Ec22	a + exp(sowndiv)	-4912.516	3	27.333	9831.339	9915.613	0.00
Plant invader abundance	Ed28	a + exp(sowndiv)	-4912.516	4	20.500	9833.551	9917.825	0.00
Plant invader abundance	Ee40	a + exp(sowndiv)	-4912.516	4	20.500	9833.551	9917.825	0.00
Plant invader abundance	Ef40	a + exp(sowndiv)	-4912.516	4	20.500	9833.551	9917.825	0.00
Plant invader abundance	Eg46	a + exp(sowndiv)	-4912.516	5	16.400	9835.821	9920.095	0.00
Mycorrhiza diversity	L2	sowndiv + funcgr + leg	22.380	5	15.400	-33.915	0.000	0.16
Mycorrhiza diversity	Pa2	a + b * sowndiv	20.038	3	25.667	-33.747	0.168	0.15
Mycorrhiza diversity	LG2	SSlogis(sowndiv, Asym, xmid, scal)	20.753	4	19.250	-32.951	0.965	0.10
Mycorrhiza diversity	Pa4	b * sowndiv^c	19.561	3	25.667	-32.793	1.122	0.09
Mycorrhiza diversity	AS2	SSasympOff(sowndiv, Asym, lrc, c0)	20.644	4	19.250	-32.733	1.182	0.09
Mycorrhiza diversity	AS1	SSasympt(sowndiv, Asym, R0, lrc)	20.644	4	19.250	-32.733	1.182	0.09
Mycorrhiza diversity	Pa3	a + sowndiv^c	19.470	3	25.667	-32.611	1.305	0.08
Mycorrhiza diversity	M2	d + a * sowndiv/(b + sowndiv)	20.555	4	19.250	-32.554	1.362	0.08
Mycorrhiza diversity	Pa1	a + b * sowndiv^c	20.262	4	19.250	-31.968	1.947	0.06
Mycorrhiza diversity	E2	a + b * exp(sowndiv)	18.554	3	25.667	-30.779	3.136	0.03
Mycorrhiza diversity	M1	a * sowndiv/(b + sowndiv)	18.030	3	25.667	-29.731	4.184	0.02
Mycorrhiza diversity	M1a	SSmicmen(sowndiv, Vm, k)	18.030	3	25.667	-29.731	4.184	0.02
Mycorrhiza diversity	AS3	SSasympOrig(sowndiv, Asym, lrc)	17.712	3	25.667	-29.095	4.821	0.01
Mycorrhiza diversity	L0	block + (sowndiv + funcgr + grass + leg)^2	31.426	15	5.133	-24.983	8.932	0.00
Mycorrhiza diversity	Pa5	sowndiv^c	-29.466	2	38.500	63.094	97.009	0.00
Mycorrhiza diversity	E5	b * exp(sowndiv)	-57.516	2	38.500	119.193	153.109	0.00
Mycorrhiza diversity	E4	a + exp(sowndiv)	-4604.318	2	38.500	9212.799	9246.714	0.00
Aboveground herbivore diversity	L0	block + (sowndiv + funcgr + grass + leg)^2	52.874	15	3.333	-61.630	0.000	0.73
Aboveground herbivore diversity	L2	sowndiv + funcgr + leg	35.489	5	10.000	-59.614	2.016	0.27
Aboveground herbivore diversity	Pa4	b * sowndiv^c	24.661	3	16.667	-42.801	18.829	0.00
Aboveground herbivore diversity	Pa1	a + b * sowndiv^c	24.816	4	12.500	-40.743	20.886	0.00

Supplementary Table 2 (continued)

Long variable name	model name	model formula	LL	K	N2K	AICc	deltaAICc	w_ic
Aboveground herbivore diversity	M2	d + a * sowndiv/(b + sowndiv)	24.509	4	12.500	-40.129	21.500	0.00
Aboveground herbivore diversity	AS1	SSasymp(sowndiv, Asym, R0, lrc)	24.437	4	12.500	-39.985	21.644	0.00
Aboveground herbivore diversity	AS2	SSasympOff(sowndiv, Asym, lrc, c0)	24.437	4	12.500	-39.985	21.644	0.00
Aboveground herbivore diversity	LG2	SSlogis(sowndiv, Asym, xmid, scal)	23.986	4	12.500	-39.084	22.546	0.00
Aboveground herbivore diversity	Pa3	a + sowndiv^c	22.637	3	16.667	-38.753	22.877	0.00
Aboveground herbivore diversity	Pa2	a + b * sowndiv	21.592	3	16.667	-36.662	24.967	0.00
Aboveground herbivore diversity	M1a	SSmicmen(sowndiv, Vm, k)	19.284	3	16.667	-32.047	29.583	0.00
Aboveground herbivore diversity	M1	a * sowndiv/(b + sowndiv)	19.284	3	16.667	-32.047	29.583	0.00
Aboveground herbivore diversity	AS3	SSasympOrig(sowndiv, Asym, lrc)	15.873	3	16.667	-25.225	36.405	0.00
Aboveground herbivore diversity	E2	a + b * exp(sowndiv)	12.252	3	16.667	-17.982	43.647	0.00
Aboveground herbivore diversity	E5	b * exp(sowndiv)	-19.712	2	25.000	43.678	105.308	0.00
Aboveground herbivore diversity	Pa5	sowndiv^c	-41.029	2	25.000	86.313	147.942	0.00
Aboveground herbivore diversity	E4	a + exp(sowndiv)	-3007.804	2	25.000	6019.863	6081.492	0.00
Aboveground carnivore diversity	Pa3	a + sowndiv^c	10.999	3	16.667	-15.476	0.000	0.30
Aboveground carnivore diversity	Pa4	b * sowndiv^c	10.926	3	16.667	-15.330	0.146	0.28
Aboveground carnivore diversity	Pa1	a + b * sowndiv^c	10.999	4	12.500	-13.109	2.367	0.09
Aboveground carnivore diversity	M2	d + a * sowndiv/(b + sowndiv)	10.665	4	12.500	-12.441	3.035	0.07
Aboveground carnivore diversity	L2	sowndiv + funcgr + leg	11.623	5	10.000	-11.883	3.593	0.05
Aboveground carnivore diversity	AS1	SSasymp(sowndiv, Asym, R0, lrc)	10.328	4	12.500	-11.768	3.708	0.05
Aboveground carnivore diversity	AS2	SSasympOff(sowndiv, Asym, lrc, c0)	10.328	4	12.500	-11.768	3.708	0.05
Aboveground carnivore diversity	M1a	SSmicmen(sowndiv, Vm, k)	9.010	3	16.667	-11.498	3.978	0.04
Aboveground carnivore diversity	M1	a * sowndiv/(b + sowndiv)	9.010	3	16.667	-11.498	3.978	0.04
Aboveground carnivore diversity	LG2	SSlogis(sowndiv, Asym, xmid, scal)	9.969	4	12.500	-11.050	4.426	0.03
Aboveground carnivore diversity	Pa2	a + b * sowndiv	7.027	3	16.667	-7.533	7.943	0.01
Aboveground carnivore diversity	AS3	SSasympOrig(sowndiv, Asym, lrc)	6.274	3	16.667	-6.027	9.449	0.00
Aboveground carnivore diversity	L0	block + (sowndiv + funcgr + grass + leg)^2	23.529	15	3.333	-2.941	12.535	0.00
Aboveground carnivore diversity	E2	a + b * exp(sowndiv)	2.305	3	16.667	1.911	17.387	0.00
Aboveground carnivore diversity	Pa5	sowndiv^c	-29.955	2	25.000	64.165	79.641	0.00
Aboveground carnivore diversity	E5	b * exp(sowndiv)	-42.534	2	25.000	89.324	104.800	0.00
Aboveground carnivore diversity	E4	a + exp(sowndiv)	-3007.804	2	25.000	6019.863	6035.339	0.00
Aboveground omnivore diversity	L2	sowndiv + funcgr + leg	13.132	5	10.000	-14.901	0.000	0.77
Aboveground omnivore diversity	L0	block + (sowndiv + funcgr + grass + leg)^2	27.336	15	3.333	-10.555	4.346	0.09
Aboveground omnivore diversity	Pa4	b * sowndiv^c	7.052	3	16.667	-7.582	7.318	0.02

Supplementary Table 2 (continued)

Long variable name	model name	model formula	LL	K	N2K	AICc	deltAICc	w_ic
Aboveground omnivore diversity	Pa3	a + sowndiv^c	7.031	3	16.667	-7.540	7.361	0.02
Aboveground omnivore diversity	Pa2	a + b * sowndiv	6.959	3	16.667	-7.397	7.504	0.02
Aboveground omnivore diversity	M1	a * sowndiv/(b + sowndiv)	6.461	3	16.667	-6.401	8.500	0.01
Aboveground omnivore diversity	M1a	SSmicmen(sowndiv, Vm, k)	6.461	3	16.667	-6.401	8.500	0.01
Aboveground omnivore diversity	E2	a + b * exp(sowndiv)	6.437	3	16.667	-6.352	8.548	0.01
Aboveground omnivore diversity	AS3	SSasympOrig(sowndiv, Asym, lrc)	6.222	3	16.667	-5.923	8.978	0.01
Aboveground omnivore diversity	LG2	SSlogis(sowndiv, Asym, xmid, scal)	7.393	4	12.500	-5.897	9.004	0.01
Aboveground omnivore diversity	AS2	SSasympOff(sowndiv, Asym, lrc, c0)	7.361	4	12.500	-5.833	9.067	0.01
Aboveground omnivore diversity	AS1	SSasymp(sowndiv, Asym, R0, lrc)	7.361	4	12.500	-5.833	9.067	0.01
Aboveground omnivore diversity	M2	d + a * sowndiv/(b + sowndiv)	7.300	4	12.500	-5.711	9.189	0.01
Aboveground omnivore diversity	Pa1	a + b * sowndiv^c	7.158	4	12.500	-5.427	9.474	0.01
Aboveground omnivore diversity	Pa5	sowndiv^c	-26.421	2	25.000	57.098	71.999	0.00
Aboveground omnivore diversity	E5	b * exp(sowndiv)	-35.181	2	25.000	74.616	89.517	0.00
Aboveground omnivore diversity	E4	a + exp(sowndiv)	-3007.804	2	25.000	6019.863	6034.763	0.00
Aboveground parasitoid diversity	L2	sowndiv + funcgr + leg	23.314	5	10.000	-35.263	0.000	0.89
Aboveground parasitoid diversity	Pa2	a + b * sowndiv	17.439	3	16.667	-28.356	6.907	0.03
Aboveground parasitoid diversity	Pa1	a + b * sowndiv^c	17.859	4	12.500	-26.829	8.435	0.01
Aboveground parasitoid diversity	M2	d + a * sowndiv/(b + sowndiv)	17.739	4	12.500	-26.590	8.674	0.01
Aboveground parasitoid diversity	AS1	SSasymp(sowndiv, Asym, R0, lrc)	17.732	4	12.500	-26.574	8.689	0.01
Aboveground parasitoid diversity	AS2	SSasympOff(sowndiv, Asym, lrc, c0)	17.732	4	12.500	-26.574	8.689	0.01
Aboveground parasitoid diversity	Pa4	b * sowndiv^c	16.517	3	16.667	-26.512	8.751	0.01
Aboveground parasitoid diversity	LG2	SSlogis(sowndiv, Asym, xmid, scal)	17.675	4	12.500	-26.461	8.802	0.01
Aboveground parasitoid diversity	Pa3	a + sowndiv^c	15.857	3	16.667	-25.192	10.071	0.01
Aboveground parasitoid diversity	E2	a + b * exp(sowndiv)	13.889	3	16.667	-21.256	14.008	0.00
Aboveground parasitoid diversity	L0	block + (sowndiv + funcgr + grass + leg)^2	31.429	15	3.333	-18.740	16.523	0.00
Aboveground parasitoid diversity	M1a	SSmicmen(sowndiv, Vm, k)	11.677	3	16.667	-16.832	18.431	0.00
Aboveground parasitoid diversity	M1	a * sowndiv/(b + sowndiv)	11.677	3	16.667	-16.832	18.431	0.00
Aboveground parasitoid diversity	AS3	SSasympOrig(sowndiv, Asym, lrc)	9.146	3	16.667	-11.770	23.493	0.00
Aboveground parasitoid diversity	Pa5	sowndiv^c	-30.274	2	25.000	64.804	100.068	0.00
Aboveground parasitoid diversity	E5	b * exp(sowndiv)	-34.364	2	25.000	72.983	108.247	0.00
Aboveground parasitoid diversity	E4	a + exp(sowndiv)	-3007.804	2	25.000	6019.863	6055.126	0.00
Pollinator diversity	L2	sowndiv + funcgr + leg	11.991	5	10.000	-12.617	0.000	0.37
Pollinator diversity	L0	block + (sowndiv + funcgr + grass + leg)^2	27.788	15	3.333	-11.458	1.159	0.20

Supplementary Table 2 (continued)

Long variable name	model name	model formula	LL	K	N2K	AICc	deltAICc	w_ic
Pollinator diversity	Pa3	a + sowndiv^c	8.073	3	16.667	-9.625	2.992	0.08
Pollinator diversity	M1a	SSmicmen(sowndiv, Vm, k)	7.859	3	16.667	-9.197	3.421	0.07
Pollinator diversity	M1	a * sowndiv/(b + sowndiv)	7.859	3	16.667	-9.197	3.421	0.07
Pollinator diversity	Pa4	b * sowndiv^c	7.690	3	16.667	-8.859	3.758	0.06
Pollinator diversity	M2	d + a * sowndiv/(b + sowndiv)	8.443	4	12.500	-7.997	4.621	0.04
Pollinator diversity	AS1	SSasymp(sowndiv, Asym, R0, lrc)	8.440	4	12.500	-7.992	4.626	0.04
Pollinator diversity	AS2	SSasympOff(sowndiv, Asym, lrc, c0)	8.440	4	12.500	-7.992	4.626	0.04
Pollinator diversity	LG2	SSlogis(sowndiv, Asym, xmid, scal)	8.344	4	12.500	-7.798	4.819	0.03
Pollinator diversity	AS3	SSasympOrig(sowndiv, Asym, lrc)	6.485	3	16.667	-6.449	6.168	0.02
Pollinator diversity	Pa2	a + b * sowndiv	3.711	3	16.667	-0.900	11.718	0.00
Pollinator diversity	E2	a + b * exp(sowndiv)	0.265	3	16.667	5.992	18.609	0.00
Pollinator diversity	E5	b * exp(sowndiv)	-33.144	2	25.000	70.544	83.161	0.00
Pollinator diversity	Pa5	sowndiv^c	-36.253	2	25.000	76.761	89.378	0.00
Pollinator diversity	E4	a + exp(sowndiv)	-3007.804	2	25.000	6019.863	6032.480	0.00
Plant invader diversity	Eb1511	a + exp(c * sowndiv)	42.190	6	13.667	-71.260	0.000	0.19
Plant invader diversity	Pm1321	a + sowndiv^c	42.108	6	13.667	-71.096	0.164	0.18
Plant invader diversity	Pm1221	a + b * sowndiv	41.797	6	13.667	-70.475	0.785	0.13
Plant invader diversity	Pr3321	a + sowndiv^c	44.003	8	10.250	-70.033	1.226	0.11
Plant invader diversity	Ef3911	a + exp(c * sowndiv)	43.404	8	10.250	-68.836	2.424	0.06
Plant invader diversity	Pr3221	a + b * sowndiv	43.172	8	10.250	-68.371	2.888	0.05
Plant invader diversity	Pq2821	a + sowndiv^c	42.912	8	10.250	-67.852	3.407	0.04
Plant invader diversity	Pq2721	a + b * sowndiv	42.862	8	10.250	-67.752	3.508	0.03
Plant invader diversity	Pq2921	b * sowndiv^c	42.607	8	10.250	-67.241	4.019	0.03
Plant invader diversity	Pm1421	b * sowndiv^c	40.154	6	13.667	-67.188	4.072	0.03
Plant invader diversity	Ps3921	b * sowndiv^c	44.981	10	8.200	-66.864	4.396	0.02
Plant invader diversity	Ps3621	a + b * sowndiv^c	50.295	14	5.857	-66.322	4.938	0.02
Plant invader diversity	Eb1521	a + exp(c * sowndiv)	39.694	6	13.667	-66.268	4.992	0.02
Plant invader diversity	Pr3421	b * sowndiv^c	42.008	8	10.250	-66.043	5.216	0.01
Plant invader diversity	M1521	d + a * sowndiv/(b + sowndiv)	45.848	11	7.455	-65.925	5.335	0.01
Plant invader diversity	Pm1331	a + sowndiv^c	39.374	6	13.667	-65.628	5.632	0.01
Plant invader diversity	Pm1231	a + b * sowndiv	39.356	6	13.667	-65.592	5.668	0.01
Plant invader diversity	Ps3721	a + b * sowndiv	43.727	10	8.200	-64.355	6.905	0.01
Plant invader diversity	LO21	block + (sowndiv + funcgr + grass + leg)^2	52.320	16	5.125	-64.270	6.989	0.01

Supplementary Table 2 (continued)

Long variable name	model name	model formula	LL	K	N2K	AICc	deltAICc	w_ic
Plant invader diversity	Pp2121	a + b * sowndiv^c	45.014	11	7.455	-64.257	7.002	0.01
Plant invader diversity	Pm1131	a + b * sowndiv^c	41.113	8	10.250	-64.254	7.005	0.01
Plant invader diversity	M1132	d + a * sowndiv/(b + sowndiv)	41.025	8	10.250	-64.077	7.182	0.01
Plant invader diversity	Pr3331	a + sowndiv^c	40.833	8	10.250	-63.693	7.567	0.00
Plant invader diversity	Pp2421	b * sowndiv^c	40.805	8	10.250	-63.638	7.622	0.00
Plant invader diversity	Ef3921	a + exp(c * sowndiv)	40.653	8	10.250	-63.334	7.926	0.00
Plant invader diversity	Pr3231	a + b * sowndiv	40.436	8	10.250	-62.900	8.360	0.00
Plant invader diversity	Pq2731	a + b * sowndiv	40.410	8	10.250	-62.848	8.412	0.00
Plant invader diversity	Pq2831	a + sowndiv^c	40.274	8	10.250	-62.576	8.683	0.00
Plant invader diversity	Pq2931	b * sowndiv^c	40.026	8	10.250	-62.080	9.180	0.00
Plant invader diversity	Ps3821	a + sowndiv^c	42.527	10	8.200	-61.955	9.304	0.00
Plant invader diversity	Ps3931	b * sowndiv^c	41.813	10	8.200	-60.528	10.732	0.00
Plant invader diversity	Pp2321	a + sowndiv^c	39.062	8	10.250	-60.152	11.107	0.00
Plant invader diversity	Pm1431	b * sowndiv^c	36.628	6	13.667	-60.137	11.123	0.00
Plant invader diversity	Pp2221	a + b * sowndiv	38.794	8	10.250	-59.615	11.645	0.00
Plant invader diversity	M1532	d + a * sowndiv/(b + sowndiv)	42.512	11	7.455	-59.252	12.007	0.00
Plant invader diversity	Ps3731	a + b * sowndiv	41.047	10	8.200	-58.995	12.265	0.00
Plant invader diversity	Ps3831	a + sowndiv^c	41.027	10	8.200	-58.955	12.304	0.00
Plant invader diversity	Pr3431	b * sowndiv^c	38.217	8	10.250	-58.461	12.799	0.00
Plant invader diversity	L02	block + (sowndiv + funcgr + grass + leg)^2	49.350	16	5.125	-58.330	12.930	0.00
Plant invader diversity	Pn1821	a + sowndiv^c	35.507	6	13.667	-57.893	13.366	0.00
Plant invader diversity	M1432	d + a * sowndiv/(b + sowndiv)	41.584	11	7.455	-57.397	13.863	0.00
Plant invader diversity	Pp2431	b * sowndiv^c	37.352	8	10.250	-56.731	14.528	0.00
Plant invader diversity	Pc321	a + sowndiv^c	32.510	4	20.500	-56.500	14.759	0.00
Plant invader diversity	M1321	d + a * sowndiv/(b + sowndiv)	39.997	11	7.455	-54.222	17.037	0.00
Plant invader diversity	M711	a * sowndiv/(b + sowndiv)	36.073	8	10.250	-54.174	17.086	0.00
Plant invader diversity	L011	block + (sowndiv + funcgr + grass + leg)^2	47.231	16	5.125	-54.092	17.168	0.00
Plant invader diversity	M211	d + a * sowndiv/(b + sowndiv)	32.394	5	16.400	-53.998	17.261	0.00
Plant invader diversity	Pn1831	a + sowndiv^c	33.497	6	13.667	-53.875	17.385	0.00
Plant invader diversity	Pn1921	b * sowndiv^c	33.483	6	13.667	-53.845	17.414	0.00
Plant invader diversity	Pp2231	a + b * sowndiv	35.895	8	10.250	-53.817	17.443	0.00
Plant invader diversity	Pp2331	a + sowndiv^c	35.757	8	10.250	-53.541	17.719	0.00
Plant invader diversity	Pe821	a + sowndiv^c	33.070	6	13.667	-53.020	18.240	0.00

