Supporting Information

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SI Methods

Land-Use Intensity Index. The land-use intensity index (LUI) sums the intensity of fertilization (F), the frequency of mowing (M), and the intensity of livestock grazing (G) in each plot. Pesticides were not applied to any of the plots, and were therefore not included. F was quantified as kilograms of nitrogen (N) applied per hectare and included both organic and inorganic N; rates varied between 0 and 163 kg of $\mathrm{N{\cdot}ha^{-1}}$. To convert organic fertilizer inputs to kilograms of N per hectare, the volume of cattle slurry was multiplied by 3.2 kg of $\mathrm{N{\cdot}m^{-3}}$ and that of cattle manure was multiplied by 0.6 kg of $\mathrm{N{\cdot}m^{-3}}$. G was calculated based on the number of days of grazing, the density of grazing animals per hectare, and the type of grazing animal, which was expressed as livestock units (LU), and varied between 0 and 1,430 LU. Grazing animals were converted to LU as follows: cattle <1 y old, 0.3 LU; cattle aged 2 y, 0.6 LU; cattle >2 y old, 1 LU; sheep and goats <1 y old, 0.05 LU; sheep and goats >1 y old, 0.1 LU; horses <3 y old, 0.7 LU; horses >3 y old, 1.1 LU. M was the number of cuts per year and ranged from one to three. The intensities of these three land-use components were standardized by their means across regions and across 3 y (2006–2008) and summed to produce the LUI:

$$\mathrm{LUI} = \sqrt{\frac{F}{F_{G\ 2006\text{–}2008}} + \frac{G}{G_{G\ 2006\text{–}2008}} + \frac{M}{M_{G\ 2006\text{–}2008}}},$$

where $F_{G\ 2006\text{–}2008}$, $G_{G\ 2006\text{–}2008}$, and $M_{G\ 2006\text{–}2008}$ are the global mean values for fertilization, grazing, and mowing across all regions and across 3 y: $F_{G\ 2006\text{–}2008} = 23$ kg of $\mathrm{N{\cdot}ha^{-1}}$, $G_{G\ 2006\text{–}2008} = 129$ grazing days (i.e., equivalent to grazing one cow >2 y old per hectare for 129 d), and $M_{G\ 2006\text{–}2008} = 1.0$ cut per year. The square-root transformation was applied to produce a more even distribution and to reduce the influence of outliers. Standardizing by means within regions gave almost identical values ($R^2 = 0.97$), as did standardizing by the maximum rather than the mean ($R^2 = 0.86$) (1).

Sensitivity Analyses. In addition to the main analysis using a mean of scaled species richness values, we used a threshold-based approach to calculate multidiversity because it has been argued that this is more appropriate for multifunctionality indices (2, 3). In each plot, the species richness of each taxonomic group was scored as to whether it passed a certain threshold, which was defined as a proportion of the maximum species richness attained by that group in any plot across all regions. For each plot, the multidiversity score was the proportion of groups that exceeded the given threshold (i.e., the proportion of taxonomic groups that were at high diversity). We used thresholds of 30%, 50%, 60%, and 70% of the maximum species richness for each group (Table S3). Using these different thresholds resulted in very similar model selection. In all cases, asymptotic exponential models were the best (all models in the 95% confidence set modeled an asymptotic exponential relationship between LUI and multidiversity) and the SD in LUI ($\mathrm{LUI_{sd}}$) was included in the best-fit models (Table S3). This shows that using a threshold did not qualitatively change our results. In addition to using a threshold, we tested whether standardizing species richness values by calculating z-scores (i.e., subtracting the mean and dividing by the SD) changed the results compared with standardizing by the maximum. The alternative standardization gave almost exactly the same results (Table S3).

We also calculated multidiversity of rare (bottom 90%) and common (top 10%) species separately for each region. Species that are restricted to a single region might, in fact, be common within a region but appear rare across regions. To account for this, we designated species as rare or common for each of the three regions and then calculated multidiversity of rare and common species separately per region. We then combined the multidiversity values from the different regions and analyzed them in a single analysis using the same models as before. This gave similar results to defining the rare and common species across regions. Regardless of whether rare species were defined across regions or separately within regions, multidiversity was best predicted with an asymptotic exponential model and changing land use over time was beneficial for rare species multidiversity (Table S3). For the multidiversity of common species, variation in LUI over time had positive effects when the common species were defined across or within regions. In both cases, overall mean LUI did not have strong effects on multidiversity, but the shape of the relationship varied, the model with the lowest Akaike's information criterion (corrected for small sample sizes), AICc, in the analysis of multidiversity of common species defined within regions had a quadratic term for LUI (Table S3). This model predicted that the lowest multidiversity was found at intermediate LUI; however, the quadratic relationship was not well supported, because the second best model (<1 AICc unit higher than the best model) suggested a continuous, decelerating decline in multidiversity with LUI. Because it is not possible to separate models that differ in <2 AICc units, we can only conclude that the common species multidiversity, defined within regions, declines nonlinearly with increasing LUI and that variation in LUI has an important effect. Thus, both methods of defining common species gave similar results, although the species that are common across regions seem less sensitive to overall LUI.

Our measure of multidiversity gives equal weight to all of the groups used to calculate it; therefore, we also explored the sensitivity of our measure to alternative groupings. Using the subset of 27 plots, we aggregated the data into progressively larger taxonomic groups and checked whether calculating multidiversity among these larger groups changed the result. Multidiversity values calculated using these different groupings were very closely correlated (Fig. S6).

Individual Components of Land Use and Land-Use Variation. Although the models containing the integrated index of LUI had better fits than the models with the individual components of land use (grazing, fertilization, and mowing) fitted separately (Table S2), we did some additional modeling to determine which of these components was most important in affecting multidiversity. We therefore analyzed multidiversity only with models containing the individual land-use components: All possible combinations of linear and quadratic terms for grazing, fertilization, and mowing were fitted, along with the $\mathrm{LUI_{sd}}$, which was fitted only as a linear term (all the models containing the individual components are listed in Table S1). All of the variables seemed to be important, because the best-fit model contained linear terms for mowing and grazing and a quadratic term for fertilization, along with the $\mathrm{LUI_{sd}}$. Examining the AICc weights of the terms revealed some differences, with grazing and mowing having higher weights than fertilization (Fig. S2). Variation in LUI remained important in this set of models. We also plotted the effects of the different components of LUI using partial regression plots, which is the most appropriate way to show the effects of variables that are correlated with each other (4) (Fig. S2). This showed that mowing and grazing had strong negative effects on multidiversity, whereas fertilization had much smaller effects, with high rates of fertilization not negative for multidiversity. High fertilization is usually associated with high mowing frequency (1), but these results show that the high rates of fertilization themselves may not have as negative effects as high mowing intensity. It is often predicted that diversity is maximized at intermediate grazing intensity and not at the lowest grazing intensities (5). We do not find evidence for this here, but we note that we have no grasslands that are never grazed or mown and that cessation of grazing in our species-rich, lightly grazed grasslands would likely lead to shrub encroachment and a decline in the diversity of many groups.

To investigate the effects of $\mathrm{LUI}_{\mathrm{sd}}$ further, we fitted a series of asymptotic exponential models with parameters modeled as a function of the SD in the individual components of land use (grazing, fertilization, and mowing). We selected all of the models in the 95% confidence set (Table S2), and as well as fitting models in which the intercept, intercept and asymptote, intercept and rate constant, or all three parameters depended on the $\mathrm{LUI}_{\mathrm{sd}}$, we also fitted sets of models in which these parameters depended on all possible combinations of SD in fertilization, mowing, or grazing: a total of 33 models. This led to the same model selection as in the overall analysis (i.e., models containing variation in the individual components provided much worse fits than models with $\mathrm{LUI}_{\mathrm{sd}}$). This indicates that temporal variation in LUI is much better captured with our overall metric than with measures of variability in different types of land use. However, to identify whether variation in some types of land use was more important, we removed the models containing $\mathrm{LUI}_{\mathrm{sd}}$ from the set of models and selected only among models with the temporal SDs of the individual components. This revealed that the SD in grazing intensity over time was most important (100% of AICc weights) and that variation in the other components was less important (SD of fertilization intensity = 43% and SD of mowing intensity = 57%). The effect size of the SD of grazing intensity was also larger, because it increased the intercept of the asymptotic exponential by 1.71 ± 1.1, which is larger than the effect of fertilization (1.05 ± 1.1) or mowing (0.83 ± 0.82); these parameters come from a model with the intercept modeled as a function of the SD in grazing, mowing, and fertilization.