Supplementary Table 2 (continued)

Long variable name	model name	model formula	LL	K	N2K	AICc	deltAICc	w_ic
Plant invader diversity	Pc331	a + sowndiv^c	30.552	4	20.500	-52.585	18.675	0.00
Plant invader diversity	Pf131	a + sowndiv^c	31.353	5	16.400	-51.916	19.344	0.00
Plant invader diversity	Pe721	a + b * sowndiv	32.441	6	13.667	-51.762	19.498	0.00
Plant invader diversity	Pc421	b * sowndiv^c	30.120	4	20.500	-51.720	19.540	0.00
Plant invader diversity	Pf121	a + b * sowndiv	31.167	5	16.400	-51.544	19.716	0.00
Plant invader diversity	Pe921	b * sowndiv^c	32.278	6	13.667	-51.435	19.825	0.00
Plant invader diversity	M222	d + a * sowndiv/(b + sowndiv)	30.841	5	16.400	-50.893	20.367	0.00
Plant invader diversity	M1332	d + a * sowndiv/(b + sowndiv)	38.254	11	7.455	-50.737	20.523	0.00
Plant invader diversity	Pf141	b * sowndiv^c	30.666	5	16.400	-50.543	20.716	0.00
Plant invader diversity	L22	sowndiv + funcgr + leg	31.622	6	13.667	-50.124	21.136	0.00
Plant invader diversity	M921	a * sowndiv/(b + sowndiv)	36.556	10	8.200	-50.013	21.246	0.00
Plant invader diversity	M111	d + a * sowndiv/(b + sowndiv)	32.758	7	11.714	-50.002	21.257	0.00
Plant invader diversity	Pf111	a + b * sowndiv^c	32.754	7	11.714	-49.994	21.266	0.00
Plant invader diversity	Pj331	a + sowndiv^c	32.596	7	11.714	-49.677	21.582	0.00
Plant invader diversity	Pi291	b * sowndiv^c	32.433	7	11.714	-49.352	21.907	0.00
Plant invader diversity	Pe621	a + b * sowndiv^c	33.502	8	10.250	-49.031	22.228	0.00
Plant invader diversity	M1221	d + a * sowndiv/(b + sowndiv)	33.386	8	10.250	-48.800	22.460	0.00
Plant invader diversity	Pj321	a + b * sowndiv	32.135	7	11.714	-48.757	22.503	0.00
Plant invader diversity	Pi281	a + sowndiv^c	32.133	7	11.714	-48.753	22.507	0.00
Plant invader diversity	Ec2121	a + exp(c * sowndiv)	30.935	6	13.667	-48.750	22.510	0.00
Plant invader diversity	Pi271	a + b * sowndiv	32.085	7	11.714	-48.656	22.604	0.00
Plant invader diversity	Pj341	b * sowndiv^c	31.937	7	11.714	-48.361	22.899	0.00
Plant invader diversity	Pe731	a + b * sowndiv	30.724	6	13.667	-48.328	22.932	0.00
Plant invader diversity	M722	a * sowndiv/(b + sowndiv)	33.108	8	10.250	-48.244	23.015	0.00
Plant invader diversity	L21	sowndiv + funcgr + leg	30.445	6	13.667	-47.770	23.490	0.00
Plant invader diversity	Pe931	b * sowndiv^c	30.401	6	13.667	-47.683	23.577	0.00
Plant invader diversity	M611	a * sowndiv/(b + sowndiv)	32.773	8	10.250	-47.574	23.686	0.00
Plant invader diversity	Pk391	b * sowndiv^c	33.934	9	9.111	-47.369	23.891	0.00
Plant invader diversity	Pe831	a + sowndiv^c	30.055	6	13.667	-46.990	24.270	0.00
Plant invader diversity	L211	sowndiv + funcgr + leg	29.753	6	13.667	-46.387	24.873	0.00
Plant invader diversity	Pn1931	b * sowndiv^c	29.519	6	13.667	-45.918	25.342	0.00
Plant invader diversity	Pk381	a + sowndiv^c	32.851	9	9.111	-45.201	26.058	0.00
Plant invader diversity	Pe631	a + b * sowndiv^c	31.490	8	10.250	-45.008	26.252	0.00

Supplementary Table 2 (continued)

Long variable name	model name	model formula	LL	K	N2K	AICc	deltAICc	w_ic
Plant invader diversity	M1232	d + a * sowndiv/(b + sowndiv)	31.487	8	10.250	-45.001	26.258	0.00
Plant invader diversity	Pk371	a + b * sowndiv	32.696	9	9.111	-44.891	26.368	0.00
Plant invader diversity	M151	d + a * sowndiv/(b + sowndiv)	33.979	10	8.200	-44.860	26.400	0.00
Plant invader diversity	Pc431	b * sowndiv^c	26.004	4	20.500	-43.489	27.770	0.00
Plant invader diversity	M141	d + a * sowndiv/(b + sowndiv)	33.087	10	8.200	-43.076	28.184	0.00
Plant invader diversity	M7	a * sowndiv/(b + sowndiv)	29.219	7	11.714	-42.925	28.334	0.00
Plant invader diversity	L222	sowndiv + funcgr + leg	27.856	6	13.667	-42.592	28.668	0.00
Plant invader diversity	M821	a * sowndiv/(b + sowndiv)	30.058	8	10.250	-42.143	29.117	0.00
Plant invader diversity	Ph241	b * sowndiv^c	28.541	7	11.714	-41.569	29.691	0.00
Plant invader diversity	M511	a * sowndiv/(b + sowndiv)	27.249	6	13.667	-41.379	29.881	0.00
Plant invader diversity	M622	a * sowndiv/(b + sowndiv)	29.625	8	10.250	-41.277	29.983	0.00
Plant invader diversity	M4	a * sowndiv/(b + sowndiv)	25.145	5	16.400	-39.500	31.760	0.00
Plant invader diversity	M422	a * sowndiv/(b + sowndiv)	26.254	6	13.667	-39.388	31.872	0.00
Plant invader diversity	Pn1721	a + b * sowndiv	26.045	6	13.667	-38.971	32.289	0.00
Plant invader diversity	Ph231	a + sowndiv^c	27.199	7	11.714	-38.884	32.376	0.00
Plant invader diversity	M91	a * sowndiv/(b + sowndiv)	29.600	9	9.111	-38.701	32.559	0.00
Plant invader diversity	Ph221	a + b * sowndiv	26.755	7	11.714	-37.996	33.264	0.00
Plant invader diversity	Pg181	a + sowndiv^c	24.388	5	16.400	-37.987	33.273	0.00
Plant invader diversity	E31	a + exp(c * sowndiv)	23.217	4	20.500	-37.915	33.345	0.00
Plant invader diversity	M161	d + a * sowndiv/(b + sowndiv)	34.505	13	6.308	-37.658	33.602	0.00
Plant invader diversity	Ea921	a + exp(c * sowndiv)	25.080	6	13.667	-37.041	34.219	0.00
Plant invader diversity	M522	a * sowndiv/(b + sowndiv)	24.795	6	13.667	-36.470	34.789	0.00
Plant invader diversity	Pg191	b * sowndiv^c	23.547	5	16.400	-36.304	34.955	0.00
Plant invader diversity	Pa3	a + sowndiv^c	21.156	3	27.333	-36.004	35.255	0.00
Plant invader diversity	Pb31	a + sowndiv^c	21.156	3	27.333	-36.004	35.255	0.00
Plant invader diversity	Pc221	a + b * sowndiv	22.216	4	20.500	-35.913	35.347	0.00
Plant invader diversity	M81	a * sowndiv/(b + sowndiv)	25.500	7	11.714	-35.487	35.772	0.00
Plant invader diversity	M832	a * sowndiv/(b + sowndiv)	26.651	8	10.250	-35.329	35.931	0.00
Plant invader diversity	Pn1731	a + b * sowndiv	24.020	6	13.667	-34.920	36.340	0.00
Plant invader diversity	M2	d + a * sowndiv/(b + sowndiv)	21.557	4	20.500	-34.594	36.666	0.00
Plant invader diversity	L0	block + (sowndiv + funcgr + grass + leg)^2	35.931	15	5.467	-34.589	36.671	0.00
Plant invader diversity	Pa4	b * sowndiv^c	20.304	3	27.333	-34.300	36.960	0.00
Plant invader diversity	Pb41	b * sowndiv^c	20.304	3	27.333	-34.300	36.960	0.00

Supplementary Table 2 (continued)

Long variable name	model name	model formula	LL	K	N2K	AICc	deltAICc	w_ic
Plant invader diversity	M131	d + a * sowndiv/(b + sowndiv)	28.679	10	8.200	-34.260	36.999	0.00
Plant invader diversity	M6	a * sowndiv/(b + sowndiv)	24.859	7	11.714	-34.205	37.054	0.00
Plant invader diversity	E32	a + exp(c * sowndiv)	21.201	4	20.500	-33.882	37.378	0.00
Plant invader diversity	AS1	SSasymp(sowndiv, Asym, R0, lrc)	21.171	4	20.500	-33.823	37.437	0.00
Plant invader diversity	Pr3521	sowndiv^c	22.137	5	16.400	-33.484	37.776	0.00
Plant invader diversity	Pd81	a + sowndiv^c	21.684	5	16.400	-32.579	38.681	0.00
Plant invader diversity	BIEXP	SSbiexp(sowndiv, A1, lrc1, A2, lrc2)	21.683	5	16.400	-32.577	38.682	0.00
Plant invader diversity	Pp2521	sowndiv^c	21.663	5	16.400	-32.536	38.724	0.00
Plant invader diversity	Pd91	b * sowndiv^c	21.630	5	16.400	-32.471	38.788	0.00
Plant invader diversity	Pm1521	sowndiv^c	20.270	4	20.500	-32.020	39.239	0.00
Plant invader diversity	Ps4021	sowndiv^c	22.558	6	13.667	-31.995	39.264	0.00
Plant invader diversity	Pd71	a + b * sowndiv	21.336	5	16.400	-31.883	39.377	0.00
Plant invader diversity	L2	sowndiv + funcgr + leg	21.275	5	16.400	-31.760	39.499	0.00
Plant invader diversity	Pc231	a + b * sowndiv	20.107	4	20.500	-31.694	39.565	0.00
Plant invader diversity	Pq3021	sowndiv^c	20.801	5	16.400	-30.813	40.447	0.00
Plant invader diversity	M121	d + a * sowndiv/(b + sowndiv)	22.143	7	11.714	-28.772	42.487	0.00
Plant invader diversity	Pd61	a + b * sowndiv^c	22.040	7	11.714	-28.567	42.692	0.00
Plant invader diversity	Pn2021	sowndiv^c	17.174	4	20.500	-25.829	45.431	0.00
Plant invader diversity	Pc521	sowndiv^c	15.825	3	27.333	-25.342	45.918	0.00
Plant invader diversity	Ef4211	exp(c * sowndiv)	17.786	5	16.400	-24.783	46.477	0.00
Plant invader diversity	E21	a + b * exp(sowndiv)	16.353	4	20.500	-24.187	47.073	0.00
Plant invader diversity	Pe1021	sowndiv^c	16.103	4	20.500	-23.687	47.572	0.00
Plant invader diversity	Ef4221	exp(c * sowndiv)	16.998	5	16.400	-23.207	48.053	0.00
Plant invader diversity	M311	a * sowndiv/(b + sowndiv)	17.325	6	13.667	-21.531	49.729	0.00
Plant invader diversity	Ea1221	exp(c * sowndiv)	15.011	4	20.500	-21.502	49.758	0.00
Plant invader diversity	Pg171	a + b * sowndiv	15.865	5	16.400	-20.941	50.318	0.00
Plant invader diversity	Ea121	exp(c * sowndiv)	14.628	4	20.500	-20.736	50.523	0.00
Plant invader diversity	M1a	SSmicmen(sowndiv, Vm, k)	13.122	3	27.333	-19.936	51.324	0.00
Plant invader diversity	M1	a * sowndiv/(b + sowndiv)	13.122	3	27.333	-19.936	51.324	0.00
Plant invader diversity	Ed3021	exp(c * sowndiv)	15.314	5	16.400	-19.839	51.421	0.00
Plant invader diversity	E22	a + b * exp(sowndiv)	13.986	4	20.500	-19.453	51.806	0.00
Plant invader diversity	Pa2	a + b * sowndiv	12.881	3	27.333	-19.453	51.806	0.00
Plant invader diversity	Pb21	a + b * sowndiv	12.881	3	27.333	-19.453	51.806	0.00

Supplementary Table 2 (continued)

Long variable name	model name	model formula	LL	K	N2K	AICc	deltAICc	w_ic
Plant invader diversity	M3	a * sowndiv/(b + sowndiv)	14.237	5	16.400	-17.685	53.575	0.00
Plant invader diversity	Eb1811	exp(c * sowndiv)	12.401	4	20.500	-16.283	54.976	0.00
Plant invader diversity	M321	a * sowndiv/(b + sowndiv)	14.335	6	13.667	-15.549	55.711	0.00
Plant invader diversity	Ea12	exp(c * sowndiv)	9.941	3	27.333	-13.573	57.686	0.00
Plant invader diversity	Eb1821	exp(c * sowndiv)	10.935	4	20.500	-13.351	57.909	0.00
Plant invader diversity	Ec2421	exp(c * sowndiv)	9.886	4	20.500	-11.252	60.008	0.00
Plant invader diversity	E61	exp(c * sowndiv)	8.675	3	27.333	-11.042	60.218	0.00
Plant invader diversity	Ec2411	exp(c * sowndiv)	9.415	4	20.500	-10.311	60.949	0.00
Plant invader diversity	E62	exp(c * sowndiv)	7.984	3	27.333	-9.661	61.598	0.00
Plant invader diversity	E2	a + b * exp(sowndiv)	6.446	3	27.333	-6.584	64.676	0.00
Plant invader diversity	Eb18	exp(c * sowndiv)	5.873	3	27.333	-5.439	65.820	0.00
Plant invader diversity	Ec24	exp(c * sowndiv)	4.719	3	27.333	-3.131	68.129	0.00
Plant invader diversity	Pr3531	sowndiv^c	5.287	5	16.400	0.215	71.474	0.00
Plant invader diversity	Pm1531	sowndiv^c	3.927	4	20.500	0.666	71.926	0.00
Plant invader diversity	Pp2531	sowndiv^c	4.725	5	16.400	1.340	72.599	0.00
Plant invader diversity	Pq3031	sowndiv^c	4.610	5	16.400	1.569	72.829	0.00
Plant invader diversity	Ps4031	sowndiv^c	5.329	6	13.667	2.462	73.722	0.00
Plant invader diversity	Pc531	sowndiv^c	1.714	3	27.333	2.880	74.139	0.00
Plant invader diversity	Pn2031	sowndiv^c	2.426	4	20.500	3.667	74.927	0.00
Plant invader diversity	Pe1031	sowndiv^c	1.832	4	20.500	4.855	76.115	0.00
Plant invader diversity	Pj351	sowndiv^c	-11.079	4	20.500	30.677	101.937	0.00
Plant invader diversity	Pf151	sowndiv^c	-12.329	3	27.333	30.967	102.226	0.00
Plant invader diversity	Pi301	sowndiv^c	-11.612	4	20.500	31.743	103.003	0.00
Plant invader diversity	Pg201	sowndiv^c	-12.821	3	27.333	31.949	103.209	0.00
Plant invader diversity	Ph251	sowndiv^c	-11.817	4	20.500	32.153	103.412	0.00
Plant invader diversity	Pk401	sowndiv^c	-11.079	5	16.400	32.947	104.207	0.00
Plant invader diversity	Pa5	sowndiv^c	-14.534	2	41.000	33.219	104.479	0.00
Plant invader diversity	Pb51	sowndiv^c	-14.534	2	41.000	33.219	104.479	0.00
Plant invader diversity	Pd101	sowndiv^c	-14.530	3	27.333	35.367	106.626	0.00
Plant invader diversity	M932	a * sowndiv/(b + sowndiv)	-20.171	10	8.200	63.440	134.700	0.00
Plant invader diversity	E52	b * exp(sowndiv)	-29.160	3	27.333	64.628	135.888	0.00
Plant invader diversity	M5	a * sowndiv/(b + sowndiv)	-38.464	5	16.400	87.718	158.978	0.00
Plant invader diversity	E5	b * exp(sowndiv)	-44.289	2	41.000	92.730	163.990	0.00

Supplementary Table 2 (continued)

Long variable name	model name	model formula	LL	K	N2K	AICc	deltAICc	w_ic
Plant invader diversity	Ec2221	a + exp(sowndiv)	-794.669	4	20.500	1597.858	1669.118	0.00
Plant invader diversity	Ee342	a + exp(sowndiv)	-794.639	5	16.400	1600.068	1671.328	0.00
Plant invader diversity	Ed2821	a + exp(sowndiv)	-794.663	5	16.400	1600.116	1671.375	0.00
Plant invader diversity	Eg4621	a + exp(sowndiv)	-794.639	6	13.667	1602.398	1673.658	0.00
Plant invader diversity	E42	a + exp(sowndiv)	-801.469	3	27.333	1609.245	1680.505	0.00
Plant invader diversity	Eb1621	a + exp(sowndiv)	-801.223	4	20.500	1610.966	1682.226	0.00
Plant invader diversity	Ea1021	a + exp(sowndiv)	-801.392	4	20.500	1611.303	1682.563	0.00
Plant invader diversity	Ef4021	a + exp(sowndiv)	-800.985	5	16.400	1612.760	1684.019	0.00
Plant invader diversity	E51	b * exp(sowndiv)	-1715.803	3	27.333	3437.914	3509.174	0.00
Plant invader diversity	Eb1611	a + exp(sowndiv)	-1765.168	4	20.500	3538.856	3610.115	0.00
Plant invader diversity	Ef4011	a + exp(sowndiv)	-1765.167	5	16.400	3541.123	3612.383	0.00
Plant invader diversity	Ee341	a + exp(sowndiv)	-1765.168	5	16.400	3541.126	3612.385	0.00
Plant invader diversity	E41	a + exp(sowndiv)	-1768.390	3	27.333	3543.087	3614.347	0.00
Plant invader diversity	Eg4611	a + exp(sowndiv)	-1765.167	6	13.667	3543.453	3614.713	0.00
Plant invader diversity	Ea1011	a + exp(sowndiv)	-1768.089	4	20.500	3544.698	3615.958	0.00
Plant invader diversity	Ec2211	a + exp(sowndiv)	-1768.390	4	20.500	3545.299	3616.559	0.00
Plant invader diversity	Ed2811	a + exp(sowndiv)	-1768.089	5	16.400	3546.968	3618.227	0.00
Plant invader diversity	Ef3721	a + b * exp(c * sowndiv)	-2712.751	11	7.455	5451.272	5522.532	0.00
Plant invader diversity	E4	a + exp(sowndiv)	-4912.516	2	41.000	9829.183	9900.443	0.00
Plant invader diversity	Ea10	a + exp(sowndiv)	-4912.516	3	27.333	9831.339	9902.598	0.00
Plant invader diversity	Eb16	a + exp(sowndiv)	-4912.516	3	27.333	9831.339	9902.598	0.00
Plant invader diversity	Ec22	a + exp(sowndiv)	-4912.516	3	27.333	9831.339	9902.598	0.00
Plant invader diversity	Ed28	a + exp(sowndiv)	-4912.516	4	20.500	9833.551	9904.810	0.00
Plant invader diversity	Ee40	a + exp(sowndiv)	-4912.516	4	20.500	9833.551	9904.810	0.00
Plant invader diversity	Ef40	a + exp(sowndiv)	-4912.516	4	20.500	9833.551	9904.810	0.00
Plant invader diversity	Eg46	a + exp(sowndiv)	-4912.516	5	16.400	9835.821	9907.080	0.00
Aboveground pathogen diversity	M3	a * sowndiv/(b + sowndiv)	23.455	5	16.400	-36.120	0.000	0.09
Aboveground pathogen diversity	M311	a * sowndiv/(b + sowndiv)	24.298	6	13.667	-35.476	0.644	0.07
Aboveground pathogen diversity	M321	a * sowndiv/(b + sowndiv)	24.040	6	13.667	-34.960	1.160	0.05
Aboveground pathogen diversity	Pn1821	a + sowndiv^c	23.840	6	13.667	-34.560	1.560	0.04
Aboveground pathogen diversity	Pg181	a + sowndiv^c	22.670	5	16.400	-34.551	1.569	0.04
Aboveground pathogen diversity	M1	a * sowndiv/(b + sowndiv)	20.409	3	27.333	-34.509	1.611	0.04
Aboveground pathogen diversity	M1a	SSmicmen(sowndiv, Vm, k)	20.409	3	27.333	-34.509	1.611	0.04

Supplementary Table 2 (continued)

Long variable name	model name	model formula	LL	K	N2K	AICc	deltAICc	w_ic
Aboveground pathogen diversity	Pn1921	b * sowndiv^c	23.573	6	13.667	-34.026	2.094	0.03
Aboveground pathogen diversity	Pg191	b * sowndiv^c	22.330	5	16.400	-33.871	2.249	0.03
Aboveground pathogen diversity	Pn1831	a + sowndiv^c	23.494	6	13.667	-33.867	2.253	0.03
Aboveground pathogen diversity	Pn1931	b * sowndiv^c	23.176	6	13.667	-33.231	2.889	0.02
Aboveground pathogen diversity	Pd81	a + sowndiv^c	21.787	5	16.400	-32.784	3.336	0.02
Aboveground pathogen diversity	Pd91	b * sowndiv^c	21.620	5	16.400	-32.451	3.669	0.02
Aboveground pathogen diversity	M5	a * sowndiv/(b + sowndiv)	21.606	5	16.400	-32.423	3.697	0.01
Aboveground pathogen diversity	AS3	SSasympOrig(sowndiv, Asym, lrc)	19.359	3	27.333	-32.410	3.710	0.01
Aboveground pathogen diversity	Pa3	a + sowndiv^c	19.336	3	27.333	-32.365	3.755	0.01
Aboveground pathogen diversity	Pb31	a + sowndiv^c	19.336	3	27.333	-32.365	3.755	0.01
Aboveground pathogen diversity	M2	d + a * sowndiv/(b + sowndiv)	20.411	4	20.500	-32.303	3.817	0.01
Aboveground pathogen diversity	Pe821	a + sowndiv^c	22.687	6	13.667	-32.255	3.865	0.01
Aboveground pathogen diversity	Pc321	a + sowndiv^c	20.372	4	20.500	-32.224	3.896	0.01
Aboveground pathogen diversity	M81	a * sowndiv/(b + sowndiv)	23.843	7	11.714	-32.172	3.948	0.01
Aboveground pathogen diversity	Ph231	a + sowndiv^c	23.833	7	11.714	-32.153	3.967	0.01
Aboveground pathogen diversity	Pe921	b * sowndiv^c	22.539	6	13.667	-31.959	4.161	0.01
Aboveground pathogen diversity	Pj331	a + sowndiv^c	23.734	7	11.714	-31.955	4.165	0.01
Aboveground pathogen diversity	Pe831	a + sowndiv^c	22.536	6	13.667	-31.952	4.168	0.01
Aboveground pathogen diversity	Ph241	b * sowndiv^c	23.681	7	11.714	-31.848	4.272	0.01
Aboveground pathogen diversity	Pc331	a + sowndiv^c	20.160	4	20.500	-31.800	4.320	0.01
Aboveground pathogen diversity	Pp2321	a + sowndiv^c	24.864	8	10.250	-31.756	4.364	0.01
Aboveground pathogen diversity	Pj341	b * sowndiv^c	23.606	7	11.714	-31.698	4.422	0.01
Aboveground pathogen diversity	Pe931	b * sowndiv^c	22.380	6	13.667	-31.640	4.480	0.01
Aboveground pathogen diversity	Pr3321	a + sowndiv^c	24.783	8	10.250	-31.594	4.526	0.01
Aboveground pathogen diversity	M511	a * sowndiv/(b + sowndiv)	22.321	6	13.667	-31.522	4.598	0.01
Aboveground pathogen diversity	Pp2421	b * sowndiv/(b + sowndiv)	24.727	8	10.250	-31.481	4.639	0.01
Aboveground pathogen diversity	M6	a * sowndiv/(b + sowndiv)	23.490	7	11.714	-31.467	4.653	0.01
Aboveground pathogen diversity	Pr3421	b * sowndiv^c	24.675	8	10.250	-31.377	4.743	0.01
Aboveground pathogen diversity	M522	a * sowndiv/(b + sowndiv)	22.188	6	13.667	-31.255	4.865	0.01
Aboveground pathogen diversity	M821	a * sowndiv/(b + sowndiv)	24.613	8	10.250	-31.254	4.866	0.01
Aboveground pathogen diversity	M211	d + a * sowndiv/(b + sowndiv)	21.015	5	16.400	-31.241	4.879	0.01
Aboveground pathogen diversity	Pp2331	a + sowndiv^c	24.574	8	10.250	-31.175	4.945	0.01
Aboveground pathogen diversity	Pc421	b * sowndiv^c	19.801	4	20.500	-31.082	5.038	0.01

Supplementary Table 2 (continued)

Long variable name	model name	model formula	LL	K	N2K	AICc	deltAICc	w_ic
Aboveground pathogen diversity	Pr3331	a + sowndiv^c	24.510	8	10.250	-31.047	5.073	0.01
Aboveground pathogen diversity	Pa4	b * sowndiv^c	18.654	3	27.333	-31.000	5.120	0.01
Aboveground pathogen diversity	Pb41	b * sowndiv^c	18.654	3	27.333	-31.000	5.120	0.01
Aboveground pathogen diversity	M222	d + a * sowndiv/(b + sowndiv)	20.873	5	16.400	-30.957	5.163	0.01
Aboveground pathogen diversity	Pp2431	b * sowndiv^c	24.429	8	10.250	-30.886	5.234	0.01
Aboveground pathogen diversity	Pr3431	b * sowndiv^c	24.381	8	10.250	-30.789	5.331	0.01
Aboveground pathogen diversity	M832	a * sowndiv/(b + sowndiv)	24.380	8	10.250	-30.788	5.332	0.01
Aboveground pathogen diversity	AS2	SSasympOff(sowndiv, Asym, lrc, c0)	19.634	4	20.500	-30.749	5.371	0.01
Aboveground pathogen diversity	AS1	SSasymp(sowndiv, Asym, R0, lrc)	19.634	4	20.500	-30.749	5.371	0.01
Aboveground pathogen diversity	M611	a * sowndiv/(b + sowndiv)	24.317	8	10.250	-30.662	5.458	0.01
Aboveground pathogen diversity	Pc431	b * sowndiv^c	19.481	4	20.500	-30.443	5.677	0.01
Aboveground pathogen diversity	Pd71	a + b * sowndiv	20.601	5	16.400	-30.412	5.708	0.01
Aboveground pathogen diversity	M622	a * sowndiv/(b + sowndiv)	24.079	8	10.250	-30.185	5.935	0.00
Aboveground pathogen diversity	Pe721	a + b * sowndiv	21.641	6	13.667	-30.162	5.958	0.00
Aboveground pathogen diversity	M4	a * sowndiv/(b + sowndiv)	20.462	5	16.400	-30.134	5.986	0.00
Aboveground pathogen diversity	Ph221	a + b * sowndiv	22.665	7	11.714	-29.816	6.304	0.00
Aboveground pathogen diversity	Pe731	a + b * sowndiv	21.441	6	13.667	-29.762	6.359	0.00
Aboveground pathogen diversity	Pp2221	a + b * sowndiv	23.845	8	10.250	-29.717	6.403	0.00
Aboveground pathogen diversity	Pp2231	a + b * sowndiv	23.498	8	10.250	-29.024	7.096	0.00
Aboveground pathogen diversity	M411	a * sowndiv/(b + sowndiv)	21.071	6	13.667	-29.023	7.097	0.00
Aboveground pathogen diversity	Pf131	a + sowndiv^c	19.810	5	16.400	-28.831	7.289	0.00
Aboveground pathogen diversity	M422	a * sowndiv/(b + sowndiv)	20.940	6	13.667	-28.760	7.360	0.00
Aboveground pathogen diversity	Pm1321	a + sowndiv^c	20.855	6	13.667	-28.589	7.531	0.00
Aboveground pathogen diversity	Pi281	a + sowndiv^c	21.968	7	11.714	-28.423	7.697	0.00
Aboveground pathogen diversity	Pm1331	a + sowndiv^c	20.693	6	13.667	-28.266	7.854	0.00
Aboveground pathogen diversity	Pr3221	a + b * sowndiv	23.079	8	10.250	-28.185	7.935	0.00
Aboveground pathogen diversity	Pj321	a + b * sowndiv	21.801	7	11.714	-28.088	8.032	0.00
Aboveground pathogen diversity	M7	a * sowndiv/(b + sowndiv)	21.785	7	11.714	-28.056	8.064	0.00
Aboveground pathogen diversity	Pi291	b * sowndiv^c	21.782	7	11.714	-28.050	8.070	0.00
Aboveground pathogen diversity	Pf141	b * sowndiv^c	19.373	5	16.400	-27.957	8.163	0.00
Aboveground pathogen diversity	Pk381	a + sowndiv^c	24.217	9	9.111	-27.934	8.186	0.00
Aboveground pathogen diversity	Pn1721	a + b * sowndiv	20.518	6	13.667	-27.916	8.204	0.00
Aboveground pathogen diversity	Pm1421	b * sowndiv^c	20.495	6	13.667	-27.870	8.250	0.00

Supplementary Table 2 (continued)

Long variable name	model name	model formula	LL	K	N2K	AICc	deltAICc	w_ic
Aboveground pathogen diversity	Pq2821	a + sowndiv^c	22.887	8	10.250	-27.802	8.318	0.00
Aboveground pathogen diversity	M121	d + a * sowndiv/(b + sowndiv)	21.639	7	11.714	-27.764	8.356	0.00
Aboveground pathogen diversity	Pk391	b * sowndiv^c	24.048	9	9.111	-27.596	8.524	0.00
Aboveground pathogen diversity	Ea911	a + exp(c * sowndiv)	20.314	6	13.667	-27.508	8.613	0.00
Aboveground pathogen diversity	Pq2921	b * sowndiv^c	22.722	8	10.250	-27.472	8.648	0.00
Aboveground pathogen diversity	Pq2831	a + sowndiv^c	22.710	8	10.250	-27.447	8.673	0.00
Aboveground pathogen diversity	Pm1431	b * sowndiv^c	20.280	6	13.667	-27.439	8.681	0.00
Aboveground pathogen diversity	Ps3821	a + sowndiv^c	25.248	10	8.200	-27.398	8.722	0.00
Aboveground pathogen diversity	Pr3231	a + b * sowndiv	22.662	8	10.250	-27.351	8.769	0.00
Aboveground pathogen diversity	M91	a * sowndiv/(b + sowndiv)	23.911	9	9.111	-27.321	8.799	0.00
Aboveground pathogen diversity	Pq2931	b * sowndiv^c	22.537	8	10.250	-27.101	9.019	0.00
Aboveground pathogen diversity	Ps3921	b * sowndiv^c	25.096	10	8.200	-27.093	9.027	0.00
Aboveground pathogen diversity	M711	a * sowndiv/(b + sowndiv)	22.509	8	10.250	-27.045	9.075	0.00
Aboveground pathogen diversity	Ef3921	a + exp(c * sowndiv)	22.444	8	10.250	-26.915	9.205	0.00
Aboveground pathogen diversity	Ps3831	a + sowndiv^c	24.955	10	8.200	-26.812	9.308	0.00
Aboveground pathogen diversity	M722	a * sowndiv/(b + sowndiv)	22.353	8	10.250	-26.733	9.387	0.00
Aboveground pathogen diversity	Pg171	a + b * sowndiv	18.736	5	16.400	-26.683	9.438	0.00
Aboveground pathogen diversity	Ps3931	b * sowndiv^c	24.795	10	8.200	-26.491	9.629	0.00
Aboveground pathogen diversity	Pn1731	a + b * sowndiv	19.745	6	13.667	-26.370	9.750	0.00
Aboveground pathogen diversity	M921	a * sowndiv/(b + sowndiv)	24.716	10	8.200	-26.333	9.787	0.00
Aboveground pathogen diversity	Pi271	a + b * sowndiv	20.763	7	11.714	-26.013	10.107	0.00
Aboveground pathogen diversity	Ea921	a + exp(c * sowndiv)	19.511	6	13.667	-25.901	10.219	0.00
Aboveground pathogen diversity	M932	a * sowndiv/(b + sowndiv)	24.477	10	8.200	-25.855	10.265	0.00
Aboveground pathogen diversity	Pq2721	a + b * sowndiv	21.824	8	10.250	-25.674	10.446	0.00
Aboveground pathogen diversity	Pk371	a + b * sowndiv	23.022	9	9.111	-25.543	10.577	0.00
Aboveground pathogen diversity	M131	d + a * sowndiv/(b + sowndiv)	24.312	10	8.200	-25.525	10.595	0.00
Aboveground pathogen diversity	L2	sowndiv + funcgr + leg	18.120	5	16.400	-25.451	10.669	0.00
Aboveground pathogen diversity	M111	d + a * sowndiv/(b + sowndiv)	20.474	7	11.714	-25.435	10.685	0.00
Aboveground pathogen diversity	Ps3721	a + b * sowndiv	24.209	10	8.200	-25.320	10.800	0.00
Aboveground pathogen diversity	Pq2731	a + b * sowndiv	21.598	8	10.250	-25.223	10.897	0.00
Aboveground pathogen diversity	L211	sowndiv + funcgr + leg	19.140	6	13.667	-25.159	10.961	0.00
Aboveground pathogen diversity	Ph211	a + b * sowndiv^c	23.941	10	8.200	-24.783	11.337	0.00
Aboveground pathogen diversity	M151	d + a * sowndiv/(b + sowndiv)	23.928	10	8.200	-24.757	11.363	0.00

Supplementary Table 2 (continued)

Long variable name	model name	model formula	LL	K	N2K	AICc	deltAICc	w_ic
Aboveground pathogen diversity	Ps3731	a + b * sowndiv	23.857	10	8.200	-24.615	11.505	0.00
Aboveground pathogen diversity	L222	sowndiv + funcgr + leg	18.728	6	13.667	-24.337	11.783	0.00
Aboveground pathogen diversity	M1521	d + a * sowndiv/(b + sowndiv)	24.749	11	7.455	-23.727	12.393	0.00
Aboveground pathogen diversity	Pp2131	a + b * sowndiv^c	24.694	11	7.455	-23.617	12.503	0.00
Aboveground pathogen diversity	L21	sowndiv + funcgr + leg	18.346	6	13.667	-23.572	12.548	0.00
Aboveground pathogen diversity	L22	sowndiv + funcgr + leg	18.328	6	13.667	-23.536	12.584	0.00
Aboveground pathogen diversity	M1532	d + a * sowndiv/(b + sowndiv)	24.554	11	7.455	-23.336	12.784	0.00
Aboveground pathogen diversity	M1021	d + a * sowndiv/(b + sowndiv)	19.879	8	10.250	-21.786	14.334	0.00
Aboveground pathogen diversity	Pm1221	a + b * sowndiv	16.919	6	13.667	-20.718	15.402	0.00
Aboveground pathogen diversity	Eb1511	a + exp(c * sowndiv)	16.569	6	13.667	-20.018	16.102	0.00
Aboveground pathogen diversity	Pf121	a + b * sowndiv	15.305	5	16.400	-19.820	16.300	0.00
Aboveground pathogen diversity	Pm1231	a + b * sowndiv	16.342	6	13.667	-19.564	16.556	0.00
Aboveground pathogen diversity	Eb1521	a + exp(c * sowndiv)	15.956	6	13.667	-18.793	17.327	0.00
Aboveground pathogen diversity	Pc221	a + b * sowndiv	13.633	4	20.500	-18.747	17.374	0.00
Aboveground pathogen diversity	E31	a + exp(c * sowndiv)	13.189	4	20.500	-17.859	18.261	0.00
Aboveground pathogen diversity	Pa2	a + b * sowndiv	11.759	3	27.333	-17.211	18.909	0.00
Aboveground pathogen diversity	Pb21	a + b * sowndiv	11.759	3	27.333	-17.211	18.909	0.00
Aboveground pathogen diversity	Pc231	a + b * sowndiv	12.629	4	20.500	-16.738	19.382	0.00
Aboveground pathogen diversity	E32	a + exp(c * sowndiv)	12.130	4	20.500	-15.741	20.379	0.00
Aboveground pathogen diversity	M1421	d + a * sowndiv/(b + sowndiv)	20.480	11	7.455	-15.189	20.931	0.00
Aboveground pathogen diversity	L0	block + (sowndiv + funcgr + grass + leg)^2	25.507	15	5.467	-13.741	22.379	0.00
Aboveground pathogen diversity	L011	block + (sowndiv + funcgr + grass + leg)^2	26.267	16	5.125	-12.165	23.955	0.00
Aboveground pathogen diversity	L021	block + (sowndiv + funcgr + grass + leg)^2	25.967	16	5.125	-11.565	24.555	0.00
Aboveground pathogen diversity	L01	block + (sowndiv + funcgr + grass + leg)^2	25.791	16	5.125	-11.212	24.908	0.00
Aboveground pathogen diversity	L02	block + (sowndiv + funcgr + grass + leg)^2	25.782	16	5.125	-11.195	24.925	0.00
Aboveground pathogen diversity	E21	a + b * exp(sowndiv)	9.634	4	20.500	-10.748	25.372	0.00
Aboveground pathogen diversity	E22	a + b * exp(sowndiv)	8.329	4	20.500	-8.138	27.982	0.00
Aboveground pathogen diversity	E2	a + b * exp(sowndiv)	7.061	3	27.333	-7.814	28.306	0.00
Aboveground pathogen diversity	Pe1021	sowndiv^c	-24.247	4	20.500	57.014	93.134	0.00
Aboveground pathogen diversity	Pp2521	sowndiv^c	-23.671	5	16.400	58.131	94.251	0.00
Aboveground pathogen diversity	Pr3521	sowndiv^c	-23.959	5	16.400	58.707	94.827	0.00
Aboveground pathogen diversity	Pq3021	sowndiv^c	-24.237	5	16.400	59.264	95.384	0.00
Aboveground pathogen diversity	Ps4021	sowndiv^c	-23.484	6	13.667	60.089	96.209	0.00

Supplementary Table 2 (continued)

Long variable name	model name	model formula	LL	K	N2K	AICc	deltAICc	w_ic
Aboveground pathogen diversity	Pn2021	sowndiv^c	-26.605	4	20.500	61.730	97.850	0.00
Aboveground pathogen diversity	Pm1521	sowndiv^c	-30.156	4	20.500	68.831	104.951	0.00
Aboveground pathogen diversity	Pc521	sowndiv^c	-32.738	3	27.333	71.783	107.903	0.00
Aboveground pathogen diversity	Ec2411	exp(c * sowndiv)	-33.392	4	20.500	75.304	111.424	0.00
Aboveground pathogen diversity	Pe1031	sowndiv^c	-35.017	4	20.500	78.554	114.674	0.00
Aboveground pathogen diversity	Pp2531	sowndiv^c	-34.750	5	16.400	80.288	116.409	0.00
Aboveground pathogen diversity	Pq3031	sowndiv^c	-35.014	5	16.400	80.818	116.938	0.00
Aboveground pathogen diversity	Pr3531	sowndiv^c	-35.278	5	16.400	81.345	117.465	0.00
Aboveground pathogen diversity	Ed3021	exp(c * sowndiv)	-35.570	5	16.400	81.930	118.050	0.00
Aboveground pathogen diversity	Ps4031	sowndiv^c	-34.665	6	13.667	82.451	118.571	0.00
Aboveground pathogen diversity	Ec2421	exp(c * sowndiv)	-36.985	4	20.500	82.489	118.609	0.00
Aboveground pathogen diversity	Ec24	exp(c * sowndiv)	-38.386	3	27.333	83.080	119.200	0.00
Aboveground pathogen diversity	Pn2031	sowndiv^c	-38.002	4	20.500	84.523	120.643	0.00
Aboveground pathogen diversity	Ef4211	exp(c * sowndiv)	-37.203	5	16.400	85.195	121.315	0.00
Aboveground pathogen diversity	Ef4221	exp(c * sowndiv)	-37.583	5	16.400	85.956	122.076	0.00
Aboveground pathogen diversity	Ea121	exp(c * sowndiv)	-39.144	4	20.500	86.808	122.928	0.00
Aboveground pathogen diversity	Ea1221	exp(c * sowndiv)	-39.154	4	20.500	86.828	122.948	0.00
Aboveground pathogen diversity	Ea12	exp(c * sowndiv)	-40.980	3	27.333	88.267	124.387	0.00
Aboveground pathogen diversity	Pd101	sowndiv^c	-41.203	3	27.333	88.713	124.833	0.00
Aboveground pathogen diversity	Pm1531	sowndiv^c	-40.496	4	20.500	89.512	125.632	0.00
Aboveground pathogen diversity	Ph251	sowndiv^c	-40.939	4	20.500	90.398	126.518	0.00
Aboveground pathogen diversity	Pj351	sowndiv^c	-41.130	4	20.500	90.780	126.900	0.00
Aboveground pathogen diversity	Pg201	sowndiv^c	-42.259	3	27.333	90.825	126.945	0.00
Aboveground pathogen diversity	Pi301	sowndiv^c	-41.194	4	20.500	90.907	127.027	0.00
Aboveground pathogen diversity	Pk401	sowndiv^c	-40.879	5	16.400	92.547	128.667	0.00
Aboveground pathogen diversity	Pc531	sowndiv^c	-43.450	3	27.333	93.208	129.328	0.00
Aboveground pathogen diversity	Pb51	sowndiv^c	-44.666	2	41.000	93.484	129.604	0.00
Aboveground pathogen diversity	Pa5	sowndiv^c	-44.666	2	41.000	93.484	129.604	0.00
Aboveground pathogen diversity	Pf151	sowndiv^c	-43.663	3	27.333	93.635	129.755	0.00
Aboveground pathogen diversity	Eb1811	exp(c * sowndiv)	-43.076	4	20.500	94.671	130.791	0.00
Aboveground pathogen diversity	Eb18	exp(c * sowndiv)	-46.159	3	27.333	98.625	134.745	0.00
Aboveground pathogen diversity	Eb1821	exp(c * sowndiv)	-46.373	4	20.500	101.265	137.385	0.00
Aboveground pathogen diversity	E62	exp(c * sowndiv)	-49.204	3	27.333	104.716	140.836	0.00