Effect of Changes in Abundance. We further investigated whether the patterns in species richness that we found could have been driven only by changes in abundance or whether there was an effect on species richness, per se. Typically, rarefaction would be used to correct species richness values for abundance, but in our dataset, minimum abundance values in a plot were low (often one or two individuals) for many taxonomic groups, making rarefaction problematic. We therefore used the approach of Richardson and Richards (6), which generates an expected diversity for each group in each plot, assuming that only abundance drives the species richness patterns. This approach pools all individuals of every species into one large group and then randomly samples individuals from this species pool to form the local communities. The randomization is constrained so that total abundance in each sample and for each species remains fixed at observed values. We used this randomization to produce expected species richness values for each group in each plot. We used the data from the 17 groups (minus mycorrhizal fungi, for which there were no abundance data) measured on the 150 grassland plots for this analysis.

Having derived expected species richness values, we then calculated multidiversity using the expected species richness. If changes in abundance drive the multidiversity pattern, multidiversity calculated from expected values should show the same pattern as the original multidiversity index. Multidiversity calculated from expected values was not correlated with LUI (Fig. S3*A*). We also calculated observed and expected species richness for each group in each plot. This is the species richness value, corrected for abundance. We plotted observed minus expected values for each group against LUI (Fig. S4). For many of the groups, these observed minus expected values did still decrease with increasing LUI, indicating that there is an LUI effect on species richness, per se, for these groups. However, for other taxonomic groups (butterflies and birds), the species richness response did seem to be driven by abundance because observed minus expected values did not decline with increasing LUI. We then calculated multidiversity from the observed minus expected values. Because many of these values were negative (observed species richness less than expected), we first recoded negative values as 0. These multidiversity values did show a similar pattern to the overall index: an exponential decline with increasing LUI and a positive effect of $\mathrm{LUI}_{\mathrm{sd}}$ (Fig. S3*B* and Table S3). These analyses indicate that the species richness response of some of the groups was driven by abundance and, therefore, that some of the response of multidiversity was driven by abundance changes in these groups. However, there were also effects on species richness, per se, and our overall conclusions about the response of multidiversity to LUI were not solely driven by abundance changes.

1. Blüthgen N, et al. (2012) A quantitative index of land-use intensity in grasslands: Integrating mowing, grazing and fertilization. *Basic Appl Ecol* 13(3):207–220.
2. Zavaleta ES, Pasari JR, Hulvey KB, Tilman GD (2010) Sustaining multiple ecosystem functions in grassland communities requires higher biodiversity. *Proc Natl Acad Sci USA* 107(4):1443–1446.
3. Gamfeldt L, Hillebrand H, Jonsson PR (2008) Multiple functions increase the importance of biodiversity for overall ecosystem functioning. *Ecology* 89(5):1223–1231.
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6. Richardson JML, Richards MH (2008) A randomisation program to compare species-richness values. *Insect Conservation and Diversity* 1(3):135–141.

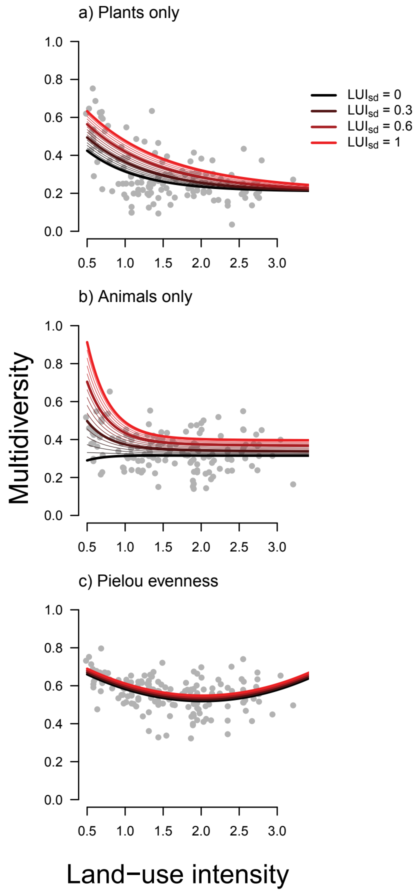

Fig. S1. Effect of LUI on multidiversity based on only plants (*A*), only animals (*B*), or evenness of species abundances (*C*). Parameters were calculated using multimodel averaging across models in the 95% confidence set and were averaged across regions. (*C*) Multimodel averaging is based on quadratic models, whose AICc weights sum to 39%. Multimodel averaging could not be done with all models in the 95% confidence set because the other models were power law models, and it would not be possible to average parameters across these different models. Note, therefore, that the quadratic relationship may not be well supported because models predicting a continuous, decelerating decline in multidiversity with increasing LUI are also included in the 95% confidence set of models.

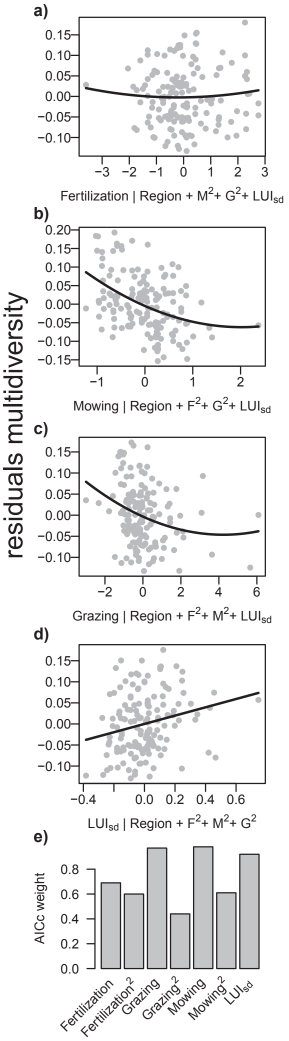

Fig. S2. Effects of individual land-use components on multidiversity: fertilization (*A*), mowing (*B*), grazing (*C*), and temporal variation in LUI_{sd} (*D*). The effects are shown as partial regression plots in which both the *x* axis and *y* axis are corrected for all of the other variables (i.e., in *A*, they are corrected for mowing, grazing, and LUI_{sd}). (*E*) Importance of each variable in *A*–*D* (linear and quadratic terms) in its effect on multidiversity is shown. Importance is calculated by summing the AICc weights of all of the models containing the term. Note that the importance of the quadratic term for mowing decreases from 61% AICc weights to 53% when the outlier with the highest mowing residuals (*B*) is removed from the analysis. This suggests that there is not strong support for a nonlinear effect of mowing.

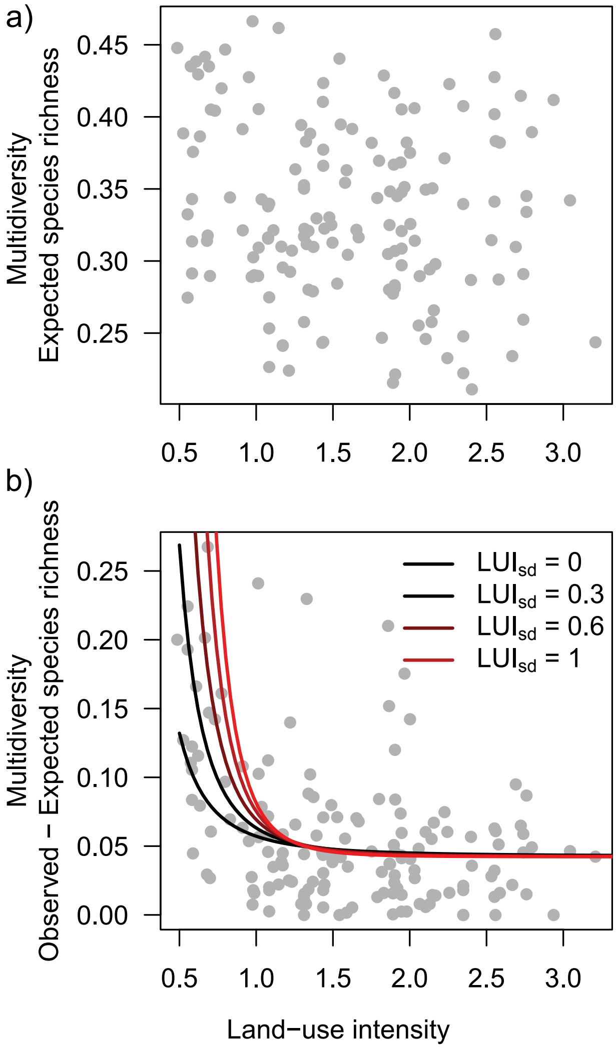

Fig. S3. Effect of abundance changes on multidiversity. (*A*) Multidiversity calculated from the species richness values expected if species richness is driven solely by abundance (more information regarding the calculation of expected values is provided in *SI Methods*). There was no effect of LUI measured using the LUI index on multidiversity calculated from expected values (Table S3). (*B*) Multidiversity calculated using abundance-corrected species richness values: observed minus expected species richness (*SI Methods*). The best-fit model for multidiversity against LUI is shown: Multidiversity follows an asymptotic exponential relationship with LUI, and the intercept depends on LUI_{sd} (Table S3).

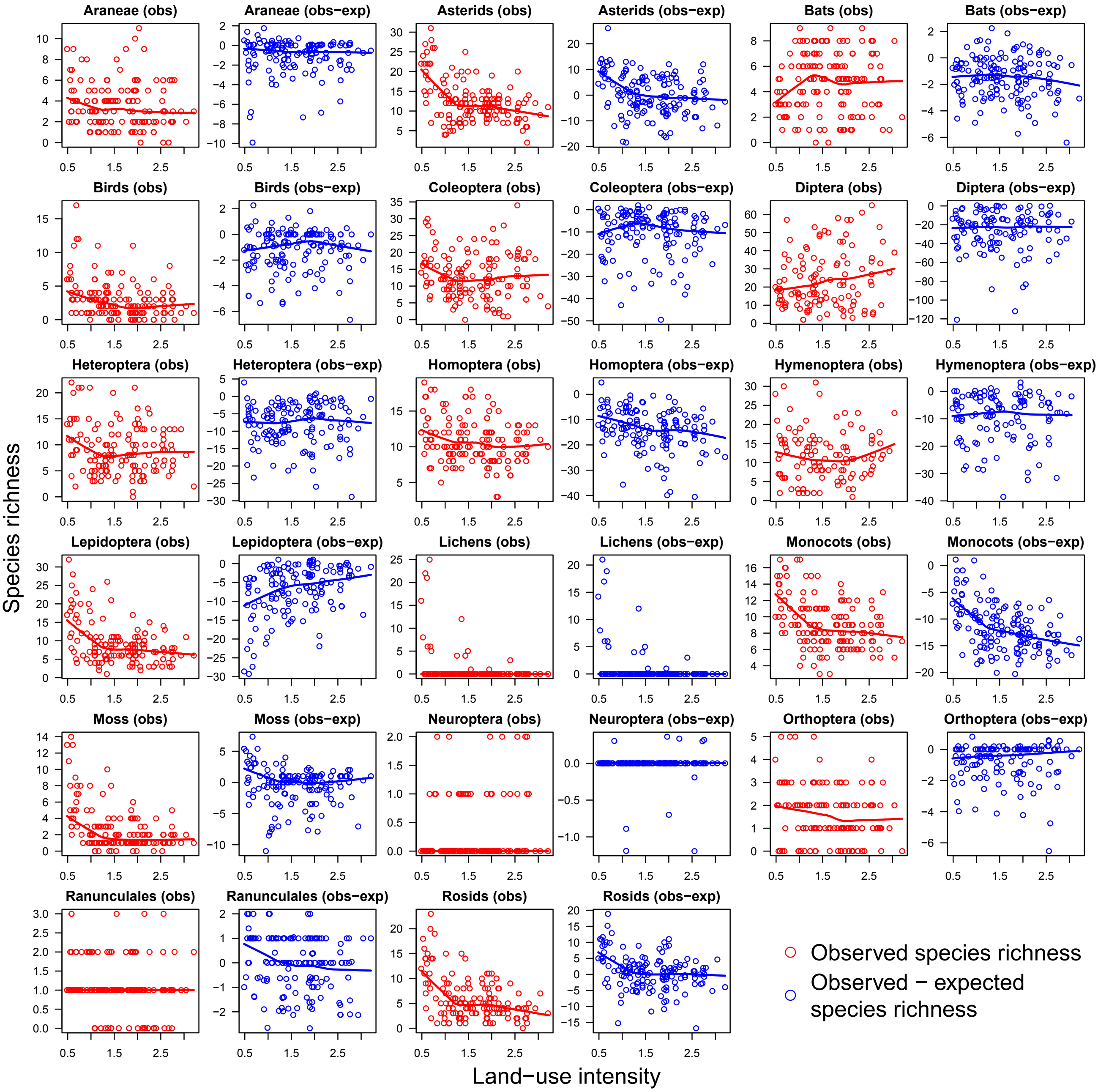

Fig. S4. Observed and abundance-corrected species richness for each of 17 taxonomic groups measured in the 150 grasslands. For each group, the points in red show the observed species richness against LUI. The points in blue show the observed (obs) minus expected (exp) species richness (more information regarding the calculation of expected values is provided in *SI Methods*). The solid line shows a locally weighted polynomial regression fitted to the data with span = 2/3, function "lowess" in R.

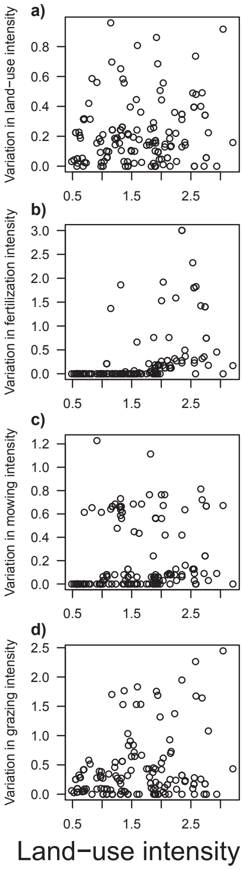

Fig. S5. Relationship between mean LUI and LUI_{sd} across 3 y (*A*, $\rho = 0.12$), SD in mowing frequency across 3 y (*C*, $\rho = 0.33$), SD in grazing intensity (*D*, $\rho = 0.12$), and SD in fertilization intensity (*B*, $\rho = 0.73$). Examples of plots with high interannual variation in LUI are shown: to produce a LUI_{sd} of 0.9 and a mean LUI of 3: 2 y of heavy grazing (1,428 $\mathrm{LU \cdot ha^{-1}}$) and mowing once a year, and 1 y of grazing moderately (461 $\mathrm{LU \cdot ha^{-1}}$); to produce a LUI_{sd} of 0.8 and a mean LUI of 1.9: 2 y of grazing at 671 $\mathrm{LU \cdot ha^{-1}}$ and 1 y of grazing at 80 $\mathrm{LU \cdot ha^{-1}}$; and to produce a LUI_{sd} of 0.65 and a mean LUI of 1.3: 1 y of grazing lightly (56 $\mathrm{LU \cdot ha^{-1}}$), 1 y of mowing once a year, and 1 y of fertilizing at 62 kg of $\mathrm{N \cdot ha^{-1}}$ and mowing once per year.