Supplementary Table 2 (continued)

Long variable name	model name	model formula	LL	K	N2K	AICc	deltAICc	w_ic
Aboveground pathogen diversity	E61	exp(c * sowndiv)	-53.489	3	27.333	113.286	149.406	0.00
Aboveground pathogen diversity	E51	b * exp(sowndiv)	-66.114	3	27.333	138.536	174.656	0.00
Aboveground pathogen diversity	E5	b * exp(sowndiv)	-67.256	2	41.000	138.664	174.784	0.00
Aboveground pathogen diversity	E52	b * exp(sowndiv)	-66.864	3	27.333	140.036	176.156	0.00
Aboveground pathogen diversity	Ec2221	a + exp(sowndiv)	-794.242	4	20.500	1597.004	1633.124	0.00
Aboveground pathogen diversity	Ed2821	a + exp(sowndiv)	-794.235	5	16.400	1599.260	1635.380	0.00
Aboveground pathogen diversity	Ee342	a + exp(sowndiv)	-794.242	5	16.400	1599.274	1635.394	0.00
Aboveground pathogen diversity	Eg4621	a + exp(sowndiv)	-794.235	6	13.667	1601.589	1637.709	0.00
Aboveground pathogen diversity	E42	a + exp(sowndiv)	-800.847	3	27.333	1608.002	1644.122	0.00
Aboveground pathogen diversity	Eb1621	a + exp(sowndiv)	-800.726	4	20.500	1609.972	1646.092	0.00
Aboveground pathogen diversity	Ea1021	a + exp(sowndiv)	-800.775	4	20.500	1610.069	1646.189	0.00
Aboveground pathogen diversity	Ef4021	a + exp(sowndiv)	-800.548	5	16.400	1611.886	1648.006	0.00
Aboveground pathogen diversity	Ea1011	a + exp(sowndiv)	-1753.602	4	20.500	3515.722	3551.843	0.00
Aboveground pathogen diversity	E41	a + exp(sowndiv)	-1755.331	3	27.333	3516.971	3553.091	0.00
Aboveground pathogen diversity	Ef4011	a + exp(sowndiv)	-1753.528	5	16.400	3517.846	3553.966	0.00
Aboveground pathogen diversity	Ed2811	a + exp(sowndiv)	-1753.601	5	16.400	3517.992	3554.113	0.00
Aboveground pathogen diversity	Eb1611	a + exp(sowndiv)	-1755.297	4	20.500	3519.114	3555.234	0.00
Aboveground pathogen diversity	Ec2211	a + exp(sowndiv)	-1755.331	4	20.500	3519.182	3555.302	0.00
Aboveground pathogen diversity	Eg4611	a + exp(sowndiv)	-1753.528	6	13.667	3520.177	3556.297	0.00
Aboveground pathogen diversity	Ee341	a + exp(sowndiv)	-1755.297	5	16.400	3521.384	3557.504	0.00
Aboveground pathogen diversity	Ef3721	a + b * exp(c * sowndiv)	-2748.242	11	7.455	5522.255	5558.375	0.00
Aboveground pathogen diversity	Ec1921	a + b * exp(c * sowndiv)	-2913.733	8	10.250	5845.439	5881.559	0.00
Aboveground pathogen diversity	E4	a + exp(sowndiv)	-4912.516	2	41.000	9829.183	9865.303	0.00
Aboveground pathogen diversity	Ea10	a + exp(sowndiv)	-4912.516	3	27.333	9831.339	9867.459	0.00
Aboveground pathogen diversity	Eb16	a + exp(sowndiv)	-4912.516	3	27.333	9831.339	9867.459	0.00
Aboveground pathogen diversity	Ec22	a + exp(sowndiv)	-4912.516	3	27.333	9831.339	9867.459	0.00
Aboveground pathogen diversity	Ed28	a + exp(sowndiv)	-4912.516	4	20.500	9833.551	9869.671	0.00
Aboveground pathogen diversity	Ee40	a + exp(sowndiv)	-4912.516	4	20.500	9833.551	9869.671	0.00
Aboveground pathogen diversity	Ef40	a + exp(sowndiv)	-4912.516	4	20.500	9833.551	9869.671	0.00
Aboveground pathogen diversity	Eg46	a + exp(sowndiv)	-4912.516	5	16.400	9835.821	9871.941	0.00
Herbivory	L22	sowndiv + funcgr + leg	41.196	6	13.667	-69.272	0.000	0.36
Herbivory	L21	sowndiv + funcgr + leg	41.049	6	13.667	-68.977	0.295	0.31
Herbivory	L211	sowndiv + funcgr + leg	39.526	6	13.667	-65.931	3.341	0.07

Supplementary Table 2 (continued)

Long variable name	model name	model formula	LL	K	N2K	AICc	deltAICc	w_ic
Herbivory	L222	sowndiv + funcgr + leg	38.649	6	13.667	-64.177	5.095	0.03
Herbivory	Ea911	a + exp(c * sowndiv)	38.151	6	13.667	-63.181	6.091	0.02
Herbivory	Pn1721	a + b * sowndiv	38.148	6	13.667	-63.175	6.097	0.02
Herbivory	L2	sowndiv + funcgr + leg	36.909	5	16.400	-63.029	6.244	0.02
Herbivory	Pn1921	b * sowndiv^c	37.775	6	13.667	-62.430	6.842	0.01
Herbivory	Pn1821	a + sowndiv^c	37.751	6	13.667	-62.382	6.891	0.01
Herbivory	Ea921	a + exp(c * sowndiv)	37.555	6	13.667	-61.990	7.283	0.01
Herbivory	Pn1731	a + b * sowndiv	37.552	6	13.667	-61.984	7.288	0.01
Herbivory	M311	a * sowndiv/(b + sowndiv)	37.483	6	13.667	-61.846	7.426	0.01
Herbivory	Pp2421	b * sowndiv^c	39.799	8	10.250	-61.625	7.647	0.01
Herbivory	Pn1931	b * sowndiv^c	37.236	6	13.667	-61.353	7.919	0.01
Herbivory	Pn1831	a + sowndiv^c	37.214	6	13.667	-61.308	7.964	0.01
Herbivory	Pp2221	a + b * sowndiv	39.532	8	10.250	-61.092	8.181	0.01
Herbivory	Pp2321	a + sowndiv^c	39.418	8	10.250	-60.863	8.409	0.01
Herbivory	Pg171	a + b * sowndiv	35.818	5	16.400	-60.847	8.425	0.01
Herbivory	M321	a * sowndiv/(b + sowndiv)	36.966	6	13.667	-60.813	8.460	0.01
Herbivory	M3	a * sowndiv/(b + sowndiv)	35.678	5	16.400	-60.567	8.705	0.00
Herbivory	Pg191	b * sowndiv^c	35.636	5	16.400	-60.482	8.790	0.00
Herbivory	Pg181	a + sowndiv^c	35.633	5	16.400	-60.477	8.796	0.00
Herbivory	M611	a * sowndiv/(b + sowndiv)	38.902	8	10.250	-59.831	9.442	0.00
Herbivory	Pp2431	b * sowndiv^c	38.837	8	10.250	-59.701	9.571	0.00
Herbivory	Pr3221	a + b * sowndiv	38.713	8	10.250	-59.453	9.819	0.00
Herbivory	Ef3911	a + exp(c * sowndiv)	38.702	8	10.250	-59.431	9.841	0.00
Herbivory	Pp2231	a + b * sowndiv	38.668	8	10.250	-59.363	9.910	0.00
Herbivory	Pp2331	a + sowndiv^c	38.636	8	10.250	-59.299	9.974	0.00
Herbivory	Pr3421	b * sowndiv^c	38.448	8	10.250	-58.924	10.349	0.00
Herbivory	Pr3321	a + sowndiv^c	38.379	8	10.250	-58.786	10.486	0.00
Herbivory	M821	a * sowndiv/(b + sowndiv)	38.320	8	10.250	-58.667	10.606	0.00
Herbivory	Ph241	b * sowndiv^c	37.078	7	11.714	-58.642	10.630	0.00
Herbivory	Ps3921	b * sowndiv^c	40.762	10	8.200	-58.425	10.847	0.00
Herbivory	Ph231	a + sowndiv^c	36.963	7	11.714	-58.412	10.861	0.00
Herbivory	M1321	d + a * sowndiv/(b + sowndiv)	42.085	11	7.455	-58.399	10.873	0.00
Herbivory	Ph221	a + b * sowndiv	36.922	7	11.714	-58.331	10.941	0.00

Supplementary Table 2 (continued)

Long variable name	model name	model formula	LL	K	N2K	AICc	deltAICc	w_ic
Herbivory	Pc221	a + b * sowndiv	33.422	4	20.500	-58.324	10.949	0.00
Herbivory	E31	a + exp(c * sowndiv)	33.417	4	20.500	-58.314	10.959	0.00
Herbivory	Pr3231	a + b * sowndiv	37.969	8	10.250	-57.966	11.306	0.00
Herbivory	Ef3921	a + exp(c * sowndiv)	37.964	8	10.250	-57.956	11.317	0.00
Herbivory	Ps3721	a + b * sowndiv	40.357	10	8.200	-57.616	11.656	0.00
Herbivory	E21	a + b * exp(sowndiv)	33.041	4	20.500	-57.564	11.709	0.00
Herbivory	Pc231	a + b * sowndiv	33.023	4	20.500	-57.526	11.747	0.00
Herbivory	E32	a + exp(c * sowndiv)	33.015	4	20.500	-57.510	11.762	0.00
Herbivory	Pc421	b * sowndiv^c	32.996	4	20.500	-57.472	11.801	0.00
Herbivory	Pr3431	b * sowndiv^c	37.714	8	10.250	-57.455	11.818	0.00
Herbivory	Pr3331	a + sowndiv^c	37.674	8	10.250	-57.376	11.896	0.00
Herbivory	M832	a * sowndiv/(b + sowndiv)	37.670	8	10.250	-57.367	11.906	0.00
Herbivory	Pc321	a + sowndiv^c	32.888	4	20.500	-57.256	12.016	0.00
Herbivory	M1232	d + a * sowndiv/(b + sowndiv)	37.588	8	10.250	-57.203	12.069	0.00
Herbivory	Ps3821	a + sowndiv^c	40.103	10	8.200	-57.108	12.165	0.00
Herbivory	Pc431	b * sowndiv^c	32.780	4	20.500	-57.040	12.232	0.00
Herbivory	Pj321	a + b * sowndiv	36.242	7	11.714	-56.970	12.303	0.00
Herbivory	M121	d + a * sowndiv/(b + sowndiv)	36.217	7	11.714	-56.921	12.351	0.00
Herbivory	Pc331	a + sowndiv^c	32.672	4	20.500	-56.824	12.449	0.00
Herbivory	M81	a * sowndiv/(b + sowndiv)	36.168	7	11.714	-56.822	12.451	0.00
Herbivory	E22	a + b * exp(sowndiv)	32.629	4	20.500	-56.739	12.533	0.00
Herbivory	Pj331	a + sowndiv^c	36.002	7	11.714	-56.490	12.783	0.00
Herbivory	Pj341	b * sowndiv^c	35.998	7	11.714	-56.482	12.790	0.00
Herbivory	AS3	SSasympOrig(sowndiv, Asym, lrc)	31.389	3	27.333	-56.469	12.803	0.00
Herbivory	Pc121	a + b * sowndiv^c	33.425	5	16.400	-56.061	13.211	0.00
Herbivory	M921	a * sowndiv/(b + sowndiv)	39.558	10	8.200	-56.017	13.256	0.00
Herbivory	Pb21	a + b * sowndiv	31.149	3	27.333	-55.990	13.282	0.00
Herbivory	Pa2	a + b * sowndiv	31.149	3	27.333	-55.990	13.282	0.00
Herbivory	Pa4	b * sowndiv^c	31.106	3	27.333	-55.903	13.369	0.00
Herbivory	Pb41	b * sowndiv^c	31.106	3	27.333	-55.903	13.369	0.00
Herbivory	Pa3	a + sowndiv^c	31.090	3	27.333	-55.872	13.401	0.00
Herbivory	Pb31	a + sowndiv^c	31.090	3	27.333	-55.872	13.401	0.00
Herbivory	Ps3931	b * sowndiv^c	39.477	10	8.200	-55.854	13.418	0.00

Supplementary Table 2 (continued)

Long variable name	model name	model formula	LL	K	N2K	AICc	deltAICc	w_ic
Herbivory	M1a	SSmicmen(sowndiv, Vm, k)	31.046	3	27.333	-55.785	13.487	0.00
Herbivory	M1	a * sowndiv/(b + sowndiv)	31.046	3	27.333	-55.785	13.487	0.00
Herbivory	Pm1421	b * sowndiv^c	34.360	6	13.667	-55.601	13.671	0.00
Herbivory	Ps3731	a + b * sowndiv	39.251	10	8.200	-55.403	13.869	0.00
Herbivory	Pm1321	a + sowndiv^c	34.213	6	13.667	-55.305	13.967	0.00
Herbivory	E2	a + b * exp(sowndiv)	30.806	3	27.333	-55.304	13.968	0.00
Herbivory	Ps3831	a + sowndiv^c	39.127	10	8.200	-55.155	14.117	0.00
Herbivory	Pm1221	a + b * sowndiv	34.134	6	13.667	-55.147	14.125	0.00
Herbivory	Eb1511	a + exp(c * sowndiv)	34.102	6	13.667	-55.084	14.189	0.00
Herbivory	Pm1431	b * sowndiv^c	34.013	6	13.667	-54.907	14.366	0.00
Herbivory	M1121	d + a * sowndiv/(b + sowndiv)	36.378	8	10.250	-54.784	14.488	0.00
Herbivory	Pm1331	a + sowndiv^c	33.898	6	13.667	-54.676	14.596	0.00
Herbivory	Pk391	b * sowndiv^c	37.538	9	9.111	-54.576	14.696	0.00
Herbivory	Pk371	a + b * sowndiv	37.370	9	9.111	-54.239	15.033	0.00
Herbivory	Pm1231	a + b * sowndiv	33.650	6	13.667	-54.180	15.093	0.00
Herbivory	Pk381	a + sowndiv^c	37.327	9	9.111	-54.155	15.118	0.00
Herbivory	Eb1521	a + exp(c * sowndiv)	33.621	6	13.667	-54.123	15.150	0.00
Herbivory	Pe921	b * sowndiv^c	33.542	6	13.667	-53.964	15.308	0.00
Herbivory	M411	a * sowndiv/(b + sowndiv)	33.541	6	13.667	-53.963	15.310	0.00
Herbivory	Pe721	a + b * sowndiv	33.516	6	13.667	-53.912	15.360	0.00
Herbivory	Pa1	a + b * sowndiv^c	31.181	4	20.500	-53.842	15.431	0.00
Herbivory	Pb11	a + b * sowndiv^c	31.181	4	20.500	-53.842	15.431	0.00
Herbivory	LG2	SSlogis(sowndiv, Asym, xmid, scal)	31.162	4	20.500	-53.804	15.469	0.00
Herbivory	AS2	SSasympOff(sowndiv, Asym, lrc, c0)	31.161	4	20.500	-53.802	15.471	0.00
Herbivory	AS1	SSasymp(sowndiv, Asym, R0, lrc)	31.161	4	20.500	-53.802	15.471	0.00
Herbivory	Pe821	a + sowndiv/(b + sowndiv)	33.432	6	13.667	-53.745	15.528	0.00
Herbivory	Pf141	b * sowndiv^c	32.258	5	16.400	-53.726	15.546	0.00
Herbivory	Pf131	a + sowndiv^c	32.206	5	16.400	-53.622	15.651	0.00
Herbivory	M422	a * sowndiv/(b + sowndiv)	33.290	6	13.667	-53.461	15.812	0.00
Herbivory	M4	a * sowndiv/(b + sowndiv)	32.088	5	16.400	-53.386	15.887	0.00
Herbivory	Pe931	b * sowndiv^c	33.135	6	13.667	-53.151	16.122	0.00
Herbivory	Pe731	a + b * sowndiv	33.120	6	13.667	-53.121	16.152	0.00
Herbivory	Ec2121	a + exp(c * sowndiv)	33.118	6	13.667	-53.117	16.156	0.00

Supplementary Table 2 (continued)

Long variable name	model name	model formula	LL	K	N2K	AICc	deltAICc	w_ic
Herbivory	Pe831	a + sowndiv^c	33.061	6	13.667	-53.001	16.271	0.00
Herbivory	Pf121	a + b * sowndiv	31.879	5	16.400	-52.969	16.304	0.00
Herbivory	M511	a * sowndiv/(b + sowndiv)	33.007	6	13.667	-52.893	16.379	0.00
Herbivory	Ph211	a + b * sowndiv^c	37.919	10	8.200	-52.740	16.532	0.00
Herbivory	M522	a * sowndiv/(b + sowndiv)	32.711	6	13.667	-52.302	16.971	0.00
Herbivory	Pq2721	a + b * sowndiv	35.013	8	10.250	-52.054	17.219	0.00
Herbivory	Pd91	b * sowndiv^c	31.264	5	16.400	-51.739	17.533	0.00
Herbivory	Pd71	a + b * sowndiv	31.238	5	16.400	-51.687	17.586	0.00
Herbivory	M1632	d + a * sowndiv/(b + sowndiv)	42.962	14	5.857	-51.655	17.618	0.00
Herbivory	Pd81	a + sowndiv^c	31.220	5	16.400	-51.652	17.621	0.00
Herbivory	Pq2921	b * sowndiv^c	34.785	8	10.250	-51.598	17.675	0.00
Herbivory	M5	a * sowndiv/(b + sowndiv)	31.179	5	16.400	-51.569	17.703	0.00
Herbivory	Pq2821	a + sowndiv^c	34.729	8	10.250	-51.485	17.787	0.00
Herbivory	L021	block + (sowndiv + funcgr + grass + leg)^2	45.900	16	5.125	-51.430	17.842	0.00
Herbivory	M711	a * sowndiv/(b + sowndiv)	34.527	8	10.250	-51.082	18.190	0.00
Herbivory	Pq2731	a + b * sowndiv	34.501	8	10.250	-51.029	18.244	0.00
Herbivory	Pq2931	b * sowndiv^c	34.354	8	10.250	-50.735	18.537	0.00
Herbivory	Pq2831	a + sowndiv^c	34.304	8	10.250	-50.635	18.637	0.00
Herbivory	M722	a * sowndiv/(b + sowndiv)	34.059	8	10.250	-50.146	19.126	0.00
Herbivory	Pi271	a + b * sowndiv	32.701	7	11.714	-49.888	19.384	0.00
Herbivory	Pi291	b * sowndiv^c	32.602	7	11.714	-49.690	19.583	0.00
Herbivory	Pi281	a + sowndiv^c	32.579	7	11.714	-49.644	19.629	0.00
Herbivory	M7	a * sowndiv/(b + sowndiv)	32.574	7	11.714	-49.635	19.637	0.00
Herbivory	Pd61	a + b * sowndiv^c	32.014	7	11.714	-48.514	20.759	0.00
Herbivory	L02	block + (sowndiv + funcgr + grass + leg)^2	44.424	16	5.125	-48.479	20.793	0.00
Herbivory	Pk361	a + b * sowndiv^c	39.593	13	6.308	-47.834	21.439	0.00
Herbivory	L011	block + (sowndiv + funcgr + grass + leg)^2	43.699	16	5.125	-47.030	22.243	0.00
Herbivory	Pi261	a + b * sowndiv^c	33.730	10	8.200	-44.362	24.910	0.00
Herbivory	M932	a * sowndiv/(b + sowndiv)	33.092	10	8.200	-43.086	26.186	0.00
Herbivory	L0	block + (sowndiv + funcgr + grass + leg)^2	39.591	15	5.467	-41.910	27.362	0.00
Herbivory	M622	a * sowndiv/(b + sowndiv)	23.298	8	10.250	-28.623	40.649	0.00
Herbivory	M6	a * sowndiv/(b + sowndiv)	21.048	7	11.714	-26.583	42.690	0.00
Herbivory	M91	a * sowndiv/(b + sowndiv)	18.946	9	9.111	-17.392	51.881	0.00