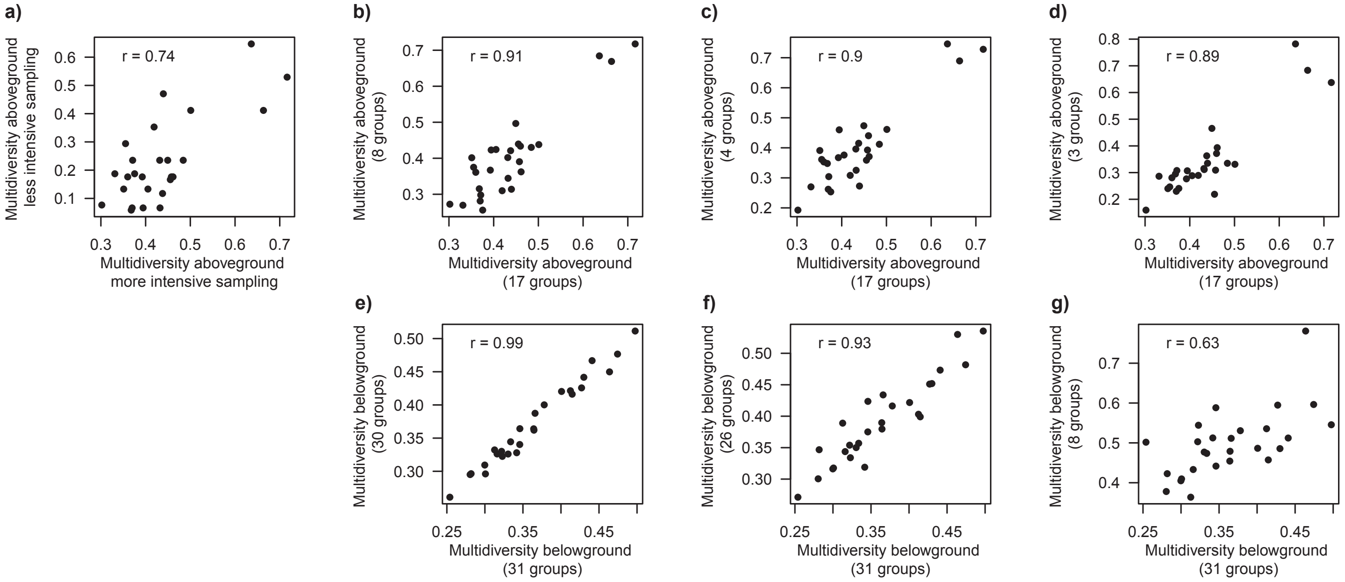

Fig. S6. Relationship among different measures of multidiversity on the subset of 27 plots for multidiversity aboveground (*A*–*D*) and multidiversity belowground (*E*–*G*). In each graph, *r* values show Pearson correlation coefficients. (*A*) No extra taxonomic groups were measured aboveground on the subset of 27 plots; however, several insect groups were measured more intensively on the subset of 27 plots than they were on all 150 plots (full details are provided in Table S4). Multidiversity is calculated with the species richness values from the more intensive sampling "Multidiversity aboveground 27 plots" and is calculated with the same 17 groups but with species richness values from the less intensive sampling "Multidiversity aboveground 150 plots." The high correlation between the two measures shows that the intensity of sampling does not affect the overall results. (*B*–*G*) Multidiversity was also calculated using different taxonomic groups, progressively aggregating groups into larger ones and summing the species richness values within the groups. Three different levels were used, and these are shown in Table S4. For example, Coleoptera formed one group in the main analysis of multidiversity. For aggregation level 1, they were aggregated with other insects and the total species richness of Hexapoda was included in the analysis; for aggregation level 2, they were aggregated with all other arthropods (insects and arachnids) and the species richness of Arthropoda was analyzed; and at aggregation level 3, they were aggregated with all other animals (also including vertebrate groups) and the species richness of animals was analyzed as one group. This tests whether our calculation of multidiversity is affected by the taxonomic groups that we chose; the close correlations among all of the measures indicate that the groups we chose for the analysis do not bias the results. Correlations between the multidiversity values used in the main analysis and the groups formed with the first aggregation are shown for aboveground groups (*B*, 17 vs. 8 groups) and belowground groups (*E*, 31 vs. 30 groups). Correlations between the multidiversity values used in the main analysis and the groups formed with the second aggregation are shown for aboveground groups (*C*, 17 vs. 4 groups) and belowground groups (*F*, 31 vs. 26 groups). Correlations between the multidiversity values used in the main analysis and the groups formed with the third aggregation are shown for aboveground groups (*D*, 17 vs. 3 groups) and belowground groups (*G*, 31 vs. 8 groups).

Table S1. All the models fit in the analyses

Model description	R code
Model with compound LUI: used for all analyses	
No LUI_{sd}	
Null	lm(y ∼ Exploratory)
Linear LUI	lm(y ∼ Exploratory + LUI)
Quadratic LUI	lm(y ∼ Exploratory + poly(LUI,2))
Cubic LUI	lm(y ∼ Exploratory + poly(LUI,3))
Negative exponential LUI	gnls(y ∼ a * exp(−b * LUI), params = list(a ∼ Exploratory, b ∼ 1), start = c (1, 1, 1, 1))
Asymptotic exponential LUI	gnls(y ∼ Asym + (R0 − Asym) * exp(−exp(lrc) * LUI), params = list(Asym + lrc ∼1, R0 ∼ Exploratory), start = c(p[c (1, 3)],p[2],1,1))
Power law LUI	gnls(y ∼ a + b * (LUIˆc), params = list(a ∼ Exploratory, b + c ∼ 1), start = c(p2[1],0,0,p2[2],p2[3]))
LUI_{sd} main effect	
LUI_{sd}	lm(y ∼ Exploratory + LUI.sd)
Linear LUI + LUI_{sd}	lm(y ∼ Exploratory + LUI + LUI.sd)
Quadratic LUI + LUI_{sd}	lm(y ∼ Exploratory + poly(LUI,2) + LUI.sd)
Cubic LUI + LUI_{sd}	lm(y ∼ Exploratory + poly(LUI,3) + LUI.sd)
Negative exponential intercept as function of LUI_{sd}	gnls(y ∼ a * exp(−b * LUI), params = list(a ∼ Exploratory + LUI.sd, b ∼ 1), start = c (1, 1, 1, 1, 1))
Asymptotic exponential intercept as function of LUI_{sd}	gnls(y ∼ Asym + (R0 − Asym) * exp(−exp(lrc) * LUI), params = list(Asym + lrc ∼ 1, R0 ∼ Exploratory + LUI.sd), start = c(p[c (1, 3)],p[2],1,1,0), control = nlc)
Asymptotic exponential asymptote as function of LUI_{sd}	gnls(y ∼ Asym + (R0 − Asym) * exp(−exp(lrc) * LUI), params = list(Asym ∼ LUI.sd, lrc ∼ 1, R0 ∼ Exploratory), start = c(p[1],0,p[3],p[2],1,1), control = nlc)
Asymptotic exponential rate constant as function of LUI_{sd}	gnls(y ∼ Asym + (R0 − Asym) * exp(−exp(lrc) * LUI), params = list(Asym ∼ 1, lrc ∼ LUI.sd, R0 ∼ Exploratory), start = c(p[c (1, 3)],0,p[2],1,1), control = nlc)
Power law intercept as function of LUI_{sd}	gnls(y ∼ a + b * (LUIˆc), params = list(a ∼ Exploratory + LUI.sd, b + c ∼ 1), start = c(p2[1],0,0,0, p2[2],p2[3]))
LUI_{sd} interaction	
Linear LUI × LUI_{sd}	lm(y ∼ Exploratory + LUI * LUI.sd)
Quadratic LUI × LUI_{sd}	lm(y ∼ Exploratory + poly(LUI,2) * LUI.sd)
Cubic LUI × LUI_{sd}	lm(y ∼ Exploratory + poly(LUI,3) * LUI.sd)
Negative exponential all parameters as function of LUI_{sd}	gnls(y ∼ a * exp(−b * LUI), params = list(a ∼ Exploratory + LUI.sd, b ∼ LUI.sd), start = c (1, 1, 1, 1, 1, 1))
Asymptotic exponential asymptote and rate constant as function of LUI_{sd}	gnls(y ∼ Asym + (R0 − Asym) * exp(−exp(lrc) * LUI), params = list(Asym + lrc ∼ LUI.sd, R0 ∼ Exploratory), start = c(p[1],0,p[2],0,p[3],1,1), control = nlc)
Asymptotic exponential asymptote and intercept as function of LUI_{sd}	gnls(y ∼ Asym + (R0 − Asym) * exp(−exp(lrc) * LUI), params = list(Asym ∼ LUI.sd, lrc ∼ 1, R0 ∼ Exploratory + LUI.sd), start = c(p[1],0,p[3],p[2],1,1,0), control = nlc)
Asymptotic exponential rate constant and intercept as function of LUI_{sd}	gnls(y ∼ Asym + (R0 − Asym) * exp(−exp(lrc) * LUI), params = list(Asym ∼ 1, lrc ∼ LUI.sd, R0 ∼ Exploratory + LUI.sd), start = c(p[1],p[3],0,p[2],1,1,0), control = nlc)
Asymptotic exponential all parameters as function of LUI_{sd}	gnls(y ∼ Asym + (R0 − Asym) * exp(−exp(lrc) * LUI), params = list(Asym + lrc ∼ LUI.sd, R0 ∼ Exploratory + LUI.sd), start = c(p[1],0,p[3],0,p[2],1,1,0), control = nlc)
Power law all parameters as function of LUI_{sd}	gnls(y ∼ a + b * (LUIˆc), params = list(a ∼ Exploratory + LUI.sd, b + c ∼ LUI.sd), start = c(p2 [1],0,0,0,p2[2],0,p2[3],0)))
Models with individual components: used for analysis of multidiversity	
Fertilization	lm(y ∼ Exploratory + Fstd)
Mowing	lm(y ∼ Exploratory + Mstd)
Grazing	lm(y ∼ Exploratory + Gstd)
Fertilization + grazing	lm(y ∼ Exploratory + Fstd + Gstd)
Fertilization + mowing	lm(y ∼ Exploratory + Fstd + Mstd)
Mowing + grazing	lm(y ∼ Exploratory + Mstd + Gstd)
Fertilization + mowing + grazing	lm(y ∼ Exploratory + Fstd + Mstd + Gstd)
Fertilization^2	lm(y ∼ Exploratory + poly(Fstd,2))
Mowing^2	lm(y ∼ Exploratory + poly(Mstd,2))
Grazing^2	lm(y ∼ Exploratory + poly(Gstd,2))
Fertilization^2 + mowing	lm(y ∼ Exploratory + poly(Fstd,2) + Mstd)
Fertilization^2 + mowing + grazing	lm(y ∼ Exploratory + poly(Fstd,2) + Mstd + Gstd)
Fertilization^2 + grazing	lm(y ∼ Exploratory + poly(Fstd,2) + Gstd)
Mowing^2 + fertilization	lm(y ∼ Exploratory + poly(Mstd,2) + Fstd)
Mowing^2 + fertilization + grazing	lm(y ∼ Exploratory + poly(Mstd,2) + Fstd + Gstd)
Mowing^2 + grazing	lm(y ∼ Exploratory + poly(Mstd,2) + Gstd)
Grazing^2 + fertilization	lm(y ∼ Exploratory + poly(Gstd,2) + Fstd)
Grazing^2 + fertilization + mowing	lm(y ∼ Exploratory + poly(Gstd,2) + Fstd + Mstd)
Grazing^2 + mowing	lm(y ∼ Exploratory + poly(Gstd,2) + Mstd)
Fertilization^2 + mowing^2	lm(y ∼ Exploratory + poly(Fstd,2) + poly(Mstd,2))
Fertilization^2 + grazing^2	lm(y ∼ Exploratory + poly(Fstd,2) + poly(Gstd,2))

Table S1. Cont.

Model description	R code
Mowing^2 + Grazing^2	lm(y ~ Exploratory + poly(Mstd,2) + poly(Gstd,2))
Fertilization^2 + mowing^2 + grazing	lm(y ~ Exploratory + poly(Fstd,2) + poly(Mstd,2) + Gstd)
Fertilization^2 + grazing^2 + mowing	lm(y ~ Exploratory + poly(Fstd,2) + poly(Gstd,2) + Mstd)
Mowing^2 + grazing^2 + fertilization	lm(y ~ Exploratory + poly(Mstd,2) + poly(Gstd,2) + Fstd)
Mowing^2 + grazing^2 + fertilization^2	lm(y ~ Exploratory + poly(Fstd,2) + poly(Mstd,2) + poly(Gstd,2))
With LUI_{sd}	
Fertilization + LUI_{sd}	lm(y ~ Exploratory + LUI.sd + Fstd)
Mowing + LUI_{sd}	lm(y ~ Exploratory + LUI.sd + Mstd)
Grazing + LUI_{sd}	lm(y ~ Exploratory + LUI.sd + Gstd)
Fertilization + grazing + LUI_{sd}	lm(y ~ Exploratory + LUI.sd + Fstd + Gstd)
Fertilization + mowing + LUI_{sd}	lm(y ~ Exploratory + LUI.sd + Fstd + Mstd)
Mowing + grazing + LUI_{sd}	lm(y ~ Exploratory + LUI.sd + Mstd + Gstd)
Fertilization + mowing + grazing + LUI_{sd}	lm(y ~ Exploratory + LUI.sd + Fstd + Mstd + Gstd)
Fertilization^2	lm(y ~ Exploratory + LUI.sd + poly(Fstd,2))
Mowing^2 + LUI_{sd}	lm(y ~ Exploratory + LUI.sd + poly(Mstd,2))
Grazing^2 + LUI_{sd}	lm(y ~ Exploratory + LUI.sd + poly(Gstd,2))
Fertilization^2 + mowing + LUI_{sd}	lm(y ~ Exploratory + LUI.sd + poly(Fstd,2) + Mstd)
Fertilization^2 + mowing + grazing + LUI_{sd}	lm(y ~ Exploratory + LUI.sd + poly(Fstd,2) + Mstd + Gstd)
Fertilization^2 + grazing + LUI_{sd}	lm(y ~ Exploratory + LUI.sd + poly(Fstd,2) + Gstd)
Mowing^2 + fertilization + LUI_{sd}	lm(y ~ Exploratory + LUI.sd + poly(Mstd,2) + Fstd)
Mowing^2 + fertilization + grazing + LUI_{sd}	lm(y ~ Exploratory + LUI.sd + poly(Mstd,2) + Fstd + Gstd)
Mowing^2 + grazing + LUI_{sd}	lm(y ~ Exploratory + LUI.sd + poly(Mstd,2) + Gstd)
Grazing^2 + fertilization + LUI_{sd}	lm(y ~ Exploratory + LUI.sd + poly(Gstd,2) + Fstd)
Grazing^2 + fertilization + mowing + LUI_{sd}	lm(y ~ Exploratory + LUI.sd + poly(Gstd,2) + Fstd + Mstd)
Grazing^2 + mowing + LUI_{sd}	lm(y ~ Exploratory + LUI.sd + poly(Gstd,2) + Mstd)
Fertilization^2 + mowing^2 + LUI_{sd}	lm(y ~ Exploratory + LUI.sd + poly(Fstd,2) + poly(Mstd,2))
Fertilization^2 + grazing^2 + LUI_{sd}	lm(y ~ Exploratory + LUI.sd + poly(Fstd,2) + poly(Gstd,2))
Mowing^2 + grazing^2 + LUI_{sd}	lm(y ~ Exploratory + LUI.sd + poly(Mstd,2) + poly(Gstd,2))
Fertilization^2 + mowing^2 + grazing + LUI_{sd}	lm(y ~ Exploratory + LUI.sd + poly(Fstd,2) + poly(Mstd,2) + Gstd)
Fertilization^2 + grazing^2 + mowing + LUI_{sd}	lm(y ~ Exploratory + LUI.sd + poly(Fstd,2) + poly(Gstd,2) + Mstd)
Mowing^2 + grazing^2 + fertilization + LUI_{sd}	lm(y ~ Exploratory + LUI.sd + poly(Mstd,2) + poly(Gstd,2) + Fstd)
Mowing^2 + grazing^2 + fertilization^2 + LUI_{sd}	lm(y ~ Exploratory + LUI.sd + poly(Fstd,2) + poly(Mstd,2) + poly(Gstd,2))

A model description is given, along with the code used to fit the models in the statistical package R. The formula for the asymptotic exponential model was:

$$y = a + (b - a)e^{-e^{c}x},$$

where a is the asymptote (Asym in R code), b is the intercept (R0), and c is the natural log of the rate constant (lrc).
The formula for the negative exponential was:

$$y = ae^{-bx},$$

where a is the intercept and b is the rate constant.
The formula for the power law models was:

$$y = a + bx^{c}.$$

For the asymptotic exponential models, starting parameters "p" were found using the self-starting function SSasym in R. For the power law models, starting parameters "p2" were found by trying a series of random starting values using the R function nls2.