Supplementary Table 2 (continued)

Long variable name	model name	model formula	LL	K	N2K	AICc	deltAICc	w_ic
Herbivory	Ed3021	exp(c * sowndiv)	-1.164	5	16.400	13.118	82.391	0.00
Herbivory	Ea12	exp(c * sowndiv)	-3.939	3	27.333	14.186	83.458	0.00
Herbivory	Ea1221	exp(c * sowndiv)	-3.010	4	20.500	14.540	83.812	0.00
Herbivory	Ef4221	exp(c * sowndiv)	-1.909	5	16.400	14.607	83.880	0.00
Herbivory	Ef4211	exp(c * sowndiv)	-2.225	5	16.400	15.239	84.512	0.00
Herbivory	Ea121	exp(c * sowndiv)	-3.435	4	20.500	15.390	84.662	0.00
Herbivory	Ec24	exp(c * sowndiv)	-5.092	3	27.333	16.492	85.765	0.00
Herbivory	Ec2411	exp(c * sowndiv)	-4.149	4	20.500	16.817	86.089	0.00
Herbivory	Ec2421	exp(c * sowndiv)	-4.203	4	20.500	16.925	86.198	0.00
Herbivory	E61	exp(c * sowndiv)	-7.970	3	27.333	22.248	91.521	0.00
Herbivory	E62	exp(c * sowndiv)	-8.125	3	27.333	22.558	91.830	0.00
Herbivory	E52	b * exp(sowndiv)	-8.651	3	27.333	23.610	92.882	0.00
Herbivory	Eb18	exp(c * sowndiv)	-8.737	3	27.333	23.782	93.054	0.00
Herbivory	Eb1811	exp(c * sowndiv)	-7.964	4	20.500	24.447	93.719	0.00
Herbivory	Eb1821	exp(c * sowndiv)	-8.125	4	20.500	24.769	94.042	0.00
Herbivory	E5	b * exp(sowndiv)	-10.336	2	41.000	24.824	94.097	0.00
Herbivory	E51	b * exp(sowndiv)	-10.130	3	27.333	26.568	95.840	0.00
Herbivory	Pr3521	sowndiv^c	-21.591	5	16.400	53.972	123.244	0.00
Herbivory	Pp2521	sowndiv^c	-21.663	5	16.400	54.115	123.387	0.00
Herbivory	Ps4021	sowndiv^c	-21.345	6	13.667	55.811	125.083	0.00
Herbivory	Pe1021	sowndiv^c	-23.804	4	20.500	56.128	125.401	0.00
Herbivory	Pn2021	sowndiv^c	-24.538	4	20.500	57.595	126.867	0.00
Herbivory	Pq3021	sowndiv^c	-23.672	5	16.400	58.134	127.406	0.00
Herbivory	Pc521	sowndiv^c	-31.123	3	27.333	68.553	137.826	0.00
Herbivory	Pm1521	sowndiv^c	-30.066	4	20.500	68.651	137.923	0.00
Herbivory	Pp2531	sowndiv^c	-37.888	5	16.400	86.565	155.837	0.00
Herbivory	Pe1031	sowndiv^c	-39.043	4	20.500	86.605	155.877	0.00
Herbivory	Pr3531	sowndiv^c	-38.356	5	16.400	87.501	156.773	0.00
Herbivory	Pq3031	sowndiv^c	-38.943	5	16.400	88.676	157.948	0.00
Herbivory	Ps4031	sowndiv^c	-37.796	6	13.667	88.712	157.985	0.00
Herbivory	Pc531	sowndiv^c	-45.620	3	27.333	97.547	166.819	0.00
Herbivory	Pg201	sowndiv^c	-46.205	3	27.333	98.718	167.990	0.00
Herbivory	Pm1531	sowndiv^c	-45.419	4	20.500	99.358	168.630	0.00

Supplementary Table 2 (continued)

Long variable name	model name	model formula	LL	K	N2K	AICc	deltAICc	w_ic
Herbivory	Pb51	sowndiv^c	-48.045	2	41.000	100.241	169.513	0.00
Herbivory	Pa5	sowndiv^c	-48.045	2	41.000	100.241	169.513	0.00
Herbivory	Pj351	sowndiv^c	-46.049	4	20.500	100.618	169.890	0.00
Herbivory	Pd101	sowndiv^c	-47.180	3	27.333	100.667	169.939	0.00
Herbivory	Ph251	sowndiv^c	-46.119	4	20.500	100.758	170.031	0.00
Herbivory	Pf151	sowndiv^c	-48.035	3	27.333	102.377	171.649	0.00
Herbivory	Pi301	sowndiv^c	-46.955	4	20.500	102.430	171.702	0.00
Herbivory	Pk401	sowndiv^c	-46.037	5	16.400	102.864	172.136	0.00
Herbivory	Ec2221	a + exp(sowndiv)	-794.227	4	20.500	1596.974	1666.247	0.00
Herbivory	Ed2821	a + exp(sowndiv)	-794.222	5	16.400	1599.233	1668.505	0.00
Herbivory	Ee342	a + exp(sowndiv)	-794.225	5	16.400	1599.239	1668.511	0.00
Herbivory	Eg4621	a + exp(sowndiv)	-794.221	6	13.667	1601.562	1670.834	0.00
Herbivory	E42	a + exp(sowndiv)	-800.854	3	27.333	1608.017	1677.289	0.00
Herbivory	Eb1621	a + exp(sowndiv)	-800.705	4	20.500	1609.929	1679.201	0.00
Herbivory	Ea1021	a + exp(sowndiv)	-800.780	4	20.500	1610.079	1679.351	0.00
Herbivory	Ef4021	a + exp(sowndiv)	-800.509	5	16.400	1611.808	1681.080	0.00
Herbivory	Ea1011	a + exp(sowndiv)	-1727.462	4	20.500	3463.443	3532.715	0.00
Herbivory	Ef4011	a + exp(sowndiv)	-1726.707	5	16.400	3464.203	3533.476	0.00
Herbivory	Eb1611	a + exp(sowndiv)	-1728.199	4	20.500	3464.917	3534.190	0.00
Herbivory	Ed2811	a + exp(sowndiv)	-1727.462	5	16.400	3465.713	3534.985	0.00
Herbivory	E41	a + exp(sowndiv)	-1729.905	3	27.333	3466.117	3535.390	0.00
Herbivory	Eg4611	a + exp(sowndiv)	-1726.707	6	13.667	3466.534	3535.806	0.00
Herbivory	Ee341	a + exp(sowndiv)	-1728.199	5	16.400	3467.187	3536.460	0.00
Herbivory	Ec2211	a + exp(sowndiv)	-1729.905	4	20.500	3468.329	3537.601	0.00
Herbivory	Ef3721	a + b * exp(c * sowndiv)	-2688.523	11	7.455	5402.817	5472.089	0.00
Herbivory	Ec1921	a + b * exp(c * sowndiv)	-2878.481	8	10.250	5774.934	5844.207	0.00
Herbivory	E4	a + exp(sowndiv)	-4912.516	2	41.000	9829.183	9898.455	0.00
Herbivory	Ea10	a + exp(sowndiv)	-4912.516	3	27.333	9831.339	9900.611	0.00
Herbivory	Eb16	a + exp(sowndiv)	-4912.516	3	27.333	9831.339	9900.611	0.00
Herbivory	Ec22	a + exp(sowndiv)	-4912.516	3	27.333	9831.339	9900.611	0.00
Herbivory	Ed28	a + exp(sowndiv)	-4912.516	4	20.500	9833.551	9902.823	0.00
Herbivory	Ee40	a + exp(sowndiv)	-4912.516	4	20.500	9833.551	9902.823	0.00
Herbivory	Ef40	a + exp(sowndiv)	-4912.516	4	20.500	9833.551	9902.823	0.00

Supplementary Table 2 (continued)

Long variable name	model name	model formula	LL	K	N2K	AICc	deltAICc	w_ic
Herbivory	Eg46	a + exp(sowndiv)	-4912.516	5	16.400	9835.821	9905.093	0.00
Parasitism	Pa2	a + b * sowndiv	5.078	3	26.000	-3.833	0.000	0.15
Parasitism	Pa4	b * sowndiv^c	4.935	3	26.000	-3.546	0.287	0.13
Parasitism	Pa3	a + sowndiv^c	4.872	3	26.000	-3.419	0.413	0.13
Parasitism	E2	a + b * exp(sowndiv)	4.726	3	26.000	-3.128	0.705	0.11
Parasitism	M1a	SSmicmen(sowndiv, Vm, k)	4.289	3	26.000	-2.254	1.578	0.07
Parasitism	M1	a * sowndiv/(b + sowndiv)	4.289	3	26.000	-2.254	1.578	0.07
Parasitism	Pa1	a + b * sowndiv^c	5.131	4	19.500	-1.714	2.119	0.05
Parasitism	M2	d + a * sowndiv/(b + sowndiv)	5.118	4	19.500	-1.687	2.145	0.05
Parasitism	AS2	SSasymp(sowndiv, Asym, lrc, c0)	5.115	4	19.500	-1.681	2.151	0.05
Parasitism	AS1	SSasymp(sowndiv, Asym, R0, lrc)	5.115	4	19.500	-1.681	2.151	0.05
Parasitism	LG2	SSlogis(sowndiv, Asym, xmid, scal)	5.105	4	19.500	-1.662	2.171	0.05
Parasitism	AS3	SSasympOrig(sowndiv, Asym, lrc)	3.811	3	26.000	-1.297	2.536	0.04
Parasitism	L2	sowndiv + funcgr + leg	5.805	5	15.600	-0.776	3.057	0.03
Parasitism	L0	block + (sowndiv + funcgr + grass + leg)^2	14.398	15	5.200	8.945	12.778	0.00
Parasitism	E5	b * exp(sowndiv)	-31.235	2	39.000	66.631	70.463	0.00
Parasitism	Pa5	sowndiv^c	-46.858	2	39.000	97.875	101.708	0.00
Parasitism	E4	a + exp(sowndiv)	-4674.831	2	39.000	9353.822	9357.655	0.00
Flower visitation	L2	sowndiv + funcgr + leg	41.249	5	14.600	-71.602	0.000	0.75
Flower visitation	Pa4	b * sowndiv^c	36.025	3	24.333	-65.703	5.900	0.04
Flower visitation	M1a	SSmicmen(sowndiv, Vm, k)	36.007	3	24.333	-65.666	5.936	0.04
Flower visitation	M1	a * sowndiv/(b + sowndiv)	36.007	3	24.333	-65.666	5.936	0.04
Flower visitation	Pa3	a + sowndiv^c	36.001	3	24.333	-65.654	5.948	0.04
Flower visitation	AS3	SSasympOrig(sowndiv, Asym, lrc)	35.673	3	24.333	-64.998	6.605	0.03
Flower visitation	Pa1	a + b * sowndiv^c	36.189	4	18.250	-63.790	7.813	0.02
Flower visitation	M2	d + a * sowndiv/(b + sowndiv)	36.122	4	18.250	-63.655	7.947	0.01
Flower visitation	AS1	SSasymp(sowndiv, Asym, R0, lrc)	36.040	4	18.250	-63.492	8.110	0.01
Flower visitation	AS2	SSasympOff(sowndiv, Asym, lrc, c0)	36.040	4	18.250	-63.492	8.110	0.01
Flower visitation	Pa2	a + b * sowndiv	34.526	3	24.333	-62.703	8.899	0.01
Flower visitation	LG2	SSlogis(sowndiv, Asym, xmid, scal)	35.602	4	18.250	-62.615	8.987	0.01
Flower visitation	E2	a + b * exp(sowndiv)	31.686	3	24.333	-57.023	14.579	0.00
Flower visitation	L0	block + (sowndiv + funcgr + grass + leg)^2	46.318	15	4.867	-54.214	17.388	0.00
Flower visitation	E5	b * exp(sowndiv)	17.632	2	36.500	-31.092	40.510	0.00

Supplementary Table 2 (continued)

Long variable name	model name	model formula	LL	K	N2K	AICc	deltaAICc	w_ic
Flower visitation	Pa5	sowndiv^c	-43.530	2	36.500	91.232	162.834	0.00
Flower visitation	E4	a + exp(sowndiv)	-4377.580	2	36.500	8759.332	8830.935	0.00
Litter decomposition	Pa4	b * sowndiv^c	10.937	3	14.667	-15.275	0.000	0.13
Litter decomposition	Pa3	a + sowndiv^c	10.937	3	14.667	-15.275	0.000	0.13
Litter decomposition	Pa2	a + b * sowndiv	10.799	3	14.667	-14.998	0.277	0.12
Litter decomposition	E3	a + exp(c * sowndiv)	10.792	3	14.667	-14.984	0.291	0.11
Litter decomposition	M1	a * sowndiv/(b + sowndiv)	10.791	3	14.667	-14.982	0.292	0.11
Litter decomposition	M1a	SSmicmen(sowndiv, Vm, k)	10.791	3	14.667	-14.982	0.292	0.11
Litter decomposition	E2	a + b * exp(sowndiv)	10.596	3	14.667	-14.592	0.682	0.09
Litter decomposition	AS3	SSasympOrig(sowndiv, Asym, lrc)	10.565	3	14.667	-14.529	0.746	0.09
Litter decomposition	M2	d + a * sowndiv/(b + sowndiv)	10.937	4	11.000	-12.849	2.426	0.04
Litter decomposition	Pa1	a + b * sowndiv^c	10.937	4	11.000	-12.849	2.426	0.04
Litter decomposition	L2	sowndiv + funcgr + leg	10.799	5	8.800	-10.019	5.256	0.01
Litter decomposition	L0	block + (sowndiv + funcgr + grass + leg)^2	23.167	15	2.933	0.809	16.084	0.00
Litter decomposition	Pa5	sowndiv^c	-16.748	2	22.000	37.789	53.064	0.00
Litter decomposition	E6	exp(c * sowndiv)	-17.601	2	22.000	39.494	54.769	0.00
Litter decomposition	E5	b * exp(sowndiv)	-31.904	2	22.000	68.101	83.376	0.00
Litter decomposition	E4	a + exp(sowndiv)	-731.905	2	22.000	1468.104	1483.378	0.00
Seed predation	Pa3	a + sowndiv^c	11.123	3	15.333	-15.675	0.000	0.13
Seed predation	Pa4	b * sowndiv^c	11.123	3	15.333	-15.674	0.000	0.13
Seed predation	E3	a + exp(c * sowndiv)	11.035	3	15.333	-15.499	0.176	0.12
Seed predation	Pa2	a + b * sowndiv	11.031	3	15.333	-15.491	0.184	0.12
Seed predation	M1a	SSmicmen(sowndiv, Vm, k)	11.017	3	15.333	-15.463	0.212	0.12
Seed predation	M1	a * sowndiv/(b + sowndiv)	11.017	3	15.333	-15.463	0.212	0.12
Seed predation	E2	a + b * exp(sowndiv)	10.904	3	15.333	-15.236	0.439	0.11
Seed predation	L2	sowndiv + funcgr + leg	12.756	5	9.200	-14.013	1.662	0.06
Seed predation	Pa1	a + b * sowndiv^c	11.123	4	11.500	-13.271	2.403	0.04
Seed predation	M2	d + a * sowndiv/(b + sowndiv)	11.123	4	11.500	-13.271	2.403	0.04
Seed predation	L0	block + (sowndiv + funcgr + grass + leg)^2	18.277	15	3.067	9.446	25.121	0.00
Seed predation	Pa5	sowndiv^c	-2.743	2	23.000	9.765	25.440	0.00
Seed predation	E6	exp(c * sowndiv)	-3.969	2	23.000	12.218	27.892	0.00
Seed predation	E5	b * exp(sowndiv)	-42.906	2	23.000	90.092	105.767	0.00
Seed predation	E4	a + exp(sowndiv)	-765.564	2	23.000	1535.407	1551.081	0.00

Supplementary Table 2 (continued)

Long variable name	model name	model formula	LL	K	N2K	AICc	deltAICc	w_ic
Pathogen infection	L021	block + (sowndiv + funcgr + grass + leg)^2	75.283	16	5.125	-110.197	0.000	1.00
Pathogen infection	Pn1821	a + sowndiv^c	40.701	6	13.667	-68.282	41.915	0.00
Pathogen infection	Pn1921	b * sowndiv^c	40.362	6	13.667	-67.604	42.594	0.00
Pathogen infection	Pp2421	b * sowndiv^c	41.321	8	10.250	-64.668	45.529	0.00
Pathogen infection	Pr3321	a + sowndiv^c	40.941	8	10.250	-63.910	46.287	0.00
Pathogen infection	Pp2321	a + sowndiv^c	40.747	8	10.250	-63.521	46.676	0.00
Pathogen infection	Pr3421	b * sowndiv^c	40.721	8	10.250	-63.470	46.727	0.00
Pathogen infection	Pp2221	a + b * sowndiv	40.561	8	10.250	-63.149	47.049	0.00
Pathogen infection	Ea911	a + exp(c * sowndiv)	37.106	6	13.667	-61.092	49.106	0.00
Pathogen infection	Ps3921	b * sowndiv^c	41.769	10	8.200	-60.440	49.757	0.00
Pathogen infection	Ps3821	a + sowndiv^c	41.671	10	8.200	-60.244	49.953	0.00
Pathogen infection	M1121	d + a * sowndiv/(b + sowndiv)	38.554	8	10.250	-59.135	51.062	0.00
Pathogen infection	Pc421	b * sowndiv^c	33.704	4	20.500	-58.889	51.308	0.00
Pathogen infection	Ps3721	a + b * sowndiv	40.948	10	8.200	-58.797	51.400	0.00
Pathogen infection	Pe821	a + sowndiv^c	35.419	6	13.667	-57.717	52.480	0.00
Pathogen infection	M1221	d + a * sowndiv/(b + sowndiv)	37.749	8	10.250	-57.526	52.671	0.00
Pathogen infection	Pc321	a + sowndiv^c	32.801	4	20.500	-57.083	53.114	0.00
Pathogen infection	Pe921	b * sowndiv^c	34.787	6	13.667	-56.454	53.743	0.00
Pathogen infection	Pm1321	a + sowndiv^c	34.370	6	13.667	-55.620	54.577	0.00
Pathogen infection	M1421	d + a * sowndiv/(b + sowndiv)	40.392	11	7.455	-55.013	55.184	0.00
Pathogen infection	Pm1421	b * sowndiv^c	33.980	6	13.667	-54.839	55.358	0.00
Pathogen infection	Pq2821	a + sowndiv^c	36.326	8	10.250	-54.680	55.518	0.00
Pathogen infection	Pe721	a + b * sowndiv	33.782	6	13.667	-54.445	55.752	0.00
Pathogen infection	Pn1931	b * sowndiv^c	33.547	6	13.667	-53.975	56.223	0.00
Pathogen infection	Pq2931	b * sowndiv^c	35.867	8	10.250	-53.762	56.435	0.00
Pathogen infection	Pn2021	sowndiv^c	30.358	4	20.500	-52.197	58.000	0.00
Pathogen infection	Pq2721	a + b * sowndiv	35.043	8	10.250	-52.112	58.085	0.00
Pathogen infection	Pn1831	a + sowndiv^c	32.524	6	13.667	-51.928	58.269	0.00
Pathogen infection	Pp2431	b * sowndiv^c	34.308	8	10.250	-50.643	59.555	0.00
Pathogen infection	Pr3431	b * sowndiv^c	34.290	8	10.250	-50.607	59.590	0.00
Pathogen infection	Pr3331	a + sowndiv^c	34.182	8	10.250	-50.392	59.805	0.00
Pathogen infection	Pp2521	sowndiv^c	30.497	5	16.400	-50.205	59.992	0.00
Pathogen infection	Ea921	a + exp(c * sowndiv)	31.598	6	13.667	-50.077	60.120	0.00

Supplementary Table 2 (continued)

Long variable name	model name	model formula	LL	K	N2K	AICc	deltAICc	w_ic
Pathogen infection	Pr3521	sowndiv^c	30.370	5	16.400	-49.951	60.246	0.00
Pathogen infection	Pr3221	a + b * sowndiv	33.907	8	10.250	-49.842	60.355	0.00
Pathogen infection	Pp2331	a + sowndiv^c	33.676	8	10.250	-49.380	60.817	0.00
Pathogen infection	Ps4021	sowndiv^c	30.962	6	13.667	-48.805	61.392	0.00
Pathogen infection	L011	block + (sowndiv + funcgr + grass + leg)^2	44.572	16	5.125	-48.775	61.422	0.00
Pathogen infection	Eb1511	a + exp(c * sowndiv)	30.925	6	13.667	-48.731	61.467	0.00
Pathogen infection	Pm1221	a + b * sowndiv	30.729	6	13.667	-48.338	61.859	0.00
Pathogen infection	Pp2231	a + b * sowndiv	32.303	8	10.250	-46.634	63.563	0.00
Pathogen infection	Pe1021	sowndiv^c	27.528	4	20.500	-46.536	63.661	0.00
Pathogen infection	Ps3931	b * sowndiv^c	34.761	10	8.200	-46.424	63.773	0.00
Pathogen infection	Pc521	sowndiv^c	26.032	3	27.333	-45.757	64.440	0.00
Pathogen infection	Ps3831	a + sowndiv^c	34.280	10	8.200	-45.461	64.736	0.00
Pathogen infection	Ef3921	a + exp(c * sowndiv)	31.632	8	10.250	-45.292	64.905	0.00
Pathogen infection	Pq3021	sowndiv^c	27.839	5	16.400	-44.888	65.309	0.00
Pathogen infection	Pm1521	sowndiv^c	26.078	4	20.500	-43.637	66.560	0.00
Pathogen infection	Pc331	a + sowndiv^c	25.683	4	20.500	-42.847	67.350	0.00
Pathogen infection	Ps3731	a + b * sowndiv	32.937	10	8.200	-42.776	67.421	0.00
Pathogen infection	Pc431	b * sowndiv^c	24.561	4	20.500	-40.603	69.594	0.00
Pathogen infection	Pe831	a + sowndiv^c	26.793	6	13.667	-40.466	69.731	0.00
Pathogen infection	Pe931	b * sowndiv^c	26.500	6	13.667	-39.881	70.316	0.00
Pathogen infection	M611	a * sowndiv/(b + sowndiv)	28.756	8	10.250	-39.540	70.658	0.00
Pathogen infection	Pm1331	a + sowndiv^c	26.197	6	13.667	-39.274	70.923	0.00
Pathogen infection	Ec2121	a + exp(c * sowndiv)	25.890	6	13.667	-38.659	71.538	0.00
Pathogen infection	Pe731	a + b * sowndiv	25.650	6	13.667	-38.179	72.018	0.00
Pathogen infection	M1132	d + a * sowndiv/(b + sowndiv)	27.988	8	10.250	-38.004	72.193	0.00
Pathogen infection	M1232	d + a * sowndiv/(b + sowndiv)	27.931	8	10.250	-37.890	72.307	0.00
Pathogen infection	Pm1431	b * sowndiv^c	25.263	6	13.667	-37.406	72.791	0.00
Pathogen infection	M511	a * sowndiv/(b + sowndiv)	25.251	6	13.667	-37.383	72.815	0.00
Pathogen infection	Pn1721	a + b * sowndiv	24.872	6	13.667	-36.625	73.573	0.00
Pathogen infection	Pq2831	a + sowndiv^c	27.265	8	10.250	-36.558	73.639	0.00
Pathogen infection	Pq2931	b * sowndiv^c	27.138	8	10.250	-36.303	73.894	0.00
Pathogen infection	M921	a * sowndiv/(b + sowndiv)	29.658	10	8.200	-36.217	73.980	0.00
Pathogen infection	M622	a * sowndiv/(b + sowndiv)	26.472	8	10.250	-34.971	75.226	0.00

Supplementary Table 2 (continued)

Long variable name	model name	model formula	LL	K	N2K	AICc	deltAICc	w_ic
Pathogen infection	Pq2731	a + b * sowndiv	26.271	8	10.250	-34.569	75.628	0.00
Pathogen infection	Eb1521	a + exp(c * sowndiv)	23.337	6	13.667	-33.555	76.643	0.00
Pathogen infection	M711	a * sowndiv/(b + sowndiv)	25.706	8	10.250	-33.439	76.758	0.00
Pathogen infection	Pm1231	a + b * sowndiv	23.104	6	13.667	-33.087	77.110	0.00
Pathogen infection	L211	sowndiv + funcgr + leg	23.014	6	13.667	-32.908	77.289	0.00
Pathogen infection	Pr3231	a + b * sowndiv	25.261	8	10.250	-32.550	77.647	0.00
Pathogen infection	M932	a * sowndiv/(b + sowndiv)	27.698	10	8.200	-32.297	77.900	0.00
Pathogen infection	M1432	d + a * sowndiv/(b + sowndiv)	29.024	11	7.455	-32.277	77.920	0.00
Pathogen infection	E31	a + exp(c * sowndiv)	20.338	4	20.500	-32.157	78.040	0.00
Pathogen infection	Pc221	a + b * sowndiv	19.850	4	20.500	-31.180	79.017	0.00
Pathogen infection	M522	a * sowndiv/(b + sowndiv)	21.678	6	13.667	-30.236	79.962	0.00
Pathogen infection	M821	a * sowndiv/(b + sowndiv)	22.538	8	10.250	-27.104	83.093	0.00
Pathogen infection	L222	sowndiv + funcgr + leg	19.643	6	13.667	-26.166	84.031	0.00
Pathogen infection	Ea121	exp(c * sowndiv)	17.244	4	20.500	-25.969	84.228	0.00
Pathogen infection	M722	a * sowndiv/(b + sowndiv)	21.935	8	10.250	-25.897	84.300	0.00
Pathogen infection	Pn1731	a + b * sowndiv	18.971	6	13.667	-24.821	85.376	0.00
Pathogen infection	Ef4211	exp(c * sowndiv)	17.249	5	16.400	-23.709	86.488	0.00
Pathogen infection	E32	a + exp(c * sowndiv)	15.635	4	20.500	-22.750	87.447	0.00
Pathogen infection	M832	a * sowndiv/(b + sowndiv)	20.337	8	10.250	-22.702	87.495	0.00
Pathogen infection	Pc231	a + b * sowndiv	15.027	4	20.500	-21.534	88.663	0.00
Pathogen infection	L21	sowndiv + funcgr + leg	16.897	6	13.667	-20.673	89.524	0.00
Pathogen infection	Pg181	a + sowndiv^c	15.187	5	16.400	-19.584	90.613	0.00
Pathogen infection	Pg191	b * sowndiv^c	14.896	5	16.400	-19.002	91.196	0.00
Pathogen infection	M311	a * sowndiv/(b + sowndiv)	16.050	6	13.667	-18.981	91.217	0.00
Pathogen infection	L22	sowndiv + funcgr + leg	15.925	6	13.667	-18.729	91.468	0.00
Pathogen infection	M411	a * sowndiv/(b + sowndiv)	15.832	6	13.667	-18.545	91.652	0.00
Pathogen infection	Ph241	b * sowndiv^c	16.305	7	11.714	-17.096	93.101	0.00
Pathogen infection	Pj341	b * sowndiv^c	15.805	7	11.714	-16.097	94.100	0.00
Pathogen infection	M101	d + a * sowndiv/(b + sowndiv)	15.631	7	11.714	-15.748	94.449	0.00
Pathogen infection	Pj331	a + sowndiv^c	15.625	7	11.714	-15.736	94.461	0.00
Pathogen infection	Ec2411	exp(c * sowndiv)	12.014	4	20.500	-15.509	94.688	0.00
Pathogen infection	Ph231	a + sowndiv^c	15.301	7	11.714	-15.088	95.109	0.00
Pathogen infection	E61	exp(c * sowndiv)	10.465	3	27.333	-14.623	95.574	0.00

Supplementary Table 2 (continued)

Long variable name	model name	model formula	LL	K	N2K	AICc	deltAICc	w_ic
Pathogen infection	Pk391	b * sowndiv^c	16.812	9	9.111	-13.124	97.073	0.00
Pathogen infection	Eb1811	exp(c * sowndiv)	10.468	4	20.500	-12.416	97.781	0.00
Pathogen infection	E22	a + b * exp(sowndiv)	10.274	4	20.500	-12.028	98.169	0.00
Pathogen infection	Pk381	a + sowndiv^c	16.002	9	9.111	-11.504	98.693	0.00
Pathogen infection	Ea1221	exp(c * sowndiv)	9.960	4	20.500	-11.401	98.796	0.00
Pathogen infection	Ph221	a + b * sowndiv	13.254	7	11.714	-10.994	99.203	0.00
Pathogen infection	M151	d + a * sowndiv/(b + sowndiv)	16.376	10	8.200	-9.654	100.543	0.00
Pathogen infection	Ef4221	exp(c * sowndiv)	10.073	5	16.400	-9.356	100.841	0.00
Pathogen infection	M6	a * sowndiv/(b + sowndiv)	12.411	7	11.714	-9.309	100.888	0.00
Pathogen infection	Ed3021	exp(c * sowndiv)	10.002	5	16.400	-9.215	100.982	0.00
Pathogen infection	M161	d + a * sowndiv/(b + sowndiv)	20.154	13	6.308	-8.955	101.242	0.00
Pathogen infection	M422	a * sowndiv/(b + sowndiv)	10.737	6	13.667	-8.353	101.844	0.00
Pathogen infection	Pk371	a + b * sowndiv	14.054	9	9.111	-7.608	102.589	0.00
Pathogen infection	M321	a * sowndiv/(b + sowndiv)	9.854	6	13.667	-6.587	103.610	0.00
Pathogen infection	Pa3	a + sowndiv^c	5.973	3	27.333	-5.639	104.559	0.00
Pathogen infection	Pb31	a + sowndiv^c	5.973	3	27.333	-5.639	104.559	0.00
Pathogen infection	M3	a * sowndiv/(b + sowndiv)	8.073	5	16.400	-5.356	104.841	0.00
Pathogen infection	AS1	SSasymp(sowndiv, Asym, R0, lrc)	6.870	4	20.500	-5.221	104.976	0.00
Pathogen infection	M2	d + a * sowndiv/(b + sowndiv)	6.683	4	20.500	-4.846	105.351	0.00
Pathogen infection	M81	a * sowndiv/(b + sowndiv)	10.018	7	11.714	-4.522	105.675	0.00
Pathogen infection	Pa4	b * sowndiv^c	5.278	3	27.333	-4.247	105.950	0.00
Pathogen infection	Pb41	b * sowndiv^c	5.278	3	27.333	-4.247	105.950	0.00
Pathogen infection	Pb11	a + b * sowndiv^c	6.155	4	20.500	-3.791	106.406	0.00
Pathogen infection	L2	sowndiv + funcgr + leg	6.919	5	16.400	-3.049	107.148	0.00
Pathogen infection	Pd91	b * sowndiv^c	6.652	5	16.400	-2.515	107.682	0.00
Pathogen infection	Pd81	a + sowndiv^c	6.645	5	16.400	-2.501	107.696	0.00
Pathogen infection	Pf131	a + sowndiv^c	6.268	5	16.400	-1.746	108.451	0.00
Pathogen infection	Pf141	b * sowndiv^c	5.673	5	16.400	-0.557	109.640	0.00
Pathogen infection	Pd71	a + b * sowndiv	5.597	5	16.400	-0.404	109.793	0.00
Pathogen infection	L0	block + (sowndiv + funcgr + grass + leg)^2	18.527	15	5.467	0.219	110.416	0.00
Pathogen infection	Pn2031	sowndiv^c	3.933	4	20.500	0.654	110.851	0.00
Pathogen infection	Pi291	b * sowndiv^c	7.348	7	11.714	0.817	111.014	0.00
Pathogen infection	M111	d + a * sowndiv/(b + sowndiv)	7.242	7	11.714	1.029	111.226	0.00

Supplementary Table 2 (continued)

Long variable name	model name	model formula	LL	K	N2K	AICc	deltAICc	w_ic
Pathogen infection	M121	d + a * sowndiv/(b + sowndiv)	7.242	7	11.714	1.030	111.227	0.00
Pathogen infection	Pi281	a + sowndiv^c	7.224	7	11.714	1.065	111.262	0.00
Pathogen infection	Pj321	a + b * sowndiv	7.222	7	11.714	1.069	111.266	0.00
Pathogen infection	M5	a * sowndiv/(b + sowndiv)	4.745	5	16.400	1.299	111.496	0.00
Pathogen infection	Ec2421	exp(c * sowndiv)	3.570	4	20.500	1.379	111.577	0.00
Pathogen infection	Ea12	exp(c * sowndiv)	2.367	3	27.333	1.574	111.771	0.00
Pathogen infection	Pf121	a + b * sowndiv	4.472	5	16.400	1.845	112.042	0.00
Pathogen infection	Pe1031	sowndiv^c	2.939	4	20.500	2.641	112.838	0.00
Pathogen infection	Pd61	a + b * sowndiv^c	6.362	7	11.714	2.789	112.986	0.00
Pathogen infection	Pr3531	sowndiv^c	3.963	5	16.400	2.863	113.060	0.00
Pathogen infection	Pp2531	sowndiv^c	3.934	5	16.400	2.922	113.119	0.00
Pathogen infection	Pi271	a + b * sowndiv	6.179	7	11.714	3.155	113.352	0.00
Pathogen infection	Pg171	a + b * sowndiv	3.781	5	16.400	3.227	113.425	0.00
Pathogen infection	Pc531	sowndiv^c	1.501	3	27.333	3.307	113.504	0.00
Pathogen infection	Pq3031	sowndiv^c	3.040	5	16.400	4.710	114.907	0.00
Pathogen infection	Pm1531	sowndiv^c	1.865	4	20.500	4.790	114.987	0.00
Pathogen infection	Ps4031	sowndiv^c	4.085	6	13.667	4.951	115.148	0.00
Pathogen infection	M7	a * sowndiv/(b + sowndiv)	5.081	7	11.714	5.351	115.548	0.00
Pathogen infection	Pb21	a + b * sowndiv	0.410	3	27.333	5.487	115.684	0.00
Pathogen infection	Pa2	a + b * sowndiv	0.410	3	27.333	5.487	115.684	0.00
Pathogen infection	M1	a * sowndiv/(b + sowndiv)	0.260	3	27.333	5.788	115.985	0.00
Pathogen infection	M1a	SSmicmen(sowndiv, Vm, k)	0.260	3	27.333	5.788	115.985	0.00
Pathogen infection	E62	exp(c * sowndiv)	-0.331	3	27.333	6.970	117.167	0.00
Pathogen infection	M4	a * sowndiv/(b + sowndiv)	1.345	5	16.400	8.100	118.297	0.00
Pathogen infection	Eb1821	exp(c * sowndiv)	0.004	4	20.500	8.511	118.708	0.00
Pathogen infection	E2	a + b * exp(sowndiv)	-4.382	3	27.333	15.071	125.268	0.00
Pathogen infection	Ec24	exp(c * sowndiv)	-4.515	3	27.333	15.338	125.535	0.00
Pathogen infection	Eb18	exp(c * sowndiv)	-8.313	3	27.333	22.933	133.130	0.00
Pathogen infection	Pg201	sowndiv^c	-22.795	3	27.333	51.897	162.094	0.00
Pathogen infection	Pb51	sowndiv^c	-24.119	2	41.000	52.389	162.586	0.00
Pathogen infection	Pa5	sowndiv^c	-24.119	2	41.000	52.389	162.586	0.00
Pathogen infection	E52	b * exp(sowndiv)	-23.229	3	27.333	52.766	162.964	0.00
Pathogen infection	Pd101	sowndiv^c	-23.764	3	27.333	53.836	164.033	0.00

Supplementary Table 2 (continued)

Long variable name	model name	model formula	LL	K	N2K	AICc	deltAICc	w_ic
Pathogen infection	Ph251	sowndiv^c	-22.746	4	20.500	54.012	164.209	0.00
Pathogen infection	Pj351	sowndiv^c	-22.791	4	20.500	54.102	164.299	0.00
Pathogen infection	Pf151	sowndiv^c	-24.119	3	27.333	54.545	164.742	0.00
Pathogen infection	Pj301	sowndiv^c	-23.643	4	20.500	55.805	166.002	0.00
Pathogen infection	Pk401	sowndiv^c	-22.604	5	16.400	55.997	166.194	0.00
Pathogen infection	E51	b * exp(sowndiv)	-26.121	3	27.333	58.550	168.747	0.00
Pathogen infection	M91	a * sowndiv/(b + sowndiv)	-30.729	9	9.111	81.958	192.156	0.00
Pathogen infection	E5	b * exp(sowndiv)	-45.555	2	41.000	95.262	205.459	0.00
Pathogen infection	Ec2221	a + exp(sowndiv)	-794.917	4	20.500	1598.354	1708.551	0.00
Pathogen infection	Ed2821	a + exp(sowndiv)	-794.801	5	16.400	1600.391	1710.588	0.00
Pathogen infection	Ee342	a + exp(sowndiv)	-794.913	5	16.400	1600.615	1710.812	0.00
Pathogen infection	Eg4621	a + exp(sowndiv)	-794.796	6	13.667	1602.712	1712.909	0.00
Pathogen infection	E42	a + exp(sowndiv)	-801.579	3	27.333	1609.465	1719.662	0.00
Pathogen infection	Eb1621	a + exp(sowndiv)	-801.418	4	20.500	1611.355	1721.552	0.00
Pathogen infection	Ea1021	a + exp(sowndiv)	-801.577	4	20.500	1611.673	1721.870	0.00
Pathogen infection	Ef4021	a + exp(sowndiv)	-801.376	5	16.400	1613.542	1723.739	0.00
Pathogen infection	Ea1011	a + exp(sowndiv)	-1772.911	4	20.500	3554.342	3664.539	0.00
Pathogen infection	Ef4011	a + exp(sowndiv)	-1772.553	5	16.400	3555.894	3666.092	0.00
Pathogen infection	Ed2811	a + exp(sowndiv)	-1772.911	5	16.400	3556.612	3666.809	0.00
Pathogen infection	Eg4611	a + exp(sowndiv)	-1772.553	6	13.667	3558.225	3668.422	0.00
Pathogen infection	E41	a + exp(sowndiv)	-1784.916	3	27.333	3576.140	3686.338	0.00
Pathogen infection	Eb1611	a + exp(sowndiv)	-1784.570	4	20.500	3577.659	3687.856	0.00
Pathogen infection	Ec2211	a + exp(sowndiv)	-1784.916	4	20.500	3578.352	3688.549	0.00
Pathogen infection	Ee341	a + exp(sowndiv)	-1784.570	5	16.400	3579.929	3690.126	0.00
Pathogen infection	Ef3721	a + b * exp(c * sowndiv)	-2734.132	11	7.455	5494.035	5604.232	0.00
Pathogen infection	E4	a + exp(sowndiv)	-4912.516	2	41.000	9829.183	9939.380	0.00
Pathogen infection	Ea10	a + exp(sowndiv)	-4912.516	3	27.333	9831.339	9941.536	0.00
Pathogen infection	Eb16	a + exp(sowndiv)	-4912.516	3	27.333	9831.339	9941.536	0.00
Pathogen infection	Ec22	a + exp(sowndiv)	-4912.516	3	27.333	9831.339	9941.536	0.00
Pathogen infection	Ed28	a + exp(sowndiv)	-4912.516	4	20.500	9833.551	9943.748	0.00
Pathogen infection	Ee40	a + exp(sowndiv)	-4912.516	4	20.500	9833.551	9943.748	0.00
Pathogen infection	Ef40	a + exp(sowndiv)	-4912.516	4	20.500	9833.551	9943.748	0.00
Pathogen infection	Eg46	a + exp(sowndiv)	-4912.516	5	16.400	9835.821	9946.018	0.00

Supplementary Table 2 (continued)