Table S2. Best-fit models in the analysis of multidiversity

Type	LUI	LUI_{sd}	Fertilization	Mowing	Grazing	AICc	AICc weight, %	Pseudo-R^2, %
150 plots, 18 taxonomic groups								
Multidiversity measures								
Multidiversity (richness, all species)								
AE	AE	Intercept				−390	47	49
AE	AE	Intercept, asymptote				−389	26	50
AE	AE	Rate, asymptote				−388	16	49
AE	AE	Intercept, asymptote, rate				−386	8	50
Multidiversity (rare species)								
AE	AE	Rate				−387	33	53
AE	AE	Asymptote, rate				−386	22	54
AE	AE	Asymptote, intercept				−385	15	53
AE	AE	Intercept				−385	13	53
AE	AE	Rate, intercept				−384	9	53
AE	AE	Rate, intercept, asymptote				−384	7	54
Multidiversity (common species)								
AE	AE	Intercept				−376	37	29
AE	AE	Asymptote, intercept				−374	15	29
AE	AE	Rate, intercept				−374	14	29
AE	AE	Asymptote, intercept, rate				−372	5	29
AE	AE	Asymptote				−371	3	26
AE	AE	Asymptote, rate				−370	2	27
AE	AE	Rate				−370	2	26
LM		Linear	Quadratic	Linear		−370	2	27
LM		Linear		Linear		−370	2	25
AE	AE					−369	1	25
LM		Linear		Quadratic		−369	1	25
NE	NE	Intercept				−369	1	24
LM	Quadratic	Linear				−368	1	25
LM			Quadratic			−368	1	25
LM		Linear	Linear	Linear		−368	1	25
LM		Linear	Quadratic	Linear	Linear	−368	1	27
LM		Linear		Linear	Linear	−368	1	25
LM		Linear	Quadratic	Quadratic		−368	1	27
LM				Linear		−368	1	23
	Linear	Linear				−368	1	24
NE						−368	1	25
LM		Intercept, rate		Quadratic		−367	1	24
Multidiversity (Pielou evenness, *J**)								
LM	Quadratic	Linear				−336	21	28
LM	Quadratic					−335	18	27
PL	PL	Intercept				−335	17	28
LM	Cubic	Linear				−335	13	29
LM	Cubic					−334	11	28
PL	PL					−334	11	26
LM	Quadratic	LUI × LUI_{sd}				−332	4	29
Multidiversity (plants)								
AE	AE	Rate				−346	33	70
AE	AE	Intercept				−345	21	69
AE	AE	Rate, intercept				−345	19	70
AE	AE	Asymptote, rate				−344	11	70
AE	AE	Asymptote, intercept, rate				−343	7	70
AE	AE	Asymptote, intercept				−343	7	69
Multidiversity (animals)								
AE	AE	Asymptote, intercept				−297	36	20
AE	AE	Intercept				−295	13	18
AE	AE	Rate				−295	13	18
AE	AE	Asymptote, intercept, rate				−295	12	20
AE	AE	Asymptote				−294	8	18
AE	AE	Asymptote, rate				−294	7	19
AE	AE	Intercept, rate				−293	5	18
PL	PL	Intercept				−292	2	16

Table S2. Cont.

Type	LUI	LUI_{sd}	Fertilization	Mowing	Grazing	AICc	AICc weight, %	Pseudo-R^2, %
Individual groups								
Arbuscular mycorrhizal fungi								
Null						184	33	3
Araneae								
PL	PL					−56	13	10
Asterids								
AE	AE	Intercept				−228	48	63
Bats								
NE	NE					−75	12	51
Birds								
LM	Quadratic	Linear				−167	24	33
Coleoptera								
AE	AE					−66	35	12
Diptera								
NE	NE	Intercept				−16	27	19
Heteroptera								
AE	AE	Asymptote				−46	19	15
Homoptera								
AE	AE					−112	23	11
Hymenoptera								
AE	AE	Asymptote, intercept				−52	29	27
Lepidoptera								
AE	AE	Rate				−181	39	56
Lichens								
NE	NE	Asymptote, intercept, rate				−275	39	61
Monocotyledons								
AE	AE					−145	27	36
Mosses								
AE	AE	Intercept, rate				−196	52	61
Neuroptera								
NE	NE	Asymptote, intercept, rate				27	48	11
Orthoptera								
AE	AE	Intercept				−8	40	16
Ranunculales								
LM	Quadratic					−32	18	17
Rosids								
AE	AE	Intercept				−166	33	52
27 plots, 49 taxonomic groups								
Multidiversity aboveground								
AE	AE	Asymptote				−75	45	81
AE	AE					−74	23	77
AE	AE	Intercept				−73	18	80
AE	AE	Rate				−73	14	80
Multidiversity belowground (top five models are shown)								
LM				Linear		−67	13	22
Null						−66	9	10
LM					Grazing	−66	9	19
LM				Quadratic		−66	9	29
LM			Linear			−65	5	15

Different measures of multidiversity are shown for the analysis with 150 plots and 18 taxonomic groups measured and for the subset of 27 plots where 49 taxonomic groups were measured. Models in the 95% confidence set of models are shown (i.e., the set of models whose combined AIC weights sum to 95%). AICc values are corrected for small sample sizes. LUI × LUI_{sd} indicates an interaction between the terms. All model formulae are provided in Table S1. AE, asymptotic exponential; LM, linear model; NE, negative exponential; PL, power law.

*Calculated as $J = \frac{-\sum_{i=1}^{R} p_i \ln p_i}{\ln S}$, where S is the number of species, p_i is the proportional abundance of the ith species, and R is the total number of species.

Table S3. Best-fit models for the analysis of multidiversity, calculated using other thresholds, mean scaled species richness values, or after correcting species richness for abundance

Type	LUI	LUI_{sd}	Fertilization	Mowing	Grazing	AICc	AICc weight, %	Pseudo-R^2, %
150 plots, 18 taxonomic groups								
Multidiversity measures								
Standardization with z-scores								
AE	AE	Intercept				77	52	55
AE	AE	Intercept, asymptote				79	19	55
AE	AE	Rate, intercept				79	19	55
AE	AE	Intercept, asymptote, rate				81	7	55
50% threshold								
AE	AE	Intercept				−231	43	46
AE	AE	Intercept, rate				−230	24	47
AE	AE	Asymptote, intercept				−230	21	47
AE	AE	Asymptote, intercept, rate				−229	10	47
30% threshold								
AE	AE	Intercept				−192	54	41
AE	AE	Asymptote, intercept				−190	20	42
AE	AE	Rate, intercept				−190	18	41
AE	AE	Asymptote, intercept, rate				−188	6	42
60% threshold								
AE	AE	Rate				−292	34	47
AE	AE	Intercept, rate				−292	33	48
AE	AE	Asymptote, rate				−290	12	47
AE	AE	Asymptote, intercept, rate				−290	11	48
AE	AE	Intercept				−289	7	46
70% threshold								
AE	AE	Intercept				−355	35	34
AE	AE	Rate				−353	14	33
AE	AE	Asymptote, intercept				−353	12	34
AE	AE	Intercept, rate				−352	12	34
AE	AE					−352	10	32
AE	AE	Asymptote				−351	7	33
AE	AE	Asymptote, rate				−351	6	33
Multidiversity of rare species (least abundant 50% of species)								
AE	AE	Rate				−375	60	45
AE	AE	Asymptote, rate				−373	20	45
AE	AE	Intercept				−371	9	43
AE	AE	Rate, intercept				−370	4	43
AE	AE	Asymptote, intercept				−370	4	43
Multidiversity of rare species (by region)								
AE	AE	Asymptote				−287	29	39
AE	AE	Asymptote, intercept				−287	29	40
AE	AE	Asymptote, rate				−286	22	39
AE	AE	Asymptote, intercept, rate				−284	9	40
PL	PL	Intercept				−283	5	37
AE	AE	Rate				−282	4	37
Multidiversity of common species (by region)								
LM	Quadratic	Linear				−316	23	24
PL	PL	Intercept				−315	14	24
LM	Quadratic	Linear				−314	9	25
LM	Cubic	Linear				−314	8	24
LM	Linear	Linear				−313	6	22
NE	NE	Intercept				−313	6	22
PL	PL	Intercept, rate				−313	6	25
AE	AE	Asymptote, rate				−312	4	24
LM	Linear	$LUI \times LUI_{sd}$				−312	3	22
LM		Linear	Quadratic	Linear	Linear	−312	3	24
AE	AE	Rate				−312	3	22
NE	NE	Intercept, rate				−311	2	22
LM		Linear		Linear	Linear	−311	2	22
AE	AE	Intercept, rate				−311	2	23
LM		Linear	Quadratic	Quadratic	Linear	−310	1	25
LM		Linear	Quadratic	Linear	Quadratic	−310	1	25
LM	Cubic	$LUI \times LUI_{sd}$				−310	1	26

Table S3. Cont.