Long variable name	model name	model formula	LL	K	N2K	AICc	deltAICc	w_ic
Plant invasion	Pa4	b * sowndiv^c	35.226	3	26.667	-64.136	0.000	0.29
Plant invasion	Pa3	a + sowndiv^c	35.036	3	26.667	-63.757	0.380	0.24
Plant invasion	AS1	SSasymp(sowndiv, Asym, R0, lrc)	36.012	4	20.000	-63.491	0.645	0.21
Plant invasion	M2	d + a * sowndiv/(b + sowndiv)	35.790	4	20.000	-63.047	1.089	0.17
Plant invasion	BIEXP	SSbiexp(sowndiv, A1, lrc1, A2, lrc2)	36.014	5	16.000	-61.218	2.918	0.07
Plant invasion	M1	a * sowndiv/(b + sowndiv)	32.131	3	26.667	-57.946	6.190	0.01
Plant invasion	M1a	SSmicmen(sowndiv, Vm, k)	32.131	3	26.667	-57.946	6.190	0.01
Plant invasion	Pa2	a + b * sowndiv	29.147	3	26.667	-51.978	12.159	0.00
Plant invasion	L2	sowndiv + funcgr + leg	30.911	5	16.000	-51.012	13.125	0.00
Plant invasion	E2	a + b * exp(sowndiv)	26.742	3	26.667	-47.168	16.969	0.00
Plant invasion	L0	block + (sowndiv + funcgr + grass + leg)^2	37.835	15	5.333	-38.170	25.967	0.00
Plant invasion	E5	b * exp(sowndiv)	13.224	2	40.000	-22.293	41.844	0.00
Plant invasion	Pa5	sowndiv^c	-34.269	2	40.000	72.694	136.830	0.00
Plant invasion	E4	a + exp(sowndiv)	-4793.686	2	40.000	9591.527	9655.664	0.00
Bioturbation	L22	sowndiv + funcgr + leg	51.391	6	13.667	-89.662	0.000	0.54
Bioturbation	L21	sowndiv + funcgr + leg	51.249	6	13.667	-89.377	0.285	0.46
Bioturbation	Pg191	b * sowndiv^c	33.746	5	16.400	-56.703	32.958	0.00
Bioturbation	Pg181	a + sowndiv^c	33.689	5	16.400	-56.589	33.073	0.00
Bioturbation	L2	sowndiv + funcgr + leg	33.180	5	16.400	-55.570	34.092	0.00
Bioturbation	M6	a * sowndiv/(b + sowndiv)	35.506	7	11.714	-55.499	34.162	0.00
Bioturbation	Pg171	a + b * sowndiv	33.072	5	16.400	-55.355	34.306	0.00
Bioturbation	Pn1831	a + sowndiv^c	34.117	6	13.667	-55.114	34.547	0.00
Bioturbation	Pn1931	b * sowndiv^c	34.103	6	13.667	-55.087	34.575	0.00
Bioturbation	Pn1921	b * sowndiv^c	33.896	6	13.667	-54.671	34.990	0.00
Bioturbation	Pn1821	a + sowndiv^c	33.807	6	13.667	-54.493	35.168	0.00
Bioturbation	M611	a * sowndiv/(b + sowndiv)	36.172	8	10.250	-54.372	35.289	0.00
Bioturbation	L222	sowndiv + funcgr + leg	33.556	6	13.667	-53.993	35.669	0.00
Bioturbation	L211	sowndiv + funcgr + leg	33.494	6	13.667	-53.868	35.793	0.00
Bioturbation	Pn1721	a + b * sowndiv	33.471	6	13.667	-53.822	35.839	0.00
Bioturbation	Ea911	a + exp(c * sowndiv)	33.428	6	13.667	-53.736	35.925	0.00
Bioturbation	Pn1731	a + b * sowndiv	33.328	6	13.667	-53.536	36.125	0.00
Bioturbation	M622	a * sowndiv/(b + sowndiv)	35.594	8	10.250	-53.216	36.446	0.00
Bioturbation	Pj321	a + b * sowndiv	34.315	7	11.714	-53.117	36.545	0.00

Supplementary Table 2 (continued)

Long variable name	model name	model formula	LL	K	N2K	AICc	deltAICc	w_ic
Bioturbation	Pj341	b * sowndiv^c	34.126	7	11.714	-52.739	36.923	0.00
Bioturbation	M311	a * sowndiv/(b + sowndiv)	32.900	6	13.667	-52.680	36.981	0.00
Bioturbation	Pj331	a + sowndiv^c	34.078	7	11.714	-52.642	37.020	0.00
Bioturbation	Ea921	a + exp(c * sowndiv)	32.774	6	13.667	-52.428	37.234	0.00
Bioturbation	Ph231	a + sowndiv^c	33.871	7	11.714	-52.228	37.433	0.00
Bioturbation	M91	a * sowndiv/(b + sowndiv)	36.353	9	9.111	-52.205	37.456	0.00
Bioturbation	Ph221	a + b * sowndiv	33.799	7	11.714	-52.084	37.578	0.00
Bioturbation	Ph241	b * sowndiv^c	33.798	7	11.714	-52.082	37.580	0.00
Bioturbation	Pr3231	a + b * sowndiv	34.861	8	10.250	-51.749	37.913	0.00
Bioturbation	Pr3431	b * sowndiv^c	34.599	8	10.250	-51.225	38.437	0.00
Bioturbation	M81	a * sowndiv/(b + sowndiv)	33.345	7	11.714	-51.177	38.484	0.00
Bioturbation	Pr3331	a + sowndiv^c	34.468	8	10.250	-50.964	38.697	0.00
Bioturbation	Pr3221	a + b * sowndiv	34.446	8	10.250	-50.919	38.743	0.00
Bioturbation	Pp2231	a + b * sowndiv	34.374	8	10.250	-50.776	38.885	0.00
Bioturbation	Ef3921	a + exp(c * sowndiv)	34.286	8	10.250	-50.600	39.061	0.00
Bioturbation	Pr3321	a + sowndiv^c	34.260	8	10.250	-50.547	39.115	0.00
Bioturbation	Pr3421	b * sowndiv^c	34.256	8	10.250	-50.539	39.122	0.00
Bioturbation	Pp2431	b * sowndiv^c	34.170	8	10.250	-50.368	39.294	0.00
Bioturbation	Pp2331	a + sowndiv^c	34.168	8	10.250	-50.363	39.298	0.00
Bioturbation	Pp2321	a + sowndiv^c	34.128	8	10.250	-50.283	39.378	0.00
Bioturbation	Pp2221	a + b * sowndiv	33.942	8	10.250	-49.912	39.749	0.00
Bioturbation	M832	a * sowndiv/(b + sowndiv)	33.928	8	10.250	-49.883	39.779	0.00
Bioturbation	M932	a * sowndiv/(b + sowndiv)	36.474	10	8.200	-49.849	39.813	0.00
Bioturbation	L0	block + (sowndiv + funcgr + grass + leg)^2	42.835	15	5.467	-48.397	41.264	0.00
Bioturbation	Pk371	a + b * sowndiv	34.366	9	9.111	-48.233	41.429	0.00
Bioturbation	Pk381	a + sowndiv^c	34.321	9	9.111	-48.141	41.520	0.00
Bioturbation	Pk391	b * sowndiv^c	34.235	9	9.111	-47.971	41.691	0.00
Bioturbation	L011	block + (sowndiv + funcgr + grass + leg)^2	43.917	16	5.125	-47.465	42.196	0.00
Bioturbation	Ps3731	a + b * sowndiv	34.915	10	8.200	-46.732	42.929	0.00
Bioturbation	M1321	d + a * sowndiv/(b + sowndiv)	36.179	11	7.455	-46.586	43.076	0.00
Bioturbation	Ps3931	b * sowndiv^c	34.628	10	8.200	-46.158	43.504	0.00
Bioturbation	Ps3831	a + sowndiv^c	34.591	10	8.200	-46.084	43.577	0.00
Bioturbation	Ps3821	a + sowndiv^c	34.570	10	8.200	-46.041	43.620	0.00

Supplementary Table 2 (continued)

Long variable name	model name	model formula	LL	K	N2K	AICc	deltAICc	w_ic
Bioturbation	Ps3721	a + b * sowndiv	34.499	10	8.200	-45.899	43.763	0.00
Bioturbation	Ps3921	b * sowndiv^c	34.424	10	8.200	-45.750	43.912	0.00
Bioturbation	L021	block + (sowndiv + funcgr + grass + leg)^2	43.031	16	5.125	-45.694	43.968	0.00
Bioturbation	M5	a * sowndiv/(b + sowndiv)	27.553	5	16.400	-44.317	45.344	0.00
Bioturbation	Pd81	a + sowndiv^c	27.499	5	16.400	-44.209	45.452	0.00
Bioturbation	Pd91	b * sowndiv^c	27.287	5	16.400	-43.785	45.877	0.00
Bioturbation	Pi291	b * sowndiv^c	29.352	7	11.714	-43.190	46.471	0.00
Bioturbation	Pd71	a + b * sowndiv	26.938	5	16.400	-43.086	46.576	0.00
Bioturbation	M522	a * sowndiv/(b + sowndiv)	27.886	6	13.667	-42.652	47.010	0.00
Bioturbation	Pq2931	b * sowndiv^c	30.223	8	10.250	-42.473	47.189	0.00
Bioturbation	M7	a * sowndiv/(b + sowndiv)	28.974	7	11.714	-42.434	47.227	0.00
Bioturbation	Pe831	a + sowndiv^c	27.710	6	13.667	-42.300	47.361	0.00
Bioturbation	Pe821	a + sowndiv^c	27.683	6	13.667	-42.247	47.415	0.00
Bioturbation	M511	a * sowndiv/(b + sowndiv)	27.665	6	13.667	-42.211	47.451	0.00
Bioturbation	Pe931	b * sowndiv^c	27.575	6	13.667	-42.031	47.631	0.00
Bioturbation	Pe921	b * sowndiv^c	27.461	6	13.667	-41.803	47.859	0.00
Bioturbation	Pi281	a + sowndiv^c	28.605	7	11.714	-41.696	47.966	0.00
Bioturbation	Pa4	b * sowndiv^c	23.999	3	27.333	-41.691	47.971	0.00
Bioturbation	Pb41	b * sowndiv^c	23.999	3	27.333	-41.691	47.971	0.00
Bioturbation	Pe731	a + b * sowndiv	27.306	6	13.667	-41.493	48.169	0.00
Bioturbation	Ec2121	a + exp(c * sowndiv)	27.304	6	13.667	-41.487	48.174	0.00
Bioturbation	Pa3	a + sowndiv^c	23.847	3	27.333	-41.386	48.276	0.00
Bioturbation	Pb31	a + sowndiv^c	23.847	3	27.333	-41.386	48.276	0.00
Bioturbation	Pi271	a + b * sowndiv	28.428	7	11.714	-41.343	48.318	0.00
Bioturbation	M121	d + a * sowndiv/(b + sowndiv)	28.340	7	11.714	-41.166	48.495	0.00
Bioturbation	Pe721	a + b * sowndiv	27.103	6	13.667	-41.086	48.576	0.00
Bioturbation	LG2	SSlogis(sowndiv, Asym, xmid, scal)	24.773	4	20.500	-41.027	48.635	0.00
Bioturbation	Pq2921	b * sowndiv^c	29.356	8	10.250	-40.739	48.923	0.00
Bioturbation	M722	a * sowndiv/(b + sowndiv)	29.351	8	10.250	-40.729	48.933	0.00
Bioturbation	M1a	SSmicmen(sowndiv, Vm, k)	23.445	3	27.333	-40.583	49.079	0.00
Bioturbation	M1	a * sowndiv/(b + sowndiv)	23.445	3	27.333	-40.583	49.079	0.00
Bioturbation	AS2	SSasympOff(sowndiv, Asym, lrc, c0)	24.431	4	20.500	-40.342	49.319	0.00
Bioturbation	AS1	SSasymp(sowndiv, Asym, R0, lrc)	24.431	4	20.500	-40.342	49.319	0.00

Supplementary Table 2 (continued)

Long variable name	model name	model formula	LL	K	N2K	AICc	deltAICc	w_ic
Bioturbation	LG1	SSfpl(sowndiv, A, B, xmid, scal)	25.560	5	16.400	-40.330	49.332	0.00
Bioturbation	Pc421	b * sowndiv^c	24.402	4	20.500	-40.285	49.376	0.00
Bioturbation	M711	a * sowndiv/(b + sowndiv)	29.104	8	10.250	-40.235	49.427	0.00
Bioturbation	Pq2731	a + b * sowndiv	29.051	8	10.250	-40.128	49.533	0.00
Bioturbation	M2	d + a * sowndiv/(b + sowndiv)	24.277	4	20.500	-40.035	49.626	0.00
Bioturbation	Pq2831	a + sowndiv^c	28.994	8	10.250	-40.016	49.646	0.00
Bioturbation	Pc321	a + sowndiv^c	24.205	4	20.500	-39.890	49.771	0.00
Bioturbation	Pc431	b * sowndiv^c	24.168	4	20.500	-39.817	49.844	0.00
Bioturbation	Pd61	a + b * sowndiv^c	27.661	7	11.714	-39.808	49.854	0.00
Bioturbation	Pc331	a + sowndiv^c	24.111	4	20.500	-39.702	49.960	0.00
Bioturbation	Pb21	a + b * sowndiv	22.976	3	27.333	-39.645	50.017	0.00
Bioturbation	Pa2	a + b * sowndiv	22.976	3	27.333	-39.645	50.017	0.00
Bioturbation	AS3	SSasympOrig(sowndiv, Asym, lrc)	22.956	3	27.333	-39.604	50.058	0.00
Bioturbation	Pa1	a + b * sowndiv^c	24.000	4	20.500	-39.481	50.180	0.00
Bioturbation	Pb11	a + b * sowndiv^c	24.000	4	20.500	-39.481	50.180	0.00
Bioturbation	Pq2821	a + sowndiv^c	28.682	8	10.250	-39.391	50.271	0.00
Bioturbation	M1232	d + a * sowndiv/(b + sowndiv)	28.620	8	10.250	-39.268	50.394	0.00
Bioturbation	M1221	d + a * sowndiv/(b + sowndiv)	28.493	8	10.250	-39.014	50.647	0.00
Bioturbation	Pq2721	a + b * sowndiv	28.478	8	10.250	-38.984	50.678	0.00
Bioturbation	Pc221	a + b * sowndiv	23.599	4	20.500	-38.678	50.984	0.00
Bioturbation	M211	d + a * sowndiv/(b + sowndiv)	24.642	5	16.400	-38.495	51.166	0.00
Bioturbation	E31	a + exp(c * sowndiv)	23.462	4	20.500	-38.404	51.257	0.00
Bioturbation	M222	d + a * sowndiv/(b + sowndiv)	24.497	5	16.400	-38.205	51.456	0.00
Bioturbation	Pc121	a + b * sowndiv^c	24.405	5	16.400	-38.021	51.640	0.00
Bioturbation	Pc231	a + b * sowndiv	23.004	4	20.500	-37.489	52.172	0.00
Bioturbation	Pf131	a + sowndiv^c	24.040	5	16.400	-37.290	52.372	0.00
Bioturbation	E32	a + exp(c * sowndiv)	22.878	4	20.500	-37.236	52.426	0.00
Bioturbation	Pf141	b * sowndiv^c	24.009	5	16.400	-37.228	52.434	0.00
Bioturbation	M4	a * sowndiv/(b + sowndiv)	23.648	5	16.400	-36.506	53.156	0.00
Bioturbation	Pf121	a + b * sowndiv	23.611	5	16.400	-36.433	53.228	0.00
Bioturbation	Pm1321	a + sowndiv^c	24.552	6	13.667	-35.983	53.678	0.00
Bioturbation	E2	a + b * exp(sowndiv)	21.086	3	27.333	-35.865	53.797	0.00
Bioturbation	Pm1421	b * sowndiv^c	24.411	6	13.667	-35.702	53.959	0.00

Supplementary Table 2 (continued)

Long variable name	model name	model formula	LL	K	N2K	AICc	deltAICc	w_ic
Bioturbation	Pm1331	a + sowndiv^c	24.220	6	13.667	-35.319	54.343	0.00
Bioturbation	Pm1431	b * sowndiv^c	24.218	6	13.667	-35.316	54.345	0.00
Bioturbation	M1432	d + a * sowndiv/(b + sowndiv)	30.418	11	7.455	-35.064	54.598	0.00
Bioturbation	Pm1221	a + b * sowndiv	23.977	6	13.667	-34.834	54.828	0.00
Bioturbation	Eb1511	a + exp(c * sowndiv)	23.941	6	13.667	-34.762	54.899	0.00
Bioturbation	M422	a * sowndiv/(b + sowndiv)	23.871	6	13.667	-34.621	55.040	0.00
Bioturbation	Pm1231	a + b * sowndiv	23.791	6	13.667	-34.462	55.199	0.00
Bioturbation	Eb1521	a + exp(c * sowndiv)	23.782	6	13.667	-34.444	55.217	0.00
Bioturbation	E22	a + b * exp(sowndiv)	21.156	4	20.500	-33.793	55.869	0.00
Bioturbation	Ef4211	exp(c * sowndiv)	21.157	5	16.400	-31.524	58.137	0.00
Bioturbation	Ef4221	exp(c * sowndiv)	16.334	5	16.400	-21.879	67.782	0.00
Bioturbation	Ea121	exp(c * sowndiv)	13.914	4	20.500	-19.308	70.354	0.00
Bioturbation	Ed3021	exp(c * sowndiv)	15.004	5	16.400	-19.219	70.443	0.00
Bioturbation	Ec2411	exp(c * sowndiv)	13.139	4	20.500	-17.759	71.902	0.00
Bioturbation	Ec2421	exp(c * sowndiv)	11.048	4	20.500	-13.576	76.085	0.00
Bioturbation	Ec24	exp(c * sowndiv)	7.669	3	27.333	-9.030	80.632	0.00
Bioturbation	Ea1221	exp(c * sowndiv)	8.355	4	20.500	-8.190	81.472	0.00
Bioturbation	E61	exp(c * sowndiv)	6.736	3	27.333	-7.165	82.497	0.00
Bioturbation	Eb1811	exp(c * sowndiv)	7.513	4	20.500	-6.507	83.155	0.00
Bioturbation	Ea12	exp(c * sowndiv)	4.914	3	27.333	-3.521	86.141	0.00
Bioturbation	E51	b * exp(sowndiv)	4.582	3	27.333	-2.857	86.805	0.00
Bioturbation	E62	exp(c * sowndiv)	4.096	3	27.333	-1.885	87.777	0.00
Bioturbation	E5	b * exp(sowndiv)	2.777	2	41.000	-1.401	88.260	0.00
Bioturbation	Eb1821	exp(c * sowndiv)	4.545	4	20.500	-0.571	89.091	0.00
Bioturbation	E52	b * exp(sowndiv)	2.818	3	27.333	0.671	90.332	0.00
Bioturbation	Eb18	exp(c * sowndiv)	2.171	3	27.333	1.965	91.627	0.00
Bioturbation	Pp2521	sowndiv^c	-24.896	5	16.400	60.581	150.243	0.00
Bioturbation	Ps4021	sowndiv^c	-24.707	6	13.667	62.534	152.196	0.00
Bioturbation	Pr3521	sowndiv^c	-26.207	5	16.400	63.204	152.866	0.00
Bioturbation	Pq3021	sowndiv^c	-26.584	5	16.400	63.957	153.619	0.00
Bioturbation	Pe1021	sowndiv^c	-28.744	4	20.500	66.007	155.669	0.00
Bioturbation	Pn2021	sowndiv^c	-29.447	4	20.500	67.414	157.075	0.00
Bioturbation	Pm1521	sowndiv^c	-37.625	4	20.500	83.770	173.431	0.00

Supplementary Table 2 (continued)