Type	LUI	LUI$_{sd}$	Fertilization	Mowing	Grazing	AICc	AICc weight, %	Pseudo-R^2, %
LM		Linear		Linear	Quadratic	−309	1	22
Multidiversity based on expected species richness values (i.e., the effect of abundance alone on multidiversity), top five models shown*								
LM		Linear	Quadratic	Linear		−454	26	32
LM		Linear	Quadratic	Linear	Linear	−453	17	33
LM		Linear		Linear	Quadratic	−452	11	34
LM		Linear	Quadratic	Quadratic		−452	9	33
LM		Linear	Quadratic	Quadratic	Linear	−451	6	33
Multidiversity based on species richness values corrected for abundance (observed − expected)								
PL	PL	Intercept, rate				−501	37	39
PL	PL					−500	26	36
PL	PL	Intercept				−498	11	36
AE	AE	Intercept, rate				−497	6	37
AE	AE	Intercept				−497	6	36
AE	AE	Asymptote, intercept				−495	3	36
LM	Cubic					−495	3	35
AE	AE	Asymptote, intercept, rate				−495	2	37
LM	Quadratic					−494	1	33

Unless otherwise stated, the models whose AICc weights sum to 95% are shown. All model formulae and definitions are provided in Table S1.

*AIC weights for individual terms: fertilization (93%), fertilization^2 (93%), grazing (47%), grazing^2 (20%), mowing (84%), mowing^2 (22%), LUI$_{sd}$ (82%), compound LUI (0%).

Table S4. All the taxonomic groups included in the analyses at the two scales

Taxa	Aggregation level 1	Aggregation level 2	Aggregation level 3	Compartment	Sampling method	No. of plots measured	Year of measurement and sampling intensity	Authors
All 150 plots								
Araneae	Arachnida	Arthropoda	Animalia	Above	Sweep netting	150	2008: twice per plot	Lange, Pašalić, Türke, Lange, Pašalić, Türke, Gossner, Weisser
Coleoptera	Hexapoda	Arthropoda	Animalia	Above	Sweep netting	150	2008–2009: twice per plot per year	Lange, Pašalić, Türke, Lange, Pašalić, Türke, Gossner, Weisser
Diptera	Hexapoda	Arthropoda	Animalia	Above	Flower visitor observation	119	2008: one to three times per plot	Werner, Weiner, Blüthgen
Heteroptera	Hexapoda	Arthropoda	Animalia	Above	Sweep netting	150	2008–2010: twice per plot per year	Lange, Pašalić, Türke, Lange, Pašalić, Türke, Gossner, Weisser
Homoptera	Hexapoda	Arthropoda	Animalia	Above	Sweep netting	150	2008: twice per plot	Lange, Pašalić, Türke, Gossner, Weisser
Hymenoptera	Hexapoda	Arthropoda	Animalia	Above	Sweep netting (Symphyta) and flower visitor observation	119	2008: twice per plot	Combined data: Werner, Weiner, Blüthgen, Lange, Pašalić, Türke, Gossner, Weisser
Lepidoptera	Hexapoda	Arthropoda	Animalia	Above	Butterfly netting along a transect	137	2008: three surveys	Börschig, Krauss, Klein
Neuroptera	Hexapoda	Arthropoda	Animalia	Above	Sweep netting	150	2008: twice per plot	Lange, Pašalić, Türke, Gossner, Weisser
Orthoptera	Hexapoda	Arthropoda	Animalia	Above	Sweep netting	150	2008: twice per plot	Lange, Pašalić, Türke, Gossner, Weisser
Aves	Aves	Chordata	Animalia	Above	Observation: cumulative species list over 3 y	150	2008–2010: five times per plot per year	Böhm, Renner, Kalko
Chiroptera	Mammalia	Chordata	Animalia	Above	Monitoring of echolocation: cumulative species list over 3 y	150	2008–2010	Jung, Kalko
Glomeromycota	Glomeromycota	Glomeromycota	Fungi	Below	Terminal restriction fragment length polymorphism analysis	75	2008: once per plot*	Barto, Rillig
Lichens	Lichen	Lichen	Lichen	Above	% cover 4 × 4-m subplot	150	2009: once per plot	Boch, Prati, Fischer
Bryophyta	Bryophyta	Embryophta	Plantae	Above	% cover 4 × 4-m subplot	150	2009: once per plot	Müller, Boch, Prati, Fischer M
Asterids	Dicotyledons	Embryophta	Plantae	Above	% cover 4 × 4-m subplot	148	2009: once per plot	Müller, Boch, Socher, Prati, Fischer M, Klaus, Kleinebecker, Hölzel
Ranunculales	Dicotyledons	Embryophta	Plantae	Above	% cover 4 × 4-m subplot	148	2009: once per plot	Müller, Boch, Socher, Prati, Fischer M, Klaus, Kleinebecker, Hölzel
Rosids	Dicotyledons	Embryophta	Plantae	Above	% cover 4 × 4-m subplot	148	2009: once per plot	Müller, Boch, Socher, Prati, Fischer M, Klaus, Kleinebecker, Hölzel

Table S4. Cont.

Taxa	Aggregation level 1	Aggregation level 2	Aggregation level 3	Compartment	Sampling method	No. of plots measured	Year of measurement and sampling intensity	Authors
Monocotyledons	Monocotyledons	Embryophta	Plantae	Above	% cover 4 × 4-m subplot	148	2009: once per plot	Müller, Boch, Socher, Prati, Fischer M, Klaus, Kleinebecker, Hölzel
Subset of 27 plots								
Araneae	Arachnida	Arthropoda	Animalia	Above	Sweep netting and pitfall trapping	27	2008: twice per plot	Lange, Pašalić, Türke, Gossner, Weisser
Coleoptera	Hexapoda	Arthropoda	Animalia	Above	Sweep netting and pitfall trapping	27		Combined data: Krauss, Lange, Pašalić, Türke, Gossner, Weisser, Rothenwöhrer, Scherber, Tscharntke
Diptera	Hexapoda	Arthropoda	Animalia	Above	Flower visitor observation	22	2008: one to three times per plot	Werner, Weiner, Blüthgen
Heteroptera	Hexapoda	Arthropoda	Animalia	Above	Sweep netting and pitfall trapping	27	2008: twice per plot	Lange, Pašalić, Türke, Gossner, Weisser
Homoptera	Hexapoda	Arthropoda	Animalia	Above	Sweep netting and pitfall trapping	27	2008: twice per plot	Lange, Pašalić, Türke, Gossner, Weisser
Hymenoptera	Hexapoda	Arthropoda	Animalia	Above	Flower visitor observation and trap nesting hymenoptera	27	Trap nests: 2008, four surveys Flower visitors, 2008, one to three times per plot	Combined data: Steckel, Bellach, Westphal, Scherber, Steffan-Dewenter, Tscharntke, Werner, Weiner, Blüthgen
Lepidoptera	Hexapoda	Arthropoda	Animalia	Above	Butterfly netting along a transect	26	2008: three times per plot	Börschig, Krauss, Klein
Neuroptera	Hexapoda	Arthropoda	Animalia	Above	Sweep netting and pitfall trapping	27	2008: twice per plot	Lange, Pašalić, Türke, Gossner, Weisser
Orthoptera	Hexapoda	Arthropoda	Animalia	Above	Sweep netting and pitfall trapping	27	2008: twice per plot	Lange, Pašalić, Türke, Gossner, Weisser
Aves	Aves	Chordata	Animalia	Above	Observation: cumulative species list over 3 y	27	2008–2010: five times per plot per year	Böhm, Renner, Kalko
Chiroptera	Mammalia	Chordata	Animalia	Above	Monitoring of echolocation: cumulative species list over 3 y	27	2008–2010	Jung, Kalko
Lichens	Lichen	Lichen	Lichen	Above	% cover 4 × 4-m subplot	27	2009: once per plot	Boch, Prati, Fischer
Bryophyta	Bryophyta	Embryophta	Plantae	Above	% cover 4 × 4-m subplot	27	2009: once per plot	Müller, Boch, Prati, Fischer
Asterids	Dicotyledons	Embryophta	Plantae	Above	% cover 4 × 4-m subplot	25	2009: once per plot	Müller, Boch, Socher, Prati, Fischer
Ranunculales	Dicotyledons	Embryophta	Plantae	Above	% cover 4 × 4-m subplot	25	2009: once per plot	Müller, Boch, Socher, Prati, Fischer
Rosids	Dicotyledons	Embryophta	Plantae	Above	% cover 4 × 4-m subplot	25	2009: once per plot	Müller, Boch, Socher, Prati, Fischer
Monocotyledons	Monocotyledons	Embryophta	Plantae	Above	% cover 4 × 4-m subplot	25	2009: once per plot	Müller, Boch, Socher, Prati, Fischer
Lumbricidae	Clitellata	Annelida	Animalia	Below	Hand sorting from soil cores 20 × 10 cm	26	2008: two soil cores per plot	Birkhofer, Diekötter, Wolters