Long variable name	model name	model formula	LL	K	N2K	AICc	deltAICc	w_ic
Bioturbation	Pe1031	sowndiv^c	-38.048	4	20.500	84.616	174.277	0.00
Bioturbation	Pp2531	sowndiv^c	-37.204	5	16.400	85.198	174.860	0.00
Bioturbation	Pq3031	sowndiv^c	-37.236	5	16.400	85.261	174.922	0.00
Bioturbation	Pr3531	sowndiv^c	-37.381	5	16.400	85.551	175.212	0.00
Bioturbation	Pc521	sowndiv^c	-40.052	3	27.333	86.412	176.074	0.00
Bioturbation	Ps4031	sowndiv^c	-37.205	6	13.667	87.529	177.191	0.00
Bioturbation	Pn2031	sowndiv^c	-43.222	4	20.500	94.963	184.625	0.00
Bioturbation	Pc531	sowndiv^c	-49.415	3	27.333	105.137	194.798	0.00
Bioturbation	Pd101	sowndiv^c	-50.173	3	27.333	106.654	196.315	0.00
Bioturbation	Pm1531	sowndiv^c	-49.112	4	20.500	106.743	196.405	0.00
Bioturbation	Pj351	sowndiv^c	-49.668	4	20.500	107.855	197.516	0.00
Bioturbation	Ph251	sowndiv^c	-50.103	4	20.500	108.726	198.388	0.00
Bioturbation	Pi301	sowndiv^c	-50.165	4	20.500	108.850	198.512	0.00
Bioturbation	Pb51	sowndiv^c	-52.563	2	41.000	109.278	198.939	0.00
Bioturbation	Pa5	sowndiv^c	-52.563	2	41.000	109.278	198.939	0.00
Bioturbation	Pk401	sowndiv^c	-49.652	5	16.400	110.093	199.755	0.00
Bioturbation	Pg201	sowndiv^c	-52.124	3	27.333	110.555	200.217	0.00
Bioturbation	Pf151	sowndiv^c	-52.405	3	27.333	111.117	200.778	0.00
Bioturbation	Ec2221	a + exp(sowndiv)	-794.448	4	20.500	1597.415	1687.077	0.00
Bioturbation	Ed2821	a + exp(sowndiv)	-794.410	5	16.400	1599.609	1689.271	0.00
Bioturbation	Ee342	a + exp(sowndiv)	-794.442	5	16.400	1599.673	1689.335	0.00
Bioturbation	Eg4621	a + exp(sowndiv)	-794.410	6	13.667	1601.939	1691.601	0.00
Bioturbation	E42	a + exp(sowndiv)	-801.242	3	27.333	1608.791	1698.453	0.00
Bioturbation	Eb1621	a + exp(sowndiv)	-801.072	4	20.500	1610.663	1700.325	0.00
Bioturbation	Ea1021	a + exp(sowndiv)	-801.210	4	20.500	1610.940	1700.602	0.00
Bioturbation	Ef4021	a + exp(sowndiv)	-800.951	5	16.400	1612.692	1702.353	0.00
Bioturbation	Ea1011	a + exp(sowndiv)	-1726.313	4	20.500	3461.145	3550.806	0.00
Bioturbation	Ef4011	a + exp(sowndiv)	-1726.127	5	16.400	3463.043	3552.704	0.00
Bioturbation	Ed2811	a + exp(sowndiv)	-1726.313	5	16.400	3463.415	3553.076	0.00
Bioturbation	Eg4611	a + exp(sowndiv)	-1726.127	6	13.667	3465.373	3555.035	0.00
Bioturbation	Eb1611	a + exp(sowndiv)	-1744.127	4	20.500	3496.773	3586.434	0.00
Bioturbation	Ee341	a + exp(sowndiv)	-1744.127	5	16.400	3499.043	3588.704	0.00
Bioturbation	E41	a + exp(sowndiv)	-1746.568	3	27.333	3499.445	3589.106	0.00

Supplementary Table 2 (continued)

Long variable name	model name	model formula	LL	K	N2K	AICc	deltAICc	w_ic
Bioturbation	Ec2211	a + exp(sowndiv)	-1746.568	4	20.500	3501.656	3591.318	0.00
Bioturbation	Ef3721	a + b * exp(c * sowndiv)	-2690.078	11	7.455	5405.927	5495.588	0.00
Bioturbation	E4	a + exp(sowndiv)	-4912.516	2	41.000	9829.183	9918.845	0.00
Bioturbation	Ea10	a + exp(sowndiv)	-4912.516	3	27.333	9831.339	9921.000	0.00
Bioturbation	Eb16	a + exp(sowndiv)	-4912.516	3	27.333	9831.339	9921.000	0.00
Bioturbation	Ec22	a + exp(sowndiv)	-4912.516	3	27.333	9831.339	9921.000	0.00
Bioturbation	Ed28	a + exp(sowndiv)	-4912.516	4	20.500	9833.551	9923.212	0.00
Bioturbation	Ee40	a + exp(sowndiv)	-4912.516	4	20.500	9833.551	9923.212	0.00
Bioturbation	Ef40	a + exp(sowndiv)	-4912.516	4	20.500	9833.551	9923.212	0.00
Bioturbation	Eg46	a + exp(sowndiv)	-4912.516	5	16.400	9835.821	9925.482	0.00
Ant activity	L2	sowndiv + funcgr + leg	13.401	5	16.200	-16.001	0.000	0.96
Ant activity	Pa2	a + b * sowndiv	6.621	3	27.000	-6.929	9.072	0.01
Ant activity	Pa3	a + sowndiv^c	6.047	3	27.000	-5.783	10.218	0.01
Ant activity	E2	a + b * exp(sowndiv)	5.979	3	27.000	-5.645	10.356	0.01
Ant activity	Pa4	b * sowndiv^c	5.939	3	27.000	-5.567	10.434	0.01
Ant activity	AS1	SSasymp(sowndiv, Asym, R0, lrc)	6.701	4	20.250	-4.876	11.125	0.00
Ant activity	Pa1	a + b * sowndiv^c	6.689	4	20.250	-4.852	11.149	0.00
Ant activity	L0	block + (sowndiv + funcgr + grass + leg)^2	20.443	15	5.400	-3.502	12.499	0.00
Ant activity	M1a	SSmicmen(sowndiv, Vm, k)	4.842	3	27.000	-3.371	12.630	0.00
Ant activity	M1	a * sowndiv/(b + sowndiv)	4.842	3	27.000	-3.371	12.630	0.00
Ant activity	BIEXP	SSbiexp(sowndiv, A1, lrc1, A2, lrc2)	6.702	5	16.200	-2.605	13.396	0.00
Ant activity	Pa5	sowndiv^c	-36.660	2	40.500	77.473	93.474	0.00
Ant activity	E5	b * exp(sowndiv)	-40.907	2	40.500	85.967	101.968	0.00
Ant activity	E4	a + exp(sowndiv)	-4853.104	2	40.500	9710.361	9726.362	0.00

Supplementary Table 3 | Parameter estimates of minimal adequate 1-, 2- and 3-parameter power models (in a separate file)

Supplementary Table 4 | Parameter estimates of common two-parameter power models. Shown are the estimates of the exponent, z, in models of the form $y=b \times S^z$, where b is an estimated constant and S is the plant species richness of the community. Response, response variable; Compartment, above- or belowground. Measure, abundance or species richness ("diversity"). SE, the standard error of each estimate. Response variables are scaled to [0;1], plant species richness ranges from 1-60 plant species. For example, collembolan abundance

Response	Compartment	Measure	Estimate	SE
Herbivorous invertebrates	aboveground	abundance	0.35	0.05
Carnivorous invertebrates	aboveground	abundance	0.18	0.06
Omnivorous invertebrates	aboveground	abundance	0.12	0.07
Hyperparasitoids	aboveground	abundance	-0.06	0.17
Parasitoids	aboveground	abundance	0.34	0.09
Plant invaders	aboveground	abundance	-0.29	0.09
Pollinators	aboveground	abundance	0.06	0.08
Voles	aboveground	abundance	0.18	0.17
Herbivorous invertebrates	aboveground	diversity	0.39	0.04
Carnivorous invertebrates	aboveground	diversity	0.21	0.04
Omnivorous invertebrates	aboveground	diversity	0.07	0.05
Parasitoids	aboveground	diversity	0.21	0.04
Plant invaders	aboveground	diversity	-0.37	0.07
Pollinators	aboveground	diversity	0.22	0.05
Plant-pathogenic fungi	aboveground	diversity	0.20	0.03
Bacterivorous Nematodes	belowground	abundance	0.08	0.09
Fungivorous Nematodes	belowground	abundance	-0.05	0.10
Omnivorous Nematodes	belowground	abundance	0.02	0.09
Plant-feeding Nematodes	belowground	abundance	0.06	0.07
Predatory Nematodes	belowground	abundance	0.92	0.21
Collembolans	belowground	abundance	0.11	0.06
Earthworms	belowground	abundance	0.07	0.08
Gamasida	belowground	abundance	0.28	0.12
Herbivorous macrofauna	belowground	abundance	0.19	0.08
Predatory macrofauna	belowground	abundance	0.09	0.10
Saprophagous macrofauna	belowground	abundance	0.18	0.08
Mites	belowground	abundance	-0.01	0.09
Bacterivorous Nematodes	belowground	diversity	0.11	0.06
Fungivorous Nematodes	belowground	diversity	0.02	0.05
Omnivorous Nematodes	belowground	diversity	0.03	0.08
Plant-feeding Nematodes	belowground	diversity	0.12	0.05
Predatory Nematodes	belowground	diversity	0.16	0.15
Collembolans	belowground	diversity	0.10	0.04
Earthworms	belowground	diversity	0.01	0.04
Herbivorous macrofauna	belowground	diversity	0.18	0.05
Predatory macrofauna	belowground	diversity	0.04	0.05
Saprophagous macrofauna	belowground	diversity	0.14	0.05
Mycorrhiza	belowground	diversity	0.08	0.04

Supplementary Table 5a | Multivariate comparisons of organism abundances.
Columns are (from left to right): ID, variable number; Response variables (herbivore abundance etc.); "1-2" the successive difference contrast between variables 1 and 2 (herbivores vs. carnivores); "2-3" etc. accordingly. Table entries in rows 1-10 are contrast coefficients for successive difference contrasts. The two bottom rows contain the relevant information, namely the F and P values for the hypotheses tested. For example, herbivores and carnivore abundance (1 vs. 2) differ significantly at P<0.01.

ID	Response variable	1-2	2-3	3-4	4-5	5-6	6-7	7-8	8-9	9-10
1	Herbivores	-0.90	-0.80	-0.70	-0.60	-0.50	-0.40	-0.30	-0.20	-0.10
2	Carnivores	0.10	-0.80	-0.70	-0.60	-0.50	-0.40	-0.30	-0.20	-0.10
3	Omnivores	0.10	0.20	-0.70	-0.60	-0.50	-0.40	-0.30	-0.20	-0.10
4	Parasitoids	0.10	0.20	0.30	-0.60	-0.50	-0.40	-0.30	-0.20	-0.10
5	Pollinators	0.10	0.20	0.30	0.40	-0.50	-0.40	-0.30	-0.20	-0.10
6	Voles	0.10	0.20	0.30	0.40	0.50	-0.40	-0.30	-0.20	-0.10
7	Plant invaders	0.10	0.20	0.30	0.40	0.50	0.60	-0.30	-0.20	-0.10
8	Herbivorous macrofauna	0.10	0.20	0.30	0.40	0.50	0.60	0.70	-0.20	-0.10
9	Predatory macrofauna	0.10	0.20	0.30	0.40	0.50	0.60	0.70	0.80	-0.10
10	Saprophagous macrofauna	0.10	0.20	0.30	0.40	0.50	0.60	0.70	0.80	0.90
	F-Value	**23.74**	**19.61**	**16.22**	**24.45**	**15.09**	**9.98**	**0.03**	**1.52**	**0.13**
	P-Value	**<0.01**	**<0.01**	**<0.01**	**<0.01**	**<0.01**	**<0.01**	**0.85**	**0.22**	**0.73**

Supplementary Table 5b | Multivariate comparisons of organism species richness.
Columns are (from left to right): ID, variable number; Response variables (herbivore species richness etc.); "1-2" the successive difference contrast between variables 1 and 2 (herbivores vs. carnivores); "2-3" etc. accordingly. Table entries in rows 1-9 are contrast coefficients for successive difference contrasts. The two bottom rows contain the relevant information, namely the F and P values for the hypotheses tested. For example, herbivores and carnivore diversity (1 vs. 2) differ significantly at P<0.01.

ID	Response variable	1-2	2-3	3-4	4-5	5-6	6-7	7-8	8-9
1	Herbivores	-0.89	-0.78	-0.67	-0.56	-0.44	-0.33	-0.22	-0.11
2	Carnivores	0.11	-0.78	-0.67	-0.56	-0.44	-0.33	-0.22	-0.11
3	Omnivores	0.11	0.22	-0.67	-0.56	-0.44	-0.33	-0.22	-0.11
4	Parasitoids	0.11	0.22	0.33	-0.56	-0.44	-0.33	-0.22	-0.11
5	Pollinators	0.11	0.22	0.33	0.44	-0.44	-0.33	-0.22	-0.11
6	Invaders	0.11	0.22	0.33	0.44	0.56	-0.33	-0.22	-0.11
7	Herbivorous macrofauna	0.11	0.22	0.33	0.44	0.56	0.67	-0.22	-0.11
8	Predatory macrofauna	0.11	0.22	0.33	0.44	0.56	0.67	0.78	-0.11
9	Saprophagous macrofauna	0.11	0.22	0.33	0.44	0.56	0.67	0.78	0.89
	F-Value	**44.89**	**33.69**	**14.15**	**18.17**	**18.09**	**0.05**	**0.43**	**0.64**
	P-Value	**<0.01**	**<0.01**	**<0.01**	**<0.01**	**<0.01**	**0.83**	**0.52**	**0.43**

Supplementary Table 5c | Multivariate comparisons of organism interactions. Columns are (from left to right): ID, variable number; Response variables (herbivory, parasitism, etc.); "1-2" the successive difference contrast between variables 1 and 2 (herbivory vs. parasitism); "2-3" etc. accordingly. Table entries in rows 1-10 are contrast coefficients for successive difference contrasts. The two bottom rows contain the relevant information, namely the F and P values for the hypotheses tested. For example, herbivory and parasitism (1 vs. 2) are not significantly different from one another.

ID	Response variable	1-2	2-3	3-4	4-5	5-6	6-7	7-8	8-9	9-10
1	Herbivory	-0.90	-0.80	-0.70	-0.60	-0.50	-0.40	-0.30	-0.20	-0.10
2	Parasitism	0.10	-0.80	-0.70	-0.60	-0.50	-0.40	-0.30	-0.20	-0.10
3	Flower visitation	0.10	0.20	-0.70	-0.60	-0.50	-0.40	-0.30	-0.20	-0.10
4	Decomposition	0.10	0.20	0.30	-0.60	-0.50	-0.40	-0.30	-0.20	-0.10
5	Seed predation	0.10	0.20	0.30	0.40	-0.50	-0.40	-0.30	-0.20	-0.10
6	Microbial respiration	0.10	0.20	0.30	0.40	0.50	-0.40	-0.30	-0.20	-0.10
7	Pathogen damage	0.10	0.20	0.30	0.40	0.50	0.60	-0.30	-0.20	-0.10
8	Invasion	0.10	0.20	0.30	0.40	0.50	0.60	0.70	-0.20	-0.10
9	Bioturbation	0.10	0.20	0.30	0.40	0.50	0.60	0.70	0.80	-0.10
10	Ant activity	0.10	0.20	0.30	0.40	0.50	0.60	0.70	0.80	0.90
	F-Value	3.69	1.27	9.13	6.22	10.48	7.57	13.94	4.73	0.39
	P-Value	0.06	0.27	<0.01	0.02	<0.01	0.01	<0.01	0.04	0.54

Supplementary Table 6 | Sample covariance matrix used for the structural equation model presented in Fig. 3.

ID	Label	1	2	3	4	5	6	7	8	9	10
1	log (Plant species richness)	2.34									
2	Aboveground plant biomass (g/m²)	0.15	0.03								
3	Aboveground dead plant biomass (g/m²)	0.18	0.02	0.05							
4	Aboveground herbivore abundance	0.21	0.02	0.03	0.05						
5	Saprophagous macrofauna abundance	0.06	0.01	0.01	0.01	0.04					
6	Herbivorous macrofauna abundance	0.15	0.02	0.02	0.02	0.02	0.05				
7	Aboveground carnivore abundance	0.16	0.02	0.02	0.03	0.01	0.02	0.05			
8	Predatory macrofauna abundance	0.05	0.01	0.01	0.02	0.02	0.02	0.01	0.04		
9	Aboveground omnivore abundance	0.08	0.01	0.02	0.01	0.01	0.01	0.02	0.00	0.06	
10	Aboveground parasitoid abundance	0.20	0.02	0.02	0.04	0.01	0.02	0.04	0.01	0.03	0.08

Supplementary Table 7 | Sample correlation matrix used for the structural equation model presented in Fig. 3.

ID	Label	1	2	3	4	5	6	7	8	9	10
1	log (Plant species richness)	1.00									
2	Aboveground plant biomass (g/m²)	0.57	1.00								
3	Aboveground dead plant biomass (g/m²)	0.56	0.48	1.00							
4	Aboveground herbivore abundance	0.65	0.54	0.60	1.00						
5	Saprophagous macrofauna abundance	0.20	0.26	0.21	0.36	1.00					
6	Herbivorous macrofauna abundance	0.42	0.40	0.37	0.50	0.43	1.00				
7	Aboveground carnivore abundance	0.47	0.39	0.34	0.61	0.30	0.35	1.00			
8	Predatory macrofauna abundance	0.18	0.30	0.13	0.41	0.51	0.53	0.32	1.00		
9	Aboveground omnivore abundance	0.23	0.33	0.29	0.18	0.20	0.13	0.40	0.07	1.00	
10	Aboveground parasitoid abundance	0.46	0.50	0.31	0.59	0.26	0.32	0.59	0.15	0.48	1.00

Supplementary Table 8 | Unstandardized parameter estimates of the structural equation model presented in Fig. 3. S.E., standard error; C.R. critical ratio (estimate divided by S.E.)

			Estimate	S.E.	C.R.	P
Aboveground plant biomass (g/m²)	<---	log (Plant species richness)	0.06	0.01	4.817	<0.001
Aboveground herbivore abundance	<---	log (Plant species richness)	0.07	0.02	4.178	<0.001
Aboveground herbivore abundance	<---	Aboveground plant biomass (g/m²)	0.27	0.16	1.749	0.08
Aboveground dead plant biomass (g/m²)	<---	Aboveground plant biomass (g/m²)	0.30	0.18	1.696	0.09
Aboveground dead plant biomass (g/m²)	<---	log (Plant species richness)	0.06	0.02	3.055	0.002
Aboveground carnivore abundance	<---	Aboveground herbivore abundance	0.61	0.14	4.257	<0.001
Herbivorous macrofauna abundance	<---	log (Plant species richness)	0.06	0.02	3.172	0.002
Saprophagous macrofauna abundance	<---	Aboveground dead plant biomass (g/m²)	0.15	0.12	1.254	0.21
Aboveground carnivore abundance	<---	Aboveground plant biomass (g/m²)	0.11	0.18	0.64	0.522
Aboveground parasitoid abundance	<---	Aboveground herbivore abundance	0.70	0.17	4.185	<0.001
Aboveground omnivore abundance	<---	Aboveground carnivore abundance	0.42	0.14	3.017	0.003
Predatory macrofauna abundance	<---	Herbivorous macrofauna abundance	0.31	0.10	3.051	0.002
Predatory macrofauna abundance	<---	Saprophagous macrofauna abundance	0.35	0.12	2.92	0.003
Aboveground parasitoid abundance	<---	Aboveground plant biomass (g/m²)	0.27	0.21	1.336	0.182

Supplementary Table 9 | Standardized parameter estimates of the structural equation model presented in Fig. 3

			Estimate
Aboveground plant biomass (g/m²)	<---	log (Plant species richness)	0.567
Aboveground herbivore abundance	<---	log (Plant species richness)	0.529
Aboveground herbivore abundance	<---	Aboveground plant biomass (g/m²)	0.218
Aboveground dead plant biomass (g/m²)	<---	Aboveground plant biomass (g/m²)	0.237
Aboveground dead plant biomass (g/m²)	<---	log (Plant species richness)	0.426
Aboveground carnivore abundance	<---	Aboveground herbivore abundance	0.563
Herbivorous macrofauna abundance	<---	log (Plant species richness)	0.4
Saprophagous macrofauna abundance	<---	Aboveground dead plant biomass (g/m²)	0.17
Aboveground carnivore abundance	<---	Aboveground plant biomass (g/m²)	0.085
Aboveground parasitoid abundance	<---	Aboveground herbivore abundance	0.521
Aboveground omnivore abundance	<---	Aboveground carnivore abundance	0.396
Predatory macrofauna abundance	<---	Herbivorous macrofauna abundance	0.372
Predatory macrofauna abundance	<---	Saprophagous macrofauna abundance	0.356
Aboveground parasitoid abundance	<---	Aboveground plant biomass (g/m²)	0.164

Supplementary Table 10 | Intercepts for variables in the structural equation model presented in Fig. 3. S.E., standard error; C.R. critical ratio (estimate divided by S.E.)

	Estimate	S.E.	C.R.	P
Aboveground plant biomass (g/m²)	0.62	0.04	15.38	<0.001
Aboveground herbivore abundance	0.13	0.11	1.19	0.233
Aboveground dead plant biomass (g/m²)	0.05	0.12	0.38	0.707
Aboveground carnivore abundance	0.05	0.12	0.38	0.705
Herbivorous macrofauna abundance	0.37	0.06	6.55	<0.001
Saprophagous macrofauna abundance	0.46	0.06	7.95	<0.001
Aboveground omnivore abundance	0.29	0.07	4.08	<0.001
Aboveground parasitoid abundance	-0.11	0.14	-0.74	0.457
Predatory macrofauna abundance	0.20	0.07	2.78	0.005

Supplementary Notes

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