Table S4. Cont.

Taxa	Aggregation level 1	Aggregation level 2	Aggregation level 3	Compartment	Sampling method	No. of plots measured	Year of measurement and sampling intensity	Authors
Chilopoda	Myriapoda	Arthropoda	Animalia	Below	Kempson extraction from soil cores 20 × 5 cm	26	2008: one soil core per plot	Birkhofer, Diekötter, Wolters
Diplopoda	Myriapoda	Arthropoda	Animalia	Below	Kempson extraction from soil cores 20 × 5 cm	26	2008: one soil core per plot	Birkhofer, Diekötter, Wolters
Archaea	Archaea	Archaea	Archaea	Below	Protein extraction and "proteomic fingerprinting"	27	2008: once per plot*	Schulze W
Acidobacteria	Acidobacteria	Acidobacteria	Eubacteria	Below	Amplicon sequencing of partial 16S rRNA genes	18	2008: once per plot*	Fischer C, Nacke, Daniel
Actinobacteria	Actinobacteria	Actinobacteria	Eubacteria	Below	Amplicon sequencing of partial 16S rRNA genes	18	2008: once per plot*	Fischer C, Nacke, Daniel
Bacteroidetes	Bacteroidetes	Bacteroidetes	Eubacteria	Below	Amplicon sequencing of partial 16S rRNA genes	18	2008: once per plot*	Fischer C, Nacke, Daniel
Chloroflexi	Chloroflexi	Chloroflexi	Eubacteria	Below	Amplicon sequencing of partial 16S rRNA genes	18	2008: once per plot*	Fischer C, Nacke, Daniel
Cyanobacteria	Cyanobacteria	Cyanobacteria	Eubacteria	Below	Amplicon sequencing of partial 16S rRNA genes	18	2008: once per plot*	Fischer C, Nacke, Daniel
Fibrobacteres	Fibrobacteres	Fibrobacteres	Eubacteria	Below	Amplicon sequencing of partial 16S rRNA genes	18	2008: once per plot*	Fischer C, Nacke, Daniel
Firmicutes	Firmicutes	Firmicutes	Eubacteria	Below	Amplicon sequencing of partial 16S rRNA genes	18	2008: once per plot*	Fischer C, Nacke, Daniel
Nitrospira	Nitrospira	Nitrospira	Eubacteria	Below	Amplicon sequencing of partial 16S rRNA genes	18	2008: once per plot*	Fischer C, Nacke, Daniel
Proteobacteria	Proteobacteria	Proteobacteria	Eubacteria	Below	Amplicon sequencing of partial 16S rRNA genes	18	2008: once per plot*	Fischer C, Nacke, Daniel
Spirochaetes	Spirochaetes	Spirochaetes	Eubacteria	Below	Amplicon sequencing of partial 16S rRNA genes	18	2008: once per plot*	Fischer C, Nacke, Daniel
TM7	TM7	TM7	Eubacteria	Below	Amplicon sequencing of partial 16S rRNA genes	18	2008: once per plot*	Fischer C, Nacke, Daniel
Verrucomicrobia	Verrucomicrobia	Verrucomicrobia	Eubacteria	Below	Amplicon sequencing of partial 16S rRNA genes	18	2008: once per plot*	Fischer C, Nacke, Daniel
WS3	WS3	WS3	Eubacteria	Below	Amplicon sequencing of partial 16S rRNA genes	18	2008: once per plot*	Fischer C, Nacke, Daniel
Bodonidae	Kinetoplastida	Euglenozoa	Euglenozoa	Below	Terminal restriction fragment length polymorphism analysis of the 18S rRNA gene	26	2008: once per plot*	Glaser, Chatzinotas
Pezizomycotina	Pezizomycotina	Ascomycota	Fungi	Below	Amplicon sequencing of ITS rDNA genes	27	2008: once per plot*	Wubet, Christ, Buscot
Saccharomycotina	Saccharomycotina	Ascomycota	Fungi	Below	Amplicon sequencing of ITS rDNA genes	27	2008: once per plot*	Wubet, Christ, Buscot
Agaricomycotina	Agaricomycotina	Basidiomycota	Fungi	Below	Amplicon sequencing of ITS rDNA genes	27	2008: once per plot*	Wubet, Christ, Buscot
Pucciniomycotina	Pucciniomycotina	Basidiomycota	Fungi	Below	Amplicon sequencing of ITS rDNA genes	27	2008: once per plot*	Wubet, Christ, Buscot

Table S4. Cont.

Taxa	Aggregation level 1	Aggregation level 2	Aggregation level 3	Compartment	Sampling method	No. of plots measured	Year of measurement and sampling intensity	Authors
Ustilaginomycotina	Ustilaginomycotina	Basidiomycota	Fungi	Below	Amplicon sequencing of ITS rDNA genes	27	2008: once per plot*	Wubet, Christ, Buscot
Chytridiomycota	Chytridiomycota	Chytridiomycota	Fungi	Below	Amplicon sequencing of ITS rDNA genes	27	2008: once per plot*	Wubet, Christ, Buscot
Glomeromycota	Glomeromycota	Glomeromycota	Fungi	Below	Amplicon sequencing of ITS rDNA genes	27	2008: once per plot*	Wubet, Christ, Buscot
Incertae sedis	*Incertae sedis*	*Incertae sedis*	Fungi	Below	Amplicon sequencing of ITS rDNA genes	27	2008: once per plot*	Wubet, Christ, Buscot
Mucoromycotina	Mucoromycotina	*Incertae sedis*	Fungi	Below	Amplicon sequencing of ITS rDNA genes	27	2008: once per plot*	Wubet, Christ, Buscot
Chlorophyceae	Chlorophyceae	Chlorophyta	Plantae	Below	Cloning and direct sequencing of soil material	24	2008: once per plot*	Hallmann, Hodaĉ, Friedl
Trebouxiophyceae	Trebouxiophyceae	Chlorophyta	Plantae	Below	Cloning and direct sequencing of soil material	24	2008: once per plot*	Hallmann, Hodaĉ, Friedl
Chrysophyceae	Chrysophyceae	Stramenopiles	Stramenopiles	Below	Terminal restriction fragment length polymorphism analysis of the 18S rRNA gene	26	2008: once per plot*	Glaser, Chatzinotas
Virus	Virus	Virus	Virus	Below	Protein extraction and proteomic fingerprinting	27	2008: once per plot*	Schulze W

Compartment indicates whether groups were measured aboveground or belowground. Not all measures were taken on all plots; the actual number of plots measured for each group is therefore shown. In the subset of 27 plots, species richness data were aggregated into larger taxonomic units, aggregation levels 1–3, and the calculation of multidiversity was repeated with these groups to check whether the taxonomic groups used affected the calculation of multidiversity (Fig. S5). Authors who contributed data are shown for each group. TM7, Torf mittlere schicht; WS3, Wurtsmith contaminated aquifer.

*All soil microfauna were measured in the same soil samples, which were collected as part of a coordinated sampling. Five samples were taken per plot over a 20 × 20-m area and pooled to provide a single composite sample per plot